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(54) **URINE BIOMARKERS FOR PREDICTION
OF RECOVERY AFTER ACUTE KIDNEY
INJURY: PROTEOMICS**(71) Applicant: **University of Pittsburgh - Of the
Commonwealth System of Higher
Education, Pittsburgh, PA (US)**(72) Inventors: **Kai Singbartl, Pittsburgh, PA (US);
John A. Kellum, Pittsburgh, PA (US)**(21) Appl. No.: **15/399,994**(22) Filed: **Jan. 6, 2017****Related U.S. Application Data**(62) Division of application No. 13/981,747, filed on Aug.
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2800/60 (2013.01)(57) **ABSTRACT**

This invention is related to the field of the prevention and treatment of kidney disease. The treatment of kidney disease may be tailored depending upon the need for, or expectation of, renal recovery. For example, renal recovery can be determined by monitoring urine biomarkers related to the development of chronic kidney disease. For example, a normalized time course of approximately fourteen Days measuring urinary proteins can be used to establish the risk of recovery versus non-recovery in patient's having suffered an acute kidney injury. Alternatively, the invention describes signature protein expression profiles to establish the probability of renal recovery and/or renal non-recovery.

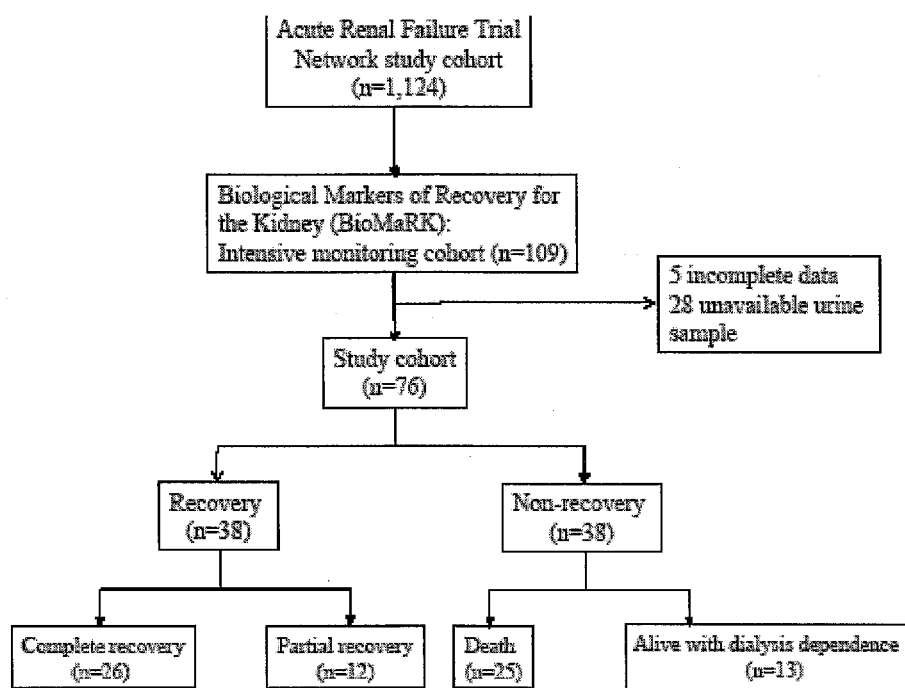


Figure 1

Arthur A vs B

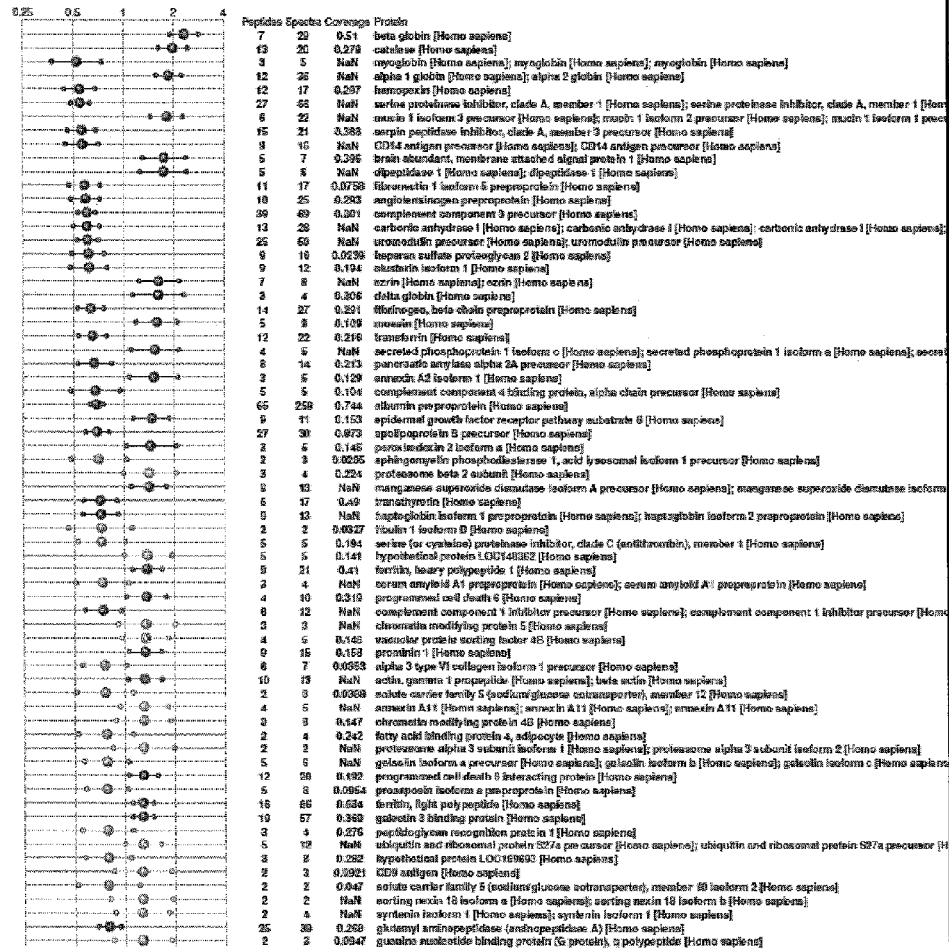


Figure 2

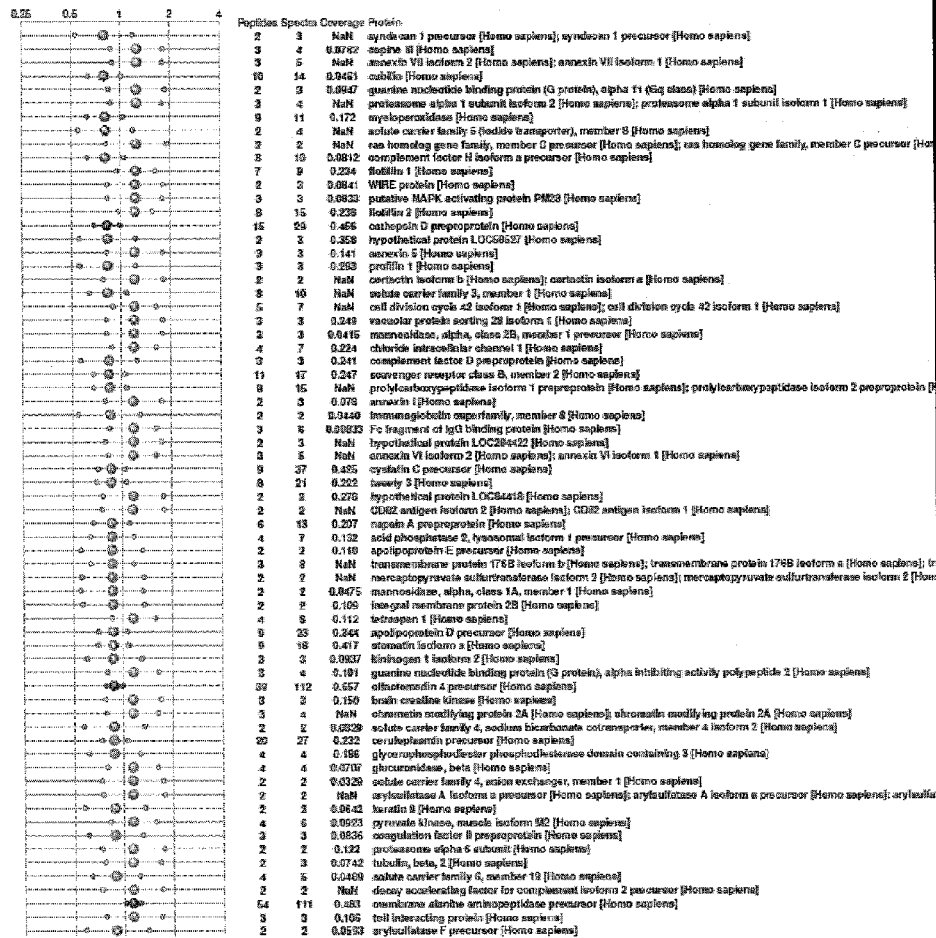


Figure 2 (cont'd)

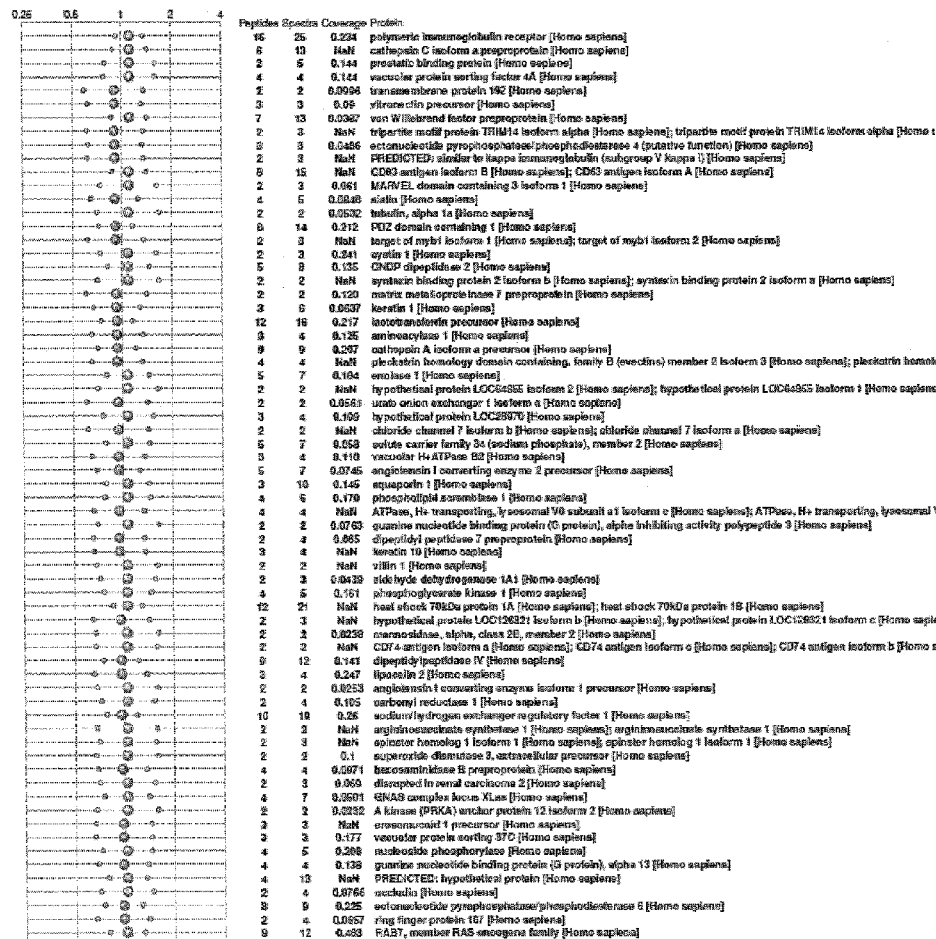


Figure 2 (cont'd)

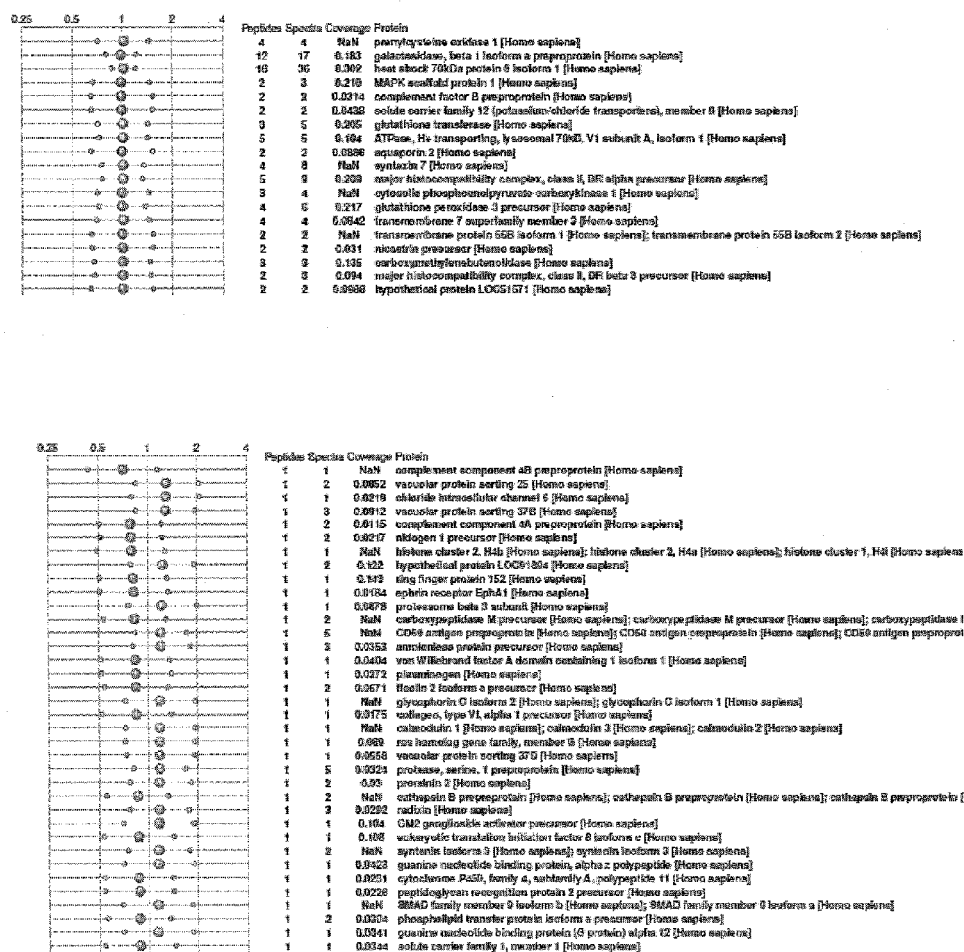


Figure 3

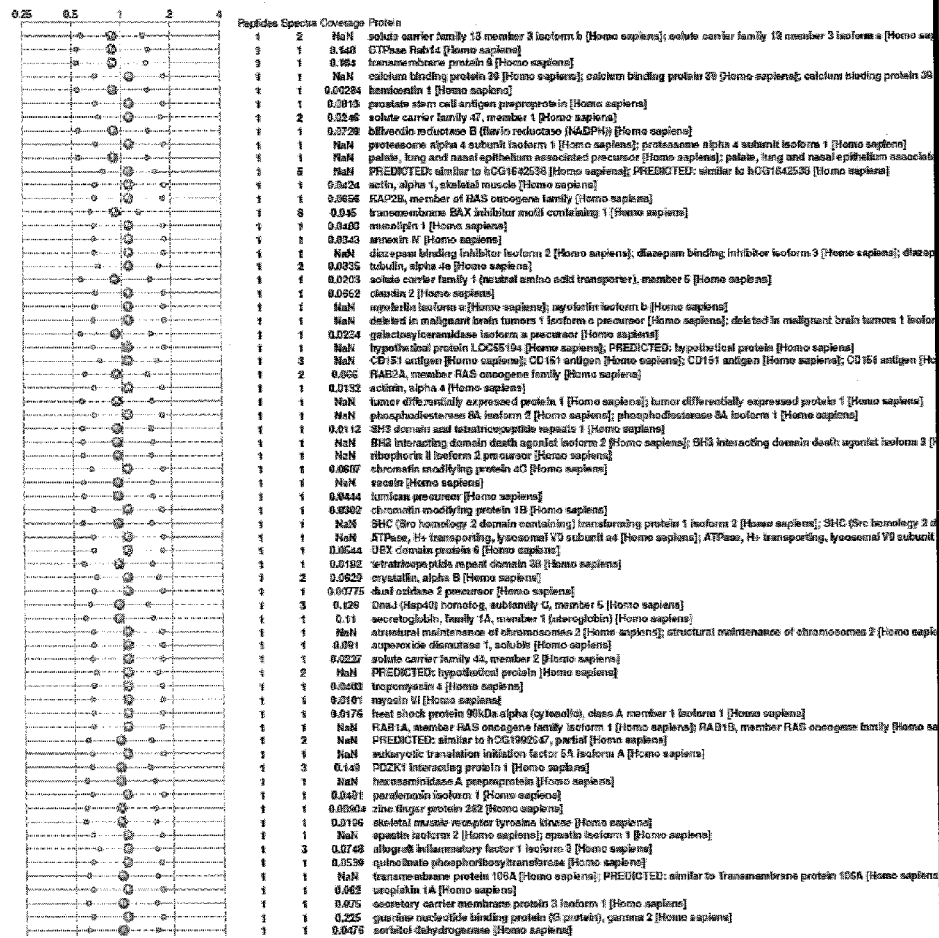


Figure 3 (cont'd)

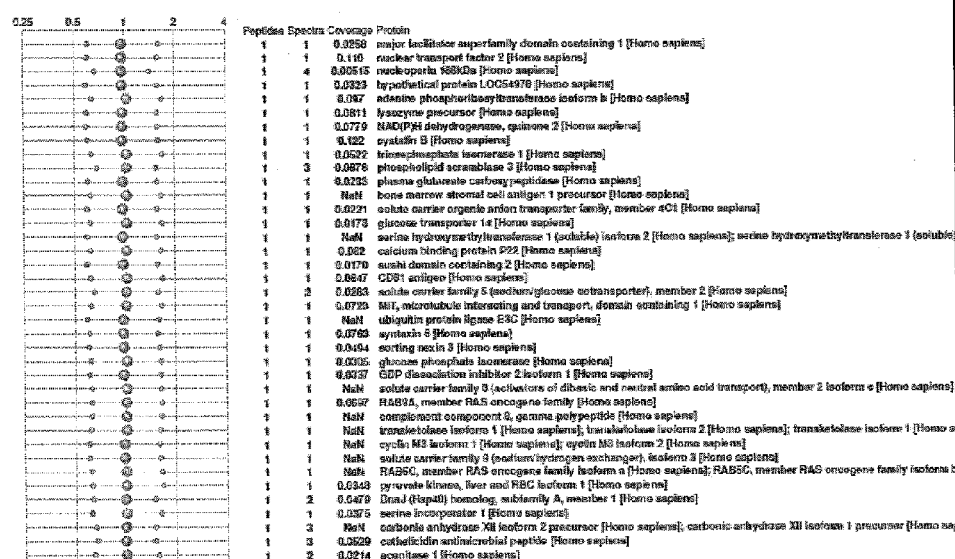


Figure 3 (cont'd)

URINE BIOMARKERS FOR PREDICTION OF RECOVERY AFTER ACUTE KIDNEY INJURY: PROTEOMICS

STATEMENT OF GOVERNMENT SUPPORT

[0001] This invention was made with government support under grant #DK 070910 awarded by the National Institutes of Health. The government has certain rights in the invention.

FIELD OF THE INVENTION

[0002] This invention is related to the field of the prevention and treatment of kidney disease. The treatment of kidney disease may be tailored depending upon the need for, or expectation of, renal recovery. For example, prediction of renal recovery can be determined by monitoring urine biomarkers related to the development of chronic kidney disease. For example, differential expression platforms can be used to identify biomarker proteins in order to establish the risk of renal recovery versus renal non-recovery in patient's having suffered an acute kidney injury.

BACKGROUND

[0003] Acute Kidney Injury (AKI) has an estimated incidence rate of approximately 2000 per million population and this rate is increasing. Ali et al. "Incidence and outcomes in acute kidney injury: a comprehensive population-based study" *J Am Soc Nephrol* 18:1292-1298 (2007). Approximately 5% of all people admitted to intensive care units around the world develop severe AKI requiring dialysis. Uchino et al., "Acute renal failure in critically ill patients: a multinational, multicenter study" *JAMA* 294:813-818 (2005). A recent, multi-center study found that fewer than only about 60% patients surviving severe AKI recovered renal function by two months. Palevsky et al., "Intensity of renal support in critically ill patients with acute kidney injury" *N Engl J Med* 359:7-20 (2008). Thus, a large number of patients with AKI go on to have end-stage renal disease (ESRD).

[0004] However, since only a fraction of patients with AKI fail to recover renal function, interventions aimed at improving recovery or providing renal support (e.g. early dialysis) cannot be targeted appropriately without some means of determining which patients will recover and which will not. Unfortunately, clinical risk prediction for recovery after AKI is extremely limited. Research efforts to treat AKI and prevent ESRD could be tailored according to long-term prognosis. In other words, with an accurate prediction of which patients will not recover kidney function, medical efforts could focus the development and application of aggressive treatment interventions on just these patients. Conversely, patients with a favorable prognosis would be spared from more aggressive interventions and their potential adverse effects.

[0005] Thus, development of a biomarker or biomarker panel that allows early prediction of recovery of kidney function would be an extremely valuable clinical tool. What is needed in the art are a panel of biomarkers to predict renal recovery after AKI.

SUMMARY

[0006] This invention is related to the field of the prevention and treatment of kidney disease. The treatment of

kidney disease may be tailored depending upon the need for, or expectation of, renal recovery. For example, prediction of renal recovery can be determined by monitoring urine biomarkers related to the development of chronic kidney disease. For example, differential expression platforms can be used to identify biomarker proteins in order to establish the risk of renal recovery versus renal non-recovery in patient's having suffered an acute kidney injury.

[0007] In one embodiment, the present invention contemplates a composition comprising an renal injury biomarker, wherein said biomarker comprises at least a fragment of a protein selected from the group consisting of ferritin, beta globin, catalase, alpha globin, epidermal growth factor receptor pathway substrate 8, mucin isoform precursor, ezrin, delta globin, moesin, phosphoprotein isoform, annexin A2, myoglobin, hemopexin, serine proteinase inhibitor, serpine peptidase inhibitor, CD14 antigen precursor, fibronectin isoform preprotein, angiotensinogen preprotein, complement component precursor, carbonic anhydrase, uromodulin precursor, complement factor H, complement component 4 BP, heparan sulfate proteoglycan 2, olfactomedian-4, leucine rich alpha-2 glycoprotein, ring finger protein 167, inter-alpha globulin inhibitor H4, heparan sulfate proteoglycan 2, N-acylshingosine aminohydrolase, serine proteinase inhibitor clade A member 1, mucin 1, clusterin isoform 1, brain abundant membrane attached signal protein 1, dipeptidase 1, fibronectin 1 isoform 5 preprotein, angiotensinogen preproprotein, carbonic anhydrase, and uromodulin precursor. In one embodiment, the composition further comprises a urine sample. In one embodiment, the urine sample is collected between 1 day and 14 days after a kidney injury. In one embodiment, the urine sample is a human urine sample. In one embodiment, the biomarker is at least 2.5 fold higher as compared to an expected level in a renal recovery group. In one embodiment, the biomarker is at least 2.0 fold higher as compared to an expected level in a renal recovery group. In one embodiment, the biomarker is at least 1.5 fold higher as compared to an expected level in a renal recovery group. In one embodiment, the biomarker is at least 1.25 fold higher as compared to an expected level in a renal recovery group. In one embodiment, the biomarker is at least 2.5 fold lower as compared to an expected level in a renal recovery group. In one embodiment, the biomarker is at least 2.0 fold lower as compared to an expected level in a renal recovery group. In one embodiment, the biomarker is at least 1.5 fold lower as compared to an expected level in a renal recovery group. In one embodiment, the biomarker is at least 1.25 fold lower as compared to an expected level in a renal recovery group.

[0008] In one embodiment, the present invention contemplates a method, comprising: a) providing; i) a patient exhibiting at least one symptom of an acute renal injury; and ii) a biological fluid sample obtained from said patient, wherein said sample comprises a renal injury biomarker; b) measuring a renal recovery biomarker value; c) comparing said renal biomarker value to an expected value from a renal recovery group; and d) predicting a probability of renal recovery for said patient based upon said comparison. In one embodiment, the probability of renal recovery is greater than 90%. In one embodiment, the probability of renal recovery is greater than 75%. In one embodiment, the probability of renal recovery is greater than 50%. In one embodiment, the probability of renal recovery is less than 50%. In one embodiment, the probability of renal recovery is less than

25%. In one embodiment, the probability of renal recovery is less than 10%. In one embodiment, the biomarker comprises at least a fragment of a protein selected from the group consisting of ferritin, beta globin, catalase, alpha globin, epidermal growth factor receptor pathway substrate 8, mucin isoform precursor, ezrin, delta globin, moesin, phosphoprotein isoform, annexin A2, myoglobin, hemopexin, serine proteinase inhibitor, serpine peptidase inhibitor, CD14 antigen precursor, fibronectin isoform preprotein, angiotensinogen preprotein, complement component precursor, carbonic anhydrase, uromodulin precursor, complement factor H, complement component 4 BP, heparan sulfate proteoglycan 2, olfactomedian-4, leucine rich alpha-2 glycoprotein, ring finger protein 167, inter-alpha globulin inhibitor H4, heparan sulfate proteoglycan 2, N-acylshingosine aminohydrolase, serine proteinase inhibitor clade A member 1, mucin 1, clusterin isoform 1, brain abundant membrane attached signal protein 1, dipeptidase 1, fibronectin 1 isoform 5 preprotein, angiotensinogen preproprotein, carbonic anhydrase, and uromodulin precursor.

[0009] In one embodiment, the present invention contemplates a kit, comprising; a) a first container comprising an antibody specifically directed to a renal injury biomarker, wherein said biomarker comprises at least a fragment of a protein selected from the group consisting of ferritin, beta globin, catalase, alpha globin, epidermal growth factor receptor pathway substrate 8, mucin isoform precursor, ezrin, delta globin, moesin, phosphoprotein isoform, annexin A2, myoglobin, hemopexin, serine proteinase inhibitor, serpine peptidase inhibitor, CD14 antigen precursor, fibronectin isoform preprotein, angiotensinogen preprotein, complement component precursor, carbonic anhydrase, uromodulin precursor, complement factor H, complement component 4 BP, heparan sulfate proteoglycan 2, olfactomedian-4, leucine rich alpha-2 glycoprotein, ring finger protein 167, inter-alpha globulin inhibitor H4, heparan sulfate proteoglycan 2, N-acylshingosine aminohydrolase, serine proteinase inhibitor clade A member 1, mucin 1, clusterin isoform 1, brain abundant membrane attached signal protein 1, dipeptidase 1, fibronectin 1 isoform 5 preprotein, angiotensinogen preproprotein, carbonic anhydrase, and uromodulin precursor; b) instructions for determining whether said biomarker is overexpressed as compared to an expected value from a renal recovery group; c) instructions for determining whether said biomarker is underexpressed as compared to an expected value from a renal recovery group; and d) instructions for determining the probability of renal recovery. In one embodiment, the antibody is a monoclonal antibody. In one embodiment, the monoclonal antibody is specifically directed to said biomarker protein fragment.

[0010] In one embodiment, the present invention contemplates a signature expression profile comprising a urinary protein biomarker panel, wherein said profile predicts renal recovery. In one embodiment, the biomarker panel comprises a plurality of overexpressed urinary proteins. In one embodiment, the biomarker panel comprises a plurality of underexpressed urinary proteins. In one embodiment, the plurality of overexpressed urinary proteins are selected from the group consisting of beta globin, catalase, alpha globin, mucin isoform precursor, ezrin, delta globin, moesin, phosphoprotein isoform, and annexin A2. In one embodiment, the plurality of underexpressed urinary proteins are selected from the group consisting of myoglobin, hemopexin, serine

proteinase inhibitor, serpine peptidase inhibitor, CD14 antigen precursor, fibronectin isoform preprotein, angiotensinogen preprotein, complement component precursor, carbonic anhydrase, and uromodulin precursor.

[0011] In one embodiment, the present invention contemplates a signature expression profile comprising a urinary protein biomarker panel, wherein said profile predicts renal non-recovery. In one embodiment, the biomarker panel comprises a plurality of overexpressed urinary proteins. In one embodiment, the biomarker panel comprises a plurality of underexpressed urinary proteins. In one embodiment, the plurality of overexpressed urinary proteins are selected from the group consisting of beta globin, catalase, alpha globin, mucin isoform precursor, ezrin, delta globin, moesin, phosphoprotein isoform, and annexin A2. In one embodiment, the plurality of underexpressed urinary proteins are selected from the group consisting of myoglobin, hemopexin, serine proteinase inhibitor, serpine peptidase inhibitor, CD14 antigen precursor, fibronectin isoform preprotein, angiotensinogen preprotein, complement component precursor, carbonic anhydrase, and uromodulin precursor.

[0012] In one embodiment, the present invention contemplates a method, comprising: a) providing; i) a patient exhibiting at least one symptom of an acute renal injury; and ii) a biological fluid sample obtained from said patient, wherein said sample comprises a plurality of renal biomarker nucleic acids; b) expressing said plurality of renal biomarker nucleic acids, thereby creating a signature expression profile; and c) predicting a probability of renal recovery for said patient based upon said signature expression profile. In one embodiment, the signature expression profile predicts a probability of renal recovery of greater than 90%. In one embodiment, the signature expression profile predicts a probability of renal recovery of greater than 75%. In one embodiment, the signature expression profile predicts a probability of renal recovery of greater than 50%. In one embodiment, the signature expression profile predicts a probability of renal recovery of less than 50%. In one embodiment, the signature expression profile predicts a probability of renal recovery of less than 25%. In one embodiment, the signature expression profile predicts a probability of renal recovery of less than 10%. In one embodiment, the signature expression profile comprises a plurality of overexpressed urinary proteins. In one embodiment, the signature expression profile comprises a plurality of underexpressed urinary proteins. In one embodiment, the plurality of overexpressed urinary proteins are selected from the group consisting of beta globin, catalase, alpha globin, mucin isoform precursor, ezrin, delta globin, moesin, phosphoprotein isoform, and annexin A2. In one embodiment, the plurality of underexpressed urinary proteins are selected from the group consisting of myoglobin, hemopexin, serine proteinase inhibitor, serpine peptidase inhibitor, CD14 antigen precursor, fibronectin isoform preprotein, angiotensinogen preprotein, complement component precursor, carbonic anhydrase, and uromodulin precursor.

[0013] In one embodiment, the present invention contemplates a kit, comprising; a) a first container comprising reagents for creating a signature expression profile using a biological sample, wherein said signature expression profile comprises a plurality of renal biomarker nucleic acids; b) a second container comprising monoclonal antibodies specific for said renal biomarker nucleic acids; c) a set of instructions for creating said signature expression profile; d) a set of

instructions for determining overexpressed renal biomarker nucleic acids; e) a set of instructions for determining under-expressed renal biomarker nucleic acids; f) a set of instructions for predicting the probability of renal recovery; and g) a set of instructions for predicting the probability of renal non-recovery.

Definitions

[0014] As used herein, an “injury to renal function” is an abrupt (i.e., for example, within 14 Days, preferably within 7 Days, more preferably within 72 hours, and still more preferably within 48 hours) measurable reduction in a measure of renal function. Such an injury to renal function may be identified, for example, by a decrease in glomerular filtration rate (GFR) or estimated GFR (eGFR), a reduction in urine output, an increase in serum creatinine, an increase in serum cystatin C, a requirement for renal replacement therapy (i.e., for example, dialysis), etc.

[0015] As used herein, an “improvement in renal function” is an abrupt (i.e., for example, within 14 Days, preferably within 7 Days, more preferably within 72 hours, and still more preferably within 48 hours) measurable increase in a measure of renal function. Preferred methods for measuring and/or estimating GFR are described herein-after.

[0016] As used herein, “reduced renal function” is an abrupt (i.e., for example, within 14 Days, preferably within 7 Days, more preferably within 72 hours, and still more preferably within 48 hours) reduction in kidney function identified by an absolute increase in serum creatinine of greater than or equal to 0.1 mg/dL ($\geq 8.8 \mu\text{mol/L}$), a percentage increase in serum creatinine of greater than or equal to 20% (1.2-fold from baseline), or a reduction in urine output (documented oliguria of less than 0.5 ml/kg per hour).

[0017] As used herein, “acute renal failure” or “ARF” is an abrupt (i.e., for example, within 14 Days, preferably within 7 Days, more preferably within 72 hours, and still more preferably within 48 hours) reduction in kidney function identified by an absolute increase in serum creatinine of greater than or equal to 0.3 mg/dl ($\geq 26.4 \mu\text{mol/L}$), a percentage increase in serum creatinine of greater than or equal to 50% (1.5-fold from baseline), or a reduction in urine output (documented oliguria of less than 0.5 ml/kg per hour for at least 6 hours). This term is synonymous with “acute kidney injury” or “AKI.”

[0018] As used herein, the term “relating a signal to the presence or amount” of an analyte refers to assay measurements using a standard curve calculated with known concentrations of the analyte of interest. The skilled artisan will understand that the signals obtained from an assay are often a direct result of complexes formed between, for example, one or more antibodies and a target biomolecule (i.e., for example, an analyte) and/or polypeptides containing an epitope(s) to which, for example, antibodies bind. While such assays may detect a full length biomarker and the assay result may be expressed as a concentration of a biomarker of interest, the signal from the assay is actually a result of all such “immunoreactive” polypeptides present in the sample.

[0019] As the term is used herein, an assay is “configured to detect” an analyte if an assay can generate a detectable signal indicative of the presence or amount of a physiologically relevant concentration of the analyte. For example, an antibody epitope is usually on the order of 8 amino acids,

such that an immunoassay can be configured to detect a marker of interest that will also detect polypeptides related to the marker sequence, so long as those polypeptides contain the epitope(s) necessary to bind to the antibody or antibodies used in the assay.

[0020] The term “related marker” or “biomarker” as used herein with regard to a physiological substance such as one of the proteins as described herein. A related marker may also refer to one or more fragments, variants, etc., of a particular protein and/or peptide or its biosynthetic parent that may be detected as a surrogate for the marker itself or as independent biomarkers. The term also refers to one or more polypeptides present in a biological sample that are derived from the biomarker precursor complexed to additional species, such as binding proteins, receptors, heparin, lipids, sugars, etc.

[0021] The term “subject” or “patient” as used herein, refers to a human or non-human organism. Thus, the methods and compositions described herein are equally applicable to both human and veterinary disease. Further, while a subject or patient is preferably a living organism, the invention described herein may be used in post-mortem analysis as well. Preferred subjects or patients are humans, which as used herein refer to living humans that are receiving medical care for a disease or condition.

[0022] The term “analyte” as used herein, refers to any measured compound or molecule. Preferably, an analyte is measured in a sample (i.e., for example, a body fluid sample). Such a sample may be obtained from a subject or patient, or may be obtained from biological materials intended to be provided to the subject or patient. For example, a sample may be obtained from a kidney being evaluated for possible transplantation into a subject, such that an analyte measurement may be used to evaluate the kidney for preexisting damage.

[0023] The term “body fluid sample” as used herein, refers to any sample of bodily fluid obtained for the purpose of diagnosis, prognosis, classification or evaluation of a subject of interest, such as a patient or transplant donor. In certain embodiments, such a sample may be obtained for the purpose of determining the outcome of an ongoing medical condition or the effect of a treatment regimen on a medical condition. Preferred body fluid samples include but are not limited to, blood, serum, plasma, cerebrospinal fluid, urine, saliva, sputum, or pleural effusions. In addition, certain body fluid samples may be more readily analyzed following a fractionation or purification procedure, for example, separation of whole blood into serum or plasma components.

[0024] The term “diagnosis” as used herein, refers to methods by which trained medical personnel can estimate and/or determine the probability (i.e., for example, a likelihood) of whether or not a patient is suffering from a given disease or condition. In the case of the present invention, “diagnosis” includes correlating the results of an assay (i.e., for example, an immunoassay) for a renal biomarker of the present invention, optionally together with other clinical indicia, to determine the occurrence or nonoccurrence of an acute renal injury or acute renal failure for a subject or patient from which a sample was obtained and assayed. That such a diagnosis is “determined” is not meant to imply that the diagnosis is 100% accurate. Thus, for example, a measured biomarker level below a predetermined diagnostic threshold may indicate a greater likelihood of the occurrence of a disease in the subject relative to a measured biomarker

level above the predetermined diagnostic threshold may indicate a lesser likelihood of the occurrence of the same disease.

[0025] The term “prognosis” as used herein, refers to a probability (i.e., for example, a likelihood) that a specific clinical outcome will occur. For example, a level or a change in level of a prognostic indicator, which in turn is associated with an increased probability of morbidity (e.g., worsening renal function, future ARF, or death) is referred to as being “indicative of an increased likelihood” of an adverse outcome in a patient.

[0026] The term “RIFLE” criteria, as used herein, refers to any quantitative clinical evaluation of renal status used to establish renal classifications of Risk, Injury, Failure, Loss, & End Stage Renal Disease based upon a uniform definition of acute kidney injury (AKI). Kellum, Crit. Care Med. 36: S141-45 (2008); and Ricci et al., Kidney Int. 73, 538-546 (2008), each hereby incorporated by reference in its entirety.

[0027] The term, “modified RIFLE criteria”, as used herein, provide alternative classifications for stratifying AKI patients, and may include, Stage I, Stage II, and/or Stage III. Mehta et al., Crit. Care 11:R31 (2007), hereby incorporated by reference in its entirety.

[0028] The term, “Stage I”, as used herein, refers to a risk stratification comprising a RIFLE Risk category, characterized by an increase in serum creatinine of more than or equal to 0.3 mg/dL ($\geq 26.4 \mu\text{mol/L}$) and/or an increase to more than or equal to 150% (1.5-fold) from baseline. Alternatively, the category may be defined by a urine output less than 0.5 mL/kg per hour for more than 6 hours.

[0029] The term, “Stage II”, as used herein, refers a risk stratification comprising a RIFLE Injury category, characterized by an increase in serum creatinine to more than 200% (>2 -fold) from baseline. Alternatively, the category may be defined by a urine output less than 0.5 mL/kg per hour for more than 12 hours.

[0030] The term, “Stage III”, as used herein, refers to a risk stratification comprising a RIFLE Failure category, characterized by an increase in serum creatinine to more than 300% (>3 -fold) from baseline and/or serum creatinine $\geq 354 \mu\text{mol/L}$ accompanied by an acute increase of at least 44 $\mu\text{mol/L}$. Alternatively, the category may be defined by a urine output less than 0.3 mL/kg per hour for 24 hours or anuria for 12 hours.

[0031] The term “Risk category”, as used herein, refers to a RIFLE classification wherein, in terms of serum creatinine, means any increase of at least 1.5 fold from baseline, or urine production of $<0.5 \text{ mL/kg body weight/hr}$ for approximately 6 hours.

[0032] The term “Injury category” as used herein includes, refers to a RIFLE classification wherein, in terms of serum creatinine, means any increase of at least 2.0 fold from baseline or urine production $<0.5 \text{ mL/kg/hr}$ for 12 h.

[0033] The term “Failure category” as used herein includes, refers to a RIFLE classification wherein, in terms of serum creatinine means any increase of at least 3.0 fold from baseline or a urine creatinine $>355 \mu\text{mol/l}$ (with a rise of >44) or urine output below 0.3 mL/kg/hr for 24 h, or anuria for at least 12 hours.

[0034] The term “Loss category” as used herein, refers to a clinical outcome risk and/or a RIFLE classification wherein the clinical outcome risk is characterized by a persistent need for renal replacement therapy for more than four weeks.

[0035] The term “End Stage Renal Disease category” or “ESRD category” as used herein, refers to a clinical outcome risk and/or a RIFLE classification characterized by a need for dialysis for more than 3 months.

[0036] The term “clinical outcome risk” as used herein, refers to a medical prognosis directed towards either renal recovery or renal non-recovery.

[0037] The term “renal biomarker” as used herein, refers to any biological compound related to the progressive development of chronic kidney disease. In particular, a renal biomarker may be a kidney injury marker. For example, a renal biomarker may comprise a urinary protein, or any metabolite and/or derivative thereof, wherein the renal biomarker is either overexpressed or underexpressed as a result of an AKI.

[0038] The term “positive going biomarker” as that term is used herein, refers to any biomarker that is determined to be elevated in subjects suffering from a disease or condition, relative to subjects not suffering from that disease or condition.

[0039] The term “negative going biomarker” as that term is used herein, refer to any biomarker that is determined to be reduced in subjects suffering from a disease or condition, relative to subjects not suffering from that disease or condition.

[0040] The term “positive going renal biomarker value” as used herein, refers to any increased likelihood (i.e., for example, increased probability) of suffering a future injury to renal function assigned to a subject when the measured biomarker concentration is above a specified threshold value, relative to a likelihood assigned when the measured biomarker concentration is below the specified threshold value. Alternatively, when the measured biomarker concentration is below a specified threshold value, an increased likelihood of a non-occurrence of an injury to renal function may be assigned to the subject relative to the likelihood assigned when the measured biomarker concentration is above the specified threshold value. Alternatively, when the measured biomarker concentration is below the threshold value, an improvement of renal function may be assigned to the subject. A positive going kidney injury marker may include, but not be limited to, an increased likelihood of one or more of: acute kidney injury, progression to a worsening stage of AKI, mortality, a requirement for renal replacement therapy, a requirement for withdrawal of renal toxins, end stage renal disease, heart failure, stroke, myocardial infarction, progression to chronic kidney disease, etc.

[0041] The term “negative going renal biomarker value” as used herein, refers to any increased likelihood (i.e., for example, an increased probability) of suffering a future injury to renal function assigned to the subject when the measured biomarker concentration is below a specified threshold value, relative to a likelihood assigned when the measured biomarker concentration is above the threshold value. Alternatively, when the measured biomarker concentration is above the threshold value, an increased likelihood of a non-occurrence of an injury to renal function may be assigned to the subject relative to the likelihood assigned when the measured biomarker concentration is below the threshold value. Alternatively, when the measured biomarker concentration is above the threshold value, an improvement of renal function may be assigned to the subject. A negative going kidney injury marker may include, but not be limited to, an increased likelihood of one or more

of: acute kidney injury, progression to a worsening stage of AKI, mortality, a requirement for renal replacement therapy, a requirement for withdrawal of renal toxins, end stage renal disease, heart failure, stroke, myocardial infarction, progression to chronic kidney disease, etc.

[0042] The term “pre-existing” and “pre-existence” as used herein, means any risk factor (i.e., for example, a renal biomarker) existing at the time a body fluid sample is obtained from the subject.

[0043] The term “predicting” as used herein, refers to a method of forming a prognosis and/or a stratification risk assignment, wherein a medically trained person analyzes biomarker information, and optionally with relevant clinical indicia and/or demographic information.

[0044] The term “acute renal disease/failure/injury” as used herein, refers to any progressive worsening of renal function over hours to Days, resulting in the retention of nitrogenous wastes (such as urea nitrogen) and creatinine in the blood. Retention of these substances may also be referred to as, azotemia. In: *Current Medical Diagnosis & Treatment 2008*, 47th Ed, McGraw Hill, New York, pages 785-815, herein incorporated by reference in their entirety.

[0045] The term “chronic renal disease/failure/injury” as used herein, refers to a medical condition wherein exemplary symptoms may include, but are not limited to, hyperphosphatemia (i.e., for example, >4.6 mg/dl) or low glomerular filtration rates (i.e., for example, <90 ml/minute per 1.73 m² of body surface). However, many CKD patients may have normal serum phosphate levels in conjunction with a sustained reduction in glomerular filtration rate for 3 or more months, or a normal GFR in conjunction with sustained evidence of a structural abnormality of the kidney. In some cases, patients diagnosed with chronic kidney disease are placed on hemodialysis to maintain normal blood homeostasis (i.e., for example, urea or phosphate levels). Alternatively, “chronic kidney disease” refers to a medical condition wherein a patient has either i) a sustained reduction in GFR <60 ml/min per 1.73 m² of body surface for 3 or more months; or ii) a structural or functional abnormality of renal function for 3 or more months even in the absence of a reduced GFR. Structural or anatomical abnormalities of the kidney could be defined as, but not limited to, persistent microalbuminuria or proteinuria or hematuria or presence of renal cysts. Chronic renal failure (chronic kidney disease) may also result from an abnormal loss of renal function over months to years. In: *Current Medical Diagnosis & Treatment 2008*, 47th Ed, McGraw Hill, New York, pages 785-815, herein incorporated by reference in their entirety.

[0046] The term “about” as used herein in the context of any of any assay measurements refers to $\pm 5\%$ of a given measurement.

[0047] The term “asymptomatic” as used herein, refers to a patient and/or subject that does not have a renal disease and/or injury, wherein a renal disease and/or injury symptom may include, but is not limited to, having a reduced glomerular filtration rate (i.e., for example, between approximately 70-89 ml/min per 1.73 m² of body surface) for less than three months.

[0048] The term “glomerular filtration rate” as used herein, refers to any measurement capable of determining kidney function. In general, a normal glomerular filtration rate ranges between approximately 120-90 ml/minute per 1.73 m² of body surface. Compromised kidney function is assumed when glomerular filtration rates are less than 90

ml/minute per 1.73 m² of body surface. Kidney failure is probable when glomerular filtration rates fall below approximately 30 ml/minute per 1.73 m² of body surface. Dialysis is frequently initiated when glomerular filtration rates fall below approximately 15 ml/minute per 1.73 m² of body surface.

[0049] The term “renal failure” as used herein, refers to any acute, sudden, and/or chronic loss of the ability of the kidneys to remove waste and concentrate urine without losing electrolytes.

[0050] The term “biological sample” as used herein, refers to any substance derived from a living organism. For example, a sample may be derived from blood as a urine sample, serum sample, a plasma sample, and or a whole blood sample. Alternatively, a sample may be derived from a tissue collected, for example, by a biopsy. Such a tissue sample may comprise, for example, kidney tissue, vascular tissue and/or heart tissue. A biological sample may also comprise body fluids including, but not limited to, urine, saliva, or perspiration.

[0051] The term “reagent” as used herein, refers to any substance employed to produce a chemical reaction so as to detect, measure, produce, etc., other substances. The term “antibody” as used herein refers to any peptide or polypeptide derived from, modeled after, or substantially encoded by, an immunoglobulin gene or immunoglobulin genes, or fragments thereof, capable of specifically binding an antigen or epitope. See, e.g. In: *Fundamental Immunology*, 3rd Edition, W. E. Paul, ed., Raven Press, N.Y. (1993); Wilson et al., *J. Immunol. Methods* 175:267-273 (1994); and Yarmush et al., *J. Biochem. Biophys. Methods* 25:85-97 (1992). The term antibody includes, but is not limited to, antigen-binding portions, i.e., “antigen binding sites” exemplified by fragments, subsequences, and/or complementarity determining regions (CDRs)) that retain capacity to bind antigen, including, but not limited to: (i) a Fab fragment, a monovalent fragment comprising VL, VH, CL or CH1 domains; (ii) a F(ab')₂ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment comprising VH and CH1 domains; (iv) a Fv fragment comprising VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., *Nature* 341:544-546 (1989)), which comprises a VH domain; or (vi) an isolated complementarity determining region (CDR). Single chain antibodies are also included by reference in the term “antibody.”

[0052] The term “epitope” as used herein, refers to any antigenic determinant capable of specific binding to an antibody. Epitopes usually display chemically active surface molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. Conformational and nonconformational epitopes may be distinguished in that the binding to the former but not the latter can be lost in the presence of denaturing solvents.

[0053] The term “correlating” as used herein, in reference to the use of biomarkers, refers to comparing the presence and/or amount of any biomarker(s) in a patient to its presence and/or amount in persons known to suffer from, or known to be at risk of, a given condition; or in persons known to be free of a given condition. Often, this takes the form of comparing an assay result in the form of a biomarker concentration to a predetermined threshold selected to be

indicative of the occurrence or nonoccurrence of a disease or the likelihood of some future outcome.

BRIEF DESCRIPTION OF THE FIGURES

[0054] FIG. 1 presents exemplary subject information relevant to the Biological Markers of Recovery for the Kidney (BioMaRK) study cohort used as the basis for some of the data analysis presented herein.

[0055] FIG. 2: Representative protein biomarker families identified by a proteomics platform.

[0056] FIG. 3 Representative single biomarker peptides Identified by a proteomics platform.

DETAILED DESCRIPTION

[0057] This invention is related to the field of the prevention and treatment of kidney disease. The treatment of kidney disease may be tailored depending upon the need for, or expectation of, renal recovery. For example, prediction of renal recovery can be determined by monitoring urine biomarkers related to the development of chronic kidney disease. For example, differential expression platforms can be used to identify biomarker proteins in order to establish the risk of renal recovery versus renal non-recovery in patient's having suffered an acute kidney injury.

[0058] Despite significant advances in the epidemiology of acute kidney injury (AKI), prognostication remains a major clinical challenge. Unfortunately, there is no reliable method to predict renal recovery. The discovery of biomarkers to aid in clinical risk prediction for recovery after AKI would represent a significant advance over current practice.

1. Kidney Injury and/or Disease

[0059] The kidney is responsible for water and solute excretion from the body. Its functions include maintenance of acid-base balance, regulation of electrolyte concentrations, control of blood volume, and regulation of blood pressure. As such, loss of kidney function through injury and/or disease results in substantial morbidity and mortality. A detailed discussion of renal injuries is provided in Harrison's Principles of Internal Medicine, 17th Ed., McGraw Hill, New York, pages 1741-1830, which are hereby incorporated by reference in their entirety. The kidneys are located in the flank (back of the upper abdomen at either side of the spinal column). They are deep within the abdomen and are protected by the spine, lower rib cage, and the strong muscles of the back. This location protects the kidneys from many external forces. They are well-padded for a reason—kidneys are highly vascular organs, which means that they have a large blood supply. If injury occurs, severe bleeding may result.

[0060] Kidneys may be injured by damage to the blood vessels that supply or drain them. This may be in the form of aneurysm, arteriovenous fistula, arterial blockage, or renal vein thrombosis. The extent of bleeding depends on the location and the degree of injury. Kidneys may also bleed profusely if they are damaged centrally (on the inside)—this is a life-threatening injury. Fortunately, most kidney injuries caused by blunt trauma occur peripherally, only causing bruising of the kidney (usually a self-limiting process).

[0061] People with undiagnosed kidney conditions—such as angiomyolipoma (benign tumor), ureteropelvic junction obstruction (congenital or acquired UPJ Obstruction), and other disorders—are more susceptible to kidney injuries and more likely to have serious complications if they occur.

Other causes of kidney injury and bleeding are medical procedures. Kidney biopsies, nephrostomy tube placements, or other surgeries can cause an abnormal connection between an artery and vein (arteriovenous fistula). This is usually a self-limiting problem, but close observation is usually needed. Injury to the kidney can also disrupt the urinary tract, causing leakage of the urine from the kidney.

[0062] Each kidney filters about 1700 liters of blood per Day and concentrates fluid and waste products into about 1 liter of urine per Day. Because of this, the kidneys receive more exposure to toxic substances in the body than almost any other organ. Therefore, they are highly susceptible to injury from toxic substances. Analgesic nephropathy is one of the most common types of toxic damage to the kidney. Exposure to lead, cleaning products, solvents, fuels, or other nephrotoxic chemicals (those which can be toxic to the kidney) can damage kidneys. Excessive buildup of body waste products, such as uric acid (that can occur with gout or with treatment of bone marrow, lymph node, or other disorders) can also damage the kidneys.

[0063] Inflammation (irritation with swelling and presence of extra immune cells) caused by immune responses to medications, infection, or other disorders may also injure the structures of the kidney, usually causing various types of glomerulonephritis or acute tubular necrosis (tissue death). Autoimmune disorders may also damage the kidneys. Injury to the kidney may result in short-term damage with minimal or no symptoms. Alternately, it can be life-threatening because of bleeding and associated shock, or it may result in acute renal failure or chronic renal failure.

[0064] Ureteral injuries (injuries to the tubes which carry urine from the kidneys to the bladder) can also be caused by trauma (blunt or penetrating), complications from medical procedures, and other diseases in the retroperitoneum such as retroperitoneal fibrosis (RPF), retroperitoneal sarcomas, or metastatic lymph node positive cancers. Medical therapies (such as OB/GYN surgeries, prior radiation or chemotherapy, and previous abdominopelvic surgeries) increase the risk for ureteral injuries.

[0065] A. Acute Kidney Failure

[0066] Acute (sudden) kidney failure is the sudden loss of the ability of the kidneys to remove waste and concentrate urine without losing electrolytes. There are many possible causes of kidney damage including, but are not limited to, decreased blood flow, which may occur with extremely low blood pressure caused by trauma, surgery, serious illnesses, septic shock, hemorrhage, burns, or dehydration, acute tubular necrosis (ATN), infections that directly injure the kidney such as acute pyelonephritis or septicemia, urinary tract obstruction (obstructive uropathy), autoimmune kidney disease such as interstitial nephritis or acute nephritic syndrome, disorders that cause clotting within the thin blood vessels of the kidney, idiopathic thrombocytopenic thrombotic purpura (ITTP), transfusion reaction, malignant hypertension, scleroderma, hemolytic-uremic syndrome, disorders of childbirth, such as bleeding placenta abruptio or placenta previa

[0067] Symptoms of acute kidney failure may include, but are not limited to, decrease in amount of urine (oliguria), urination stops (anuria), excessive urination at night, ankle, feet, and leg swelling, generalized swelling, fluid retention, decreased sensation, especially in the hands or feet, decreased appetite, metallic taste in mouth, persistent hiccups, changes in mental status or mood, agitation, drowsi-

ness, lethargy, delirium or confusion, coma, mood changes, trouble paying attention, hallucinations, slow, sluggish, movements, seizures, hand tremor (shaking), nausea or vomiting, may last for Days, bruising easily, prolonged bleeding, nosebleeds, bloody stools, flank pain (between the ribs and hips), fatigue, breath odor, or high blood pressure.

[0068] Acute renal failure (ARF) may also be referred to as acute kidney injury (AKI) and may be characterized by an abrupt (i.e., for example, typically detected within about 48 hours to 1 week) reduction in glomerular filtration rate (GFR). This loss of filtration capacity results in retention of nitrogenous (urea and creatinine) and non-nitrogenous waste products that are normally excreted by the kidney, a reduction in urine output, or both. It is reported that ARF complicates about 5% of hospital admissions, 4-15% of cardiopulmonary bypass surgeries, and up to 30% of intensive care admissions. ARF may be categorized as prerenal, intrinsic renal, or postrenal in causation. Intrinsic renal disease can be further divided into glomerular, tubular, interstitial, and vascular abnormalities. Major causes of ARF are described in association with their respective risk factors are summarized below. See, Table 4; In: Merck Manual, 17th ed., Chapter 222, and which is hereby incorporated by reference in their entirety.

TABLE 4

Representative Acute Renal Failure Risk Factors	
Type of Renal Failure	Risk Factors
Prerenal	
ECF volume depletion	Excessive diuresis, hemorrhage, GI losses, loss of intravascular fluid into the extravascular space (due to ascites, peritonitis, pancreatitis, or burns), loss of skin and mucus membranes, renal salt- and water-wasting states
Low cardiac output	Cardiomyopathy, MI, cardiac tamponade, pulmonary embolism, pulmonary hypertension, positive-pressure mechanical ventilation
Low systemic vascular resistance	Septic shock, liver failure, antihypertensive drugs
Increased renal vascular resistance	NSAIDs, cyclosporines, tacrolimus, hypercalcemia, anaphylaxis, anesthetics, renal artery obstruction, renal vein thrombosis, sepsis, hepatorenal syndrome
Decreased efferent arteriolar tone (leading to decreased GFR from reduced glomerular transcapillary pressure, especially in patients with bilateral renal artery stenosis)	ACE inhibitors or angiotensin II receptor blockers
Intrinsic Renal	
Acute tubular injury	Ischemia (prolonged or severe prerenal state): surgery, hemorrhage, arterial or venous obstruction; Toxins: NSAIDs, cyclosporines, tacrolimus, aminoglycosides, foscarnet, ethylene glycol, hemoglobin, myoglobin, ifosfamide, heavy metals, methotrexate, radiopaque contrast agents, streptozotocin
Acute glomerulonephritis	ANCA-associated: Crescentic glomerulonephritis, polyarteritis nodosa, Wegener's granulomatosis; Anti-GBM glomerulonephritis: Goodpasture's syndrome;

TABLE 4-continued

Representative Acute Renal Failure Risk Factors	
Type of Renal Failure	Risk Factors
Acute tubulointerstitial nephritis	Immune-complex: Lupus glomerulonephritis, postinfectious glomerulonephritis, cryoglobulinemic glomerulonephritis
	Drug reaction (eg, β -lactams, NSAIDs, sulfonamides, ciprofloxacin, thiazide diuretics, furosemide, phenytoin, allopurinol, pyelonephritis, papillary necrosis)
	Acute vascular nephropathy
	Vasculitis, malignant hypertension, thrombotic microangiopathies, scleroderma, atheroembolism
Infiltrative diseases	Lymphoma, sarcoidosis, leukemia
Postrenal	
Tubular precipitation	Uric acid (tumor lysis), sulfonamides, triamterene, acyclovir, indinavir, methotrexate, ethylene glycol ingestion, myeloma protein, myoglobin
Ureteral obstruction	Intrinsic: Calculi, clots, sloughed renal tissue, fungus ball, edema, malignancy, congenital defects; Extrinsic: Malignancy, retroperitoneal fibrosis, ureteral trauma during surgery or high impact injury
Bladder obstruction	Mechanical: Benign prostatic hyperplasia, prostate cancer, bladder cancer, urethral strictures, phimosis, paraphimosis, urethral valves, obstructed indwelling urinary catheter; Neurogenic: Anticholinergic drugs, upper or lower motor neuron lesion

[0069] In the case of ischemic ARF, the course of the disease may be divided into four phases. During an initiation phase, which lasts hours to Days, reduced perfusion of the kidney is evolving into injury. Glomerular ultrafiltration reduces, the flow of filtrate is reduced due to debris within the tubules, and back leakage of filtrate through injured epithelium occurs. Renal injury can be mediated during this phase by reperfusion of the kidney. Initiation is followed by an extension phase which is characterized by continued ischemic injury and inflammation and may involve endothelial damage and vascular congestion. During the maintenance phase, lasting from 1 to 2 weeks, renal cell injury occurs, and glomerular filtration and urine output reaches a minimum. A recovery phase can follow in which the renal epithelium is repaired and GFR gradually recovers. Despite this, the survival rate of subjects with ARF may be as low as about 60%.

[0070] Acute kidney injury caused by radiocontrast agents (also called contrast media) and other nephrotoxins such as cyclosporine, antibiotics including aminoglycosides and anticancer drugs such as cisplatin manifests over a period of Days to about a week. Contrast induced nephropathy (CIN, which is AKI caused by radiocontrast agents) is thought to be caused by intrarenal vasoconstriction (leading to ischemic injury) and from the generation of reactive oxygen species that are directly toxic to renal tubular epithelial cells. CIN classically presents as an acute (onset within 24-48 h) but reversible (peak 3-5 Days, resolution within 1 week) rise in blood urea nitrogen and serum creatinine.

[0071] A commonly reported criteria for defining and detecting AKI is an abrupt (typically within about 2-7 Days or within a period of hospitalization) elevation of serum creatinine. Although the use of serum creatinine elevation to define and detect AKI is well established, the magnitude of the serum creatinine elevation and the time over which it is measured to define AKI varies considerably among publications. Traditionally, relatively large increases in serum creatinine such as 100%, 200%, an increase of at least 100%

to a value over 2 mg/dL and other definitions were used to define AKI. However, the recent trend has been towards using smaller serum creatinine rises to define AKI.

[0072] For example, relationships between elevated serum creatinine and AKI has been reported to be associated with health risks. Praught et al., *Curr Opin Nephrol Hypertens* 14:265-270 (2005); and Chertow et al., *J Am Soc Nephrol* 16:3365-3370 (2005) (both references are herein incorporated by reference in their entirety). As described in these publications, acute worsening renal function (AKI) and increased risk of death and other detrimental outcomes are now known to be associated with very small increases in serum creatinine. These creatinine increases may be determined as a relative (percent) value or a nominal value. Relative increases in serum creatinine as small as 20% from the pre-injury value have been reported to indicate acutely worsening renal function (AKI) and increased health risk, but the more commonly reported value to define AKI and increased health risk is a relative increase of at least 25%. Nominal increases as small as 0.3 mg/dL, 0.2 mg/dL or even 0.1 mg/dL have been reported to indicate worsening renal function and increased risk of death. Various time periods for the serum creatinine to rise to these threshold values have been used to define AKI, for example, ranging from 2 Days, 3 Days, 7 Days, or a variable period defined as the time the patient is in the hospital or intensive care unit. These studies indicate there is not a particular threshold serum creatinine rise (or time period for the rise) for worsening renal function or AKI, but rather a continuous increase in risk with increasing magnitude of serum creatinine rise.

[0073] Another study correlated serum creatinine levels with post-surgical mortality rates. Following heart surgery, patients with a mild fall in serum creatinine (i.e., for example, between approximately -0.1 to -0.3 mg/dL) had the lowest mortality rate, wherein patients had a larger mortality rate associated with either large falls in serum creatinine (i.e., for example, more than or equal to -0.4 mg/dL), or an increase in serum creatinine. Lassnigg et al., *J Am Soc Nephrol* 15:1597-1605 (2004), herein incorporated by reference in its entirety. These findings suggested that even very subtle changes in renal function, as detected by small creatinine changes within 48 hours of surgery, can be predictive of a patient's outcome.

[0074] A unified classification system using serum creatinine to define AKI in clinical trials and in clinical practice was proposed to stratify AKI patients. Bellomo et al., *Crit Care* 8(4):R204-212 (2004), which is herein incorporated by reference in its entirety. For example, a serum creatinine rise of 25% may define contrast-induced nephropathy. McCollough et al., *Rev Cardiovasc Med*. 7(4): 177-197 (2006), herein incorporated by reference in its entirety. Although various groups propose slightly different criteria for using serum creatinine to detect AKI, the consensus is that small changes in serum creatinine, such as 0.3 mg/dL (i.e., for example, approximately 25%) are sufficient to detect AKI that characterizes a worsening renal function and that the magnitude of the serum creatinine change may be an indicator of the severity of the AKI and mortality risk.

[0075] Although serial measurement of serum creatinine over a period of Days is an accepted method of detecting and diagnosing AKI patients, serum creatinine is generally regarded to have several limitations in the diagnosis, assessment and monitoring of AKI patients. The time period for serum creatinine to rise to approximately 0.3 mg/dL (25%)

is considered diagnostic for AKI can be 48 hours or longer depending on the definition used.

[0076] Since cellular injury in AKI can occur over a period of hours, serum creatinine elevations detected at 48 hours or longer can be a late indicator of injury, and relying on serum creatinine can thus delay diagnosis of AKI. Furthermore, serum creatinine is not a good indicator of the exact kidney status and treatment needs during the most acute phases of AKI when kidney function is changing rapidly. Until defined by some embodiments of the present invention, there were no methods to determine whether some patients with AKI would recover fully, or whether some would need dialysis (either short term or long term), or whether some would have other detrimental outcomes including, but not limited to, death, major adverse cardiac events or chronic kidney disease. Because serum creatinine is a marker of filtration rate, it does not differentiate between the causes of AKI (pre-renal, intrinsic renal, post-renal obstruction, atheroembolic, etc) or the category or location of injury in intrinsic renal disease (for example, tubular, glomerular or interstitial in origin). Urine output is similarly limited.

[0077] These limitations underscore the need for better methods to detect and assess AKI, particularly in the early and subclinical stages, but also in later stages when recovery and repair of the kidney can occur. Furthermore, there is a need to better identify patients who are at risk of having an AKI.

[0078] B. Chronic Kidney Failure

[0079] Unlike acute renal failure, chronic renal failure slowly gets worse. It most often results from any disease that causes gradual loss of kidney function. It can range from mild dysfunction to severe kidney failure. Chronic renal failure may lead to end-stage renal disease (ESRD).

[0080] Chronic renal failure usually occurs over a number of years as the internal structures of the kidney are slowly damaged. In the early stages, there may be no symptoms. In fact, progression may be so slow that symptoms do not occur until kidney function is less than one-tenth of normal.

[0081] Chronic renal failure and ESRD affect more than 2 out of 1,000 people in the United States. Diabetes and high blood pressure are the two most common causes and account for most cases. Other major causes include, but are not limited to, Alport syndrome, analgesic nephropathy, glomerulonephritis of any type (one of the most common causes), kidney stones and infection, obstructive uropathy, polycystic kidney disease, or reflux nephropathy. Chronic renal failure results in an accumulation of fluid and waste products in the body, leading to a build up of nitrogen waste products in the blood (azotemia) and general ill health. Most body systems are affected by chronic renal failure.

[0082] Initial symptoms may include, but are not limited to, fatigue, frequent hiccups, general ill feeling, generalized itching (pruritus), headache, nausea, vomiting, or unintentional weight loss. Further, later symptoms may include, but are not limited to, blood in the vomit or in stools, decreased alertness, including drowsiness, confusion, delirium, orcoma, decreased sensation in the hands, feet, or other areas, easy bruising or bleeding, increased or decreased urine output, muscle twitching or cramps, seizures, or white crystals in and on the skin (uremic frost).

[0083] Circulating levels of cytokines and other inflammation markers are markedly elevated in patients with chronic renal failure. This could be caused by increased generation, decreased removal, or both. However, it is not

well established to what extent renal function per se contributes to the uremic proinflammatory milieu. Relationships between inflammation and glomerular filtration rate (GFR) were reported in 176 patients (age, 52+/-1 years; GFR, 6.5+/-0.1 mL/min) close to the initiation of renal replacement therapy. Pecoits-Filho et al., "Associations between circulating inflammatory markers and residual renal function in CRF patients" *Am J Kidney Dis.* 41(6):1212-1218 (2003). For example, circulating levels of high-sensitivity C-reactive protein (hsCRP), tumor necrosis factor-alpha (TNF-alpha), interleukin-6 (IL-6), hyaluronan, and neopterin were measured after an overnight fast. Patients subsequently were subdivided into two groups according to median GFR (6.5 mL/min). Despite the narrow range of GFR (1.8 to 16.5 mL/min), hsCRP, hyaluronan, and neopterin levels were significantly greater in the subgroup with lower GFRs, and significant negative correlations were noted between GFR and IL-6 ($\rho=-0.18$; $P<0.05$), hyaluronan ($\rho=-0.25$; $P<0.001$), and neopterin ($\rho=-0.32$; $P<0.0005$). In a multivariate analysis, age and GFR were associated with inflammation but cardiovascular disease and diabetes mellitus were not. These results show that a low GFR per se is associated with an inflammatory state, suggesting impaired renal elimination of proinflammatory cytokines, increased generation of cytokines in uremia, or an adverse effect of inflammation on renal function.

[0084] C. Dialysis

[0085] Dialysis (i.e., for example, renal replacement therapy) is a method of removing toxic substances (impurities or wastes) from the blood when the kidneys are unable to do so and can be performed using several different methods. For example, peritoneal dialysis may filter waste by using the peritoneal membrane inside the abdomen. The abdomen is filled with special solutions that help remove toxins. The solutions remain in the abdomen for a time and then are drained out. This form of dialysis can be performed at home, but must be done every Day. Alternatively, hemodialysis may be performed by circulating the blood through special filters outside the body. The blood flows across a filter, along with solutions that help remove toxins.

[0086] Dialysis uses special ways of accessing the blood in the blood vessels. The access can be temporary or permanent. Temporary access takes the form of dialysis catheters—hollow tubes placed in large veins that can support acceptable blood flows. Most catheters are used in emergency situations for short periods of time. However, catheters called tunneled catheters can be used for prolonged periods of time, often weeks to months. Permanent access is created by surgically joining an artery to a vein. This allows the vein to receive blood at high pressure, leading to a thickening of the vein's wall. This vein can handle repeated puncture and also provides excellent blood flow rates. The connection between an artery and a vein can be made using blood vessels (an arteriovenous fistula, or AVF) or a synthetic bridge (arteriovenous graft, or AVG). Blood is diverted from the access point in the body to a dialysis machine. Here, the blood flows counter-current to a special solution called the dialysate. The chemical imbalances and impurities of the blood are corrected and the blood is then returned to the body. Typically, most patients undergo hemodialysis for three sessions every week. Each session lasts 3-4 hours.

The purpose of dialysis is to assist kidney functions including, filters for the blood, removing waste products, regulat-

ing body water, maintaining electrolyte balance, or maintaining blood pH remains between 7.35 and 7.45. Further, dialysis may replace some of the functions for kidneys that aren't working properly that would otherwise result in the death of a patient.

[0087] Dialysis is most often used for patients who have kidney failure, but it can also quickly remove drugs or poisons in acute situations. This technique can be life saving in people with acute or chronic kidney failure.

II. Urinary Renal Biomarkers

[0088] Currently, no effective treatments exist to improve renal recovery, or to improve short and long-term renal outcome, after AKI. Furthermore, methods to predict recovery are also lacking. The emerging role of biomarkers for early detection of renal disease and/or renal injury may help identify new prognostic tools to predict renal clinical outcomes. Potential candidates for biomarkers of renal recovery include, but are not limited to, molecules expressed in pathways leading to regeneration and proliferation as well as markers of fibrosis and apoptosis. In addition, renal injury biomarkers may also serve to distinguish early resolution, and hence increased odds of recovery.

[0089] Acute kidney injury (AKI) has an estimated incidence rate of approximately 2000 per million population and this rate is increasing. Ali et al., "Incidence and outcomes in acute kidney injury: a comprehensive population-based study" *J Am Soc Nephrol* 18:1292-1298 (2007). Approximately 5% of all people admitted to intensive care units around the world develop severe AKI requiring dialysis. Uchino et al., "Acute renal failure in critically ill patients: a multinational, multicenter study" *JAMA* 294:813-818 (2005). A recent, United States multi-center study found that fewer than only about 60% patients surviving severe AKI recovered renal function by two months. Palevsky et al., "Intensity of renal support in critically ill patients with acute kidney injury" *N Engl J Med* 359:7-20 (2008). Thus, a large number of patients with AKI progress into end-stage renal disease (ESRD).

[0090] However, since only a fraction of patients with AKI fail to recover renal function, interventions aimed at improving recovery or at providing renal support (e.g. early dialysis) cannot be selectively targeted appropriately without some means of determining which patients will recover and which will not recover (i.e., for example, the availability of non-invasive biomarkers). Currently, clinical risk prediction for recovery after AKI is extremely limited. Thus, development of a non-invasive biomarker that allows early prediction of recovery of kidney function is a long felt need in the art of renal disease management.

[0091] The identification of such non-invasive biomarkers (i.e., for example, a urinary biomarker) would greatly improve long-term prognosis thereby tailoring research efforts to treat AKI and prevent ESRD. In other words, having the ability to predict which patients will not recover kidney function allows a clinician to focus limited resources on the development and application of aggressive treatment interventions on these predicted at-risk patients. Conversely, patients with a favorable prognosis would be spared from more aggressive interventions and their potential adverse effects, thereby releasing medical resources to those in need and reducing overall medical costs.

[0092] In one embodiment, the present invention contemplates methods and compositions for evaluating renal func-

tion in a subject. As described herein, measurement of various kidney injury markers described herein can be used for diagnosis, prognosis, risk stratification, staging, monitoring, categorizing and a determination of further diagnosis and treatment regimens in subjects suffering or at risk of suffering from an injury to renal function, reduced renal function, and/or acute renal failure (also called acute kidney injury).

[0093] Renal biomarkers as described herein may be used individually, or in panels, comprising a plurality of renal biomarkers, for risk stratification. In one embodiment, risk stratification identifies subjects at risk for a future: i) injury to renal function; ii) progression to reduced renal function; iii) progression to ARF; or iv) improvement in renal function, etc. In one embodiment, risk stratification diagnoses an existing disease, comprising identifying subjects who have: i) suffered an injury to renal function; ii) progressed to reduced renal function; or iii) progressed to ARF, etc. In one embodiment, risk stratification monitors for deterioration and/or improvement of renal function. In one embodiment, risk stratification predicts a future medical outcome including, but not limited to, an improved or worsening renal function, a decreased or increased mortality risk, a decreased or increased risk that a subject will require initiation or continuation of renal replacement therapy (i.e., hemodialysis, peritoneal dialysis, hemofiltration, and/or renal transplantation, a decreased or increased risk that a subject will recover from an injury to renal function, a decreased or increased risk that a subject will recover from ARF, a decreased or increased risk that a subject will progress to end stage renal disease, a decreased or increased risk that a subject will progress to chronic renal failure, a decreased or increased risk that a subject will suffer rejection of a transplanted kidney, etc.

III. Clinical Renal Biomarker Studies

[0094] The results of a large multicenter clinical trial has recently been reported comparing two intensities of renal support for critically ill patients with acute kidney injury (AKI) in which recovery of renal function was less than 25% at 28 days and not different between the two treatment strategies. Palevsky et al., "Intensity of renal support in critically ill patients with acute kidney injury" *N Engl J Med* 359:7-20 (2008). These results emphasize that incomplete renal recovery is a common problem in the patients who survive severe AKI. Uchino et al., "Acute renal failure in critically ill patients: a multinational, multicenter study" *JAMA*, 294: 813-818 (2005). Failure to recover renal function can have tremendous negative effects on quality of life and health care costs. Manns et al., "Cost of acute renal failure requiring dialysis in the intensive care unit: clinical and resource implications of renal recovery" *Crit Care Med*, 31:449-455 (2003). Therefore, treatments to hasten and facilitate renal recovery are eagerly being sought by both the critical care and nephrology communities. Unfortunately, there are no effective treatments to improve renal recovery. One possible barrier to progress in this area has been the inability to forecast recovery in individual patients. The ability to prognosticate in an AKI patient population would be extremely valuable both for clinical decisions as well as to guide future research on therapy to promote recovery of renal function.

[0095] One clinical study reported that patients who recovered from AKI did not appear to differ in clinical

characteristics (i.e., for example, age, gender, mechanical ventilation status, or clinical severity scores) from the non-recovery group. Bhandari et al., "Survivors of acute renal failure who do not recover renal function" *QJM*, 89:415-421 (1996). Secondary analysis from three randomized controlled trials (RCTs) comparing efficacy of continuous renal replacement therapy (RRT) versus intermittent RRT found that: i) APACHE III scores >100; ii) cardiovascular instability; and iii) pre-existing renal impairment were all associated with renal non-recovery. Mehta et al., "A randomized clinical trial of continuous versus intermittent dialysis for acute renal failure" *Kidney Int*, 60:1154-1163 (2001); Augustine et al., "A randomized controlled trial comparing intermittent with continuous dialysis in patients with ARF" *Am J Kidney Dis*, 44:1000-1007 (2004); and Uehlinger et al., "Comparison of continuous and intermittent renal replacement therapy for acute renal failure" *Nephrol Dial Transplant*, 20:1630-1637 (2005), respectively. However, these studies did not adhere to a uniform definition of, or standard timing, to assess renal recovery.

[0096] Other studies have suggested that baseline creatinine and urine output at the time of discontinuation of RRT were most predictive of recovery. Uchino et al., "Discontinuation of continuous renal replacement therapy: a post hoc analysis of a prospective multicenter observational study" *Crit Care Med*, 37:2576-2582 (2009). However, urine output was analyzed after RRT had ended based on a clinical decision rather than at a fixed time point (e.g. 14 Days post AKI) to predict renal recovery. Therefore, these data are compromised to suggest that urine output was predictive of renal recovery, and further, baseline creatinine might have been less valuable because patients with stage 4 and 5 CKD were excluded.

[0097] Recently, a number of urinary biomarkers have been investigated for the purpose of early diagnosis of AKI. Since these markers correlate with renal tubular cell injury or function, their patterns in the urine, either alone or in combination, could provide new prognostic information regarding renal recovery. For example, several reports have suggested possible candidate renal biomarkers relating to three aspects of the physiology of renal recovery:

[0098] i) inflammatory markers including; a) urinary neutrophil gelatinase-associated lipocalin (uNGAL), which has been extensively studied for predicting AKI (Supavekin et al., "Differential gene expression following early renal ischemia/reperfusion" *Kidney Int*, 63:1714-1724 (2003); Mishra et al., "Kidney NGAL is a novel early marker of acute injury following transplantation" *Pediatr Nephrol*, 21:856-863 (2006); Hirsch et al., "NGAL is an early predictive biomarker of contrast-induced nephropathy in children" *Pediatr Nephrol*, 22: 2089-2095 (2007); and Zappitelli et al., "Urine neutrophil gelatinase-associated lipocalin is an early marker of acute kidney injury in critically ill children: a prospective cohort study" *Crit Care*, 11: R84 (2007); b) matrix metalloproteinase protein-9 (MMP-9), a matrix degradation enzyme which is up-regulated after ischemic injury in animal models and links to NGAL by a disulfide bond forming urinary NGAL/MMP-9 (uNGAL/MMP-9) (Ronco et al., "Matrix metalloproteinases in kidney disease progression and repair: a case of flipping the coin" *Semin Nephrol*, 27:352-362 (2007); and c) urinary interleukin-18 (uIL-18), an inflammatory cytokine which is found to potentiate ischemic AKI and has been tested in many clinical settings (Parikh et al., "Urine IL-18 is an early diagnostic marker for

acute kidney injury and predicts mortality in the intensive care unit" *J Am Soc Nephrol*, 16:3046-3052 (2005); and Parikh et al., "Urinary IL-18 is an early predictive biomarker of acute kidney injury after cardiac surgery" *Kidney Int*, 70:199-203 (2006);

[0099] ii) growth factors including urinary hepatocyte growth factor (uHGF), a biomarker linked to renal tubular epithelial cell regeneration (Liu et al., "Hepatocyte growth factor: new arsenal in the fights against renal fibrosis?" *Kidney Int*, 70:238-240 (2006); and

[0100] iii) filtration and tubular reabsorption markers, such as cystatin C, which is freely filtered and is normally completely reabsorbed by proximal tubular epithelial cells and urine creatinine. Herget-Rosenthal et al., "Measurement of urinary cystatin C by particle-enhanced nephelometric immunoassay: precision, interferences, stability and reference range" *Ann Clin Biochem*, 41:111-118 (2004).

[0101] Despite these reports, only a few suggest biomarkers having an ability to predict AKI severity. But no study has identified a biomarker as a predictor of renal recovery. Coca et al., "Biomarkers for the diagnosis and risk stratification of acute kidney injury: a systematic review" *Kidney Int*, 73:1008-1016 (2008). The data presented herein provide heretofore unknown renal biomarkers identified by proteomic gene expression analysis. The data was obtained from urine samples collected during a clinical study as described below.

[0102] The data presented herein was collected from 109 patients in the BioMaRK clinical study where 76 patients had complete data available including urine samples. Exactly half (38 patients) recovered renal function (alive and without requirement for dialysis) by day 60. See, FIG. 1. Baseline clinical characteristics of the study patients were taken. See, Table 1.

TABLE 1

Summary of baseline and clinical characteristics of the study patients				
Characteristics	All subjects (n = 76)	Recovery (n = 38)	Non-recovery (n = 38)	P value
Age, mean (SD), -yr	58.4(17.0)	52.2(15.7)	64.7(16.2)	<0.001
Gender: Female (%)	30(39.5)	15(39.5)	15(39.5)	1.00
Race: White (%)	64(84.2)	30(79.0)	34(89.5)	0.21
Baseline serum creatinine, mean (SD) (mg/dl)	1.1(0.4)	1.1(0.4)	1.2(0.5)	0.45
BUN at initiation of RRT, mean (SD) (mg/dl)	55.6(29.9)	51.3(28.8)	59.9(30.8)	0.23
Cause of acute kidney injury				
Ischemia (%)	66(86.8)	29(76.3)	37(97.4)	0.007
Nephrotoxins (%)	16(21.3)	10(26.3)	6(16.2)	0.29
Sepsis (%)	50(65.8)	23(60.5)	27(71.1)	0.33
Multifunctional causes (%)	51(68.0)	25(65.8)	26(70.3)	0.68
Length of ICU stay before randomization-days, mean (SD)	5.4(4.1)	4.2(2.8)	6.5(4.9)	0.03
Length of hospital stay before randomization-days, mean (SD)	8.5(7.1)	6.7(5.0)	10.2(8.5)	0.08
Charlson comorbidity index ^a , mean (SD)	4.1(3.3)	3.3(3.8)	4.9(2.7)	0.008
Mechanical ventilation (%)	69(90.8)	34(89.5)	35(92.1)	1.00
Sepsis ^b (%)	47(62.7)	22(57.9)	25(67.6)	0.39
APACHE II score ^c , mean (SD)	23.4(7.2)	21.8(7.2)	25.0(6.8)	0.06
Non-renal SOFA organ-system score ^d , mean (SD)				
Respiratory	2.1(1.3)	2.1(1.5)	2.1(1.2)	0.98
Coagulation	1.5(1.3)	1.4(1.3)	1.5(1.3)	0.58
Liver	0.9(1.3)	1.2(1.5)	0.6(1.0)	0.08
Cardiovascular	2.2(1.7)	2.0(1.7)	2.5(1.6)	0.17
Central nervous system	2.2(1.4)	2.3(1.3)	2.1(1.5)	0.45
Total	8.9(4.0)	9.2(4.6)	8.5(3.3)	0.43
Cleveland Clinic ICU ARF Renal Failure score ^e , mean (SD)	11.9(3.0)	11.6(3.0)	12.2(3.0)	0.49
Intensive category ^f (%)	34(44.7)	18(47.4)	16(42.1)	0.64

Abbreviations: RRT, Renal Replacement Therapy.

ICU, Intensive Care Unit.

APACHE II, Acute Physiology and Chronic Health Evaluation II.

SOFA, Sequential Organ Failure Assessment.

ARF, Acute Renal Failure.

^aAccording to the method of Charlson et al.²³

^bDefined as sepsis plus acute organ dysfunction according to 2001 international consensus criteria for severe sepsis.²⁶

^cAccording to the method of Knaus et al.²⁹

^dNon renal SOFA score, excluding the renal part, assessed on the first day according to the method of Vincent et al.³⁰

^eAccording to the method of Thakar et al.³¹

^fIntensive strategy, intermittent hemodialysis and sustained low-efficiency dialysis were provided six times per week (every day except Sunday), and continuous venovenous hemodiafiltration was prescribed to provide a flow rate of the total effluent (the sum of the dialysate and ultrafiltrate) of 35 ml per kilogram of body weight per hour, based on the weight before the onset of acute illness.¹

[0103] Patients recovering from renal injury were more likely to be younger, had a shorter length of intensive care unit (ICU) stay before randomization, lower Charlson comorbidity index, and lower nonrenal SOFA score as compared to those not recovering renal function. By contrast, there were no statistical differences in gender, ethnicity, baseline serum creatinine, blood urea nitrogen (BUN) at initiation of RRT, length of hospital stay, length of ICU stay, requirement for mechanical ventilation, Cleveland Clinic ICU Acute Renal Failure (ARF) score, or intensity of RRT. The primary etiology of AKI was ischemia in both groups. However, a significantly lower percentage of ischemia (76.3%) was noted as the cause of AKI in the recovery group compared to 97.4% in non-recovery group. Of the 38 participants who recovered renal function, 26 (68.4%) had complete recovery. Among those failing to recover renal function, 25 patients (65.8%), did not survive past day 60.

IV. Proteomics Gene Expression Platforms

[0104] In one embodiment, the present invention contemplates a method for identifying urinary biomarkers using a proteomics platform. In one embodiment, the proteomics platform detects protein expression profiles. In one embodiment, the method further comprises comparing a first protein expression profile to a second protein expression profile. In one embodiment, the comparing identifies an overexpressed protein in the first protein expression profile relative to the second protein expression profile. In one embodiment, the comparing identifies an underexpressed protein in the first protein expression profile relative to the second protein expression profile.

[0105] A Introduction

[0106] In one embodiment, the present invention contemplates a method comprising a proteomics platform (i.e., for example, iTRAQ) capable of summarizing an analysis of relative protein biomarker expression. For example, the proteomics platform may use reporter ion peak area measurements (i.e., for example, supplied by ABI software) to estimate treatment-dependent peptide and protein biomarker relative expression. Such estimations may be accomplished using a Bayesian approach. The proteomics platform described herein includes a protein biomarker relative expression summary and a per-protein biomarker detailed analysis.

[0107] B Experiment and Model Description

[0108] 1. Experiment Design

[0109] Proteomic platforms contemplated herein may summarize data from one or more experiments addressing a common comparison. For example, a possible experimental design for such an analysis is presented below. See, Table 5.

TABLE 5

Representative Proteomic Experimental Designs				
	Experiment	Treatment	Channel	Sample
1	A	A	113	A1
2	A	A	114	A2
3	A	A	115	A3
4	A	A	116	A4
5	A	B	117	B1
6	A	B	118	B2
7	A	B	119	B4
8	A	B	121	B4

[0110] 2. Input Files

[0111] Data for proteomic analyses may be extracted from input files including but not limited to a tandem mass spectra (MSMS) summary file, such as:

Experiment	MSMS	Summary File
A		?

? indicates text missing or illegible when filed

[0112] 3. Statistical Modeling Statistical models to estimate the treatment-dependent effects may including but not limited to: $\text{LogIntensity} \sim \text{Channel} + \text{Spectrum} + \text{Protein} + \text{Peptide} + \text{Protein:Treatment} + \text{Peptide:Treatment}$.

[0113] 4. Data Summarization

[0114] The proteomics platform may comprise filtering the data supplied in the MSMS summary to remove unidentified proteins, contaminants, and/or peptides containing selected modifications. A representative analysis may provide a data summary as presented below. See, Table 6.

TABLE 6

Representative Data Summary		
	A	Combined
Supplied Spectra	4608	4608
Unidentified Spectra	0	0
Disallowed Modifications	249	249
Spectra from Contaminants	1210	1210
Missing Data	115	115
Low Confidence Spectra	0	0
Degenerate Peptides	379	379
Remaining Spectra		2655
Unique Proteins		360
Unique Peptides		1473
Model R2		0.767

[0115] C. Protein Biomarker Summary

[0116] In one embodiment, the proteomics platform may identify each protein biomarker in one or more of the MSMS summaries, for example, in decreasing order of expression change magnitude. See, FIG. 2. The median and estimated credible interval for each protein biomarker is given to the left in the table. Similar data is shown where protein biomarkers are identified by a single peptide. See FIG. 3.

[0117] D. Protein Biomarker Details

[0118] A detailed summary of each protein biomarker is given below, wherein each protein biomarker is designated as 5.####. These sections include protein biomarker relative expression estimates in addition to protein-level estimates.

5.1 beta globin [*Homo sapiens*]

Protein Accession gi|4504349

Mean Expression Ratio 2.31

Median Expression Ratio 2.31

Credible Interval (1.9, 2.82)

Associated Peptides 7

Associated Spectra 29

Coverage 0.51

[0119]

A	2.5	50	97.5	SEQ ID NO:	Sequence
1	1.6	2.2	3.0	SEQ ID NO: 1	EFTPPVQAAAYQK
3	1.8	2.4	3.1	SEQ ID NO: 2	FESFGDLSTPDA VMGNPK
4	1.8	2.4	3.2	SEQ ID NO: 3	FFESFGDLSTPD AVMGNPK
4	1.9	2.5	3.3	SEQ ID NO: 4	GTFATLSELHCD K
13	2.1	2.6	3.2	SEQ ID NO: 5	LLGNVLVCVLAH HFGK
3	1.6	2.2	2.9	SEQ ID NO: 6	VNVDEVGGEALG R
1	1.7	2.4	3.3	SEQ ID NO: 7	FRLLGNVLVCVL AHHFGK
SEQ ID NO: 8					
1	M V H L T P E E K S A V T A L W G K V N V D E V G G E A L G R L L V V Y P W T Q R F F E S F G D L S T P D A V M G N P K V K A H G K K V L G A F S D G L A H L D				
81	N L K G T F A T L S E L H C D K L H V D P E N F R L L G N V L V C V L A H H F G K E F T P P V Q A A Y Q K V V A G V A N A L A H K Y H				

5.2 catalase [*Homo sapiens*]

Protein Accession gi|4557014

Mean Expression Ratio 1.97

Median Expression Ratio 1.97

Credible Interval (1.61, 2.40)

Associated Peptides 13

Associated Spectra 20

Coverage 0.279

[0120]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	1.4	1.8	2.5	SEQ ID NO: 9	AFYVNVLNNEQR
2	1.4	2.0	2.6	SEQ ID NO: 10	DPILFPSFIHSQ K
1	1.5	2	2.8	SEQ ID NO: 11	FSTVAGESGSAD TVR
4	1.7	2.2	2.9	SEQ ID NO: 12	GPLLVDVVFSTD EMAHFDR
1	1.6	2.2	3	SEQ ID NO: 13	GPRGPLLVQDVV FTDEMAHFDR
1	1.6	2.1	3.0	SEQ ID NO: 14	IRDPILFPSFIH SQK
1	1.5	2	2.7	SEQ ID NO: 15	LFAYPDTHR
1	1.4	1.9	2.6	SEQ ID NO: 16	LSQEDPDYGIR
2	1.4	2.0	2.7	SEQ ID NO: 17	LVQDVVFSTDEMA HFDR
2	1.5	2.0	2.7	SEQ ID NO: 18	NFTEVHPDYGSH IQALLDK
1	1.4	2.0	2.7	SEQ ID NO: 19	FAEVEQIAFDPS NMPPGIEASPDK
1	1.4	1.9	2.7	SEQ ID NO: 20	VFEHIGK
1	1.4	2.0	2.7	SEQ ID NO: 21	FNTANDDNVTQV R
SEQ ID NO: 22					
1	M A D S R D P A S D Q M Q H W K E Q R A A Q K A D V L T T G A G N P V G D K L N V I T V G P R G P L L V Q D V V F T D E M A H F D R E R I P E R V V H A K G A G				
81	A F G Y F E V T H D I T K Y S K A K V F E H I G K K T P I A V R F S T V A G E S G S A D T V R D P R G F A V K F Y T E D G N W D L V G N N T P I F F I R D P I L				
161	F P S F I H S Q K R N P Q T H L K D P D M V W D F W S L R P E S L H Q V S F L F S D R G I P D G H R H M N G Y G S H T F K L V N A N G E A V Y C K F H Y K T D Q				
241	G I K N L S V E D A A R L S Q E D P D Y G I R D L F N A I A T G K Y P S W T F Y I Q V M T F N Q A E T F P F N P F D L T K V W P H K D Y P L I P V G K L V L N R				
321	N P V N Y F A E V E Q I A F D P S N M P P G I E A S P D K M L Q G R L F A Y P D T H R H R L G P N Y L H I P V N C P Y R A R V A N Y Q R D G P M C M Q D N Q G G				
401	A P N Y Y P N S F G A P E Q Q P S A L E H S I Q Y S G E V R R F N T A N D D N V T Q V R A F Y V N V L N E E Q R K R L C E N I A G H L K D A Q I F I Q K K A V K				
481	N F T E V H P D Y G S H I Q A L L D K Y N A E K P K N A I H T F V Q S G S H L A A R E K A N L				

5.3 myoglobin [*Homo sapiens*]; myoglobin [*Homo sapiens*];
myoglobin [*Homo sapiens*]
Protein Accession gil4885477 gil44955888 gil44955885

Mean Expression Ratio 0.525
Median Expression Ratio 0.526
Credible Interval (0.373, 0.736)

Associated Peptides 3
Associated Spectra 5

Coverage NaN
[0121]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.35	0.53	0.8	SEQ ID NO: 23	GLSDGEWQLVLN VWGK
2	0.36	0.53	0.77	SEQ ID NO: 24	HGATVLTLALGGI LK
2	0.31	0.45	0.65	SEQ ID NO: 25	VEADIPGHGQEV LIR

5.4 alpha 1 globin [*Homo sapiens*]; alpha 2 globin [*Homo sapiens*]
Protein Accession gil4504347 gil4504345

Mean Expression Ratio 1.86
Median Expression Ratio 1.86
Credible Interval (1.56, 2.22)

Associated Peptides 12
Associated Spectra 36

Coverage NaN
[0122]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	1.6	2.2	2.9	SEQ ID NO: 26	AAHLPAEFTPAV HASLTK
1	1.4	1.9	2.7	SEQ ID NO: 27	ALSALSDLHAHK
1	1.4	1.9	2.6	SEQ ID NO: 28	FLSFPTTK
1	1.4	1.9	2.6	SEQ ID NO: 29	FPHFDLSHGSAQ VK
1	1.4	1.9	2.7	SEQ ID NO: 30	MFLSFPTTK
7	1.6	2.1	2.6	SEQ ID NO: 31	TYFPHFDLSHGSAQVK
3	1.4	1.8	2.4	SEQ ID NO: 32	VADALTNAAVAHV DDMPNAL

-continued

A	2.5	50	97.5	Sequence ID No.	Sequence
2	1.3	1.7	2.3	SEQ ID NO: 33	VADALTNAAVAHV DDMPNALSALSD LHAH
1	1.5	2	2.7	SEQ ID NO: 34	VDDMPNALSALS DLHAHK
9	1.2	1.5	1.9	SEQ ID NO: 35	VGAHAGEYGAEALER
6	1.5	1.9	2.4	SEQ ID NO: 36	VADALTNAAVAHV DDMPNALSALSD LHAHK
2	1.4	1.8	2.4	SEQ ID NO: 37	VDPVNFK

5.5 hemopexin [*Homo sapiens*]
Protein Accession gil11321561

Mean Expression Ratio 0.547
Median Expression Ratio 0.547
Credible Interval (0.444, 0.676)

Associated Peptides 12
Associated Spectra 17

Coverage 0.297
[0123]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.4	0.55	0.77	SEQ ID NO: 38	DYFMPCPGR
1	0.4	0.55	0.76	SEQ ID NO: 39	EWFWDLATGTMK
1	0.40	0.56	0.79	SEQ ID NO: 40	FDPVRGEVPPR
1	0.39	0.54	0.76	SEQ ID NO: 41	FQGDREWFWDLA TGTMK
4	0.35	0.46	0.62	SEQ ID NO: 42	LLQDEFPFGIPSP LDAAVECHR
1	0.4	0.56	0.77	SEQ ID NO: 43	NFPSPVDAAPR
2	0.4	0.55	0.75	SEQ ID NO: 44	RLWLWDLK
1	0.39	0.55	0.77	SEQ ID NO: 45	SGAQATWTLPW PHEK
2	0.4	0.55	0.75	SEQ ID NO: 46	VAEGETKPDPDV TER
1	0.39	0.54	0.75	SEQ ID NO: 47	YYCFQGNQFLR
1	0.39	0.54	0.77	SEQ ID NO: 48	GIILDSVDAAFI CPGSSR
1	0.37	0.52	0.73	SEQ ID NO: 49	LWWLWDLK

SEQ ID NO: 50
1 M A R V L G A P V A L G L W S L C W S L A I
A T P L P P T S A H G N V A E G E T K P D P
D V T E R C S D G W S F D A T T L D D N G T
M L F F K G E F V W K S H K

5.6 serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]; serine proteinase inhibitor, clade A, member 1 [*Homo sapiens*]

Protein Accession gil50363221 gil50363219 gil50363217
gil189163542 gil189163540 gil189163538 gil189163536

Median Expression Ratio 0.551

Credible Interval (0.482, 0.627)

Associated Peptides 27

Associated Spectra 68

Coverage NaN

[0124]

A	2.5	50	97.5	Sequence ID No:	Sequence
9	0.46	0.57	0.7	SEQ ID NO: 51	DTEEDFDH VDQVTTVK
1	0.43	0.57	0.77	SEQ ID NO: 52	DTVFALVN YIFPK
2	0.40	0.53	0.71	SEQ ID NO: 53	ELDRDTVF ALVNYIFF K

-continued

A	2.5	50	97.5	Sequence ID No:	Sequence
1	0.42	0.56	0.76	SEQ ID NO: 54	GTEAAGAM FLEAIPMS IPPEVK
1	0.4	0.54	0.72	SEQ ID NO: 55	ITPNLAEF AFSLYR
2	0.43	0.57	0.75	SEQ ID NO: 56	KLSSWVLL MK
2	0.44	0.58	0.77	SEQ ID NO: 57	KQINDYVE K
1	0.43	0.57	0.77	SEQ ID NO: 58	LAEFAPSL YR
4	0.4	0.52	0.67	SEQ ID NO: 59	LGMFNIQH CK
18	0.39	0.46	0.55	SEQ ID NO: 60	LQHLENEL THDIITK
5	0.42	0.53	0.68	SEQ ID NO: 61	LVDKFLED VK
2	0.42	0.56	0.74	SEQ ID NO: 62	QINDYVEK
2	0.44	0.59	0.78	SEQ ID NO: 63	SASLHLPK
1	0.4	0.54	0.73	SEQ ID NO: 64	SVLGQLGI TK
1	0.42	0.57	0.77	SEQ ID NO: 65	TLNQPSDQ LQLTTGNG LFLSEGLK
1	0.4	0.54	0.73	SEQ ID NO: 66	TVNFGDTE EAKK
3	0.41	0.53	0.69	SEQ ID NO: 67	VFSNGADL SGVTEEAP LK
2	0.39	0.52	0.69	SEQ ID NO: 68	WERPFEVK
1	0.41	0.54	0.73	SEQ ID NO: 69	LVDKFLED VKK
1	0.39	0.53	0.71	SEQ ID NO: 70	GKWERPFE VK
1	0.42	0.57	0.76	SEQ ID NO: 71	AVLTIDEK
1	0.4	0.54	0.73	SEQ ID NO: 72	FLEDVKK
1	0.41	0.56	0.75	SEQ ID NO: 73	LSITGTYD LK
2	0.42	0.56	0.73	SEQ ID NO: 74	FLEDVK
1	0.39	0.53	0.71	SEQ ID NO: 75	EEEDFHVD QVTTVK
1	0.43	0.58	0.77	SEQ ID NO: 76	GLFLSEGL K
1	0.41	0.55	0.74	SEQ ID NO: 77	FNKPFVVF

5.7 mucin 1 isoform 3 precursor [*Homo sapiens*]; mucin 1 isoform 2 precursor [*Homo sapiens*]; mucin 1 isoform 1 precursor [*Homo sapiens*]
Protein Accession gil67189069 gil67189007 gil65301117

Mean Expression Ratio 1.81
Median Expression Ratio 1.81
Credible Interval (1.45, 2.27)

Associated Peptides 6
Associated Spectra 22

Coverage NaN
[0125]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	1.3	1.8	2.5	SEQ ID NO: 78	DISEMFLQIYK
2	1.4	1.9	2.6	SEQ ID NO: 79	HDVETQFNQYK
2	1.3	1.7	2.4	SEQ ID NO: 80	KNYGQLDIFPAR
4	1.5	1.9	2.6	SEQ ID NO: 81	NYGQLDIFPAR
1	1.3	1.8	2.4	SEQ ID NO: 82	QGGFLGLSNIK
12	1.6	2.0	2.5	SEQ ID NO: 83	EGTINVHDVETQFNQYK

5.8 serpin peptidase inhibitor, clade A, member 3 precursor [*Homo sapiens*]
Protein Accession gil50659080

Mean Expression Ratio 0.563
Median Expression Ratio 0.563
Credible Interval (0.463, 0.681)

Associated Peptides 15
Associated Spectra 21

Coverage 0.388
[0126]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.41	0.55	0.74	SEQ ID NO: 84	AVLDVFEEGTEA SAATAVK
1	0.39	0.54	0.75	SEQ ID NO: 85	DYNLNDILLQLG IEEAFTSK
1	0.42	0.58	0.8	SEQ ID NO: 86	EIGELYLPK
2	0.37	0.51	0.68	SEQ ID NO: 87	HPNSPLDEENLT QENQDR
1	0.38	0.53	0.73	SEQ ID NO: 88	ITLLSALVETR

-continued

1	0.42	0.57	0.8	SEQ ID NO: 89	KLINDYVK
1	0.4	0.55	0.76	SEQ ID NO: 90	LYGSEAFATDFQ DSAAAK
3	0.45	0.6	0.8	SEQ ID NO: 91	MEEVEAMLLPET LKR
1	0.42	0.57	0.79	SEQ ID NO: 92	MEEVEAMLLPET LKR
2	0.42	0.57	0.77	SEQ ID NO: 93	NLAVSQVVKH
2	0.42	0.56	0.76	SEQ ID NO: 94	NSPLDEENLTQE NQDR
1	0.40	0.55	0.76	SEQ ID NO: 95	SPLDEENLTQEN QDR
1	0.41	0.57	0.77	SEQ ID NO: 96	WEMPFDPQDTHQ SR
1	0.4	0.55	0.76	SEQ ID NO: 97	WRDSLEFR
1	0.41	0.57	0.78	SEQ ID NO: 98	EQLSLDRFTED AK

SEQ ID NO: 99	1	M E R M L P L L A L G L L A A G F C P A V L C H P N S P L D E E N L T Q E N Q D R G T H V D L G L A S A N V D F A F S L Y K Q L V L K A P D K N V I F S P L S I
81	S T A L A F L S L G A H N T T L T E I L K G L K F N L T E T S E A E I H Q S F Q H L L R T L N Q S S D E L Q L S M G N A M F V K E Q L S L L D R F T E D A K R L	
161	Y G S E A F A T D F Q D S A A A K K L I N D Y V K N G T R G K I T D L I K D L D S Q T M M V L V N Y I F F K A K W E M P F D P Q D T H Q S R F Y L S K K K W V M	
241	V P M M S L H H L T I P Y F R D E E L S C T V V E L K Y T G N A S A L F I L P D Q D K M E E V E A M L L P E T L K R W R D S L E F R E I G E L Y L P K F S I S R	
321	D Y N L N D I L L Q L G I E E A F T S K A D L S G I T G A R N L A V S Q V V H K A V L D V F E E G T E A S A A T A V K I T L L S A L V E T R T I V R F N R P F L	
401	M I I V P T D T Q N I F F M S K V T N P K Q A	

5.9 CD14 antigen precursor [*Homo sapiens*]; CD14 antigen precursor [*Homo sapiens*]

Protein Accession gi|91105159 gi|4557417

Mean Expression Ratio 0.567

Median Expression Ratio 0.567

Credible Interval (0.452, 0.707)

Associated Peptides 9

Associated Spectra 16

Coverage NaN

[0127]

A	2.5	50	97.5	Sequence ID No.	Sequence
4	0.4	0.53	0.71	SEQ ID NO: 100	AFPALTSL DLSDNPGL GER
1	0.41	0.58	0.81	SEQ ID NO: 101	GLMAALCP HK
1	0.42	0.58	0.8	SEQ ID NO: 102	GLMAALCP HKFPAIQN L
1	0.40	0.56	0.79	SEQ ID NO: 103	GLMAALCP HKFPAIQN LALR
2	0.43	0.58	0.8	SEQ ID NO: 104	ITGTMPLP PLEATGLA LSSLR
3	0.39	0.53	0.72	SEQ ID NO: 105	LTVGAAQV PAQLLVGA LR
1	0.4	0.56	0.78	SEQ ID NO: 106	SWLAELQQ WLKPGLK
2	0.41	0.56	0.77	SEQ ID NO: 107	TTPEPCEL DDEDFR
1	0.39	0.54	0.76	SEQ ID NO: 108	VLSIAQAH SPAFSCEQ VR

5.10 brain abundant, membrane attached signal protein 1 [*Homo sapiens*]

Protein Accession gi|30795231

Mean Expression Ratio 1.75

Median Expression Ratio 1.75

Credible Interval (1.30, 2.35)

Associated Peptides 5

Associated Spectra 7

Coverage 0.396

[0128]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	1.2	1.8	2.7	SEQ ID NO: 109	AAEAAAAP AESAAPAA GEEPSKEE GEPK
1	1.2	1.7	2.5	SEQ ID NO: 110	AEPKKAPE QEQAAPGP AAGGEAPK
2	1.3	1.8	2.6	SEQ ID NO: 111	APEQEQA PGPAAGGE APK
1	1.2	1.8	2.7	SEQ ID NO: 112	AQGPAASA EPPKPVEA PAANSQDT VTVK
2	1.3	1.8	2.6	SEQ ID NO: 113	EKPDQDAE GK
SEQ ID NO: 114					
1	M G G K L S K K K K G Y N V N D E K A K E K D K K A E G A A T E E E G T P K E S E P Q A A A E P A E A K E G K E K P D Q D A E G K A E E K E G E K D A A A A K E				
81	E A P K A E P E K T E G A A E A K A E P P K A P E Q E Q A A P G P A A G G E A P K A A E A A A P A E S A A P A A G E E P S K E E G E P K K T E A P A A P A A Q				
161	E T K S D G A P A S D S K P G S S E A A P S S K E T P A A T E A P S S T P K A Q G P A A S A E E P K P V E A P A A N S D Q T V T V K E				

5.11 dipeptidase 1 [*Homo sapiens*]; dipeptidase 1 [*Homo sapiens*]
Protein Accession gil4758190 gil89458885

Mean Expression Ratio 1.72
Median Expression Ratio 1.72
Credible Interval (1.25, 2.37)

Associated Peptides 5
Associated Spectra 6

Coverage NaN
[0129]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	1.2	1.7	2.6	SEQ ID NO: 115	AVGFGGDF DGVPR
1	1.2	1.8	2.6	SEQ ID NO: 116	DSPVIDGH NDLPWQLL DMFNRR
1	1.2	1.8	2.7	SEQ ID NO: 117	VPEGLEDV SKYPDLIA ELLR
1	1.2	1.8	2.7	SEQ ID NO: 118	YPDLIAEL LR
2	1.2	1.8	2.5	SEQ ID NO: 119	VASLIGVE GGHSIDSS LGVLR

5.12 fibronectin 1 isoform 5 preproprotein [*Homo sapiens*]
Protein Accession gil47132553

Mean Expression Ratio 0.586
Median Expression Ratio 0.585
Credible Interval (0.475, 0.724)

Associated Peptides 11
Associated Spectra 17

Coverage 0.0758
[0130]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.40	0.55	0.74	SEQ ID NO: 120	AVEENQES TPVVIQQE TTGTPR
2	0.43	0.58	0.79	SEQ ID NO: 121	EESPLLIG QQSTVSDV PR
2	0.41	0.57	0.77	SEQ ID NO: 122	ESVPISDT IIPAVPPP TDLR

-continued

1	0.45	0.63	0.88	SEQ ID NO: 123	LISWDAPA VTVR
1	0.42	0.58	0.81	SEQ ID NO: 124	QVDAVPAN GQTPIQR
1	0.43	0.59	0.82	SEQ ID NO: 125	SSPVVIDA STDAIDAPS NLR
2	0.43	0.59	0.81	SEQ ID NO: 126	TETITGFQ VDAVPANG QTIQR
2	0.42	0.57	0.78	SEQ ID NO: 127	VDVIPVNL PGEHGQR
1	0.43	0.6	0.84	SEQ ID NO: 128	VTWAPPPS IDLTNFLV R
1	0.43	0.6	0.83	SEQ ID NO: 129	DLEVVAAT PTSLIISW DAPAVTVR
1	0.37	0.51	0.7	SEQ ID NO: 130	IISCHPVG TDEEPLQF R

SEQ ID NO: 131					
1	M	L	R	G	P
	S	T	G	A	S
	V	S	Q	S	K
	R	T	Y	L	G
	N	A	L	V	C
	T	C	Y	G	
81	G	S	R	G	F
	G	N	T	Y	R
	C	I	G	A	G
	S	Y	K	I	G
	D	T	W	R	R
	P	H	E	T	
161	G	G	Y	M	L
	A	E	K	C	F
	Y	Q	G	W	M
	S	R	N	R	C
	N	D	Q	D	T
	R	T	S	Y	
241	R	I	G	D	T
	N	G	R	G	E
	P	F	T	D	V
	H	C	V	T	D
	S	G	V	V	Y
	S	V	G	M	
321	Q	W	L	K	T
	Q	E	T	A	V
	T	Y	N	G	R
	S	T	T	S	N
	Y	E	Q	D	Q
	K	Y	S	F	
401	C	T	D	H	T
	P	F	L	Y	N
	W	C	G	T	T
	E	E	I	C	T
	T	N	E	G	V
	M	Y	R	I	
481	G	D	Q	W	D
	R	G	E	W	T
	Y	N	V	N	D
	G	Q	G	R	G
	R	W	K	C	D
	P	V	D	Q	
561	C	Q	D	S	E
	V	R	Y	Q	C
	Y	P	S	S	S
	P	I	Q	W	N
	A	P	Q	P	S
	H	I	S	K	
641	Y	I	L	R	W
	L	N	S	Y	T
	Q	Q	Y	G	H
	T	S	N	T	V
	T	G	E	T	T
	P	F	S	P	

-continued	
721	L V A T S E S V T E I T A S S F V V S W V S A S D T V S G F R V E Y E L S E E G D E P Q Y L D L P S T A T S V N I P D L L P G R K Y I V N V Y Q I S E D G E Q S
801	L I L S T S Q T T A P D A P P D P T V D Q V D D T S I V V R W S R P Q A P I T G Y R I V Y S P S V E G S S T E L N L P E T A N S V T L S D L Q P G V Q Y N I T I
881	Y A V E E N Q E S T P V V I Q Q E T T G T P R S D T V P S P R D L Q F V E V T D V K V T I M W T P P E S A V T G Y R V D V I P V N L P G E H G Q R L P I S R N T
961	F A E V T G L S P G V T Y Y F K V F A V S H G R E S K P L T A Q Q T T K L D A P T N L Q F V N E T D S T V L V R W T P P R A Q I T G Y R L T V G L T R R G Q P R
1041	Q Y N V G P S V S K Y P L R N L Q P A S E Y T V S L V A I K G N Q E S P K A T G V F T T L Q P G S S I P P Y N T E V T E T T I V I T W T P A P R I G F K L G V R
1121	P S Q G G E A P R E V T S D S G S I V V S G L T P G V E Y V Y T I Q V L R D G Q E R D A P I V N K V V T P L S P P T N L H L E A N P D T G V L T V S W E R S T T
1201	P D I T G Y R I T T T P T N G Q Q G N S L E E V V H A D Q S S C T F D N L S P G L E Y N V S V Y T V K D D K E S V P I S D T I I P A V P P P T D L R F T N I G P
1281	D T M R V T W A P P P S I D L T N F L V R Y S P V K N E E D V A E L S I S P S D N A V V L T N L L P G T E Y V V S V S S V Y E Q H E S T P L R G R Q K T G L D S
1361	P T G I D F S D I T A N S F T V H W I A P R A T I T G Y R I R H H P E H F S G R P R E D R V P H S R N S I T L T N L T P G T E Y V V S I V A L N G R E E S P L L
1441	I G Q Q S T V S D V P R D L E V V A A T P T S L L I S W D A P A V T V R Y Y R I T Y G E T G G N S P V Q E F T V P G S K S T A T I S G L K P G V D Y T I T V Y A
1521	V T G R G D S P A S S K P I S I N Y R T E I D K P S Q M Q V T D V Q D N S I S V K W L P S S S P V T G Y R V T T T P K N G P G P T K T K T A G P D Q T E M T I E
1601	G L Q P T V E Y V V S V Y A Q N P S G E S Q P L V Q T A V T T I P A P T D L K F T Q V T

-continued	
	P T S L S A Q W T P P N V Q L T G Y R V R V T P K E K T G P M K E I N L
1681	A P D S S S V V V S G L M V A T K Y E V S V Y A L K D T L T S R P A Q G V V T T L E N V S P P R R A R V T D A T E T T I T I S W R T K T E T I T G F Q V D A V P
1761	A N G Q T P I Q R T I K P D V R S Y T I T G L Q P G T D Y K I Y L Y T L N D N A R S S P V V I D A S T A I D A P S N L R F L A T T P N S L L V S W Q P P R A R I
1841	T G Y I I K Y E K P G S P P R E V V P R P R P G V T E A T I T G L E P G T E Y T I Y V I A L K N N Q K S E P L I G R K K T D E L P Q L V T L P H P N L H G P E I
1921	L D V P S T V Q K T P F V T H P G Y D T G N G I Q L P G T S G Q Q P S V G Q Q M I F E E H G F R R T T P P T T A T P I R H R P R P Y P P N V G E E I Q I G H I P
2001	R E D V D Y H L Y P H G P G L N P N A S T G Q E A L S Q T T I S W A P F Q D T S E Y I I S C H P V G T D E E P L Q F R V P G T S T S A T L T G L T R G A T Y N I
2081	I V E A L K D Q Q R H K V R E E V V T V G N S V N E G L N Q P T D D S C F D P Y T V S H Y A V G D E W E R M S E S G F K L L C Q C L G F G S G H F R C D S S R W
2161	C H D N G V N Y K I G E K W D R Q G E N G Q M M S C T C L G N G K G E F K C D P H E A T C Y D D G K T Y H V G E Q W Q K E Y L G A I C S C T C F G G Q R G W R C
2241	D N C R R P G G E P S P E G T T G Q S Y N Q Y S Q R Y H Q R T N T N V N C P I E C F M P L D V Q A D R E D S R E

5.13 angiotensinogen preproprotein [*Homo sapiens*]
Protein Accession gi|4557287

Mean Expression Ratio 0.59

Median Expression Ratio 0.59

Credible Interval (0.482, 0.718)

Associated Peptides 10

Associated Spectra 25

Coverage 0.293

[0131]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.42	0.57	0.77	SEQ ID NO: 132	AAMVGMLANFLGFR
2	0.4	0.54	0.73	SEQ ID NO: 133	ADSQQLLLSTVVGVTAPGLHLK
1	0.44	0.6	0.83	SEQ ID NO: 134	ALQDQLVLVAAK
2	0.46	0.62	0.85	SEQ ID NO: 135	DPTFIPAPIQAK
1	0.45	0.63	0.87	SEQ ID NO: 136	FMQAVTGWK
1	0.42	0.56	0.78	SEQ ID NO: 137	QPFVQGLALYTPVVLPR
2	0.46	0.62	0.85	SEQ ID NO: 138	VGEVLNSIFFELEADER
2	0.43	0.58	0.79	SEQ ID NO: 139	VLSALQAVQGLLVAQGR
11	0.4	0.5	0.61	SEQ ID NO: 140	DRVYIHPFHL
1	0.44	0.6	0.84	SEQ ID NO: 141	LQAILGVPWK

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SEQ ID NO: 142	
1	M R K R A P Q S E M A P A G V S L R A T I L C L L A W A G L A A G D R V Y I H P
F	H L V I H N E S T C E Q L A K A N A G K P K D P T F I P A P I Q A K T S P V D
81 E K A L Q D Q L V L V A A K L D T E D K L R A A M V G M L A N F L G F R I Y G	
M	H S E L W G V V H G A T V L S P T A V F G T L A S L Y L G A L D H T A D R L Q
A	
161 I L G V P W K D K N C T S R L D A H K V L S A L Q A V Q G L L V A Q G R A D	
S	Q A Q L L L S T V V G V F T A P G L H L K Q P F V Q G L A L Y T P V V L P R S L
D	
241 F T E L D V A A E K I D R F M Q A V T G W K T G C S L M G A S V D S T L A F N	
T	Y V H F Q G K M K G F S L L A E P Q E F W V D N S T S V S V P M L S G M G T F Q
321 H W S D I Q D N F S V T Q V P F T E S A C L L L I Q P H Y A S D L D K V E G L T	
F	Q Q N S L N W M K K L S P R T I H L T M P Q L V L Q G S Y D L Q D L L A Q A E
401 L P A I L H T E L N L Q K L S N D R I R V G E V L N S I F F E L E A D E R E P T E	
S	T Q Q L N K P E V L E V T L N R P F L F A V Y D Q S A T A L H F L G R V A N
481 P L S T A	

5.14 complement component 3 precursor [<i>Homo sapiens</i>]	Credible Interval (0.532, 0.678)
Protein Accession gil115298678	Associated Peptides 39
Mean Expression Ratio 0.601	Associated Spectra 69
	Coverage 0.301
Median Expression Ratio 0.602	[0132]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.46	0.61	0.82	SEQ ID NO: 143	CAENCFIQK
1	0.45	0.6	0.8	SEQ ID NO: 144	DAPDHQELNLDVSLQLPSR
2	0.44	0.58	0.77	SEQ ID NO: 145	DFDFVPPVVR
1	0.45	0.6	0.81	SEQ ID NO: 146	DTWVEHWPEDECQDEENQK
11	0.35	0.43	0.53	SEQ ID NO: 147	EDIPPADLSQVPTSESTR
3	0.45	0.59	0.76	SEQ ID NO: 148	EPGQDLVVLPLSITDFIPSR
1	0.45	0.6	0.81	SEQ ID NO: 149	EYVLPSEFVIVEPTEK
1	0.46	0.6	0.81	SEQ ID NO: 150	FYHPEKEDGK
1	0.46	0.61	0.83	SEQ ID NO: 151	HQQTVTIPPK
1	0.46	0.61	0.82	SEQ ID NO: 152	IHWESASLLR
5	0.44	0.56	0.71	SEQ ID NO: 153	ILLQGTTPVAQMTEDAVDAER
3	0.48	0.62	0.81	SEQ ID NO: 154	IPIEDGSGEVVLSR
1	0.44	0.59	0.79	SEQ ID NO: 155	IWDVVEK
2	0.46	0.61	0.8	SEQ ID NO: 156	KQELSEAEQATR
2	0.47	0.62	0.83	SEQ ID NO: 157	LESEETMVLEAHDAQGDVPVTVTVHD
					FPGK
1	0.46	0.61	0.82	SEQ ID NO: 158	LMNIFL K
3	0.48	0.62	0.81	SEQ ID NO: 159	QKPDGVFQEDAPVIHQEMIGGLR
1	0.47	0.63	0.85	SEQ ID NO: 160	SGQSEDRQPVPGQMTLK
1	0.45	0.59	0.8	SEQ ID NO: 161	SITDFIPSR
2	0.45	0.59	0.78	SEQ ID NO: 162	SNLDEDIAEENIVSR
1	0.44	0.59	0.79	SEQ ID NO: 163	SWDIPELVNMGQWK
1	0.45	0.61	0.81	SEQ ID NO: 164	TELRPGETLNVNF
2	0.46	0.61	0.81	SEQ ID NO: 165	TELRPGETLNVNLLR
2	0.47	0.63	0.83	SEQ ID NO: 166	TVMVNIEPPEGIPVK
1	0.46	0.61	0.81	SEQ ID NO: 167	VFTVNPDGSPAYR
1	0.45	0.61	0.82	SEQ ID NO: 168	VIFGIQDGEQR
1	0.45	0.6	0.8	SEQ ID NO: 169	VLLDGVQNPR
3	0.44	0.58	0.75	SEQ ID NO: 170	VQLSNDFDEYIMAEQTIK
3	0.45	0.58	0.76	SEQ ID NO: 171	VTIKPAPETEK
1	0.46	0.61	0.81	SEQ ID NO: 172	AGDFLEANYMNLQR
1	0.45	0.6	0.8	SEQ ID NO: 173	GICVADPPFEVTVMQDFFIDLR
1	0.46	0.61	0.81	SEQ ID NO: 174	LKGPLLNK

-continued

1	0.41	0.54	0.72	SEQ ID NO: 175	FYYIYNEK
1	0.47	0.63	0.84	SEQ ID NO: 176	QPVPGQQMTLK
1	0.46	0.62	0.83	SEQ ID NO: 177	RIPIEDGSGEVVLSR
1	0.47	0.62	0.83	SEQ ID NO: 178	VSHSEDDCLAFK
1	0.45	0.6	0.8	SEQ ID NO: 179	LSINTHPSQKPL
1	0.45	0.6	0.8	SEQ ID NO: 180	GLSSDFWGEKPNLSY
1	0.48	0.64	0.85	SEQ ID NO: 181	QIHFTK

SEQ ID NO: 182

1 M G P T S G P S L L L L L L L T H L P L A L G S P M Y S I I T P N I L R L E S E E T M
V L E A H D A Q G D V P V T V T V H D F P G K K L V L S S E K T V L T P A T

81 N H M G N V T F T I P A N R E F K S E K G R N K F V T V Q A T F G T Q V V E K
V V L V S L Q S G Y L F I Q T D K T I Y T P G S T V L Y R I F T V N H K L L P V G

161 R T V M V N I E N P E G I P V K Q D S L S S Q N Q L G V L P L S W D I P E L V N
M G Q W K I R A Y Y E N S P Q Q V F S T E F E V K E Y V L P S F E V I V E P T E

241 K F Y Y I Y N E K G L E V T I T A R F L Y G K K V E G T A F V I F G I Q D G E Q
R I S L P E S L K R I P I E D G S G E V V L S R K V L L D G V Q N P R A E D L V

321 G K S L Y V S A T V I L H S G S D M V Q A E R S G I P I V T S P Y Q I H F T K T P
K Y F K P G M P F D L M V F V T N P D G S P A Y R V P V A V Q G E D T V Q S L

401 T Q G D G V A K L S I N T H P S Q K P L S I T V R T K K Q E L S E A E Q A T R T
M Q A L P Y S T V G N S N N Y L H L S V L R T E L R P G E T L N V N F L L R M D

481 R A H E A K I R Y Y T Y L I M N K G R L L K A G R Q V R E P G Q D L V V L P L
S I T T D F I P S F R L V A Y Y T L I G A S G Q R E V V A D S V W V D V K D S C V

561 G S L V V K S G Q S E D R Q P V P G Q Q M T L K I E G D H G A R V V L V A V D
K G V F V L N K K N K L T Q S K I W D V V E K A D I G C T P G S G K D Y A G V F S

641 D A G L T F T S S S G Q Q T A Q R A E L Q C P Q P A A R R R R S V Q L T E K R
M D K V G K Y P K E L R K C C E D G M R E N P M R F S C Q R R T R F I S L G E A C

721 K K V F L D C C N Y I T E L R R Q H A R A S H L G L A R S N L D E D I I A E E N
I V S R S E F P E S W L W N V E D L K E P P K N G I S T K L M N I F L K D S I T

801 T W E I L A V S M S D K K G I C V A D P F E V T V M Q D F F I D L R L P Y S V V
R N E Q V E I R A V L Y N Y R Q N Q E L K V R V E L L H N P A F C S L A T T K R

881 R H Q Q T V T I P P K S S L S V P Y V I V P L K T G L Q E V E V K A A V Y H H F
I S D G V R K S L K V V P E G I R M N K T V A V R T L D P E R L G R E G V Q K E

961 D I P P A D L S D Q V P D T E S E T R I L L Q G T P V A Q M T E D A V D A E R L
K H L I V T P S G C G E Q N M I G M T P T V I A V H Y L D E T E Q W E K F G L E

1041 K R Q G A L E L I K K G Y T Q Q L A F R Q P S S A F A A F V K R A P S T W L T
A Y V V K V F S L A V N L I A I D S Q V L C G A V K W L I L E K Q K P D G V F Q E

1121 D A P V I H Q E M I G G L R N N N E K D M A L T A F V L I S L Q E A K D I C E
E Q V N S L P G S I T K A G D F L E A N Y M N L Q R S Y T V A I A G Y A L A Q M G

1201 R L K G P L L N K F L T T A K D K N R W E D P G K Q L Y N V E A T S Y A L L
A L L Q L K D F D F V P P V V R W L N E Q R Y Y G G G Y G S T Q A T F M V F Q A
L A

1281 Q Y Q K D A P D H Q E L N L D V S L Q L P S R S S K I T H R I H W E S A S L L
R S E E T K E N E G F T V T A E G K G Q G T L S V V T M Y H A K A K D Q L T C N
K

1361 F D L K V T I K P A P E T E K R P Q D A K N T M I L E I C T R Y R G D Q D A T
M S I L D I S M M T G F A P D T D D L K Q L A N G V D R Y I S K Y E L D K A F S D

1441 R N T L I T Y L D K V S H S E D D C L A F K V H Q Y F N V E L I Q P G A V K V
Y A Y Y N L E E S C T R F Y H P E K E D G K L N K L C R D E L C R C A E E N C F I

1521 Q K S D D K V T L E E R L D K A C E P G V D Y V Y K T R L V K V Q L S N D F
D E Y I M A I E Q T I K S G S D E V Q V G Q Q R T F I S P I K C R E A L K L E E K K

1601 H Y L M W G L S S D F W G E K P N L S Y I I G K D T W V E H W P E E D E C Q
D E E N Q K Q C Q D L G A F T E S M V V F G C P N

5.15 carbonic anhydrase I [*Homo sapiens*]; carbonic anhydrase I [*Homo sapiens*]; carbonic anhydrase I [*Homo sapiens*]; carbonic anhydrase I [*Homo sapiens*]
Protein Accession gi|4502517 gi|92447434 gi|92447432 gi|92447430

Mean Expression Ratio 0.602

Median Expression Ratio 0.604

Credible Interval (0.499, 0.718)

Associated Peptides 13

Associated Spectra 28

Coverage NaN

[0133]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.47	0.63	0.85	SEQ ID NO: 183	ADGLAVIGVLMK	
3	0.47	0.63	0.83	SEQ ID NO: 184	EIINVGHSPHVNFDNDNR	
1	0.43	0.59	0.82	SEQ ID NO: 185	ESISVSSEQLAQFR	
1	0.43	0.58	0.8	SEQ ID NO: 186	HDTSLKPISVSYNPATAK	
1	0.43	0.59	0.8	SEQ ID NO: 187	LFQPHF	
6	0.45	0.58	0.74	SEQ ID NO: 188	LYPIANGNNQSPVDIK	
2	0.45	0.6	0.81	SEQ ID NO: 189	NGPEQWSK	
2	0.46	0.62	0.83	SEQ ID NO: 190	SFHVNFEDNDNR	
1	0.43	0.6	0.82	SEQ ID NO: 191	SLLSNVEGDNAVPMQHNN	
1	0.41	0.57	0.78	SEQ ID NO: 192	VLDALQAIK	
2	0.45	0.61	0.81	SEQ ID NO: 193	YSAELHVAHW	
1	0.46	0.63	0.87	SEQ ID NO: 194	YSAELHVAHWNSAK	
5	0.41	0.53	0.68	SEQ ID NO: 195	SLLSNVEGDNAVPMQHNNRPTQPLK	

5.16 uromodulin precursor [*Homo sapiens*]; uromodulin precursor [*Homo sapiens*]
Protein Accession gi|59850812 gi|56550049

Mean Expression Ratio 0.608

Median Expression Ratio 0.607

Credible Interval (0.528, 0.701)

Associated Peptides 25

Associated Spectra 50

Coverage NaN

[0134]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.47	0.63	0.86	SEQ ID NO: 196	ACSYPLDMK	
9	0.51	0.64	0.79	SEQ ID NO: 197	DSTIQVVENGESSQGR	
3	0.46	0.6	0.8	SEQ ID NO: 198	DWVSVVTPAR	
1	0.45	0.59	0.8	SEQ ID NO: 199	FSVQMFR	
1	0.44	0.59	0.8	SEQ ID NO: 200	INFACSYPLDMK	
4	0.47	0.6	0.78	SEQ ID NO: 201	LADEIIIR	
1	0.45	0.62	0.83	SEQ ID NO: 202	LECGANDMK	
1	0.46	0.61	0.83	SEQ ID NO: 203	LSPGLGCTDVDECAEPGLSHCH	
2	0.46	0.61	0.8	SEQ ID NO: 204	LYVGTMLDGGDLRS	
5	0.45	0.58	0.73	SEQ ID NO: 205	MAETCVPVLR	
1	0.44	0.59	0.8	SEQ ID NO: 206	SCVCPEGFR	
1	0.43	0.59	0.79	SEQ ID NO: 207	SENTLYLADEIIIR	
3	0.46	0.6	0.79	SEQ ID NO: 208	STEYGEYACDSDLR	
1	0.45	0.6	0.8	SEQ ID NO: 209	TALQPMVSALNIR	
2	0.43	0.57	0.76	SEQ ID NO: 210	TLDEYWR	
1	0.44	0.6	0.81	SEQ ID NO: 211	VFMYLSDSR	
1	0.45	0.61	0.82	SEQ ID NO: 212	VGTMLDGGDLRS	
1	0.47	0.64	0.86	SEQ ID NO: 213	VLNLGPITR	
1	0.43	0.58	0.79	SEQ ID NO: 214	WHCQCK	
5	0.46	0.58	0.74	SEQ ID NO: 215	YFIIQDR	
1	0.48	0.64	0.86	SEQ ID NO: 216	SLGFDKVFMYSLSR	
1	0.46	0.61	0.83	SEQ ID NO: 217	SLGFDK	
1	0.46	0.62	0.83	SEQ ID NO: 218	SYPLDMK	
1	0.45	0.6	0.8	SEQ ID NO: 219	CSGFNDR	
1	0.46	0.61	0.82	SEQ ID NO: 220	DLNIK	

5.17 heparan sulfate proteoglycan 2 [*Homo sapiens*]
Protein Accession gi|126012571

Mean Expression Ratio 0.614

Median Expression Ratio 0.614

Credible Interval (0.488, 0.761)

Associated Peptides 9

Associated Spectra 16

Coverage 0.0239

[0135]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.42	0.58	0.79	SEQ ID NO: 221	DFISLGLQDGHVFR
2	0.43	0.6	0.82	SEQ ID NO: 222	FHDDGFLAFPGHVF
1	0.42	0.6	0.83	SEQ ID NO: 223	FHDDGFLAFPGHVFSR
1	0.45	0.63	0.9	SEQ ID NO: 224	GSIQVDGEELVSGR
2	0.47	0.64	0.88	SEQ ID NO: 225	GSVYIGGAPDVATLTGGR
2	0.42	0.59	0.8	SEQ ID NO: 226	LVSEDPINDGEWHR
2	0.44	0.61	0.83	SEQ ID NO: 227	PGAPPPQPLDLQHR
3	0.44	0.59	0.8	SEQ ID NO: 228	SLPEVPETIELEVR
1	0.44	0.63	0.87	SEQ ID NO: 229	IGGAPDVATLTGGR

SEQ ID NO: 230

1 M G W R A A G A L L L L A L L L H G R L L A V T H G L R A Y D G L S L P E D I E T
V T A S Q M R W T H S Y L S D D E D M L A D S I S G D D L G S G D L G S G D F Q

81 M V Y F R A L V N F T R S I E Y S P Q L E D A G S R E F R E V S E A V V D T L E
S E Y L K I P G D Q V V S V V F I K E L D G W V F V E L D V G S E G N A D G A Q

161 I Q E M L L R V I S S G S V A S Y V T S P Q G F Q F R R L G T V P Q F P R A C T
E A E F A C H S Y N E C V A L E Y R C D R R P D C R D M S D E L N C E E P V L G

241 I S P T F S L L V E T T S L P P R P E T T I M R Q P P V T H A P Q P L L P G S V R P
L P C G P Q E A A C R N G H C I P R D Y L C D G Q E D C E D G S D E L D C G

321 P P P P C E P N E F P C G N G H C A L K L W R C D G D F D C E D R T D E A N C
P T K R P E E V C G P T Q F R C V S T N M C I P A S F H C D E E S D C P D R S D E

401 F G C M P P Q V V T P P R E S I Q A S R G Q T V T F T C V A I G V P T P I I N W R
L N W G H I P S H P R V T V T S E G G R G T L I I R D V K E S D Q G A Y T C E

481 A M N A R G M V F G I P D G V L E L V P Q R G P C P D G H F Y L E H S A A C L
P C F C F G I T S V C Q S T R R F R D Q I R L R F D Q P D D F K G V N V T M P A Q

561 P G T P P L S S T Q L Q I D P S L H E F Q L V D L S R R F L V H D S F W A L P E
Q F L G N K V D S Y G G S L R Y N V R Y E L A R G M L E P V Q R P D V V L M G A

641 G Y R L L S R G H T P T Q P G A L N Q R Q V Q F S E E H W V H E S G R P V Q R
A E L L Q V L Q S L E A V L I Q T V Y N T K M A S V G L S D I A M D T T V T H A T

721 S H G R A H S V E E C R C P I G Y S G L S C E S C D A H F T R V P G G P Y L G T
C S G C N C N G H A S S C D P V Y G H C L N C Q H N T E G P Q C N K C K A G F F

801 G D A M K A T A T S C R P C P C P Y I D A S R R F S D T C F L D T D G Q A T C
D A C A P G Y T G R R C E S C A P G Y E G N P I Q P G G K C R P V N Q E I V R C D

881 E R G S M G T S G E A C R C K N N V V G R L C N E C A D G S F H L S T R N P D
G C L K C F C M G V S R H C T S S S W S R A Q L H G A S E E P G H F S L T N A A S

961 T H T T N E G I F S P T P G E L G F S S F H R L L S G P Y F W S L P S R F L G D K
V T S Y G G E L R F T V T Q R S Q P G S T P L H G Q P L V V L Q G N N I I L E

1041 H H V A Q E P S P G Q P S T F I V P F R E Q A W Q R P D G Q P A T R E H L L M
A L A G I D T L L I R A S Y A Q Q P A E S R V S G I S M D V A V P E E T G Q D P A

1121 L E V E Q C S C P P G Y R G P S C Q D C D T G Y T R T P S G L Y L G T C E R C
S C H G H S E A C E P E T G A C Q G C Q H H T E G P R C E Q C Q P G Y Y G D A Q R

1201 G T P Q D C Q L C P C Y G D P A A G Q A A H T C F L D T D G H P T C D A C S
P G H S G R H C E R C A P G Y Y G N P S Q G Q P C Q R D S Q V P G P I G C N C D P
Q

1281 G S V S S Q C D A A G Q C Q C K A Q V E G L T C S H C R P H H F H L S A S N
P D G C L P C F C M G I T Q Q C A S S A Y T R H L I S T H F A P G D F Q G F A L V N

1361 P Q R N S R L T G E F T V E P V P E G A Q L S F G N F A Q L G H E S F Y W Q L
P E T Y Q G D K V A A Y G G K L R Y T L S Y T A G P Q G S P L S D P D V Q I T G N

1441 N I M L V A S Q P A L Q G P E R R S Y E I M F R E E F W R R P D G Q P A T R E
H L L M A L A D L D E L L I R A T F S S V P L A A S I S A V S L E V A Q P G P S N

1521 R P R A L E V E E C R C P P G Y I G L S C Q D C A P G Y T R T G S G L Y L G H
C E L C E C N G H S D L C H P E T G A C S Q C Q H N A A G E F C E L C A P G Y Y G

1601 D A T A G T P E D C Q P C A C P L T N P E N M F S R T C E S L G A G G Y R C T
A C E P G Y T G Q Y C E Q C G P G Y V G N P S V Q G G Q C L P E T N Q A P L V V E

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1681 V H P A R S I V P Q G G S H S L R C Q V S G S P P H Y F Y W S R E D G R P V P
S G T Q Q R H Q G S E L H F P S V Q P S D A G V Y I C T C R N L H Q S N T S R A E

1761 L L V T E A P S K P I T V T V E E Q R S Q S V R P G A D V T F I C T A K S K S P
A Y T L V W T R L H N G K L P T R A M D F N G I L T I R N V Q L S D A G T Y V C

1841 T G S N M F A M D Q G T A T L H V Q A S G T L S A P V V S I H P P Q L T V Q P
G Q L A E F R C S A T G S P T P T L E W T G G P G G Q L P A K A Q I H G G I L R L

1921 P A V E P T D Q A Q Y L C R A H S S A G Q Q V A R A V L H V H G G G G P R V
Q V S P E R T Q V H A G R T V R L Y C R A A G V P S A T I T W R K E G G S L P P Q
A

2001 R S E R T D I A T L L I P A I T T A D A G F Y L C V A T S P A G T A Q A R I Q V
V V L S A S D A S P P P V K I E S S S P S V T E G Q T L D L N C V V A G S A H A

2081 Q V T W Y R R G G S L P P H T Q V H G S R L R L P Q V S P A D S G E Y V C R
V E N G S G P K E A S I T V S V L H G T H S G P S Y T P V P G S T R P I R I E P S S

2161 S H V A E G Q T L D L N C V V P G Q A H A Q V T W H K R G G S L P A R H Q T
H G S L L R L H Q V T P A D S G E Y V C H V V G T S G P L E A S V L V T I E A S V I

2241 P G P I P P V R I E S S S S T V A E G Q T L D L S C V V A G Q A H A Q V T W Y
K R G G S L P A R H Q V R G S R L Y I F Q A S P A D A G Q Y V C R A S N G M E A S

2321 I T V T V T G T Q G A N L A Y P A G S T Q P I R I E P S S S Q V A E G Q T L D L
N C V V P G Q S H A Q V T W H K R G G S L P V R H Q T H G S L L R L Y Q A S P A

2401 D S G E Y V C R V L G S S V P L E A S V L V T I E P A G S V P A L G V T P T V
R I E S S S S Q V A E G Q T L D L N C L V A G Q A H A Q V T W H K R G G S L P A R

2481 H Q V H G S R L R L L Q V T P A D S G E Y V C R V V G S S G T Q E A S V L V
T I Q Q R L S G S H S Q G V A Y P V R I E S S S A S L A N G H T L D L N C L V A S Q

2561 A P H T I T W Y K R G G S L P S R H Q I V G S R L R I P Q V T P A D S G E Y V
C H V S N G A G S R E T S L I V T I Q G S G S S H V P S V S P P I R I E S S S P T

2641 V V E G Q T L D L N C V V A R Q P Q A I I T W Y K R G G S L P S R H Q T H G S
H L R L H Q M S V A D S G E Y V C R A N N N I D A L E A S I V I S V S P S A G S P

2721 S A P G S S M P I R I E S S S S H V A E G E T L D L N C V V P G Q A H A Q V T
W H K R G G S L P S H H Q T R G S R L R L H H V S P A D S G E Y V C R V M G S S G

2801 P L E A S V L V T I E A S G S S A V H V P A P G G A P P I R I E P S S S R V A E
G Q T L D L K C V V P G Q A H A Q V T W H K R G G N L P A R H Q V H G P L L R L

2881 N Q V S P A D S G E Y S C Q V T G S S G T L E A S V L V T I E P S S P G P I P A
P G L A Q P I Y I E A S S S H V T E G Q T L D L N C V V P G Q A H A Q V T W Y K

2961 R G G S L P A R H Q T H G S Q L R L H L V S P A D S G E Y V C R A A S G P G P
E Q E A S F T V T V P P S E G S S Y R L R S P V I S I D P P S S T V Q Q G Q D A S

3041 F K C L I H D G A A P I S L E W K T R N Q E L E D N V H I S P N G S I I T I V G
T R P S N H G T Y R C V A S N A Y G V A Q S V V N L S V H G P P T V S V L P E G

3121 P V W V K V G K A V T L E C V S A G E P R S S A R W T R I S S T P A K L E Q R
T Y G L M D S H A V L Q I S S A K P S D A G T Y V C L A Q N A L G T A Q K Q V E V

3201 I V D T G A M A P G A P Q V Q A E E A E L T V E A G H T A T L R C S A T G S P
A P T I H W S K L R S P L P W Q H R L E G D T L I I P R V A Q Q D S G Q Y I C N A

3281 T S P A G H A E A T I I L H V E S P P Y A T T V P E H A S V Q A G E T V Q L Q
C L A H G T P P L T F Q W S R V G S S L P G R A T A R N E L L H F E R A A P E D S

3361 G R Y R C R V T N K V G S A E A F A Q L L V Q G P P G S L P A T S I P A G S T
P T V Q V T P Q L E T K S I G A S V E F H C A V P S D R G T Q L R W F K E G G Q L

3441 P P G H S V Q D G V L R I Q N L D Q S C Q G T Y I C Q A H G P W G K A Q A S
A Q L V I Q A L P S V L I N I R T S V Q T V V V G H A V E F E C L A L G D P K P Q V

3521 T W S K V G G H L R P G I V Q S G G V V R I A H V E L A D A G Q Y R C T A T
N A A G T T Q S H V L L L V Q A L P Q I S M P Q E V R V P A G S A A V F P C I A S G

3601 Y P T P D I S W S K L D G S L P P D S R L E N N M L M L P S V R P Q D A G T Y
V C T A T N R Q G K V K A F A H L Q V P E R V V P Y F T Q T P Y S F L P L P T I K

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3681 DAYRKFEIKITFRPDSADGMLLYNGQKRVPGSPTNLANR
QPDFISFGLVGGRRPEFRFDAGSGMATIRHPTPLALGHFHTV

3761 TLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLG
GYPDYGAIPKAGLSSGFIGCVRELRIQGEEIVFHDNLNLTAH

3841 GISHCPTCRDRPCQNGGQCHDSESSSYVCVCPAGFTGSR
CEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGLR

3921 CEEGVTVTTPSLSGAGSYLALPALTNTHHELRLDVEFKP
LAPDGVLLFSSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLA

4001 VLRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRS
SPGKSQGLNLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGE
V

4081 SVNGKRRLDLTYSFLGSQGIGQCYDSSPCERQPCQHGATC
MPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPC LHGGTCQ

4161 GTRCLCLPGFSGPRCQQQSGHGI AESDWHLEGS GGNDAP
GQYGAYFHDDGFLAFP GHVFSRSLPEVPETIELEVRTSTAS

4241 GLLLWQGV E VGEAGQ GKDFISLGLQDGH LVFRYQLGSG
EARLVSEDPINDGEWHRVTALREGRRGSIQVDGEE LVSGRSP

4321 GPNVAVNAKGSVYIGGAPDVA TL TGGRFSSGITGCVKNL
VLHSARPGAPPPQPLDLLQHRAQAGANTRPCPS

5.18 clusterin isoform 1 [*Homo sapiens*]
Protein Accession gi|42716297

Mean Expression Ratio 0.62

Median Expression Ratio 0.619

Credible Interval (0.484, 0.788)

Associated Peptides 9

Associated Spectra 12

Coverage 0.194

[0136]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.42	0.59	0.82	SEQ ID NO: 231	ASSIIDELFQDR
1	0.45	0.63	0.89	SEQ ID NO: 232	ASSIIDELFQDRF
1	0.44	0.62	0.87	SEQ ID NO: 233	EILSVDCSTNNPSQAK
1	0.45	0.63	0.9	SEQ ID NO: 234	ELDESLQVAER
3	0.42	0.57	0.77	SEQ ID NO: 235	LFSDSPITVTVPEVSR
1	0.44	0.63	0.89	SEQ ID NO: 236	MLDVMQDHF
1	0.44	0.63	0.89	SEQ ID NO: 237	PITVTVPEVSR
1	0.44	0.62	0.88	SEQ ID NO: 238	VTTVASHTSDSDVPSGVTEVVVK
1	0.43	0.6	0.85	SEQ ID NO: 239	RPHFFFPK
SEQ ID NO: 240					
1MQVCSQPQRGCVREQSAINTAPPSAHNAASPGGARGHRVP LTEACKDSRIGGMMKTL L LFVGL L LTWESGQVLGDQTVSD					
81NELQEMSNQGSKYVNKEIQNAVNGVKQIKTLIEKTNEERK TLLSNLEEA KKKKEDALNETRESETKLKELPGVCNETMMA					
161LWEECKPCLKQTCMKFYARVCRSGSGLVGRQLEEF LNQS SPFYFWMNGDRIDS LLEND RQQTHMLDVMQDHF SRASSIID					
241ELFQDRFFFTREPQDTYHYLPFSLPHRRPHFFFFPKSRIVRSL MPFSPYEPLNFHAMFPFL EMIHEAQQA MDIHFHSPAFQ					
321HPPTTEFIREGDDDRDTVCREIRHNSTGCLRMKDQCDKCREI LSVDCSTNNPSQAKLRRELDESLQVAERLTRKYNEL LKSY					

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401	Q	W	K	M	L	N	T	S	S	L	L	E	Q	L	N	E	Q	F	N	W	V	S	R	L	A	N	L	T	Q	G	E	D	Q	Y	Y	L	R	V				
	T	T	V	A	S	H	T	S	D	S	D	V	P	S	G	V	T	E	V	V	V	K	L	F	D	S	D	P	I	T	V	T	V	P	V	E	V	S	R	K	N	P
481	K	F	M	E	T	V	A	E	K	A	L	Q	E	Y	R	K	K	H	R	E	E																					

5.19 ezrin [*Homo sapiens*]; ezrin [*Homo sapiens*]
Protein Accession gi|21614499 gi|161702986

Mean Expression Ratio 1.62
Median Expression Ratio 1.61
Credible Interval (1.23, 2.13)
Associated Peptides 7
Associated Spectra 8
Coverage NaN
[0137]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	1.2	1.7	2.5	SEQ ID NO: 241	FYPEDVAEELIQDITQK
1	1.1	1.6	2.3	SEQ ID NO: 242	KEDEVEEWQHR
1	1.1	1.6	2.4	SEQ ID NO: 243	QLLTLSSELSQAR

-continued						
A	2.5	50	97.5	Sequence	ID No.	Sequence
1	1.1	1.6	2.4	SEQ ID NO: 244		QQLETEK
1	1.2	1.7	2.4	SEQ ID NO: 245		GFPTWLK
1	1.1	1.6	2.3	SEQ ID NO: 246		IAQDLEMYGINYFEIK
1	1.1	1.6	2.3	SEQ ID NO: 247		ILQLCMGNHELYMR

5.20 delta globin [*Homo sapiens*]
Protein Accession gi|4504351

Mean Expression Ratio 1.60
Median Expression Ratio 1.60
Credible Interval (1.12, 2.29)
Associated Peptides 3
Associated Spectra 4
Coverage 0.306
[0138]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	1.2	1.7	2.6	SEQ ID NO: 248	F F E S F G D L S S P D A V M G N P K
1	1.1	1.6	2.5	SEQ ID NO: 249	V N V D A V G G E A L G R
1	1.1	1.6	2.5	SEQ ID NO: 250	G T F S Q L S E L H C D K
SEQ ID NO: 251					
1 M V H L T P E E K T A V N A L W G K V N V D A V G G E A L G R L L V V Y P W T					
Q R F F E S F G D L S S P D A V M G N P K V K A H G K K V L G A F S D G L A H L D					
81 N L K G T F S Q L S E L H C D K L H V D P E N F R L L G N V L V C V L A R N F G					
K E F T P Q M Q A A Y Q K V V A G V A N A L A H K Y H					

5.21 fibrinogen, beta chain preproprotein [*Homo sapiens*]
Protein Accession gi|70906435

Mean Expression Ratio 0.633
Median Expression Ratio 0.633
Credible Interval (0.527, 0.76)
Associated Peptides 14
Associated Spectra 27
Coverage 0.291
[0139]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.49	0.66	0.87	SEQ ID NO: 252	AHYGGFTVQNEANK
1	0.46	0.62	0.85	SEQ ID NO: 253	DNENVVNEYSSELEK
1	0.5	0.68	0.92	SEQ ID NO: 254	ETVNSNIPTNLR

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1	0.47	0.64	0.88	SEQ ID NO: 255	GGETSEMYLIQPDSSVKPYR
7	0.47	0.59	0.75	SEQ ID NO: 256	HQLYIDETVNSNIPTNLR
1	0.47	0.65	0.9	SEQ ID NO: 257	IDETVNSNIPTNLR
2	0.45	0.6	0.8	SEQ ID NO: 258	LIQPDSSVKPYR
2	0.44	0.59	0.8	SEQ ID NO: 259	MGPTELLIEMEDWK
1	0.45	0.62	0.85	SEQ ID NO: 260	NYCGLPGEYWLGN DK
1	0.45	0.62	0.86	SEQ ID NO: 261	QGFGNVATNTDGK
1	0.46	0.63	0.87	SEQ ID NO: 262	YIDETVNSNIPTNLR
4	0.45	0.6	0.78	SEQ ID NO: 263	QGVNDNEEGFFSAR
1	0.47	0.65	0.9	SEQ ID NO: 264	LES DVSAQMEYCR
1	0.46	0.64	0.88	SEQ ID NO: 265	SILENLR
SEQ ID NO: 266					
1 M K R M V S W S F H K L K T M K H L L L L L L C V F L V K S Q G V N D N E E G					
F F S A R G H R P L D K K R E E A P S L R P A P P P I S G G G Y R A R P A K A A A					
81 T Q K K V E R K A P D A G G C L H A D P D L G V L C P T G C Q L Q E A L L Q Q					
E R P I R N S V D E L N N N V E A V S Q T S S S S F Q Y M Y L L K D L W Q K R Q K					
161 Q V K D N E N V V N E Y S S E L E K H Q L Y I D E T V N S N I P T N L R V L R S					
I L E N L R S K I Q K L E S D V S A Q M E Y C R T P C T V S C N I P V V S G K E					
241 C E E I I R K G G E T S E M Y L I Q P D S S V K P Y R V Y C D M N T E N G G W					
T V I Q N R Q D G S V D F G R K W D P Y K Q G F G N V A T N T D G K N Y C G L P					
G					
321 E Y W L G N D K I S Q L T R M G P T E L L I E M E D W K G D K V K A H Y G G					
F T V Q N E A N K Y Q I S V N K Y R G T A G N A L M D G A S Q L M G E N R T M T					
I H					
401 N G M F F S T Y D R D N D G W L T S D P R K Q C S K E D G G G W W Y N R C H					
A A N P N G R Y Y W G G Q Y T W D M A K H G T D D G V V W M N W K G S W Y S					
M R K M					
481 S M K I R P F F P Q Q					

5.22 moesin [*Homo sapiens*]
Protein Accession gi|4505257

Credible Interval (1.18, 2.08)

Associated Peptides 5

Mean Expression Ratio 1.57

Associated Spectra 9

Median Expression Ratio 1.57

[0140]

A	2.5	50	97.5	Sequence ID No.	Sequence
4	1.3	1.8	2.4	SEQ ID NO: 267	FYPEDVSEELIQDITQR
2	1.1	1.5	2.2	SEQ ID NO: 268	GSELWLGV DALGLNIYE QNDR
1	1.1	1.6	2.3	SEQ ID NO: 269	TQEQLALEMAELTAR
1	1.1	1.6	2.3	SEQ ID NO: 270	ERQEAEEAK
1	1.1	1.6	2.3	SEQ ID NO: 271	KTQEQLALEMAELTAR
SEQ ID NO: 272					
1 M P K T I S V R V T T M D A E L E F A I Q P N T T G K Q L F D Q V V K T I G L R E					
V W F F G L Q Y Q D T K G F S T W L K L N K K V T A Q D V R K E S P L L F K F					
81 R A K F Y P E D V S E E L I Q D I T Q R L F F L Q V K E G I L N D D I Y C P P E T					
A V L L A S Y A V Q S K Y G D F N K E V H K S G Y L A G D K L L P Q R V L E Q					
161 H K L N K D Q W E E R I Q V W H E E H R G M L R E D A V L E Y L K I A Q D L					
E M Y G V N Y F S I K N K K G S E L W L G V D A L G L N I Y E Q N D R L T P K I G					
F					
241 P W S E I R N I S F N D K K F V I K P I D K K A P D F V F Y A P R L R I N K R I L					
A L C M G N H E L Y M R R R K P D T I E V Q Q M K A Q A R E E K H Q K Q M E R					
321 A M L E N E K K K R E M A E K E K E K I E R E K E E L M E R L K Q I E E Q T K					
K A Q Q E L E E Q T R R A L E L E Q E R K R A Q S E A E K L A K E R Q E A E E A K					

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401 E A L L Q A S R D Q K K T Q E Q L A L E M A E L T A R I S Q L E M A R Q K K E
S E A V E W Q Q K A Q M V Q E D L E K T R A E L K T A M S T P H V A E P A E N E
Q
481 D E Q D E N G A E A S A D L R A D A M A K D R S E E E R T T E A E K N E R V
Q K H L K A L T S E L A N A R D E S K K T A N D M I H A E N M R L G R D K Y K T
L R
561 Q I R Q G N T K Q R I D E F E S M

5.23 transferrin [*Homo sapiens*]

Credible Interval (0.535, 0.786)

Protein Accession gil4557871

Associated Peptides 12

Mean Expression Ratio 0.648

Associated Spectra 22

Coverage 0.216

Median Expression Ratio 0.648

[0141]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.46	0.64	0.88	SEQ ID NO: 273	CSTSSLLEACTFR
1	0.46	0.63	0.88	SEQ ID NO: 274	DCHLAQVPSHTVVAR
3	0.47	0.62	0.83	SEQ ID NO: 275	EDLIWELLNQAQEHFGK
2	0.45	0.61	0.83	SEQ ID NO: 276	EGTCPEAPTDECKPVK
3	0.53	0.7	0.93	SEQ ID NO: 277	HQTVPQNTGGK
2	0.47	0.63	0.85	SEQ ID NO: 278	HSTIFENLANK
3	0.48	0.64	0.86	SEQ ID NO: 279	KPVEEYANCHLAR
1	0.47	0.64	0.9	SEQ ID NO: 280	MYLGYEYVTAIR
1	0.48	0.66	0.9	SEQ ID NO: 281	NIPIGLLYCDLPEPR
2	0.47	0.64	0.87	SEQ ID NO: 282	NLNEKDYELLCLDGTR
2	0.47	0.63	0.86	SEQ ID NO: 283	SAGWNIPIGLLYCDLPEPR
1	0.48	0.66	0.91	SEQ ID NO: 284	YLGEYVVK
SEQUENCE ID NO: 285					
1 M R L A V G A L L V C A V L G L C L A V P D K T V R W C A V S E H E A T K C Q S F R D H M K S V I P S D G P S V A C V K K A S Y L D C I R A I A A N E A D A V T					
81 L D A G L V Y D A Y L A P N N L K P V V A E F Y G S K E D P Q T F Y Y A V A V V K K D S G F Q M N Q L R G K K S C H T G L G R S A G W N I P I G L L Y C D L P E					
161 P R K P L E K A V A N F F S G S C A P C A D G T D F P Q L C Q L C P G C G C S T L N Q Y F G Y S G A F K C L K D G A G D V A F V K H S T I F E N L A N K A D R D					
241 Q Y E L L C L D N T R K P V D E Y K D C H L A Q V P S H T V V A R S M G G K E D L I W E L L N Q A Q E H F G K D K S K E F Q L F S S P H G K D L L F K D S A H G					
321 F L K V P P R M D A K M Y L G Y E Y V T A I R N L R E G T C P E A P T D E C K P V K W C A L S H H E R L K C D E W S V N S V G K I E C V S A E T T E D C I A K I					
401 M N G E A D A M S L D G G F V Y I A G K C G L V P V L A E N Y N K S D N C E D T P E A G Y F A V A V V K K S A S D L T W D N L K G K K S C H T A V G R T A G W N G L N L C E P N N K E G Y Y G Y T G A F R C L V E K G D V A F V K H Q T V P Q N					
561 T G G K N P D P W A K N L N E K D Y E L L C L D G T R K P V E E Y A N C H L A R A P N H A V V T R K D K E A C V H K I L R Q Q Q H L F G S N V T D C S G N F C L					
641 F R S E T K D L L F R D D T V C L A K L H D R N T Y E K Y L G E E Y V K A V G N L R K C S T S S L L E A C T F R R P					

Median Expression Ratio 1.52

Credible Interval (1.10, 2.13)

Associated Peptides 4

Associated Spectra 5

Coverage NaN

[0142]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
2	1	1.5	2.1	SEQ	ID NO:	286	AIPVAQDLNAPSDWDSR
1	1.1	1.7	2.5	SEQ	ID NO:	287	GKDSYETSQLDDOSAETHSHK

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A	2.5	50	97.5	Sequence	ID	No.	Sequence
1	1.0	1.5	2.3	SEQ	ID NO:	288	KANDESNEHSDVIDSQELSK
1	1.1	1.6	2.4	SEQ	ID NO:	289	SKEEDK

5.25 pancreatic amylase alpha 2A precursor [*Homo sapiens*]
Protein Accession gi|4502085

Mean Expression Ratio 0.664

Median Expression Ratio 0.664

Credible Interval (0.527, 0.841)

Associated Peptides 8

Associated Spectra 14

Coverage 0.213

[0143]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.46	0.63	0.86	SEQ ID NO: 290	ALVFVDNHDNQ R
1	0.49	0.69	0.97	SEQ ID NO: 291	EV TINPDTTCGNDWVCEHR
5	0.48	0.64	0.84	SEQ ID NO: 292	IAEYMNHLIDIGVAGFR
1	0.47	0.66	0.95	SEQ ID NO: 293	LTGLLDLAL E K
2	0.46	0.64	0.89	SEQ ID NO: 294	LTGLLDLAL E KD YVR
1	0.48	0.68	0.95	SEQ ID NO: 295	NVVDGQPFTN WYDNGSNQVAFGR
1	0.47	0.66	0.93	SEQ ID NO: 296	NWGEGWGFVPSDR
1	0.46	0.66	0.93	SEQ ID NO: 297	WVDIALECE R
SEQ ID NO: 298					
1 M K F F L L L F T I G F C W A Q Y S P N T Q Q G R T S I V H L F E W R W V D I A L					
E C E R Y L A P K G F G G V Q V S P P N E N V A I Y N P F R P W W E R Y Q P V					
81 S Y K L C T R S G N E D E F R N M V T R C N N V G V R I Y V D A V I N H M C G					
N A V S A G T S S T C G S Y F N P G S R D F P A V P Y S G W D F N D G K C K T G S					
161 G D I E N Y N D A T Q V R D C R L T G L L D L A L E K D Y V R S K I A E Y M N					
H L I D I G V A G F R L D A S K H M W P G D I K A I L D K L H N L N S N W F P A G					
241 S K P F I Y Q E V I D L G G E P I K S S D Y F G N G R V T E F K Y G A K L G T V					
I R K W N G E K M S Y L K N W G E G W G F V P S D R A L V F V D N H D N Q R G					
H					
321 G A G G A S I L T F W D A R L Y K M A V G F M L A H P Y G F T R V M S S Y R					
W P R Q F Q N G N D V N D W V G P P N N N G V I K E V T I N P D T T C G N D W V					
C E					
401 H R W R Q I R N M V I F R N V V D G Q P P T N W Y D N G S N Q V A F G R G N					
R G F I V F N N D D W S F S L T L Q T G L P A G T Y C D V I S G D K I N G N C T G I					
481 K I Y V S D D G K A H F S I S N S A E D P F I A I H A E S K L					

5.26 annexin A2 isoform 1 [*Homo sapiens*]
Protein Accession gi|50845388
Mean Expression Ratio 1.50
Median Expression Ratio 1.5
Credible Interval (1.07, 2.11)
Associated Peptides 3
Associated Spectra 5
Coverage 0.129
[0144]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	1.1	1.6	2.4	SEQ ID NO: 299	GLGTDEDSLIEIICSR
2	1.0	1.5	2.2	SEQ ID NO: 300	RAEDGSVIDYELIDQDAR
1	1.0	1.5	2.4	SEQ ID NO: 301	SYSPTYDMLIESIR
SEQ ID NO: 302					
1	MGRQLAGCGDAGKKASFKMSTVHEILCKLSLEGDHSTPPS AYGSVKAYTNFDAERDALNIETAIKTKGVDEVTIVNLTN				

5.27 complement component 4 binding protein, alpha chain precursor [*Homo sapiens*]
Protein Accession gi|4502503
Mean Expression Ratio 0.673
Median Expression Ratio 0.675

Credible Interval (0.48, 0.94)
Associated Peptides 5
Associated Spectra 5
Coverage 0.104
[0145]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.44	0.66	0.99	SEQ ID NO: 303	EDVYVVGTVLR
1	0.42	0.64	0.95	SEQ ID NO: 304	LSLEIEQLELQR
1	0.45	0.68	1.0	SEQ ID NO: 305	PSAICQGDGTWSPR
1	0.44	0.67	1	SEQ ID NO: 306	YTCLPGYVR
1	0.44	0.66	1	SEQ ID NO: 307	CEWETPEGCEQVLTGK
SEQUENCE ID NO: 308					
1	MHPPKTPSGALHRKRKMAAWPFSLWKVSDPILFQMTLIA ALLPAVLGNCGPPPTLSFAAPMDITLTETRFKTGTTLKYT				
81	CLPGYVRSHSTQTLTCNSDGEWVYNTFCIYKRCRHPGELR NGQVEIKTDLSTFGSQIEFSCSEGFFLIGSTTSRCEVQDRG				
161	VGWVSHPLPQCEIVKCKPPPDIRNGRHSGEENFYAYGFSVT YSCDPRFSLGLGHASICTVENETIGVWRPSPPTCEKITCR				
241	KPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIH CDADSKWNPSPPACEPNSCINLPDIPHASWETYPRTKED				
321	VYVVGTVLRYRCHPGYKPTTDEPTTVICQKNLRWTPYQG CEALCCPEPKLNNGEITQHRKSRPANHCYFYFGDEISFSCH				
401	ET5RFSAICQGDGTWSPRTPSCGDICNFPKIAHGHYKQS SSYSFFKEEIIYECDKGYILVGQAKLSCSYSHWSAPAPQC				

5.28 albumin preproprotein [*Homo sapiens*]

Protein Accession gi|4502027

Mean Expression Ratio 0.681

Median Expression Ratio 0.681

Credible Interval (0.626, 0.74)

Associated Peptides 65

Associated Spectra 259

Coverage 0.744

[0146]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.49	0.64	0.86	SEQ ID NO: 309	AAFTECCQAADK
5	0.46	0.58	0.74	SEQ ID NO: 310	ADDKETCFAEEGK
1	0.49	0.64	0.85	SEQ ID NO: 311	ADDKETCFAEEGKK
3	0.55	0.7	0.9	SEQ ID NO: 312	AEFAEVSK
10	0.56	0.68	0.83	SEQ ID NO: 313	ALVLIAFAYLQQCPFEDHVK
1	0.52	0.69	0.9	SEQ ID NO: 314	AQYLQQCPFEDHVK
9	0.51	0.63	0.77	SEQ ID NO: 315	AVMDDFAAFVEK
1	0.5	0.66	0.87	SEQ ID NO: 316	CCTESLVNR
5	0.62	0.78	0.99	SEQ ID NO: 317	CIAEVENDEMPADLPSLAADFVESK
7	0.61	0.76	0.94	SEQ ID NO: 318	CTAFHDNEETFLK
1	0.5	0.66	0.87	SEQ ID NO: 319	DDNPNLPR
2	0.52	0.69	0.9	SEQ ID NO: 320	DLGEENFK
2	0.48	0.63	0.82	SEQ ID NO: 321	ECCEKPLLEK
2	0.56	0.74	0.96	SEQ ID NO: 322	ETCFAEEGK
2	0.5	0.65	0.85	SEQ ID NO: 323	ETCFAEEGKK
1	0.51	0.68	0.89	SEQ ID NO: 324	ETYGEMADCCAK
4	0.49	0.63	0.8	SEQ ID NO: 325	FKDLGEENFK
3	0.49	0.64	0.82	SEQ ID NO: 326	FQNALLVR
1	0.52	0.69	0.9	SEQ ID NO: 327	FSALEVDETYVPK
1	0.53	0.7	0.92	SEQ ID NO: 328	FYAPELLFFAK
1	0.54	0.72	0.96	SEQ ID NO: 329	HDNEETFLK
2	0.53	0.7	0.91	SEQ ID NO: 330	HPDYSVVLRLR
1	0.55	0.72	0.95	SEQ ID NO: 331	IAEVENDEMPADLPSLAADFVESK
4	0.54	0.68	0.87	SEQ ID NO: 332	KQTALVELVK
15	0.55	0.65	0.79	SEQ ID NO: 333	KVPQVSTPTLVEVSR
2	0.5	0.65	0.85	SEQ ID NO: 334	KYLYEIAR
2	0.51	0.67	0.87	SEQ ID NO: 335	LCTVATLR
3	0.52	0.66	0.86	SEQ ID NO: 336	LDELRDEGK
1	0.48	0.64	0.85	SEQ ID NO: 337	LKECCEKPLLEK
4	0.52	0.67	0.85	SEQ ID NO: 338	LVNEVTEFAK
7	0.52	0.64	0.8	SEQ ID NO: 339	LVRPEVDVMCTAFHDNEETFLK
2	0.54	0.7	0.9	SEQ ID NO: 340	LVTDLTK
3	0.51	0.66	0.86	SEQ ID NO: 341	MPCAEDYLSVVLNQLCVLHEK

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A	2.5	50	97.5	Sequence ID No.	Sequence
7	0.6	0.74	0.92	SEQ ID NO: 342	NECFLQHK
1	0.54	0.7	0.93	SEQ ID NO: 343	PLVEEPQNLIK
4	0.51	0.65	0.83	SEQ ID NO: 344	QEPERNECFLQHK
2	0.53	0.7	0.91	SEQ ID NO: 345	QLCVLHEK
2	0.54	0.7	0.91	SEQ ID NO: 346	QTALVELVK
4	0.49	0.63	0.8	SEQ ID NO: 347	RPCFSALEVDETYVVK
1	0.52	0.69	0.91	SEQ ID NO: 348	SALEVDETYVVK
18	0.5	0.59	0.7	SEQ ID NO: 349	SHCIAEVENDEMPADLPSLAADFVESK
23	0.64	0.75	0.88	SEQ ID NO: 350	SLHTLFGDK
1	0.52	0.69	0.9	SEQ ID NO: 351	TAFHDNEETFLK
2	0.52	0.69	0.9	SEQ ID NO: 352	TCVADESAENCDK
2	0.52	0.68	0.9	SEQ ID NO: 353	TFHADICTLSEK
1	0.53	0.7	0.93	SEQ ID NO: 354	VFDEFKPL
1	0.51	0.68	0.9	SEQ ID NO: 355	VFDEFKPLVEEPQNL
46	0.59	0.67	0.75	SEQ ID NO: 356	VFDEFKPLVEEPQNLIK
4	0.52	0.67	0.86	SEQ ID NO: 357	VHTECCHGDLLECADDR
4	0.57	0.72	0.93	SEQ ID NO: 358	VPQVSTPTLVEVSR
1	0.52	0.7	0.93	SEQ ID NO: 359	VSTPTLVEVSR
1	0.52	0.69	0.91	SEQ ID NO: 360	YLYEIAR
1	0.52	0.69	0.91	SEQ ID NO: 361	YTKKVPQVSTPTLVEVSR
9	0.62	0.76	0.94	SEQ ID NO: 362	DVFLGMFLYEYAR
2	0.51	0.67	0.87	SEQ ID NO: 363	QNCLEFQGLGEYK
2	0.54	0.71	0.92	SEQ ID NO: 364	YICENQDSISSK
1	0.52	0.68	0.91	SEQ ID NO: 365	CASLQK
1	0.51	0.68	0.9	SEQ ID NO: 366	KLVAASQAALGL
1	0.51	0.67	0.89	SEQ ID NO: 367	LQQCPFEDHVK
3	0.52	0.67	0.86	SEQ ID NO: 368	FYAPELFFFAKR
1	0.52	0.7	0.92	SEQ ID NO: 369	AACLLPKLDELRL
1	0.53	0.7	0.92	SEQ ID NO: 370	VFDEFK
1	0.51	0.67	0.9	SEQ ID NO: 371	RHPDYSVVLRL
1	0.51	0.68	0.9	SEQ ID NO: 372	RHPYFYAPELFFFAK
1	0.52	0.69	0.91	SEQ ID NO: 373	AACLLPK
				SEQ ID NO: 374	
1	MKWVTFISLLFLFSSAYSRGVFRDAHKSEVAHRFKDLGEE NFKALVLIIFAQYLQQCPFEDHVKLVNEVTEFAKTCVAD				
81	ESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQE PERNECFLQHKDDPNLPRLVRPEVDVMCTAFHDNEETFLK				
161	KYLEIARRHPYFYAPELFFFAKRYKAAFTECCQAADKA ACLLPKLDELRLDEGKASSAKQRLKASLQKFGERAFKAWAV				

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A	2.5	50	97.5	Sequence ID No.	Sequence
241	ARLSQRFPKAEFAEVSKLVTDLTQVHTECCHGDLLECAD				DRADLAKYICENQDSISSKLEKCEKPLEKSHCIAEVEND
321	EMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEY				ARRHPDYSVVLRLAKTYETTLEKCCAAADPHECYAKVFE
401	FKPLVEEPQNLIKQNCLEFEQLGEYKFNALLVRYTKKVP				QVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEYLSVV
481	LNQLCVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDET				YVPKEFNAETFTFHADICTLSEKERQIKKQATALVELVKHK
561	PKATKEQLKAVMDDFAAFVEKCKADDKETCFEAEGKK				LVAASQAALGL

5.29 epidermal growth factor receptor pathway substrate 8
[Homo sapiens]
Protein Accession gil56682953

Mean Expression Ratio 1.46

Median Expression Ratio 1.46

Credible Interval (1.13, 1.86)

Associated Peptides 9

Associated Spectra 11

Coverage 0.153

[0147]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	1.1	1.6	2.3	SEQ ID NO: 376	APAPAPPGETVTQVDVR
1	1.1	1.5	2.1	SEQ ID NO: 377	EQFIPPYVPR
2	1.1	1.5	2.0	SEQ ID NO: 378	ISAAASDSGVESFDEGSSH
1	1.0	1.5	2.1	SEQ ID NO: 379	NILDIVRPPEGLGR
1	1.0	1.4	2.0	SEQ ID NO: 380	SQMEEVQDELIHR
1	1	1.4	2.0	SEQ ID NO: 381	VWTQDMILQVDDR
1	1	1.4	2	SEQ ID NO: 382	DDILEILDDR
2	1.0	1.4	2.0	SEQ ID NO: 383	MISNADPSIPPPPR
1	1.0	1.5	2.0	SEQ ID NO: 384	ANLISEDIESAISDSK
1				SEQ ID NO: 385	MNGHISNHPSSFGMYPQMNQYGSPTFSQTDREHGSKTS
					AKALYEQRKNYARDSVSSVSDISQYRVEHLTTFVLDKDA
81					MITVDDGIRKLKLLDAKGVWTQDMILQVDDRAVSLIDLE
					SKNELENFPLNTIQHCQAVMHSCSYDSVLALVCKEPTQNK
161					PDLHLFQCDEVKANLISEDIESAISDSKGGKQKRRPDALR
					MISNADPSIPPPPRAPAPAPPGETVTQVDVRSRVAWSAWA
241					ADQGDFEKPRQYHEQEETPEMMAARIDRDVQILNHILDDI
					EFFITKLQKAAEAFSELSKRKKNKKGRKGPGEVLTIRA
321					KPPPPDEFDFCFQKFKHGFNLLAKLKSHIQNPSAADLVHF
					LFTPLNMVVQATGGPELASSVLSPLLNKDTIDFLNYTVNG
401					DERQLWMSLGGTWMKARAEWPKEQFIPPYVPRFRNGWE
					PPMLNFMGATMEQDLYQLAESVANVAEHQRKQEIKRLSTEH
					S
481					SVSEYHPADGYAFSSNIYTRGSHLDQGEAAVAFKPTSNR
					HIDRNYEPLKTQPKKYAKSKYDFVARNNSELSVLKDDILEI
561					LDDRQWQWVNRNASGDSGFVPNNILDIVRPPEGLGRAD
					PPYHTIQQRMEYGRPADTPPAPSPPTTPAPVPVPLPPS

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A	2.5	50	97.5	Sequence ID No.	Sequence
641					TPAPVPVSKVPANITRONSSSSDSGGSIVRDSQRHKQLPV DRRKSQMEEVQDELIHRLTIGRSAAQKKFHVPRQNPVIN
721					ITYD5TPEDVKTWLQSKGFNPVTVNSLGVNLGAQLFSLN KDELRTVCPEGARVYSQITVQKAALEDSSGSSELQEIMRRR
801					QEKISAAASDSGVESFDEGSSH

5.30 apolipoprotein B precursor [*Homo sapiens*]
Protein Accession gil105990532

Associated Peptides 27

Mean Expression Ratio 0.688

Associated Spectra 30

Median Expression Ratio 0.688

Coverage 0.073

Credible Interval (0.585, 0.815)

[0148]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.5	0.68	0.92	SEQ ID NO: 386	AHLDIAGSLEGHLR
1	0.48	0.65	0.88	SEQ ID NO: 387	ATFQTPDFIVPLTDLR
1	0.47	0.65	0.88	SEQ ID NO: 388	DKDQEVLLQTFLLDASPDKR
1	0.5	0.69	0.93	SEQ ID NO: 389	ELPVLHVPR
1	0.51	0.7	0.95	SEQ ID NO: 390	FLDMLIK
1	0.52	0.7	0.96	SEQ ID NO: 391	HSITNPLAVLCEFISQSIK
2	0.5	0.68	0.9	SEQ ID NO: 392	ILGEELGFASLHDLQLLGK
1	0.5	0.69	0.94	SEQ ID NO: 393	LELELRPTGEIEQY
1	0.52	0.7	0.96	SEQ ID NO: 394	LHVAGNLK
1	0.51	0.69	0.94	SEQ ID NO: 395	LIDVISMYR
1	0.49	0.67	0.92	SEQ ID NO: 396	LVALIPEPSAQQLR
2	0.51	0.67	0.9	SEQ ID NO: 397	NMGLPDFHIPENLFLK
1	0.51	0.69	0.94	SEQ ID NO: 398	QSMTLSSSEVQIPDFDVLGTILR
1	0.5	0.68	0.93	SEQ ID NO: 399	QTIIVVLENVQR
1	0.49	0.67	0.9	SEQ ID NO: 400	SSEVQIPDFDVLGTILR
1	0.5	0.68	0.92	SEQ ID NO: 401	TEVIPPLIENR
1	0.51	0.69	0.95	SEQ ID NO: 402	TLQGIPQMIGEVIR
1	0.52	0.7	0.96	SEQ ID NO: 403	TLSSSEVQIPDFDVLGTILR
1	0.49	0.67	0.92	SEQ ID NO: 404	TQFNNNEYSQDLDAYNTK
2	0.53	0.72	0.95	SEQ ID NO: 405	VAWHYDEEK
1	0.49	0.68	0.92	SEQ ID NO: 406	YTYNYEAESSSGVPGTADSR
1	0.51	0.7	0.95	SEQ ID NO: 407	QSFDSL VK
1	0.51	0.69	0.94	SEQ ID NO: 408	VTNMGIIIPDFAR
1	0.51	0.7	0.95	SEQ ID NO: 409	HIQNIDIQHLGK
1	0.53	0.72	0.99	SEQ ID NO: 410	VLLDQLGTTISFER

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A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.52	0.71	0.97	SEQ ID NO: 411	LALWGEHTGQLY
1	0.51	0.68	0.94	SEQ ID NO: 412	MGIIPDFAR
				SEQ ID NO: 413	
1					MDPPRPALLALLALPALLLLLLLAGARAEEMLENVSLVCP KDATRFKHLRKYYTYNYEAESSGVPGTADSRSATRINCKV
81					ELEVPLCSFILKTSQCTLKEVYGFNPEGKALLKKTKNSEE FAAAMSRYELKLAIEPGKQVFLYPEKDEPTYILNIKRGI
161					ISALLVPPETEEAKQVFLDVTYVGNCSHTFTVKTRKGNVA TEISTERDLGQCDRFKPIRTGISPLALIKGMTRPLSTLIS
241					SSQSCQYTLDAKRKHVAEAIKCEQHLFLPFSYKNKYGMV AQVTQTLKLEDTPKINSRFFGEGTKKMGLAFESTKSTSPPK
321					QAEAVLKTQLKELKLTISEQNIQRANLFPNKLVTLELGLSD EAVTSLLPQLIEVSSPITLQALVQCGQPQCSTHILQWLKR
401					VHANPLLIDVVTYLVALIPEPSAQQLREIFNMARDQRSRA TLYALSHAVNNYHKTNPTGTQELLDIANYLMEQIQDDCTG
481					DEDYTYLILRVIGNMGQTMEQLTPELKSSILKCVQSTKPS LMIQKAAIQALRKMEPKDKDQEVLLQTFLLDASPGDKRLA
561					AYLMLMRSPSQADINKIVQILPWEQNEQVKNFVASHIANI LNSEELDIQDLKKLVKEALKESQLPTVMDFRKFSRNYQLY
641					KSVSLPSLDPASAKIEGNLIFDPNNYLPKESMLKTTLTAF GFASADLIEIGLEGKGFEPTLEALFGKQGFPPDSVKNALY
721					WVNGQVPDGVSKVLVDHFGYTKDDKHEQDMVNGIMLSV EKLIKDLKSKEVPEARAYLRILGEELGFASLHDLQLLGKLLL
801					MGARTLQGI PQMIGEVIRKGSKNDFFLHYIFMENAFELPT GAGLQLQISSSGVIAPGAKAGVKLEVANMQAELVAKPSVS
881					VEFVTNMGIIIPDFARSGVQMNTNFFHESGLEAHVALKAG KLKFIIPSPKRPVKLLSGGNTLHLVSTTKTEVIPPLIENR
961					QSWSVCKQVFPGLNYCTSGAYSNASSTDSASYPLTGD RLELELRPTGEIEQYSVSATYELQREDRALVDTLKFTQAE
1041					GAKQTEATMTFKYNRQSMTLSSSEVQIPDFDVLGTILRV NDESTEGKTSYRLTLDIQNKKITEVALMGHLSCTDKERKI
1121					KGVISIPRLQAEARSEILAHWSPAKLLQMDSSATAYGS TVSKRVAWHYDEEKIEFEWNTGTNVDTKKMTSNFPVDLSD Y
1201					PKSLHMYANRLDHRVPQDTMTFRHVGSKLIVAMSSWL QKASGSLPYTQTLQDHLNSLKEFNLQNMGLPDFHIPENLFLK
1281					SDGRVKYTLNKNLSKIEIPLPFGGKSSRDLMLETVRTP ALHFKSVGFHLPSPREFQVPTFTIPKLYQLQVPLLGVLDLST
1361					NVYSNLYNWSASYSGGNTSTDHFSRLRHYHMKADSVVD LLSYNVQSGGETTYDHKNFTLSCDGSLRHKFLDSNFKFSHV
1441					EKLGNPNVSKGLLIFDASSWGPQMSASVHLDSKKKQHL FVKEVKIDGQFRVSSFYAKGTYGLSCQRDPNTGRLNGESNL
1521					RFNSSYLQGTNQITGRYEDGTLSTSTSDLQSGIINKTAS LKYENYELTLKSDTNGKYKNFATSNKMDMTFSKQNALRS
1601					EYQADYESLRFFSLLSGSLNSHGLELNADILGTDKINSGA HKATLRIGQDGISTSATNLKCSLLVLENELNAELGLSGA
1681					SMKLTNTGRFREHNAKFSLDGKAALTELSLGSAYQAMIL GVDSKNIFFNFKVSQEGKLKSNMMGSYAEMKFDHTNSLNI
1761					GLSLDFSSKLDNIYSSDKFYKQTVNLQLQPYSLVTTLNS DLKYNALDLTNNGLRLEPLKLHVAGNLKGAYQNNKHIY

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A	2.5	50	97.5	Sequence ID No.	Sequence
1841					AISSAALSASYKADTVAKVQGVESHRLNTDIAGLASAI DMSTNYNSDSLHFSNVFRSVMAPFTMTIDAHTNGNGLALW
1921					GEHTGQLYSKFLLKAEPLAFTFSHDYKGSTSHHLVSRKS ISAALEHKVSALLTPAEQTGTWKLKTQFNNNEYSQDLDAYN
2001					TKDKIGVELTGRTLADLTLLDSPIKVPLLLSEPINIIDALE MRDAVEKPPQEFFTIVAFVKYDKNQDVHSINLPPFETLQEY
2081					FERNRQTIIVVLENVQRNLKHINIDQFVRKYRAALGKLP QQANDYLNFSFNWERQVSHAKEKLTALTKKYRITENDIQIAL
2161					DDAKINFNEKLSQLQTYMIQFDQYIKDSYDLHDLKIAIA NIIDEIIEKLSLDEHYHIRVNLVKTIHDLHLFIENIDFNK
2241					SGSSTASWIQNVDTKYQIRIQIQEKLQQLKRHIQNIDIQH LAGKLQKHIEAIDVRVLLDQLGTTISFERINDVLEHVKHF
2321					VINLIGDFEVAEKINAFRAKVHELIEREYVDQQIQVLMMD KLVELAHQYKLBKETIQKLSNVLQQVKIKDYFEKLVGFIDDA
2401					VKKLNELSFKTFIEDVNKFLDMLIKKLSFDYHQFVDET NDKIREVTQRLNGEIQALELPQKAEALKPLEETKATVAVY
2481					LESLQDTKITLIINWLQEALSSASLAHMAKAFRETLEDTR DRMYQMDIQQELQRYLSLVGQVYSTLVYISDWWTLAAKN
2561					LTDFAEQYSIQDWAKRMKALVEQGFTVPEIKTILGTMPA FEVSLQALQKATFPQTPDFIVPLTDLRIPSVQINFKDLKNIK
2641					IPSRFSTPEFTILNLFHIPSFTIDFVEMKVKIIRTIDQMLNS ELQWPVPDIYLRDLKVEDIPLARITLPDFRLPEIAIPE
2721					FIIPTLNLNDFQVPDLHIPEFQLPHISHTIEVPTFGKLYSIL KIQSPLFTLDANADIGNGTTSANEAGIAASITAKGESK
2801					LEVLNFDQANAQLSNPKINPLALKESVKFSSSKYLRTHE GSEMLFFGNAIEGKSNTVASLHTEKNTLELSNGVIVKINNQ
2881					LTLDSNTKYFHKLNIPKLDFFSSQADLRNEIKTLLKAGHIA WTSSGKGSWKWACPRFSDEGTHESQISFTIEGPLTSFGLS
2961					NKINSKHLRVNQNLVYESGSLNFSKLEIQSQVDSQHVGH SVLTAKGMALFGEKAEFTGRHDAHLNGKVI GTLKNSLFFS
3041					AQPFEITASTNNEGNLKVRFPLRLTGKIDFLNNYALFLSP SAQQASWQVSARFNQYKNQNFSAAGNNENIMEAHVGINGE
3121					ANLDFLNIPLTIPEMRLPYTIIITPPLKDFSLWEKTGLKEF LKTTKQSPDLSVKAQYKKNKHRHSITNPLAVLCEFISQS
3201					IKSFDRHFEKNRNNALDFVTKSYNETKIKFDKYKAEKSH DELPRTFQIPGYTPVVNVEVSPFTIEMSAFGYVFPKAVSM
3281					PSFSILGSDVRVPSYTLILPSLELPVLHVPRNLKLSLPDFK ELCTISHIFIPAMGNITYDFSFKSSVITLNTNAELFNQS
3361					DIVAHLLSSSSSIDALQYKLEGTRLTRKRGLKLATALS LSNKFVEGSHNSTVSLTTKNMEVSVATTTKAQIPILRMNF
3441					KQELNGNTKSKPTVSSSMEFYDFNSSMLYSTAKGAVD HKLSLESLSYFYSIESSTKGDVKGSVLSREYSGTIASEANTY
3521					LNSKSTRSSVKLQGTSKIDDIWNLEVKENFAGEATLQRI YSLWEHSTKNHLQLEGLFFTNGEHTSKATLELSPWQMSALV
3601					QVHASQPSSFHDFPDLGQEVAlNANTKNQKIRWKNEVRI HSGSFQSQVELSNDQEKALDIAGSLEGHLRFLKNIIILPVY
3681					DKSLWDFLKLDTVTTSIGRRQHRLRVSTAFVYTKNPNGYSF SIPVKVLADKFIIPGLKLNLDLNSVLVMPTFHVPTDLQVPS

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A	2.5	50	97.5	Sequence ID No.	Sequence
3761					CKLDFREIQIYKKLRTSSFALNLP TLPEVKFPPEVDVLTKY SQPEDSLIPFFEITVPESQLTVSQFTLPKSVSDGIAALDL
3841					NAVANKIADFELPTIIVPEQTIEIPSIKFSVPAGIVIPSFQA LTARFEVDSPVYNATWSASLKNKADYVETVLDSTCSST
3921					VQFLEYELNVLGTHKIEDGTLASKTKGTFAHRDFSABEYE EDGKYEGLQEWEGKAHLNLIKSPAFTDLHLRYQKDKKGISTS
4001					AASPAVGTVGMDMEDDDFSKWNFYSPQSSPDKKLT I FKTEL RVRESDEETQIKVNWEEEAASGLLTS LKDNVPKATG V
4081					LYDYVNKYHWEHTGLTLREVSSKLRRNLQNNAEWVYQ GAIRQIDDDIVRFQKAASGTTGTYQEWKDKAONLYQELLTQ EG
4161					QASFQGLKDNVFDGLVRVTQEFHMKVKHLIDSLIDFLNF PRFQFPGKPGIYTREELCTMFIREVGT VLSQVYSKVHNGSE
4241					ILFSYFQDLVITLPFELRKHKLIDVISMYRELLKDLSKEA QEVFKAIQ SLKTTEVLRNLQDLLQFIFQLIEDN I KQLKEM
4321					KFTYLINIQDEINTIFS DYIPYVFKLLKENLCLNLHKFN EFIQNELQEASQELQQIHQYIMALREEYFDPSIVGWT VKY
4401					YELEEKIVSLIKNLLVALKDFHSEYIVSASNFTSQLSSQV EQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEIIKSQ
4481					AIATKKIISDYHQQFRYKLQDFSDQLSDYYEKFIAESKRL IDLSIQNYHTFLIYITELLKKLQSTTVMNPYMKLAPGELT
4561					IIL

5.31 peroxiredoxin 2 isoform a [*Homo sapiens*]
Protein Accession gi|32189392

Associated Peptides 3

Mean Expression Ratio 1.44

Associated Spectra 5

Median Expression Ratio 1.43

Coverage 0.146

Credible Interval (1.03, 2.04)

[0149]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	1.1	1.5	2.2	SEQ ID NO: 414	EGGGLGPLNIPLLDVTR
1	0.99	1.5	2.2	SEQ ID NO: 415	KEGGLGPLNIPLLDVTR
1	0.96	1.5	2.2	SEQ ID NO: 416	QITVNDLPVGR
				SEQ ID NO: 417	
1				MASGNARIGKPAPDFKATAVVDGAFKEVKLSDYKGKYVV LFFYPLDFTFVCPTETIIAFSNRAEDFRKLGCEVLGVSVD SQ	
81				FTHLAWINTPRKEGGLGPLNIPLLDVTRRLSEDYGV LKT DEGIAYRGLFIIDGKGVLRQITVNDLPVGRSVDEALRLVQ	
161				AFQYTDEHGEVCPAGWKPGSDTIKPNVDDSK EYFSKHN	

5.32 sphingomyelin phosphodiesterase 1, acid lysosomal isoform 1 precursor [*Homo sapiens*]
Protein Accession gi|56117840
Mean Expression Ratio 0.703
Median Expression Ratio 0.702
Credible Interval (0.479, 1.03)
Associated Peptides 2
Associated Spectra 3
Coverage 0.0285
[0150]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.43	0.65	0.98	SEQ ID NO: 418	AWEPWLP AEALR
1	0.45	0.69	1.1	SEQ ID NO: 419	LCNLLK
1				SEQ ID NO: 420	MPRYGASLRQSCPRSGREQQDGTAGAPGLLWMGLVLAL ALALALALALS DSRVLWAPAEAHPLSPQGHPARLHRI VPRL
81					RDVFGWGNLTCPICKGLFTAINLGLKKEPNVARVGSVAIK LCNLLKIAPPAVCQSI VHLFEDDMVEVWRRSVLSPSEACG
161					LLLGSTCGHWDIFSSWNISLPTVPKPPKPPSPAPGAPVS RILFLTDLHWDH DYLEGTDPCADPLCCRRGSGLPASR
241					PGAGYWGEYSKCDLPLRTL ESSLGLGPAGPDMVYWTG DIPAHDVWHQTRQDQLRALTTVTALVRKFLGPVPVYPAVGN
321					HESTPVNSFPFPFIEGNHSSRWLYEAMAKAWEPWLPAEA LRTLRI GGFYALSPYPGLRLISLNMNFC SRENFWLLINSTD
401					PAGQLQWL VGELQAAEDRGDKVHIIGHIPPGHCLKSWSW NYYRIVARYENTLAAQFFGH THVDEFEVYDEETLSRPLAV
481					AFLAPSATTYIGLNPGRVYQIDGNYS GSSHVLDHETYI LNL TQANIPGAIPHWQLLYRARETYGLPNTLP TAWHNLVY
561					RMRGDMQLFQTFWFLYHKGHPPSEPCGTPCRLATLCAQL SARADSPALCRHLM PDGSLPEAQSLWPRPLFC

5.33 proteasome beta 2 subunit [*Homo sapiens*]
Protein Accession gi|4506195
Mean Expression Ratio 1.41
Median Expression Ratio 1.41
Credible Interval (0.987, 2.04)

Associated Peptides 3
Associated Spectra 4
Coverage 0.224
[0151]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.97	1.5	2.3	SEQ ID NO: 421	FILNLP TFSVR
2	1.0	1.5	2.2	SEQ ID NO: 422	LIGIQGPDYVLVASDR
1	0.91	1.4	2.1	SEQ ID NO: 423	HVNLLLAGYDEHEGPALY
1				SEQ ID NO: 424	MEYLIGIQGPDYVLVASDRVAASNIVQMDDHDKMFKMSE KILLLCVGEAGDTVQFAEYI QKNVQLYKMRNGYELSPTAA
81					ANFTRRLADCLRSRTPYHVNLLLAGYDEHEGPALYYMD YLAALAKAPFAAHGYGAFLT LSI LDRYTTPTISRERAVELL
161					RKCLEELQKR FILNLP TFSVRIIDKNGIHDLDNISFPKQGS

5.34 complement component 4B preproprotein [*Homo sapiens*]

Protein Accession gi178557739

Mean Expression Ratio 0.712

Median Expression Ratio 0.711

Credible Interval (0.435, 1.15)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0152]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.39	0.65	1.1	SEQ ID NO: 425	LLSQQQADGSFQDLSPVIHR

5.35 manganese superoxide dismutase isoform A precursor [*Homo sapiens*];

manganese superoxide dismutase isoform A precursor [*Homo sapiens*]

Protein Accession gi67782307 gi67782305

Mean Expression Ratio 1.40

Median Expression Ratio 1.40

Credible Interval (1.10, 1.77)

Associated Peptides 9

Associated Spectra 13

Coverage NaN

[0153]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	1.0	1.4	1.9	SEQ ID NO: 426	AIWNVINWENVTER
2	1.1	1.5	2.1	SEQ ID NO: 427	DFGSFDKFK
1	1.0	1.4	2.0	SEQ ID NO: 428	FNGGGHINHSIFW
1	1	1.4	2	SEQ ID NO: 429	GDVTAQIALQPALK
2	1.0	1.4	2	SEQ ID NO: 430	GELLEAIKR
1	0.97	1.4	1.9	SEQ ID NO: 431	HHAAYVNNLNVTEEK
2	1	1.4	1.9	SEQ ID NO: 432	NVRPDYLK
1	1.0	1.4	2	SEQ ID NO: 433	GWLGFNK
1	0.96	1.4	1.9	SEQ ID NO: 434	YQEALAK

5.36 transthyretin [*Homo sapiens*]

Protein Accession gi4507725

Mean Expression Ratio 0.718

Median Expression Ratio 0.718

Credible Interval (0.572, 0.9)

Associated Peptides 6

Associated Spectra 17

Coverage 0.49

[0154]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.54	0.73	1	SEQ ID NO: 435	ALGISPFHEHAEEVVF
2	0.56	0.76	1.0	SEQ ID NO: 436	ALGISPFHEHAEEVVFTANDSGPR

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A	2.5	50	97.5	Sequence ID No.	Sequence
6	0.48	0.61	0.8	SEQ ID NO: 437	GSPAINVAHVFR
2	0.5	0.7	0.95	SEQ ID NO: 438	KAADDTWEPFASGK
3	0.54	0.74	1	SEQ ID NO: 439	TSESGELHGLTTEEFVEGIYK
1	0.51	0.72	1	SEQ ID NO: 440	AADDTWEPFASGK
				SEQ ID NO: 441	
1	MASHRLLLLCLAGLVFVSEAGPTGTGESKCPLMKVLDVAV RGSPAINVAHVFRKAADDTWEPFASGKTSESGELHGLTT				

5.37 haptoglobin isoform 1 preproprotein [*Homo sapiens*];
haptoglobin isoform 2 preproprotein [*Homo sapiens*]
Protein Accession gi|4826762 gi|186910296

Credible Interval (0.565, 0.918)

Associated Peptides 9

Associated Spectra 13

Mean Expression Ratio 0.721

Coverage NaN

Median Expression Ratio 0.72

[0155]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.52	0.74	1.1	SEQ ID NO: 442	AVHDLEEDTWYATGILSPDK
1	0.51	0.73	1.0	SEQ ID NO: 443	GSFPWQAK
1	0.5	0.71	1.0	SEQ ID NO: 444	HYEGSTVPEKK
2	0.54	0.74	1.0	SEQ ID NO: 445	ILGGHLDK
1	0.48	0.67	0.95	SEQ ID NO: 446	SPVGVQPILNEHTFCAGMSK
1	0.52	0.72	1.0	SEQ ID NO: 447	VMPICLPSKDYAEVGR
1	0.52	0.73	1.0	SEQ ID NO: 448	VTIQDWVQK
3	0.51	0.69	0.93	SEQ ID NO: 449	YVMLPVADQDQCIR
2	0.5	0.7	0.97	SEQ ID NO: 450	FTDHLK

5.38 fibulin 1 isoform D [*Homo sapiens*]

Protein Accession gi|34734066

Mean Expression Ratio 0.726

Median Expression Ratio 0.728

Credible Interval (0.464, 1.12)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0327

[0156]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.42	0.68	1.1	SEQ ID NO: 451	EFTRPEEIIIFLR
1	0.45	0.73	1.2	SEQ ID NO: 452	IIFDITEGNLR
				SEQ ID NO: 453	
1	MERAAPSRVRPLPLLLGLALLAAGVDADVLLLEACCADG HRMATHQKDCSLPYATESKECRMVQEQCCHSQLEELHCA				

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A	2.5	50	97.5	Sequence ID No.	Sequence
81	GISLANEQDRCATPHGDNASLEATFVKRCCHCCLLGRAAQ AQGQSCEYSMLMGYQCGQVFRACCVKSQETGDLDVGGLQE				
161	TDKIIIEVEEEQEDPYLNDRCRGGGPKQQCRDTGDEVVC SCFVGYYQLSDGVSCEDVNECITGSHSCLRGESCINTVGSF				
241	RCQRDSSCGTGYELTEDNSCKDIDECESGIHNCLPDFICQ NTLGSFRCPKQLCKSGFIQDALGNCIDINECLISAPCP				
321	IGHTCINTEGSYTCQKNVPNCGRGYHLNEEGTRCVDVDE CAPPAEPCGKGHRCVNSPGSFRCECKTGYFFDGISRMCDV				
401	NECQRYPGRLCGHKCENTLGSYLCSCSVGFRLSVDGRSC EDINECSSSPCSQECANVYGSYQCYCRRGYQLSDVDGV				
481	DIDECALPTGGHICSYRCINIPGSFQCSCPSGGYRLAPNGR NCQDIDECVTGIHNCSINETCFNIQGGFRCLAFECPENY				
561	RRSAATLQQEKTDTVRCIKSCRPNVDTCVFDPVHTISHTV ISLPTFRETRPEEIIFLRAITPPHPASQANIIDITEGN				
641	LRDSFDIIKRYMDGMTVGVRQVRPIVGFHAVLKLEMN YVVGGVVSHRNVNVHIFVSEYWF				

5.39 serine (or cysteine) proteinase inhibitor, clade C (anti-thrombin), member 1
[Homo sapiens]
Protein Accession gi|4502261

Mean Expression Ratio 0.73

Median Expression Ratio 0.73

Credible Interval (0.529, 1.00)

Associated Peptides 5

Associated Spectra 5

Coverage 0.194

[0157]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.48	0.72	1.1	SEQ ID NO: 454	AFLEVNEEGSEAAASTAVVIAGR
1	0.49	0.74	1.1	SEQ ID NO: 455	EVPLNTIIFMGR
1	0.48	0.72	1.1	SEQ ID NO: 456	VAEGTQVLELPFK
1	0.49	0.72	1.1	SEQ ID NO: 457	ELTPEVLQEWLDELEEMMLVVHMPR
1	0.47	0.7	1.0	SEQ ID NO: 458	ATEDEGSEQIPEATNR
SEQ ID NO: 459					
1	MYSNVIGTVTSGKRKVYLLSLLIGFWDVCVTCHGSPVDICT AKPRDIPMNPICIYRSPEKKATEDEGSEQIPEATNRRV				
81	WELSKANSRFATTFYQHLADSKNDNDNIFLSPLSISTAFA MTKLGACNDTLQQLMEVFKFDITISEKTSQIHFFFAKLNC				
161	RLYRKANKSSKLVSANRLFGDKSLTFNETYQDISELVYG AKLQPLDFKENAEQSRRAINKWVSNKTEGRITDVIPSEAIN				
241	ELTVLVLVNTIYFKGLWKSKEFSPENTRKELFYKADGESCS ASMMYQEGKFRYRRAEAGTQVLELPFKGDDITMVILPKP				
321	EKSLAKVEKELTPEVLQEWLDELEEMMLVVHMPRFRIED GFSLKEQLQDMGLVDLFSPEKSKLPGIVAEGRDDLYVSDAF				
401	HKAFLEVNEEGSEAAASTAVVIAGRSINPNRVTFKANRPF LVFIREVPLNTIIFMGRVANPCVK				

5.40 hypothetical protein LOC148362 [*Homo sapiens*]
Protein Accession gil124244088
Mean Expression Ratio 1.37
Median Expression Ratio 1.37
Credible Interval (0.994, 1.92)
Associated Peptides 5
Associated Spectra 5
Coverage 0.141
[0158]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.92	1.4	2.0	SEQ ID NO: 460	LLELFTDLSCNPEMMK
1	0.94	1.4	2.1	SEQ ID NO: 461	NAADSYFSLQGFINSLDESTQESK
1	0.93	1.4	2.1	SEQ ID NO: 462	SLLQGFINSLDESTQESK
1	0.94	1.4	2.1	SEQ ID NO: 463	YIQNFK
1	0.92	1.4	2.1	SEQ ID NO: 464	IPTEAPQLELK
SEQ ID NO: 465					
1	MTHWFHRNPLKATAPVSPNYGVVTGPSASKICNDLRSSR ARLLELFTDLSCNPEMMKNAADSYFSLQGFINSLDESTQ				
81	ESKLRYIQNFKWTDTLQGQVPSAQQDAVFELISMGFNVAL WYTKYASRLAGKENITDEAKEVHRSLKIAAGIFKHLKES				
161	HLPKLITPAEKGRDLESRLIEAYVIQCQAEAEVTIARAIE LKHAPGLIAALAYETANFYQKADHTLSSLEPAYSARKWK				
241	YLHLKMCFYTAYAYCYHGETLLASDKCGEAIRSLQAEAK LYAKAEALCKEYGETKGPPTVKPSGHLFFRKLGNLVKNTL				
321	EKCQRENGFIYFQKIPTAPQLELKANYGLVEPIPFEPPT SVQWTPETLAAPDLTKRPKDDSTKPKPEEEVKPVKEPDI				
401	KPQKDTGCIYS				

5.41 ferritin, heavy polypeptide 1 [*Homo sapiens*]
Protein Accession gil56682959
Mean Expression Ratio 1.36
Median Expression Ratio 1.36
Credible Interval (1.12, 1.67)

Associated Peptides 9
Associated Spectra 21
Coverage 0.41
[0159]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	1.0	1.4	1.9	SEQ ID NO: 466	ELGDHVTNLR
1	1.1	1.5	2.1	SEQ ID NO: 467	GGRIFLQDIK
2	0.9	1.2	1.6	SEQ ID NO: 468	LCDFIETHYLNQVK
2	1.0	1.4	1.9	SEQ ID NO: 469	MGAPESGLAEYLFDK
3	1.1	1.5	1.9	SEQ ID NO: 470	NDPHLCDFIETHYLNQVK
5	1.1	1.4	1.9	SEQ ID NO: 471	NVNQSLLELHK
1	0.97	1.3	1.8	SEQ ID NO: 472	YFLHQSHOER

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A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.96	1.3	1.8	SEQ ID NO: 473	LCDFIETHY
3	1.0	1.4	1.9	SEQ ID NO: 474	IFLQDIK
				SEQ ID NO: 475	
1	MTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSY YFDRDDVALKNFAKYFLHQSHEREHAEKLMLQNQRGGR				
81	IFLQDIKKPCDDWESGLNAMECALHLEKNVNQSLLELHK LATDKNDPHLCDFIETHYLNQVKAIKELGDHVTNLRKMG				
161	APESGLAEYLFDKHTLGSDSDNES				

5.42 serum amyloid A1 preproprotein [*Homo sapiens*];
serum amyloid A1
preproprotein [*Homo sapiens*]
Protein Accession gi|40316912 gi|40316910

Mean Expression Ratio 0.738

Median Expression Ratio 0.737

Credible Interval (0.512, 1.06)
Associated Peptides 3
Associated Spectra 4
Coverage NaN
[0160]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.47	0.69	1.0	SEQ ID NO: 476	FFGHGAEDSLADQAANEWGR
1	0.48	0.73	1.1	SEQ ID NO: 477	SFFSFLGEAPDGAR
1	0.48	0.74	1.1	SEQ ID NO: 478	GPGGAWAAEVISDAR

5.43 programmed cell death 6 [*Homo sapiens*]
Protein Accession gi|7019485

Mean Expression Ratio 1.34
Median Expression Ratio 1.34
Credible Interval (1.02, 1.77)
Associated Peptides 4
Associated Spectra 10
Coverage 0.319
[0161]

A	2.5	50	97.5	Sequence ID No.	Sequence
4	0.99	1.3	1.8	SEQ ID NO: 479	LSDQFHDILIR
4	1.0	1.4	1.9	SEQ ID NO: 480	SGVISDTTELQQALSNGTWTPTFNPVTVR
1	0.99	1.4	2.1	SEQ ID NO: 481	YITDWQNVFR
1	0.93	1.3	2.0	SEQ ID NO: 482	AGVNFSEFTGVWK
				SEQ ID NO: 483	
1	MAAYSYPGPGAGPGPAAGALPDQSFLWNVFORVDKDR SGVISDTTELQQALSNGTWTPTFNPVTVRSIISMFDRENKAGV				
81	NFSEFTGVWKYITDWQNVFRTYDRDNSGMIDKNELKQAL SGFGYRLSDQFHDILIRKFPDRQGRGQIAFDQDFIQGCIVLQR				
161	LTDIFRRYDQDQGWIQVSYEQYLSMVFSIV				

5.44 complement component 1 inhibitor precursor [*Homo sapiens*]; complement component 1 inhibitor precursor [*Homo sapiens*]

Protein Accession gi|73858570 gi|73858568

Mean Expression Ratio 0.745

Median Expression Ratio 0.744

Credible Interval (0.58, 0.953)

Associated Peptides 8

Associated Spectra 12

Coverage NaN

[0162]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.5	0.69	0.93	SEQ ID NO: 484	GVTSVSQIFHSPDLAIR
2	0.55	0.77	1.1	SEQ ID NO: 485	KYPVAHFIDQTLK
1	0.52	0.74	1.0	SEQ ID NO: 486	LEDMEQALSPSVFK
1	0.52	0.75	1.0	SEQ ID NO: 487	LLDSLPSDTR
1	0.53	0.75	1.1	SEQ ID NO: 488	LVLLNAIYLSAK
1	0.52	0.74	1.1	SEQ ID NO: 489	QHQTVLELTETGVEAAAAAISVAR
2	0.53	0.73	1.0	SEQ ID NO: 490	QTVLELTETGVEAAAAAISVAR
1	0.53	0.76	1.1	SEQ ID NO: 491	DFTCVHQALK

5.45 chromatin modifying protein 5 [*Homo sapiens*]

Protein Accession gi|189409150

Associated Peptides 3

Mean Expression Ratio 1.34

Associated Spectra 3

Median Expression Ratio 1.34

Coverage NaN

Credible Interval (0.915, 2.00)

[0163]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.89	1.4	2.1	SEQ ID NO: 492	APPPSLTDCIGTVDSR
1	0.88	1.4	2.1	SEQ ID NO: 493	IDQIEDLQDQLEDMMEDANEIQEALSR
1	0.9	1.4	2.1	SEQ ID NO: 494	YKDQIK

5.46 vacuolar protein sorting factor 4B [*Homo sapiens*]

Protein Accession gi|17865802

Mean Expression Ratio 1.33

Median Expression Ratio 1.33

Credible Interval (0.961, 1.84)

Associated Peptides 4

Associated Spectra 5

Coverage 0.146

[0164]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.9	1.4	2.0	SEQ ID NO: 495	ENKPSIIFIDEIDSLCGSR
1	0.88	1.3	2.0	SEQ ID NO: 496	LLEPVVMSDMLR
2	0.94	1.4	2.0	SEQ ID NO: 497	LQNQLQGAIVIERPNVK
1	0.9	1.3	2	SEQ ID NO: 498	SLSNTKPTVNEHDLK
SEQ ID NO: 499					
1	MSSTSPNLQKAIDLASKAAQEDKAGNYEEALQLYQHAVQY FLHVVKYEAQGDKAKQSIRAKCTEYLDRAEKLKEYLKNKE				
81	KKAQKPVKEGQPSPADEKGNDSGEGESDDPEKKKLQNG LQGAIVIERPNVKWSDVAGLEGAKEALKEAVILPIKFPPLF				
161	TGKRTPWGILLFGPPGTGKSYLAKAVATEANNSTPFSIS SSDLVSKWLGESEKLVKNLFLQALARENKPSIIFIDEIDSLC				
241	GSRSENESEAARRIKTEFLVQMGGVVDNDGILVLGATNI PWVLDSAIRRRFEKRIYIPLPEPHARAAMFKLHGLTTQNS				
321	LTEADFRELGKRTDGYSGADISIIVRDALMQPVRKVQSAT HFKKVRGPSRADPNHLVDDLLTPCSPGDPGAIENTWMDVP				

5.47 prominin 1 [*Homo sapiens*]
Protein Accession gil5174387

Associated Peptides 9

Mean Expression Ratio 1.32

Associated Spectra 15

Median Expression Ratio 1.32

Coverage 0.158

Credible Interval (1.05, 1.66)

[0165]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	1.1	4	1.8	SEQ ID NO: 500	AFTDLNSINSVLGGGILDR
1	0.96	1.3	1.9	SEQ ID NO: 501	LLNEDWEYYLSGK
1	0.96	1.3	1.9	SEQ ID NO: 502	LTFEQVYSDCK
3	0.95	1.3	1.7	SEQ ID NO: 503	QLPPVDAELDNVNNVLR
1	0.96	1.3	1.9	SEQ ID NO: 504	SLHQQSTQLSSSLTSVK
3	1.0	1.4	1.9	SEQ ID NO: 505	TDLDGLVQQGYQSLNDIPDR
1	0.94	1.3	1.8	SEQ ID NO: 506	TLLNETPEQIK
1	0.92	1.3	1.8	SEQ ID NO: 507	VLPIEQSLSTLYQSVK
1	0.94	1.3	1.9	SEQ ID NO: 508	VNLNIFLLGAAGR
SEQ ID NO: 509					
1	MALVLGSLLLGLCGNSFSGGQPSSTDAPKAWNYELPATN YETQDSHKAGPIGILFELVHIFLVVQPRDFPEDTLRKFL				
81	QKAYESKIDYDKPETVILGLKIVYYEAGIILCCVLGLLFIIL MPLVGYYFCMCRCCKGCGEMHQKQKENGPFLLKCFAL				
161	SLLVICIIISIGIFYGFVANHQVRTRIKSRKLADSNFKDLR TLLNETPEQIKYILAQYNTTKDKAFTDLNSINSVLGGG				
241	ILDRLRPNIIPLVDEIKSMATAIKETKEALENMNSTLKS LHQQSTQLSSSLTSVKTSRSSLNDPLCLVHPSSETCNSIR				
321	LSLSQLNSNPRLQPPVDAELDNVNNVLRDLDGLVQQ GYQSLNDIPDRVQRQTTVVAGIKRVLNSIGSDIDNVQTQRL				

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A	2.5	50	97.5	Sequence ID No.	Sequence
401					PIQDILSAFSVYVNNTESYIHRNLPTLEEYDSYWWLGGV ICSLTLTIVIFYLGLLGCVCYDRHATPTTRGCVSNTGG
481					VFLMVGVGLSFLFCWILMIIVVLTFFVGANVEKLICEPYT SKELFRVLDTPYLLNEDWEYYSGLKFNKSKMKLTFEQVY
561					SDCKKNRGTYGTLHLQNSFNISEHLNINEHTGSISSELES KVNLNIFLLGAAGRKNLQDFAACGIDRMNYDSYLAQTGK
641					SPAGVNLLSFAYDLEAKANSLPPGNLNRSLKRDAQTIKTI HQQRVLPIEQSLSTLYQSVKILQRTGNGLLERVTRILASL
721					DFAQNFTTNNSSVIEETKKYGRTIIGYFEHYLQWIEFSIS EKVASCKPVATALDTAVDVFLCSYIIDPLNLFWFGIGK
801					ATVFLLPALIFAVKLAKYYRMRMSEDVYDDVETIPMKNM ENGNNGYHKDHVYGIHNPVMTSPSQH

5.48 alpha 3 type VI collagen isoform 1 precursor [*Homo sapiens*]

Protein Accession gil55743098

Mean Expression Ratio 0.756

Median Expression Ratio 0.757

Credible Interval (0.563, 1.02)

Associated Peptides 6

Associated Spectra 7

Coverage 0.0353

[0166]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.49	0.71	1.0	SEQ ID NO: 510	AAPLQGMPLGLLAPLR
1	0.51	0.75	1.1	SEQ ID NO: 511	GADQAELEIEIAFDSSLVFI PAEFR
1	0.5	0.73	1.1	SEQ ID NO: 512	GAQGPAGPAGPPGLIGEQQ ISGPR
1	0.51	0.75	1.1	SEQ ID NO: 513	ITEGVFQLLIVLTADR
1	0.51	0.75	1.1	SEQ ID NO: 514	LVDYLDVGFDTTR
2	0.56	0.8	1.1	SEQ ID NO: 515	MKPLDGSALYTGSAIDFVR

SEQ ID NO: 516

1	MRKHRHPLVAVVFLFLSGFPTTHAQQQQADVKNGAAADIIFL VDSSTWITIGEEHFQLVREFLYDVVKS LAVGENDPHFAL
81	VQFNGNPHTEFLNTYRTKQEVLSHISNMSYIGGTNQTKGKLE YIMQSHLTKAAGSRAGDGVQVIVVLT DGHSKDGLAL
161	PSAELKSADVNVFAIGVEDADEGALKEIASEPLNMHMFNLNF TSLHDIVGNLVS CVHSSVSPERAGDTETLKDITAQDS
241	ADIIFLDGSSNNTGSVNFVILDFLVNLEKLP IGTQQIRVGV VQFSDEPERTMFSLDYTSKAQVLGAVKALGFAGGELA
321	NIGLALDFVVENHFTRAGGSRVEEGVQVVLVISAGPSSDEIR YGVVALKQASVFSFGLGAQAASRAELQHIAITDDNLVF
401	TVPEFRSFGDLQEKLLPYIVGVQQRHIVLKPPTIVTQVIEVVK RDIVFLVDGSSALGLANFNFAIRDFIAKVIQRLEIGQD
481	LIQVAVAQYADTVRPEFYFNTHPTKREVI TAVRMKPLDGSAL YTGSAIDFVRNLF TSSAGYRAAEGIPKLLVLITGGK
561	SLDEISQPAQELKRSSIMAFI GNGADQAELEIEIAFDSSLVFI IPAEFRAAPLQGMPLGLLAPLR L TSGTPEVHSNKRDI
641	IFLLDGSANVGKTNFYPVVRDVMNLVNSLDIGNDIRVGLVQF SDTPVTEFSLNTYQTKSDILGHLRQLQLQGGSGLNTG
721	SALSYVYANHFTEAGGSRIREHVPQLLLLTAGQS EDSYLQAA NALTRAGILTF CVGASQANKAELEQIAFNPSLVYLM

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801	DFSSLPALPQQLIQPLTTYVSGGVEEVPLAQPESKRDILFLPD GSANLVGQFPVVRDFLYKIIDELNVKPEGTRIAVAQY
881	SDDVKVESRFDEHQSKPEILNLVKRMKIKTGKALNLGYALDYA QRYIFVKSGASRIEDGVLQFLVLLVAGRSSDRVDGPA
961	SNLKQSGVVPFIPOAKNADPAELEQIVLSPAFILAESLPKIG DLHPQIVNLLKSVHNGAPAPVSGEKDVVFLDGSSEGV
1041	RSGFPLLKEFVQRVVESLDVGQDRVRVAVVQYSDTRPEFYLN SYMKNQDVVNAVRQLTLLGGPTPTNTGALEFVLRNLI
1121	VSSAGSRITEGVPQLLIVLTADRSGDDVRNPVSVVVRKGAVPI GIGIGNADITEMQTI SFIPDFAVAIPTFRQLGTVOQV
1201	ISERVQLTREELSRLQPVLPPLSPGVGGKRDVVFLIDGSQS AGPEFYVRLIERLDYLDVGFDTTRVAVIQFSDDP
1281	KVEFLLNAHSSKDEVQNAVQRLRPKGRQINVGNALEYVSRNI FKRPLGSRIEEGVPQFLVLISSGKSDEVDPAVELK
1361	QFGVAPFTIARNADQEELVKISLSPPEYVFSVSTFRELSLEQK LLTPIITLTSEQIKLLASTRYPPPAVESDAADIVFL
1441	IDSSEGVPRDGFHIRDVFSRIVRRLNIGPSKVRVGVVQFSND VFPEFYLKTYRSQAPVLDAIRRLRLRGGSPLNTGKAL
1521	EFVARNLFVKSAGSRIEDGVPHLVVLGGKSQDDVSRFAQVI RSSGIVSLGVGDRNIDRTELQTI TNDPRLVFTVREFR
1601	ELPNIERIMNSFGPSAATPAPPGVDTPPPSRPEKKKADIVFL LDGSINFRDPSQEVLRFSVSEIVDTVYEDGDSIQVGL
1681	VQYNSDPTDEFFLKDFTSKRQIIDAINKVYKGRHANTKVGL EHLRVNHVFP EAGSRLDQRPQIAFVITGGKSVEDAQ
1761	DVSLALTQRGVKVFAVGVRNIDSEEVGKIASNSATAFRVGNVQ ELSELSEQVLETLHDAMHETLCPGVTDAAKACNLDDVI
1841	LGFDGSRDQNVFVAQKGFESKVDAILNRI SQMHRVSCSGGRSP TVRVSVVANTPSGPVEAFDFDEYQPEMLEKFRNMRSQ
1921	HPYVLTEDTLKVLNKFQSSPDSVKVVIHFTDGDADGLADLH RASENLRQEGVRALILVGLERVVNLERLMHLEFGRGF
2001	MYDRPLRLNLLDLDYELAEQLDNI AEKACCGVPCCKSGQRGDR GPIGSGPKGIPGEDGYRGYPGDEGGGGERGPPGVNG
2081	TQGFQGCPCGQGVKSGRGGFPEKGEVGEIGLDGLDGEDGDKGL PGSSGEKGNPGRGDKGPRGKGERGDVIRGDPGNP
2161	GQDSQERGPKEGTGDLGPMGVPGRDGVPGGPGETGKNGFGRR GPPGAKGNKGGPGQPFGEQEQTGRGAQGPAGPAGPPG
2241	LIGEQQISGPRGSGGAAGAPGERGRGTGPLRKGEPEGPGKGG IGNRGRGETGDDGRDGVGSEGRRGKGERGFPGYGP
2321	PKGNPGEPLNGTTGPKGIRGRNGSGPPGIVGQKGDPGYPGP AGPKGNRGDSIDQCALIQSIKDKCPCCYGLECPVFP
2401	TELAFALDTS EGVNQDTFGRMRDVVLSIVNDLTIAESNCPRGA RVAVVTYNNNEVTTEIRFADSKRKS VLLDKIKNLQVAL
2481	TSKQQSLETAMSFVARNTFKVRNGFLMRKAVVFSNTPTRAS PQLREAVLKLSDAGITPLFLTRQEDRQLINALQINNT
2561	AVGHALVLPAGRDLTDFLENVLTCHVCLDICNIDPSCGFGSWR PSFRDRRAAGSDVIDMAFILD SAETTTLPQFNEMKK
2641	YIAYLVRLQDMSDPKASQHFARVAVVQHPAESVDNASMPV KVEFSLTDYGSKEKLVDFLSRGMTQLQGTALGSAIE
2721	YTIENVFESAPNPRDLKIVVLMLTGVEVPEQQLEEAQRVILQAK CKGYFFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDK
2801	STELNEEPLMRFGRLLPFSVSSENAFYLSPDIRKQCDWFQGDQ PTKNLVKFGHKQVNVNPNVTSSPTSNPVTTTKPVTTT

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2881	KPVT	TTTTKPV	TTTTTKPV	TIINQPSVKPAAAKPAPAKPVAAKPV
	ATKMATVR	PPVAVK	PATAAKPVAAKPA	AVRPPAAAAA
2961	KPVATKPEV	PRPQAAKPAATK	PATTKPMVKMSREVQVFEITEN	
	SAKLHWERA	EPGPYPFYDLTV	TSAHDQSLVLKQNLTV	
3041	TDRVIGGLLAGQ	TYHVAVVCYLRSQVRATYHGSFSTKKSQPPP		
	PQPARSASSSTINLMV	STEPLALTETDICKLPKDEGT		
3121	CRDFILKWWYD	PNTKSCARFWYGGCGGNENKFGSQKECEKVCA		
	PVLAKPGVISV	MG		

5.49 actin, gamma 1 propeptide [*Homo sapiens*]; beta actin [*Homo sapiens*]
Protein Accession gil4501887 gil4501885

Mean Expression Ratio 1.31

Median Expression Ratio 1.31

Credible Interval (1.05, 1.67)

Associated Peptides 10

Associated Spectra 13

Coverage NaN

[0167]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.9	1.3	1.8	SEQ ID NO: 517	ANTVLSGGTTMYPGIADR	
1	0.95	1.4	1.9	SEQ ID NO: 518	DLYANTVLSGGTTMYPGIADR	
1	1	1.4	1.9	SEQ ID NO: 519	KDLYANTVLSGGTTMYPGIADR	
2	0.97	1.3	1.8	SEQ ID NO: 520	LCYVALDFEQEMATAASSSSL	EK
2	0.92	1.3	1.8	SEQ ID NO: 521	TTGIVMDSGDGVTHTVPIYEG	Y
1	0.95	1.3	1.9	SEQ ID NO: 522	TTGIVMDSGDGVTHTVPIYEG	YALPHAILR
1	0.93	1.3	1.8	SEQ ID NO: 523	TVLSGGTTMYPGIADR	
1	0.91	1.3	1.8	SEQ ID NO: 524	VALDFEQEMATAASSSSLEK	
1	0.98	1.4	2.0	SEQ ID NO: 525	VAPEEHPVLLTEAPLNPK	
2	0.97	1.3	1.8	SEQ ID NO: 526	YPIEHGIVTNWDDMEK	

5.50 solute carrier family 5 (sodium/glucose cotransporter), member 12 [*Homo sapiens*]
Protein Accession gil157671931

Mean Expression Ratio 0.762

Median Expression Ratio 0.764

Credible Interval (0.515, 1.12)

Associated Peptides 2

Associated Spectra 3

Coverage 0.0388

[0168]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.44	0.68	1	SEQ ID NO: 527	LHIFDFDVLPLR	
1	0.52	0.8	1.2	SEQ ID NO: 528	QGAESVLQNGLR	
SEQ ID NO: 529						
1	MEVKNFAVWDYVVFALFFISSGIGVFFAIKERKKATSREF					
	LVGGRQMSFGPVGSLTASFMSAVTVLGTPEVYRFGAS					
81	FLVFFIAYLFWILLTSELFLPVFYRSGITSTYEYLQLRFNK					
	PVRYAATVIYIVQITILYTGVVVYAPALALNQVTGFDLWG					
161	SVFATGIVCTFYCTLGGLKAVVWTDAPQMVMVIVGFLTVLI					
	QGSTHAGGFHNMLEQSTNGSRLHIFDFDVLPLRRHTFWT					
241	ITVGGTFTWLGIYGVNQSTIQRCISCKTEKHAKLALYFNLL					
	GLWIIILVCAVPSGLIMYSHFKDCDPWTSGIISAPDQLMP					
321	YFVMEIFATMPGLPGLFVACAFSGTLSTVASSINALATVTF					
	EDFVKSCFPHLSDKLSTWISKGLCLLFGVMCTSMAVAAS					
401	VMGGVVQASLSIHGMCGBPMLGLFSLGIVFPFVNWKGALGG					
	LLTGITLSFWVAIGAFIYPAPASKTWPLPLSTDQCICKSN					
481	VTATGPPVLSSRPGIADTWYISISLYYSAVGCLGCIVAGVI					
	ISLITGRQRGEDIQPLLRPVCNLCFWSSKKYKTLWCWG					
561	VQHDSGTEQENLENGSARKQGAESVLQNGLRRESLVHVPGY					
	DPKDKSYNNMAFETTHF					

5.51 vacuolar protein sorting 25 [*Homo sapiens*]
Protein Accession gil14150155

Mean Expression Ratio 1.31

Median Expression Ratio 1.30

Credible Interval (0.845, 2.04)

Associated Peptides 1

Associated Spectra 2

Coverage 0.0852

[0169]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.9	1.4	2.2	SEQ ID NO: 530	KLPVESIQIVLEELR	
SEQ ID NO: 531						
1	MAMSFEPWPQYRFPFFFTLQPNVDTRQKQLAAWCSLVLSF					
	CRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE					
81	LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQ					
	NNSVFTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEH					
161	KAEIITVSDGRGVKFF					

5.52 annexin A11 [*Homo sapiens*]; annexin A11 [*Homo sapiens*]; annexin A11 [*Homo sapiens*]

Protein Accession gi|4557317 gi|22165433 gi|22165431

Mean Expression Ratio 1.3

Median Expression Ratio 1.30

Credible Interval (0.93, 1.82)

Associated Peptides 4

Associated Spectra 5

Coverage NaN

[0170]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.88	1.3	2.0	SEQ ID NO: 532		AHLVAVFNEYQR
1	0.9	1.3	2	SEQ ID NO: 533		GFGTDEQAIIDCLGSR
1	0.9	1.3	2	SEQ ID NO: 534		GTITDAPGFDPLR
2	0.9	1.3	1.9	SEQ ID NO: 535		GVGTDEACLIEILASR

5.53 chromatin modifying protein 4B [*Homo sapiens*]

Protein Accession gi|28827795

Mean Expression Ratio 1.3

Median Expression Ratio 1.30

Credible Interval (0.882, 1.89)

Associated Peptides 3

Associated Spectra 3

Coverage 0.147

[0171]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.87	1.3	2.1	SEQ ID NO: 536		QLAQIDGTLSTIEFQR
1	0.85	1.3	2.0	SEQ ID NO: 537		KIEQELTAAK
1	0.87	1.3	2.1	SEQ ID NO: 538		KQEFLEK

SEQ ID NO: 539

1	MSVFGKLFAGGGKAGKGGPTPQEAIRLRDTEEMLSKKQ
	EFLEKKIEQELTAAKKHGTTNKRAALQALKRKKRYEKQLA
81	QIDGTLSTIEFQREALENANTNTEVLKNMGYAAKAMKAAH
	DNMDIDKVDELMDQDIADQQLAEIEISTAISKPVGFGEEFD
161	EDELMAELEEELEQEELDKNLLEISGPETVPLPNVPSIALP
	SKPAKKKEEEDDDMKELNENWAGSM

5.54 fatty acid binding protein 4, adipocyte [*Homo sapiens*]
Protein Accession gi|4557579

Mean Expression Ratio 0.769

Median Expression Ratio 0.771

Credible Interval (0.526, 1.12)

Associated Peptides 2

Associated Spectra 4

Coverage 0.242

[0172]

A	2.5	50	97.5	Sequence	ID No.	Sequence
3	0.49	0.73	1.1	SEQ ID NO: 540	NTEISFILGQEFDEVTTADR	
1	0.49	0.76	1.2	SEQ ID NO: 541	LVSSSENFDDYMK	

SEQ ID NO: 542

1	MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISV
	NGDVITIKSESTFKNTEISFILGQEFDEVTTADR
81	VKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVEECVMKGVTS
	TRVYERA

5.55 chloride intracellular channel 6 [*Homo sapiens*]
Protein Accession gi|27894378

Mean Expression Ratio 1.29

Median Expression Ratio 1.29

Credible Interval (0.8, 2.07)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0219

[0173]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.82	1.4	2.2	SEQ ID NO: 543	VGDGPQQEPGEDEER	

SEQ ID NO: 544

1	MAEAAEPEGVAPGPQGPPEVPAPLAERPGEPGAAGGEAEGP					
	EGSEGAEEAPRGAAAVKEAGGGGPDGPBAEARGTRGAH					
81	GETEAEEGAPEGAIEVPGGGEETSGAQVEGASPGRGAQGEPE					
	RGEAQREPEDSAAPERQEEAEQRPVPEGSASGEAGDSV					
161	DAEGPLGDNIEAEGPAGDSVEAEGRVGDSVDAEGPAGDSVD					
	AEGPLGDNIEAEGPAGDSVDAEGRVGDSVDAEGPAGDSV					
241	DAEGRVGDSVEAGDPAGDVEAGVPAGDSVEAEGPAGDSMD					
	AEGPAGRRRVSGEPQQSGDGLSPQAEAEIEVAAGESAG					
321	RSPGELAWDAEEAEVPGVKGSIEEAPGDARADAGEDRVGD					
	GPQQEPGEDEERRERSPEGPREEEAAAGGEEESPDSSPHG					
401	EASRGAAEPEAQLSNHLAEEGPAEGSGEAARVNGREDGEA					
	SEPRALGQEHDIITLFVKAGYDGESIGNCPFSQRLFMILW					
	LKGVIFNVTTVDLKRKPADLQNLAPGTNPPMTFDGEVKT					
	VNKIEEFLEEKLAAPPYPKLGTHPESNSAGNDVFAKFS					
561	AFIKNTKKDANEIHEKNLLKALRKLDNYLNSPLPDEIDAYS					
	TEDVTVSGRKFLDGDELTLADCNLLPKLHIKIVAKKYR					
641	DFEFPSEMTGIWRYLNNAYARDEFTNTCPADQEIHEYASDV					
	AKRMK					

5.56 proteasome alpha 3 subunit isoform 1 [*Homo sapiens*]; proteasome alpha 3 subunit isoform 2 [*Homo sapiens*]
Protein Accession gi|4506183 gi|23110939

Mean Expression Ratio 1.29

Median Expression Ratio 1.29

Credible Interval (0.844, 1.97)

Associated Peptides 2

Associated Spectra 2

Coverage NaN

[0174]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.85	1.4	2.2	SEQ ID NO: 545	HVGMAVAGLLADAR
1	0.82	1.3	2.1	SEQ ID NO: 546	AFELELSWVGELTNGR

5.57 gelsolin isoform a precursor [*Homo sapiens*]; gelsolin isoform b [*Homo sapiens*]; gelsolin isoform c [*Homo sapiens*]; gelsolin isoform c [*Homo sapiens*]; gelsolin isoform b [*Homo sapiens*]; gelsolin isoform b [*Homo sapiens*]; gelsolin isoform b [*Homo sapiens*]; gelsolin isoform b [*Homo sapiens*]

Protein Accession gi|4504165 gi|38044288 gi|89083782 gi|89083780 gi|89083778 gi|189083776 gi|189083774

Mean Expression Ratio 0.776

Median Expression Ratio 0.777

Credible Interval (0.57, 1.05)

Associated Peptides 5

Associated Spectra 6

Coverage NaN

[0175]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.56	0.8	1.2	SEQ ID NO: 547	AAQHGMDDDG TGQK
1	0.53	0.77	1.1	SEQ ID NO: 548	AQPVQVAEGSEPDGFWEALG GK
1	0.53	0.78	1.1	SEQ ID NO: 549	DSQEEKTEALTS AK
1	0.49	0.73	1.1	SEQ ID NO: 550	NWQGAQSTQDEVAASAILTA QLDEELGGTPVQSR
1	0.52	0.77	1.1	SEQ ID NO: 551	TAQLDEELGGTPVQSR

5.58 vacuolar protein sorting 37B [*Homo sapiens*]
Protein Accession gi|13375926

Mean Expression Ratio 1.29

Median Expression Ratio 1.28

Credible Interval (0.848, 1.94)

Associated Peptides 1

Associated Spectra 3

Coverage 0.0912

[0176]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.	93	1.4	2.0	SEQ ID NO: 552 LPELAPTAPLPYPAPPEASG PPAVAPR
SEQ ID NO: 553					
1	MAGAGSEARFAGLSLVQLNELLEDEGQLTEMVQKMEETQNVQLN KEMTLASNRS LAEGNLLYQPQLDTLKARLTQKYQEL				
81	QVLPEAYQIKKTKLDRQSSSASLETLLALLQAEGAKIEEDTENM AEKFLDGELPLDSFIDVYQSKRKLAHMRRVKIEKLQ				
161	EMVLKGQRLPQALAPLPRLPELAPTAPLPYPAPPEASGPPAVAP RRIPPPPPVPAGRLATPPTAAMSSGQAVPYPLGQC				
241	PPLPPRVGLPTQQGFSSQFVSPYPPPLPQRPPRLPPHQPGFIL Q				

5.59 programmed cell death 6 interacting protein [*Homo sapiens*]
Protein Accession gi|22027538

Mean Expression Ratio 1.28

Median Expression Ratio 1.28

Credible Interval (1.05, 1.57)

Associated Peptides 12

Associated Spectra 20

Coverage 0.192

[0177]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	1	1.3	1.8	SEQ ID NO: 554	EPSAPSIPTPAYQSSPAGGH APTPPTAPR
1	0.9	1.3	1.7	SEQ ID NO: 555	FIQQTYPSGGEEQAQYCR
3	1	1.3	1.8	SEQ ID NO: 556	FLTLAQDQGVINEEALS VTE LDR
2	0.97	1.3	1.8	SEQ ID NO: 557	FYNELTEILVR
1	0.92	1.3	1.7	SEQ ID NO: 558	HEGALETLLR
2	0.93	1.3	1.7	SEQ ID NO: 559	LQHA AELIK
1	0.93	1.3	1.8	SEQ ID NO: 560	NIQVSHQEFSK
3	0.98	1.3	1.7	SEQ ID NO: 561	NLATAYDNFVELVANLK
2	0.97	1.3	1.8	SEQ ID NO: 562	SVIEQGGIQTVDQLIK
1	0.88	1.2	1.7	SEQ ID NO: 563	FTDLFEK
1	0.95	1.3	1.8	SEQ ID NO: 564	KQEGLLK
1	0.91	1.3	1.7	SEQ ID NO: 565	YDEYVNVK
SEQ ID NO: 566					
1	MATFISVQLKKTSEVDLAKPLVKFIQQTYPSGGEEQAQYCRAA EELSKLRRRAVGRPLDKHEGALETLLRYDQICSTIEP				

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81	KFPFSENQICLTFTWKDAFDKGSFLGGSVKLALASLGYEKSCV
	LFNCAALASQIAAEQNLDNDEGLKIAAKHYQFASGAF
161	LHIKETVLSALSREPTVDISPDTVGTLSLIMLAQAQEVFFLKA
	TRDKMKDAIIAKLANQAADYFGDAFKQCQYKDTLPKE
241	VFPVLAAKHCIMQANAETHQSILAKQKKFGEEIARLQHAAEL
	IKTVASRYDEYVNVKDFSDKINRALAAAKDNDFIYH
321	DRVPDLKDLDPIGKATLVKSTPVNVPISQKFTDLFEKMPVSV
	QOSLAAYNQRKADLVNRSIAQMREATTLANGVSLASN
401	LPAAIEDVSGDTPQSIILTKSRSVIEQGGIQTVDQLIKELPEL
	LQRNREILDESRLRLDDEEATDNDLRKFKERWQRTTP
481	SNELYKPLRAEGTNFRTVLDKAVQADGQVKECYQSHRDTIVLL
	CKPEPELNAAIPSANPAKTMQGSSEVVNVLSLNLND
561	EVKKEREGLENDLKSVMFDMTSKFLTLAQDGVINEEALSUTE
	LDRVYGGITTKVQESLKKQEGLLKNIQVSHQEFSEKMK
641	QSNNEANLREEVLKNLATAYDNFVELVANLKEGTFKYNELTEI
	LVRFPQNKCSDIVFARKTERDELLKDLQSSIAREPSAP
721	SIPTPAYQSSPAGGHAPTPTPAPRTMPPTKQPPARPPPPVL
	PANRAPSATAPSPVGAGTAAPAPSQTGPSAPPPQAQG
801	PPYPTYPGYPGYCQMPMPMGYNPYAYGQYNMPPYPVYHQSPGQ
	APYPGPQQPSYPFPQPPQSSYYPQQ

5.60 prosaposin isoform a preproprotein [*Homo sapiens*]

Protein Accession gi11386147

Mean Expression Ratio 0.78

Median Expression Ratio 0.78

Credible Interval (0.587, 1.04)

Associated Peptides 5

Associated Spectra 8

Coverage 0.0954

[0178]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.51	0.72	1.0	SEQ ID NO: 567	EIVDSYLPVILDIK
1	0.55	0.8	1.2	SEQ ID NO: 568	GCSFLPDYPYQK
1	0.55	0.79	1.1	SEQ ID NO: 569	LVGYLDR
3	0.55	0.77	1.1	SEQ ID NO: 570	QEILAALEK
1	0.54	0.78	1.1	SEQ ID NO: 571	SLPCDICK
SEQ ID NO: 572					
1	MYALFLLASLLGAALAGPVLGLKECTRGSAVWCQNVKTASD				
	CGAVKHCLQTVMNKPTVKSFLPCDICKDVVTAAGDMLKDN				
81	ATEEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI				
	KGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIP				
161	ELDMTEVVAPFMANIPLLLYPQDGPGRSKPQPKDNGDVQCDC				
	IQMVTDIQTAVRTNSTFVQALVEHVKEECRLGPGMADI				
241	CKNYISQYSEIAIQMMHMQPKEICLVGFCDEVKEMPMQT				
	LVPKAVASKNVIPALELVEPIKKHEVPAKSDVYCEVCEF				
321	LVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSEECQEVV				
	DTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVMH				
401	TQPKDGGFCEVCKLVGYLDRNLEKNSTKQEI LAALEKGCS				
	FLPDYPYQKQCDQFVAEYEPVLI EILVEVMDPSFVCLKIG				
481	ACPSAHKPLLGETKCIWGPSYWCQNTETAAQCNAVEHCKRH				
	VWN				

5.61 ferritin, light polypeptide [*Homo sapiens*]

Protein Accession gi20149498

Mean Expression Ratio 1.28

Median Expression Ratio 1.28

Credible Interval (1.11, 1.47)

Associated Peptides 16

Associated Spectra 66

Coverage 0.634

[0179]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.97	1.3	1.7	SEQ ID NO: 573	AAMALEK
5	1.0	1.3	1.7	SEQ ID NO: 574	ALFQDIK
3	0.98	1.3	1.7	SEQ ID NO: 575	DDVALEGVSHFFR
3	0.93	1.2	1.6	SEQ ID NO: 576	DLHALGSAR
1	0.96	1.3	1.7	SEQ ID NO: 577	PDRDDVALEGVSHFFR
1	0.98	1.3	1.8	SEQ ID NO: 578	KLNQALLDLHALGSAR
3	1.0	1.3	1.7	SEQ ID NO: 579	KPAEDEWGK
4	0.92	1.2	1.5	SEQ ID NO: 580	LCDFLETHFLDEEVK
12	0.93	1.1	1.4	SEQ ID NO: 581	LGGPEAGLGEYLFER
1	1.0	1.4	1.9	SEQ ID NO: 582	LGGPEAGLGEYLFERLTLK
2	1.1	1.5	2.0	SEQ ID NO: 583	LGGPEAGLGEYLFERLTLK
					HD
12	1	1.2	1.5	SEQ ID NO: 584	LNQALLDLHALGSAR
1	0.96	1.3	1.7	SEQ ID NO: 585	MGDHLTNLHR
1	0.85	1.1	1.5	SEQ ID NO: 586	QALLDLHALGSAR
15	1.1	1.4	1.7	SEQ ID NO: 587	TDPHLCDFLETHFLDEEVK
1	0.96	1.3	1.7	SEQ ID NO: 588	ELAEK
SEQ ID NO: 589					
1	MSSQIRQNYSTDVEAAVNSLVNLYLQASYTSLGIFYFDRDDVAL				
	EGVSHFFRELAEKREGYERLLKMQRGRALFQ				
81	DIKKPAEDEWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPH				
	LCDFLETHFLDEEVKLIKMGDHLTNLHRLGGPEA				
161	GLGEYLFERLTLKHD				

5.62 galectin 3 binding protein [*Homo sapiens*]

Protein Accession gi15031863

Mean Expression Ratio 1.28

Median Expression Ratio 1.28

Credible Interval (1.11, 1.48)

Associated Peptides 19

Associated Spectra 57

Coverage 0.369

[0180]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	1.0	1.3	1.8	SEQ ID NO: 590	AAFQGSGPIMLDEVQCTGT
					EASLADCK
2	0.93	1.2	1.6	SEQ ID NO: 591	ALMLCEGLFVADVTDFEGWK
3	1.0	1.3	1.7	SEQ ID NO: 592	ASHEEVEGLVEK
15	1.0	1.2	1.5	SEQ ID NO: 593	ELSEALGQIFDSQR
8	0.96	1.2	1.5	SEQ ID NO: 594	GQWGTVCNLDLWDLTASVVC
					R

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1	0.95	1.3	1.7	SEQ	ID NO:	595	IDITLSSVK
1	0.92	1.2	1.7	SEQ	ID NO:	596	IYTSPTWSAFVTDSSWSAR
1	0.95	1.3	1.7	SEQ	ID NO:	597	QSFQTPQHPSFL
3	1.0	1.3	1.8	SEQ	ID NO:	598	QSFQTPQHPSFLFQDK
3	1	1.3	1.7	SEQ	ID NO:	599	QTPQHPSFLFQDK
1	0.94	1.3	1.7	SEQ	ID NO:	600	RIDITLSSVK
2	0.96	1.3	1.7	SEQ	ID NO:	601	SDLAVPSELALLK
6	1.2	1.5	1.9	SEQ	ID NO:	602	STSSFPCPAGHFNGFR
1	0.97	1.3	1.8	SEQ	ID NO:	603	TIAYENK
1	0.97	1.3	1.7	SEQ	ID NO:	604	TLQALEFHTVPF
1	0.92	1.3	1.7	SEQ	ID NO:	605	VADVTFEGWK
2	0.92	1.2	1.6	SEQ	ID NO:	606	WSHEALFQK
2	0.9	1.2	1.6	SEQ	ID NO:	607	YSSDYFQAPSDYR
1	0.96	1.3	1.8	SEQ	ID NO:	608	VEIFYR

SEQ	ID NO:	609
1	MTPPRLFWVWLLVAGTQGVNDGDMRLADGGATNQGRVEIFYRGQW	
	GTVCNDNLWDLTDAVVCRAFGFENATQALGRAAFG	
81	QSGGPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVCTN	
	ETRSTHTLDSLRELSALGQIFDSQRCGLSISVN	
161	VQGEDALGFCHTILTANLEAQLWKEPGSNVMTMSVDAECVPMV	
	RDLLRYFYRRIDITLSSVKCFHKLASAYGARQLQ	
241	GYCASLFAILLPQDPSPQMPLDLAYAVATGDALLEKLCLQFLAW	
	NFEALTQAEAWPSVPTDLLQLLLPRSDLAVPSELA	
321	LLKAVDTSWGERASHEEVEGLVEKIRFPMMLPEELFELQFNLSL	
	YWSHEALFQKKTLQALEFHTVPFQLLARYKGLNLT	
401	EDTYKPRIYTSPTWSAFVTDSSWSARKSQLVYQSRRGLPKVYSSD	
	YFQAPSDYRYYPYQSFQTPQHPSFLFQDKRVSWSL	
481	VYLPITIQSCWNYGFSCSSDELPLVGLTKSGGSDRTIAYENKALML	
	CEGLFVADVTDPEGWKAAPALDTNSSKSTSSFP	
561	CPAGHFNGFRTVIRPFYLTNSSGVD	

5.63 peptidoglycan recognition protein 1 [*Homo sapiens*]
Protein Accession gi|4827036

Mean Expression Ratio 0.784

Median Expression Ratio 0.786

Credible Interval (0.55, 1.12)

Associated Peptides 3

Associated Spectra 4

Coverage 0.276

[0181]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.51	0.77	1.2	SEQ	ID NO:	610 AAQGLLACGVAQGALR
2	0.52	0.76	1.1	SEQ	ID NO:	611 ALASECAQHLSLPLR
1	0.51	0.77	1.2	SEQ	ID NO:	612 TLGWCDVGYNFLIGEDGLVY EGR

SEQ	ID NO:	613
1	MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALAS	
	ECAQHLSLPLRYVVVSHTAGSSCNTPASCCQQARNV	
81	QHYHMKTLGWCDVGYNFLIGEDGLVYEGRWNFTHAGSHGLWNP	
	MSIGISFMGNMDRVPTPQAIRAAQGLLACGVAQGA	
161	LRSNYVLKGRDVRQRTLSPGNQLYHLIQNWPHYRSP	

5.64 ubiquitin and ribosomal protein S27a precursor [*Homo sapiens*]; ubiquitin and ribosomal protein S27a precursor [*Homo sapiens*]
Protein Accession gi|4506713 gi|208022622

Mean Expression Ratio 1.27

Median Expression Ratio 1.27

Credible Interval (0.99, 1.64)

Associated Peptides 5

Associated Spectra 12

Coverage NaN

[0182]

A	2.5	50	97.5	Sequence	ID No.	Sequence
3	0.95	1.3	1.8	SEQ	ID NO:	614 ESTLHLVLR
4	1.0	1.4	1.8	SEQ	ID NO:	615 TITLEVEPSDTIENVK
1	0.9	1.3	1.9	SEQ	ID NO:	616 TLSDDYNIQK
1	0.9	1.3	1.8	SEQ	ID NO:	617 LIFAGK
3	0.89	1.2	1.7	SEQ	ID NO:	618 MQIFVK

5.65 complement component 4A preproprotein [*Homo sapiens*]
Protein Accession gi|67190748

Mean Expression Ratio 0.787

Median Expression Ratio 0.786

Credible Interval (0.511, 1.21)

Associated Peptides 1

Associated Spectra 2

Coverage 0.0115

[0183]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.48	0.74	1.2	SEQ	ID NO:	619 LLSQQQADGSFQDPCPVLDLR

SEQ	ID NO:	620
1	MRLWGLIWASSFFTLTLQKPRLLLFSPSVVHLGVPLSGVGQL	
	QDVPRGQVVKGSVFLRNPSSNNVPCPKVDFTLSSER	
81	DFALLSLQVPLKDAKSCGLHQLLRGPEVQLVAHSPWLKDSLRS	
	TTNIQGINLLFSSRRGHLFLQTDQPIYNPQVRVRYR	
161	FALDQKMRPSTDTITVMVENSGLVRKKEVYMPSSIFQDDFV	
	IPDISEPGTWKISARFSDGLESNSSTQFEVKKYVLPN	
241	FEVKITPGKPYILTVPGHLEMDQLDIQARYIYGKPVQGVAYVR	
	FGLLDEDDGKKTFFRGLESQTKLVNGQSHISLSKAEPQ	
321	DALEKLNMGITDLQGLRLYVAAAIIESPGGEMEEAELTSWYFV	
	SSPFSLDLSKTKRHLVPGAPFLQLALVREMSGSPASG	
401	IPVKVSATVSSPGSVPEVDIQNTDGGSGQVSPPIIIPQTISE	
	LQLSVSAGSPHPAIALRTVAAPPSSGGPGFSLIERPDS	
481	RPPRVGDTLNLNLRVAVGSGATFHHYMYILSRQIVFMNREP	
	RTLTLSVSVFVDHHLAPSFYFVAFYHGDHPVANSRLV	

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561	DVQAGACEGKLELSVDGAKQYRNGESVKLHLETDLSLALVALGA
	LDTALYAAGSKSHKPLNMGKVFAMNSYDLGCGPGGG
641	DSALQVFQAAGLAFSDGDQWTLSRKRLSCPKEKTRKKRNVNF
	QKAINKLGQYASPTAKRCCQDGVTRLPMMSCEQRA
721	ARVQQPDCREPFSLSCQFAESLRKKSRLDKQAGLQRALEILQE
	EDLIDEDDIPVRSFFPENWLWRVETVDRFQILTLWL
801	DSLTTWEIHGSLSKTKGLCVATPVQLRVFREFHLHLRLPMSV
	RRFEQLRLRPVLYNYLDKNLTVSVHVSPEVGLCLAGG
881	GGLAQQVLVPAGSARPVAFSVVPTAAAVSLKVARGSPFEPV
	GDAVSKVLQIEKEGAIHREELVYELNPLDHRGRTLEI
961	PGNSDPNMI PDGDFNSYVRVTASDPLDTLGSEGLSPGCVASL
	LRLPRGCGEQMTIYLAPTLLAASRYLDKTEQWSTLPPE
1041	TKDHAVDLIQKGYMRIQQFRKADGSYAAWLSRDSSTWLTAFVL
	KVLSLAQEQVGGSPKQLQETSNWLLSQQADGSFQDP
1121	CPVLDRSMQGLVGNDETVALTAFVTIALHHGLAVFQDEGAEP
	LKQRVEASISKANSFLGEKASAGLLGAHAAITAYAL
1201	TLTKAPVDLLGVAHNNLMAMAQETGDNLYWGSVTGSQNAVSP
	TPAPRNPSPMPQAPALWIETTAYALLHLLHEGKAE
1281	MADQASAWLTRQGSFQGGFRSTQDVTIALDALSAWIASHTE
	ERGLNVTLSSTGRNGFKSHALQLNNRQIRGLEEELQF
1361	SLGSKINVKVGNSKGTLLKVLRTYNVLDKNTTCQDLQIEVTV
	KGHVEYTMEDYEDYEDYELPAKDDPDAPLPQVPTP
1441	LQLEFGRNRNRREAPKVVEEQESRVHYTVC IWRNGKVGLSGM
	AIADVTLLSGFHALRADLEKLTSLSDRYVSHFETEGP
1521	HVLLYFDSVPTSRCEVGFQAVQEVVGLVQPASATLYDYNNPE
	RRCSVFYGAQSKRLATLCSAEVCQCAEGKCPQROR
1601	ALERGLQDEDDGYRMKFCYYPVEYGFQVKVLRDSRAAFRLF
	ETKITQVLHFTKDVKAAANQMRNFLVRASCLRLLEPG
1681	KEYLIMGLDGATYDLEGHPQYLLDSNSWIEMPSERLCRSTRQ
	RAACAQLNDFLQYGTQGCQV

5.66 hypothetical protein LOC169693 [*Homo sapiens*]

Protein Accession gil23397518

Mean Expression Ratio 0.788

Median Expression Ratio 0.788

Credible Interval (0.572, 1.07)

Associated Peptides 3

Associated Spectra 8

Coverage 0.282

[0184]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
6	0.56	0.75	1	SEQ ID NO: 621	ESIAGLVVTAISEDAQR		
1	0.52	0.77	1.1	SEQ ID NO: 622	QHLAHGALPVATVDRPDF		YPPAYEESLEVEK
1	0.53	0.8	1.2	SEQ ID NO: 623	QHLAHGALPVATVDRPDF		
SEQ ID NO: 624							
1	MQNRTGLILCALALLMGLFMVCLGAFFISWGSIFDCQGSGLIAA						
	YLLLPLGFVILLSGIFWSNYRQVTESKGVLRHMLRQH						
81	LAHGALPVATVDRPDFYPPAYEESLEVEKQSCPAEREASGIPP						
	PLYTETGLFQDGNDSHPEAPPSYRESIAGLVVTAIS						
161	EDAQRGGQEC						

5.67 nidogen 1 precursor [*Homo sapiens*]

Protein Accession gil115298674

Mean Expression Ratio 0.79

Median Expression Ratio 0.788

Credible Interval (0.513, 1.22)

Associated Peptides 1

Associated Spectra 2

Coverage 0.0217

[0185]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
2	0.48	0.75	1.2	SEQ ID NO: 625	GPGQGDLEEDGDDFVS-		PALE
							LSGALR
SEQ ID NO: 626							
1	MLASSSRIRAAWTRALLPLLLAGPVGCLSRQELFPFGPGQGD						
	ELEDGDDFVSPAELSGALRFYDRSDIDAVYVTTNG						
81	IIATSEPPAKESHPLFPPTFGAVAPFLADLDTDGLGKVYYRE						
	DLSPSITQRAAECVHRGFPEISFPQSSAVVVTWESV						
161	APYQGPRSDPDQKGRNTFQAVLASDSSSYAIFLYPEDGLQFH						
	TTFSKKENNQVPAVVAFSQGSVGFGLWKSNGAYNIFA						
241	NDRESVENLAKSSNSGQGVVWFPEIGSPATNGVVPADVILGTE						
	DGAEYDDEDEDYDLATRLGLEEDVGTTPFSYKALRR						
321	GGADTVSVPSVLSPPRAATERPLGPPTERTRSFQLAVETFHQH						
	PQVIDVDEVEETGVVFSYNTDSRQTCANNRHQCSVH						
401	AECRDYATGFCCSCVAGYTNGRQCVAEGSPQRVNGKVKGRI FV						
	GSSQVPIVFENTDLHSYVVMNHGRSYTAISTIPETV						
481	GYSLLPLAPVGGIIGWMFAVEQDGFKNFISITGGEFTRQAEVTF						
	VGHPGNLVIKQRFSGIDEHGHLTIDTELEGRVPQIP						
561	FGSSVHIEPYTELYHYSTSVITSSSTREYTVTEPERDGASPSRI						
	YTYQWRQTITFQECVHDDSRPALPSTQQLSVDSVFV						
641	LYNQEEKILRYALSNSIGPVREGSPDALQNP CYI GTHGCDTNA						
	CRPGPRTQFTCECSIGFRGDGRTCYDIDECSEQSV						
721	CGSHTICNNHPGTFRCCEVGYQFSDEGTCAVAVDQRPINYCET						
	GLHNCIDIPQRAQCIYTGSSSYTCSCLPGFSGDQAC						
801	QDVDECQPSRCHPDACYNTPGFTQCCKPGYQGDGFRCPVGEV						
	EKTRCQHEREHILGAAGATDPQRP I PPGLFVPECD						
881	HGHYAPTQCHGSTGYCWCVDGRDREVEGTRTRPGMTTPCLSTVA						
	PPIHGGPAVPTAVIPLPPGTHLLFAQTGKIERLPLE						
961	GNTMRKTEAKAFHLVPAKVII GLAFCDVKMVYWTIDITEPSIGR						
	ASLHGGEPTTII RQDLGSGPEGIAVDHLGRNI FWTDS						
1041	NLDRIEVAKLDGTQRRVLFETDLVNPRGIVTDSVRGNLYWTDWN						
	RDNPKIETSYMDGTNRRILVQDDLGLPNGLTFDAFS						
1121	SQLCWVDAGTNRAECLNPSQPSRRKALEGLQYFPAVTSYGNLY						
	FTDWKMNSVVALDLAISKETDAFQPHKQTRLYGITT						
1201	ALSQCQPQGHNYCSVNNGGCTHCLATPGSRTCRCPDNTLGVDCI						
	EQK						

5.68 CD9 antigen [*Homo sapiens*]

Protein Accession gil4502693

Mean Expression Ratio 1.27

Median Expression Ratio 1.27

Credible Interval (0.856, 1.88)

Associated Peptides 2

Associated Spectra 3

Coverage 0.0921

[0186]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.91	1.4	2.1	SEQ ID NO: 627		EVQEFYK
1	0.8	1.2	2.0	SEQ ID NO: 628		AGGVEQFISDICPK
SEQ ID NO: 629						
1	MPVKGGTKCIKYLFGFNFIWLAGIAVLAIGLWLRFDST					
	KSIFEQETNNNSSFYTGYYLIGAGALMMLVGLGCCG					
81	AVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDEVIKEV					
	QEFYKDTYNKLTKDEPQRETLKAIHYALNCCGLAGGVE					
161	QFISDICPKKDVLETFVTKSCPDAIKEVFDNKFHIGAVGI					
	GIAVVMIFGMIFSMILCCAIRNRNEMV					

5.69 solute carrier family 5 (sodium/glucose cotransporter), member 10 isoform 2 [Homo sapiens]

Protein Accession gil109659836

Mean Expression Ratio 0.79

Median Expression Ratio 0.79

Credible Interval (0.519, 1.22)

Associated Peptides 2

Associated Spectra 2

Coverage 0.047

[0187]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.47	0.76	1.2	SEQ ID NO: 630		ALFPDDVGCVPSECLR
1	0.48	0.78	1.2	SEQ ID NO: 631		LVMEMLPIGLR
SEQ ID NO: 632						
1	MAANSTSDLHTPGTQLSVADIIVITVYFALNVAVGWSSCR					
	ASRNTVNGYFLAGRDMTWPIGASLFASSEGSGLFIGLA					
81	GSGAAGGLAVAGFEWNATYVLLALAWVFVPIYISSEIVTLP					
	EYIQKRYGGQRIRMYLSVLSLLSVFTKISLDLYAGALF					
161	VHICLGWNFYLSITLITLGITALYTIAGGLAAVIYTDALQTL					
	IMVVGAVILTIKAFDQIGGYGQLEAAYAQAIPSRTIANT					
241	TCHLPRTDAMHMFDPHTGDLPTWGTGFTGLTIMATWYWC					
	QVIVQRSLSARDLNHAKAGSILASYLKMLPMGLIIMPGM					
321	ISRALFPDDVGCVPSECLRACGAEVGCSNIAYPKLVMELM					
	PIGLRGLMIAVMLAALMSSLTSIFNSSSTLFTMDIWRRL					
401	RPRSGERELLLVGRVLIVALIGVSVAWIPVLQDSNSGQLFI					
	YMQSVTSSLAPPVTAVFVLGVFWRRANEQGAFWGLIAGL					
481	VVGATRLVLEFLNPAPPCGEPDTRPAVLGSIHYLHFAVALF					
	ALSGAVVAGSLLTPPPQSVQIENLTWWTLAQDVPLGTK					
561	AGDGQTPQKHAFWARVCGFNAILLMCVNIFYAYFA					

5.70 sorting nexin 18 isoform a [Homo sapiens]; sorting nexin 18 isoform b 30 [Homo sapiens]

Protein Accession gi 157057545 gi 157057543

Mean Expression Ratio 1.26

Median Expression Ratio 1.26

Credible Interval (0.82, 1.91)

Associated Peptides 2

Associated Spectra 2

Coverage NaN

[0188]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.86	1.4	2.2	SEQ ID NO: 633		APEPGPAGDGGPGAPAR
1	0.78	1.2	2.0	SEQ ID NO: 634		LVPHTHTQVPVHR

5.71 syntenin isoform 1 [Homo sapiens]; syntenin isoform 1 [Homo sapiens]

Protein Accession gi156243522 gi155749490

Mean Expression Ratio 1.26

Median Expression Ratio 1.26

Credible Interval (0.87, 1.83)

Associated Peptides 2

Associated Spectra 4

Coverage NaN

[0189]

A	2.5	50	97.5	Sequence	ID No.	Sequence
3	0.94	1.4	2.0	SEQ ID NO: 635		ANVAVVSGAPLQGQLVAR
1	0.82	1.2	1.9	SEQ ID NO: 636		VAVVSGAPLQGQLVAR

5.72 glutamyl aminopeptidase (aminopeptidase A) [Homo sapiens]

Protein Accession gi132814467

Mean Expression Ratio 0.795

Median Expression Ratio 0.794

Credible Interval (0.682, 0.932)

Associated Peptides 25

Associated Spectra 39

Coverage 0.268

[0190]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
1	0.6	0.8	1.1	SEQ ID NO: 637	AQLLDYK		
1	0.58	0.78	1.1	SEQ ID NO: 638	ASLIDDAFALAR		
2	0.62	0.81	1.1	SEQ ID NO: 639	AVHQFDSVK		
1	0.63	0.84	1.1	SEQ ID NO: 640	EESVDDKWTR		
1	0.6	0.8	1.1	SEQ ID NO: 641	ETNLLYDPK		
1	0.61	0.83	1.1	SEQ ID NO: 642	EYGALSNMPVAK		
4	0.65	0.84	1.1	SEQ ID NO: 643	IAIPDFGTGAMENWGLI TYR		
6	0.6	0.76	0.98	SEQ ID NO: 644	INPDHIGFYR		
1	0.59	0.8	1.1	SEQ ID NO: 645	KSFPFCFDEPNKK		
1	0.59	0.8	1.1	SEQ ID NO: 646	LLYGLASVK		
1	0.58	0.79	1.1	SEQ ID NO: 647	LPDFVNPVHY		
1	0.57	0.77	1.0	SEQ ID NO: 648	NMAWNWQLNWDYLVNR		
1	0.58	0.79	1.1	SEQ ID NO: 649	NNIEWLK		
1	0.61	0.83	1.1	SEQ ID NO: 650	QMGYPVLNVNGVK		
1	0.57	0.77	1.1	SEQ ID NO: 651	SFPCFDEPNKK		
1	0.56	0.75	1.0	SEQ ID NO: 652	SIVATDHEPTDAR		
1	0.57	0.78	1.0	SEQ ID NO: 653	SSHPIIVTTPDEITS VFDGISY		
3	0.57	0.75	0.99	SEQ ID NO: 654	TSDFWAALEEASR		
1	0.61	0.82	1.1	SEQ ID NO: 655	TSDFWAALEEASRLPVK		
2	0.62	0.82	1.1	SEQ ID NO: 656	YLVWLHLR		
3	0.58	0.77	1.0	SEQ ID NO: 657	YPQAGAGEKPR		
1	0.58	0.8	1.1	SEQ ID NO: 658	MLEDWIKPENFQK		
1	0.58	0.78	1.1	SEQ ID NO: 659	IQLNWDYLVNR		
1	0.57	0.77	1.0	SEQ ID NO: 660	YLDLLK		
1	0.58	0.78	1.1	SEQ ID NO: 661	QMESFFAK		
SEQ ID NO: 662							
1				MNFAEREGSKRYCIQTKHVAILCAVVVGVLIVGLAVGLTRSCD			
				SSGDGGPGTAPAPSHLPSSSTASPSGPPAQDQDICA			
81				SEDESGQWKNFRLPDFVNPVHYDLHVKPLLEEDTYTGTVSISIN			
				LSAPTRYLWLHLRETRITRLPELKRPSGDQVQVRR			
161				FEYKKQEVVVVEABEELTPSSGDGLYLLTMEFAGWLNGLVGFY			
				RTTYTENGQVKSIVATDHEPTDARKSPFCFDEPNKK			
241				ATYTIISTHPKEYGALSNMPVAKESVDDKWTRTTFEKSVPMT			
				YLVCFVHQFDSVKRISNSGKPLTIYVQPEQKHTAE			
321				YAANITKSVDFYFEEYFAMNYSLPKLDKIAIPDFGTGAMENWGL			
				ITYRETLLYDPKESASNSQQRVATVVAHELHVHWF			
401				GNIVTMDWEDLWLNFGFASFFELGVNHAETDQMRDQMLLED			
				VLPVQEDDSLMSHPITVTTTPDEITSVFDGISYS			
481				KGSSILRMLEDWIKPENFQKGCQMLEKYQFKNKTSDFWAALE			
				EASRLPVKEVMDTWTRQMGYPVLNVNGVKNITQKRF			
561				LLDPRANPSQPPSDLGWTNIPVKWEDNTSSVLFPNRSEKEGI			
				TLNSSNPSGNAPFLKINPDHIGFYRVNVEVATWDSIA			
641				TALSLNHKTFFSSADRASLIDDAFALARAQLLDYKVALNLTKYLK			
				REENFLPWQRVISAVTYIISMFEDDKELYPMIEEYF			
721				GQGVKPIADSLGWNADGHDVTKLLRSSVLGFACKMGDREALNNA			
				SSLFEQWLNGTVSLPVLNRLLVYRYGMQNSGNEISW			
801				NYTLEQYQKTSLAQEKELLYGLASVKNTVLLSRYLDLLKDTNL			
				IKTDQVFTVIRYIISYNSYGNMAWNWQLNWDYLVN			
881				RYTLNNRNLGRIVTIAEPFNTELQWQMESFFAKYPQAGAGEKP			
				REQVLETVKNNIEWLKQHRNTIREWFFNLLES			

5.73 histone cluster 2, H4b [*Homo sapiens*]; histone cluster 2, H4a [*Homo sapiens*]; histone cluster 1, H4i [*Homo sapiens*]; histone cluster 1, H4j [*Homo sapiens*]; histone cluster 1, H4e [*Homo sapiens*]; histone cluster 1, H4b [*Homo sapiens*]; histone cluster 1, H4h [*Homo sapiens*]; histone cluster 1, H4c [*Homo sapiens*]; histone cluster 1, H4k [*Homo sapiens*]; histone cluster 1, H4f [*Homo sapiens*];

histone cluster 1, H4d [*Homo sapiens*]; histone cluster 1, H4a [*Homo sapiens*]; histone cluster 4, H4 [*Homo sapiens*]; histone cluster 1, H4j [*Homo sapiens*]

Protein Accession gil77539758 gil4504323 gil4504321 gil4504317 gil4504315 gil4504313 gil4504311 gil4504309

Mean Expression Ratio 0.791

Median Expression Ratio 0.794

Credible Interval (0.489, 1.26)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0191]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
1	0.45	0.75	1.3	SEQ ID NO: 663	VFLENVIR		

5.74 guanine nucleotide binding protein (G protein), q polypeptide [*Homo sapiens*]

Protein Accession gil40254462

Mean Expression Ratio 1.25

Median Expression Ratio 1.26

Credible Interval (0.847, 1.88)

Associated Peptides 2

Associated Spectra 3

Coverage 0.0947

[0192]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
2	0.86	1.3	1.9	SEQ ID NO: 664	VADPAYLPTQQDVLR		
1	0.83	1.3	2	SEQ ID NO: 665	VPTTGIIIEYPPDLQSVIFR		
SEQ ID NO: 666							
1				MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKL			
				LLLTGESGKSTFIKQMRI IHGSGYSDCKRGFTKLVI			
81				QNIFTAMQAMIRAMDTLKI PKYEHNKAKAQLVREVDVEKVS			
				AFENPYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYY			
161				LNDLDRVADPAYLPTQQDVLRVRVPTTGIIIEYPPDLQSVIFR			
				MVDVGGQRSEERRKWIHCFENVTSIMFLVALSEYDQVLV			
241				ESDNENRMEEKALFRTIITYPWFQNSSVILFLNKKDLLEEK			
				IMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDS			
321				DKIISHTCATDTENIRFVFAAVDKTILQLNLKEYNLV			

5.75 syndecan 1 precursor [*Homo sapiens*]; syndecan 1 precursor [*Homo sapiens*]
Protein Accession gi|55749480 gi|29568086

Mean Expression Ratio 0.797
Median Expression Ratio 0.795
Credible Interval (0.536, 1.19)

Associated Peptides 2
Associated Spectra 3

Coverage NaN

[0193]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
2	0.49	0.74	1.1	SEQ ID NO: 667	EGEAVVLPEVEPGLTAR		
1	0.52	0.8	1.3	SEQ ID NO: 668	NQSPVDQGATGASQGLLDR		

5.76 copine III [*Homo sapiens*]
Protein Accession gi|4503015

Mean Expression Ratio 1.26
Median Expression Ratio 1.26
Credible Interval (0.877, 1.80)

Associated Peptides 3
Associated Spectra 4

Coverage 0.0782

[0194]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
2	0.9	1.3	1.9	SEQ ID NO: 669	DIVQFVPFR		
1	0.83	1.3	1.9	SEQ ID NO: 670	LYGPTNFSPIINHVAR		
1	0.82	1.3	1.9	SEQ ID NO: 671	VLLIITDGVITDLDETR		

SEQ ID NO: 672
1 MAAQCCTKVALNVSCANLLDKDIGSKSDPLCVLFLNTSGQQ
WYEVERTERIKNCLNPQFSKTFIDYYFEVQKLKFGVY
81 DIDNKTIELSDDDFLGECCECTLGQIVSSKKLTRPLVMKTGR
PAGKGSITISAEIKNRNVLFEMEARKLDNKDLFGKSD
161 PYLEFHKQTSNGWLMVHRTEVVKNLNPVWRPFKISLNSL
CYGDMDKTIKVECYDYDNDGSHDLIGTFQTTMTKLKEAS
241 RSSPVEPECINEKKRQKKSYKNSGVISVKQCEITVECTFL
DYIMGGCQLNFTVGVDFTGSNGDPRSPDSLHYISPNGVN
321 EYLTALWSVLGVIQDYDADKMFPAGFGAQIPQWQVSHEF
PMNFPNSNPYCNGIQGIVEAYRSLPQIKLYGPTNFSPI
401 INHVARFAAAATQQQTASQYFVLLIITDGVITDLDETRQAI
VNASRLPMSIIIVGVGGADFSAMEFLDGGSLRSPLGE
481 VAIRDIVQFVFPFQFQNAPEKALAQCVLAETPQQVVGYNFT
YKLLPPKNPATKQKQKQ

5.77 annexin VII isoform 2 [*Homo sapiens*]; annexin VII isoform 1 [*Homo sapiens*]
Protein Accession gi|4809279 gi|4502111

Mean Expression Ratio 1.26
Median Expression Ratio 1.26
Credible Interval (0.897, 1.79)

Associated Peptides 3
Associated Spectra 5

Coverage NaN

[0195]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
3	0.9	1.3	1.8	SEQ ID NO: 673	DENQSIHQMAQEDAQR		
1	0.86	1.3	2	SEQ ID NO: 674	GFGTDEQAIVDVVANR		
1	0.83	1.3	1.9	SEQ ID NO: 675	VLIETLCTR		

5.78 cubilin [*Homo sapiens*]
Protein Accession gi|26091152

Mean Expression Ratio 0.798
Median Expression Ratio 0.798
Credible Interval (0.637, 1.01)

Associated Peptides 10
Associated Spectra 14

Coverage 0.0461

[0196]

A	2.5	50	97.5	Sequence	ID	No.	Sequence
1	0.56	0.79	1.1	SEQ ID NO: 676	CNFDVLEIYGGPDFHSPR		
4	0.56	0.75	1	SEQ ID NO: 677	DFVEILDGGHEDAPLR		
1	0.58	0.81	1.1	SEQ ID NO: 678	EQLANPIVSSGNSLFLR		
1	0.57	0.8	1.1	SEQ ID NO: 679	LQVLLLTGTVGR		
1	0.57	0.8	1.1	SEQ ID NO: 680	NGGSPESPIIGQYCGNSNPR		
2	0.58	0.78	1.1	SEQ ID NO: 681	SPENPMQVSSGTNELAIR		
1	0.57	0.8	1.1	SEQ ID NO: 682	SPFFPNVYPGER		
1	0.55	0.78	1.1	SEQ ID NO: 683	VPGQSGVVEISGHPTLPYR		
1	0.57	0.8	1.1	SEQ ID NO: 684	LNDEDLSECLHQIQK		
1	0.59	0.82	1.2	SEQ ID NO: 685	YCGNTIPDSIDTSSNTAVVR		

SEQ ID NO: 686
1 M M N M S L P F L W S L L T L I F A E V N
G E A G E L E L Q R Q K R S I N L Q Q P R M
A T E R G N L V F L T G S A Q N I E F R T G
S L G K I K L N D E D L S E

-continued

81 C L H Q I Q K N K E D I I E L K G S A I G L
P Q N I S S Q I Y Q L N S K L V D L E R K F
Q G L Q Q T V D K K V C S S N P C Q N G G T
C L N L H D S F F C I C P P

161 Q W K G P L C S A D V N E C E I Y S G T P L
S C Q N G G T C V N T M G S Y S C H C P P E
T Y G P Q C A S K Y D D C E G G S V A R C V
H G I C E D L M R E Q A G E

241 P K Y S C V C D A G W M F S P N S P A C T L
D R D E C S F Q P G P C S T L V Q C F N T Q
G S F Y C G A C P T G W Q G N G Y I C E D I
N E C E I N N G G C S V A P

321 P V E C V N T P G S S H C Q A C P P G Y Q G
D G R V C T L T D I C S V S N G G C H P D A
S C S T L G S L P L C T C L P G Y T G N G
Y G P N G C V Q L S N I C L

401 S H P C L N G Q C I D T V S G Y F C K C D S
G W T G V N C T E N I N E C L S N P C L N G
G T C V D G V D S F S C E C T R L W T G A L
C Q V P Q Q V C G E S L S G

481 I N G S F S Y R S P D V G Y V H D V N C F W
V I K T E M G K V L R I T F T F F R L E S M
D N C P H E F L Q V Y D G D S S A F Q L G
R F C G S S L P H E L L S S

561 D N A L Y F H L Y S E H L R N G R G F T V R
W E T Q Q P E C G G I L T G P Y G S I K S P
G Y P G N Y P P G R D C V W I V V T S P D L
L V T F T F G T L S L E H H

641 D D C N K D Y L E I R D G P L Y Q D P L L G
K F C T T F S V P P L Q T T G P F A R I H F
H S D S Q I S D Q G F H I T Y L T S P S D L
R C G G N Y T D P E G E L F

721 L P E L S G P F T H T R Q C V Y M M K Q P Q
G E Q I Q I N F T H V E L Q C Q S D S S Q N
Y I E V R D G E T L L G K V C G N G T I S H
I K S I T N S V W I R F K I

801 D A S V E K A S F R A V Y Q V A C G D E L T
G E G V I R S P F F P N V Y P G E R T C R W
T I H Q P Q S Q V I L L N F T V F E I G S S
A H C E T D Y V E I G S S

881 I L G S P E N K K Y C G T D I P S F I T S V
Y N F L Y V T F V K S S S T E N H G F M A K
F S A E D L A C G E I L T E S T G T I Q S P
G H P N V Y P H G I N C T W

961 H I L V Q P N H L I H L M F E T F H L E F H
Y N C T N D Y L E V Y D T D S E T S L G R Y
C G K S I P P S L T S S G N S L M L V F V T
D S D L A Y E G F L I N Y E

1041 A I S A A T A C L Q D Y T D D L G T F T S P
N F P N N Y P N N W E C I Y R I T V R T G Q
L I A V H F T N F S L E E A I G N Y Y T D F
L E I R D G G Y E K S P L L

1121 G I F Y G S N L P P T I I S H S N K L W L K
F K S D Q I D T R S G F S A Y W D G S S T G
C G G N L T T S S G T F I S P N Y P M P Y Y
H S S E C Y W W L K S S H G

1201 S A F E L E F K D F H L E H H P N C T L D Y
L A V Y D G P S S N S H L L T Q L C G D E K
P P L I R S S G D S M F I K L R T D E G Q Q
G R G F K A E Y R Q T C E N

-continued

1281 V V I V N Q T Y G I L E S I G Y P N P Y S E
N Q H C N W T I R A T T G N T V N Y T F L A
F D L E H H I N C S T D Y L E L Y D G P R Q
M G R Y C G V D L P P P G S

1361 T T S S K L Q V L L L T D G V G R R E K G F
Q M Q W F V Y G C G G E L S G A T G S F S S
P G F P N R Y P P N K E C I W Y I R T D P G
S S I Q L T I H D F D V E Y

1441 H S R C N F D V L E I Y G G P D F H S P R I
A Q L C T Q R S P E N P M Q V S S T G N E L
A I R F K T D L S I N G R G F N A S W Q A V
T G G C G G I F Q A P S G E

1521 I H S P N Y P S P Y R S N T D C S W V I R V
D R N H R V L L N F T D F D L E P Q D S C I
M A Y D G L S S T M S R L A R T C G R E Q L
A N P I V S S G N S L F L R

1601 F Q S G P S R Q N R G F R A Q F R Q A C G G
H I L T S S F D T V S S P R F P A N Y P N N
Q N C S W I I Q A Q P P L N H I T L S F T H
F E L E R S T T C A R D F V

1681 E I L D G G H E D A P L R G R Y C G T D M P
H P I T S F S S A L T L R F V S D S S I S A
G G F H T T V T A S V S A C G G T F Y M A E
G I F N S P G Y P D I Y P P

1761 N V E C V W N I V S S P G N R L Q L S F I S
F Q L E D S Q D C S R D F V E I R E G N A T
G H L V G R Y C G N S F P L N Y S S I V G H
T L W V R F I S D G S G S G

1841 T G F Q A T F M K I F G N D N I V G T H G K
V A S P F W P E N Y P H N S N Y Q W T V N V
N A S H V V H G R I L E M D I E E I Q N C Y
Y D K L R I Y D G P S I H A

1921 R L I G A Y C G T Q T E S F S S T G N S L T
F H F Y S D S S I S G K G F L L E W F A V D
A P D G V L P T I A P G A C G G F L R T G D
A P V F L F S P G W P D S Y

2001 S N R V D C T W L I Q A P D S T V E L N I L
S L D I E S H R T C A Y D S L V I R D G D N
N L A Q Q L A V L C G R E I P G P I R S T G
E Y M F I R F T S D S S V T

2081 R A G F N A S F H K S C G G Y L H A D R G I
I T S P K Y P E T Y P S N L N C S W H V L V
Q S G L T I A V H F E Q P P F Q I P N G D S S
C N Q G D Y L V L R N G P D

2161 I C S P P L G P P G G N G H F C G S H A S S
T L F T S D N Q M F V Q F I S D H S N E G Q
G F K I K Y E A K S L A C G G N V Y I H D A
D S A G Y V T S P N H P H N

2241 Y P P H A D C I W I L A A P P E T R I Q L Q
F E D R F D I E V T P N C T S N Y L E L R D
G V D S D A P I L S K F C G T S L P S S Q W
S S G E V M Y L R F R S D N

2321 S P T H V G F K A K Y S I A Q C G G R V P G
Q S G V V E S I G H P T L P Y R D N L F C E
W H L Q G L S G H Y L T I S F E D F N L Q N
S S G C E K D F V E I W D N

2401 H T S G N I L G R Y C G N T I P D S I D T S
S N T A V V R F V T D G S V T A S G F R L R
F E S S M E E C G G D L Q G S I G T F T S P
N Y P N P N P H G R I C E W

-continued

2481	R I T A P E G R R I T L M F N N L R L A T H P S C N N E H V I V F N G I R S N S P Q L E K L C S S V N V S N E I K S S G N T M K V I F F T D G S R P Y G G F T A
2561	S Y T S S E D A V C G G S L P N T P E G N F T S P G Y D G V R N Y S R N L N C E W T L S N P N Q G N S S I S I H F E D F Y L E S H Q D C Q F D V L E F R V G D A
2641	D G P L M W R L C G P S K P T L P L V I P Y S Q V W I H F V T N E R V E H I G F H A K Y S F T D C G G I Q I G D S G V I T S P N Y P N A Y D S L T H C S S L L E
2721	A P Q G H T I T L T F S D F D I E P H T T C A W D S V T V R N G G S P E S P I I G Q Y C G N S N P R T I Q S G S N Q L V V T F N S D H S L Q G G G F Y A T W N T
2801	Q T L G C G G I F H S D N G T I R S P H W P Q N F P E N S R C S W T A I T H K S K H L E I S F D N N F L I P S G D G Q C Q N S F V K V W A G T E E V D K A L L A
2881	T G C G N V A P G P V I T P S N T F T A V F Q S Q E A P A Q G F S A S F V S R C G S N F T G P S G Y I I S P N Y P K Q Y D N N M N C T Y V I E A N P L S V V L L
2961	T F V S F H L E A R S A V T G S C V N D G V H I I R G Y S V M S T P F A T V C G D E M P A P L T I A G P V L L N F Y S N E Q I T D F G F K F S Y R I I S C G G V
3041	F N F S S G I I T S P A Y S Y A D Y P N D M H C L Y T I T V S D D K V I E L K F S D F D V V P S T S C S H D Y L A I Y D G A N T S D P L L G K F C G S K R P P N
3121	V K S S N N S M L L V F K T D S F Q T A K G W K M S F R Q T L G P Q Q G C G G Y L T G S N N T F A S P D S D S N G M Y D K N L N C V W I I I A P V N K V I H L T
3201	F N T F A L E A A S T R Q R C L Y D Y V K L Y D G D S E N A N L A G T F C G S T V P A P F I S S G N F L T V Q F I S D L T L E R E G F N A T Y T I M D M P C G G
3281	T Y N A T W T P Q N I S S P N S S D P D V P F S I C T W V I D S P P H Q Q V K I T V W A L Q L T S Q D C T Q N Y L Q L Q D S P Q G H G N S R F Q F C G R N A S A
3361	V P V F Y S S M S T A M V I F K S G V V N R N S R M S F T Y Q I A D C N R D Y H K A F G N L R S P G W P D N Y D N D K D C T V T L T A P Q N H T I S L F F H S L
3441	G I E N S V E C R N D F L E V R N G S N S N S P L L G K Y C G T L L P N P V F S Q N N E L Y L R F K S D S V T S D R G Y E I I W T S S P S G C G G T L Y G D R G
3521	S F T S P G Y P G T Y P N N T Y C E W V L V A P A G R L V T I N F Y F I S I D D P G D C V Q N Y L T L Y D G P N A S S P S S G P Y C G G D T S I A P F V A S S N
3601	Q V F I K F H A D Y A R R P S A F R L T W D S

5.79 guanine nucleotide binding protein (G protein), alpha 11 (Gq class) [*Homo sapiens*]

Protein Accession gi|115511049

Mean Expression Ratio 1.25

Median Expression Ratio 1.25

Credible Interval (0.849, 1.85)

Associated Peptides 2

Associated Spectra 3

Coverage 0.0947

[0197]

Sequence					Sequence																		
A	2.5	50	97.5	ID No.																			
1	0.8	1.2	1.9	SEQ ID NO: 687	SHLVDYFPEFDGPQR																		
2	0.88	1.3	2	SEQ ID NO: 688	VPTTGIIIEYPFDLENIIFR																		
SEQ ID NO: 689																							
1	M	T	L	E	S	M	M	A	C	C	L	S	D	E	V	K	E	S	K	R	I	N	A
	E	I	E	K	Q	L	R	R	D	K	R	D	A	R	R	E	L	K	L	L	L	L	G
	T	G	E	S	G	K	S	T	F	I	K	Q	M	R	I	I	H	G	A	G	Y	S	E
	E	D	K	R	G	F	T	K	L	V	Y												
81	Q	N	I	F	T	A	M	Q	A	M	I	R	A	M	E	T	L	K	I	L	Y	K	Y
	E	Q	N	K	A	N	A	L	L	I	R	E	V	D	V	E	K	V	T	T	F	E	H
	Q	Y	V	S	A	I	K	T	L	W	E	D	P	G	I	Q	E	C	Y	D	R	R	R
	E	Y	Q	L	S	D	S	A	K	Y	Y												
161	L	T	D	V	D	R	I	A	T	L	G	Y	L	P	T	Q	Q	D	V	L	R	V	R
	V	P	T	T	G	I	I	E	Y	P	F	D	L	E	N	I	I	F	R	M	V	D	V
	G	G	Q	R	S	E	R	R	K	W	I	H	C	F	E	N	V	T	S	I	M	F	L
	V	A	L	S	E	Y	D	Q	V	L	V												
241	E	S	D	N	E	N	R	M	E	E	S	K	A	L	F	R	T	I	I	T	Y	P	W
	F	Q	N	S	S	V	I	L	F	L	N	K	K	D	L	L	E	D	K	I	L	Y	S
	H	L	V	D	Y	F	P	E	F	D	G	P	Q	R	D	A	Q	A	A	R	E	F	I
	L	K	M	F	V	D	L	N	P	D	S												
321	D	K	I	I	Y	S	H	F	T	C	A	T	D	T	E	N	I	R	F	V	F	A	A
	V	K	D	T	I	L	Q	L	N	L	K	E	Y	N	L	V							

5.80 proteasome alpha 1 subunit isoform 2 [*Homo sapiens*]; proteasome alpha 1 subunit isoform 1 [*Homo sapiens*]

Protein Accession gi|4506179 gi|23110935

Mean Expression Ratio 1.25

Median Expression Ratio 1.25

Credible Interval (0.869, 1.78)

Associated Peptides 3

Associated Spectra 4

Coverage NaN

[0198]

A	2.5	50	97.5	Sequence	
				ID No.	Sequence
2	0.9	1.3	2.0	SEQ ID NO: 690	DLEFTIYDDDDVSPFLEGLEER
1	0.82	1.2	1.9	SEQ ID NO: 691	ILHVDNHIGISITAGLTADAR
1	0.84	1.3	1.9	SEQ ID NO: 692	DLEFTIYDDDDVSPFLEGLEERPQR

5.81 myeloperoxidase [*Homo sapiens*]

Protein Accession gi|4557759

Mean Expression Ratio 0.805

Median Expression Ratio 0.805

Credible Interval (0.627, 1.04)

Associated Peptides 9

Associated Spectra 11

Coverage 0.172

[0199]

			Sequence		
A	2.5	50	97.5	ID No.	Sequence
2	0.55	0.78	1.1	SEQ ID NO: 693	FCGLPQPETVQG LGTVLR
1	0.56	0.8	1.1	SEQ ID NO: 694	FPTDQLTPDQER
2	0.56	0.78	1.1	SEQ ID NO: 695	IGLDLPALNMQR
1	0.56	0.8	1.1	SEQ ID NO: 696	IVGAMVQIITYR
1	0.57	0.83	1.2	SEQ ID NO: 697	NIDIWMGGVSEPLK
1	0.56	0.8	1.1	SEQ ID NO: 698	NQINALTTSFVDASMVYGSEEPLAR
1	0.58	0.81	1.2	SEQ ID NO: 699	QALAQISLPR
1	0.55	0.79	1.1	SEQ ID NO: 700	VVLEGGIDPILR
1	0.57	0.81	1.2	SEQ ID NO: 701	VGPLLACIIGTQFR

SEO ID NO: 702

1 M G V P K F S S L R C M V D L G P C W A G G L
T A E M K F L L L A L A G L L A I L A T P Q P S
E G A A P A V L G E V D T S L V L S S M E E A
K Q L V D K A Y K E R

81 R E S I K Q R L R S G S A S P M E L L S Y F K
Q P V A A T R T A V R A A D Y L H V A L D L L
E R K L R S L W R R P F N V T D V L T P A Q L
N V L S K S S G C A Y

-continued

161	Q D V G V T C P E Q D K Y R T I T G M C N N R
	R S P T L G A S N R A F V R W L P A E Y E D G
	F S L P Y G W T P G V K R N G F P V A L A R A
	V S N E I V R F P T D
241	Q L T P D Q E R S L M F M Q W G Q L L D H D L
	D F T P E P A A R A S F V T G V N C E T S C V
	Q Q P P C F P L K I P P N D P R I K N Q A D C
	I P F F R S C P A C P
321	G S N I T I R N Q I N A L T S F V D A S M V Y
	G S E E P L A R N L R N M S N Q L G L L A V N
	Q R F Q D N G R A L L P F D N L H D D P C L L
	T N R S A R I P C F L
401	A G D T R S S E M P E L T S M H T L L L R E H
	N R L A T E L K S L N P R W D G E R L Y Q E A
	R K I V G A M V Q I I T Y R D Y L P L V L G P
	T A M R K Y L P T Y R
481	S Y N D S V D P R I A N V F T N A F R Y G H T
	L I Q P F M F R L D N R Y Q P M E P N P R V P
	L S R V F F A S W R V V L E G G I D P I L R G
	L M A T P A K L N R Q
561	N Q I A V D E I R E R L F E Q V M R I G L D L
	P A L N M Q R S R D H G L L P G Y N A W R R F C
	G L P Q P E T V G D L G T V L R N L K L A R K
	L M E Q Y G T P N N I
641	D I W M G G V S E P L K R K G R V G P L L A C
	I I G T Q F R K L R D G D R F W W E N E G V F
	S M Q Q R Q A L A Q I S L P R I I C D N T G I
	T V S K N N I F M S
721	N S Y P R D F V N C S T L P A L N L A S W R E
	A S

5.82 solute carrier family 5 (iodide transporter), member 8
[*Homo sapiens*]

Protein Accession [gil167466278](#)

Mean Expression Ratio 0.808

Median Expression Ratio 0.806

Credible Interval (0.554, 1.18)

Associated Peptides 2

Associated Spectra 4

Coverage NaN

[0200]

				Sequence	
A 2.5	50	97.5	ID No.	Sequence	
1	0.54	0.84	1.3	SEQ ID NO: 703	EDFLSNFDIFK
3	0.51	0.74	1.1	SEQ ID NO: 704	SHPVEDGGTDNPAFNHIELNSDQSGK

5.83 ras homolog gene family, member C precursor [*Homo sapiens*]; ras homolog gene family, member C precursor [*Homo sapiens*]; ras homolog gene family, member C precursor [*Homo sapiens*]; ras homolog gene family, member A [*Homo sapiens*]
Protein Accession gil28395033 gil11494251 gil11494248
gil0835049

Mean Expression Ratio 1.24
Median Expression Ratio 1.24
Credible Interval (0.815, 1.90)

Associated Peptides 2
Associated Spectra 2
Coverage NaN

[0201]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.78	1.3	2	SEQ ID NO: 705	HFCPNVPIILVGNK	
1	0.82	1.3	2.0	SEQ ID NO: 706	QVELALWDTAGQEDYDR	

5.84 complement factor H isoform a precursor [*Homo sapiens*]
Protein Accession gil62739186

Mean Expression Ratio 0.806
Median Expression Ratio 0.807
Credible Interval (0.627, 1.04)

Associated Peptides 8
Associated Spectra 10
Coverage 0.0812

[0202]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.56	0.8	1.1	SEQ ID NO: 707	EQVQSCGPPPELLNGNVK	
2	0.55	0.76	1.0	SEQ ID NO: 708	KGEWVALNPLR	
1	0.57	0.81	1.2	SEQ ID NO: 709	LIILEEHLK	
1	0.55	0.78	1.1	SEQ ID NO: 710	RPYFPVAVGK	
1	0.59	0.85	1.2	SEQ ID NO: 711	SCDNPIYPNGDYSPLR	
2	0.57	0.79	1.1	SEQ ID NO: 712	SSNLIILEEHLK	
1	0.58	0.83	1.2	SEQ ID NO: 713	TCNEGQQLLGEINYR	
1	0.55	0.79	1.1	SEQ ID NO: 714	TDCLSLPSFENAI PMGEK	
SEQ ID NO: 715						
1	M R L L A K I I C L M L W A I C V A E D C N E L P P R R N T E I L T G S W S D Q T Y P E G T Q A I Y K C R P G Y R S L G N V I M V C R K G E W V A L N P L R K C					

-continued

81	Q K R P C G H P G D T P F G T F T L T G G N V F E Y G V K A V Y T C N E G Y Q L L G E I N Y R E C D T D G W T N D I P I C E V V K C L P V T A P E N G K I V S S
161	A M E P D R E Y H F G Q A V R F V C N S G Y K I E G D E E M H C S D D G F W S K E K P K C V E I S C K S P D V I N G S P I S Q K I I Y K E N E R F Q Y K C N M G
241	Y E Y S E R G D A V C T E S G W R P L P S C E E K S C D N P Y I P N G D Y S P L R I K H R T G D E I T Y Q C R N G F Y P A T R G N T A K C T S T G W I P A P R C
321	T L K P C D Y P D I K H G G L Y H E N M R R P Y F P V A V G K Y Y S Y Y C D E H F E T P S G S Y W D H I H C T Q D G W S P A V P C L R K C Y F P Y L E N G Y N Q
401	N H G R K F V Q G K S I D V A C H P G Y A L P K A Q T T V T C M E N G W S P T P R C I R V K T C S K S S I D I E N G F I S E S Q Y T Y A L K E K A K Y Q C K L G
481	Y V T A D G E T S G S I T C G K D G W S A Q P T C I K S C D I P V F M N A R T K N D F T W F K L N D T L D Y E C H D G Y E S N T G S T T G S I V C G Y N G W S D
561	L P I C Y E R E C E L P K I D V H L V P D R K K D Q Y K V G E V L K F S C K P G F T I V G P N S V Q C Y H F G L S P D L P I C K E Q V Q S C G P P P E L L N G N
641	V K E K T K E E Y G H S E V V E Y Y C N P R F L M K G P N K I Q C V D G E W T T L P V C I V E E S T C G D I P E L E H G W A Q L S S P P Y Y Y G D S V E F N C S
721	E S F T M I G H R S I T C I H G V W T Q L P Q C V A I D K L K K C K S S N L I I L E E H L K N K K E F D H N S N I R Y R C R G K E G W I H T V C I N G R W D P E
801	V N C S M A Q I Q L C P P P P Q I P N S H N M T T T L N Y R D G E K V S V L C Q E N Y L I Q E G E E I T C K D G R W Q S I P L C V E K I P C S Q P P Q I E H G T
881	I N S S R S S Q E S Y A H G T K L S Y T C E G G F R I S E E N E T T C Y M G K W S S P P Q C E G L P C K S P P E I S H G V V A H M S D S Y Q Y G E E V T Y K C F
961	E G F G I D G P A I A K C L G E K W S H P P S C I K T D C L S L P S F E N A I P M G E K K D V Y K A G E Q V T Y T C A T Y Y K M D G A S N V T C I N S R W T G R
1041	P T C R D T S C V N P P T V Q N A Y I V S R Q M S K Y P S G E R V R Y Q C R S P Y E M F G D E E V M C L N G N W T E P P Q C K D S T G K C G P P P I D N G D I
1121	T S F P L S V Y A P A S S V E Y Q C Q N L Y Q L E G N K R I T C R N G Q W S E P P K C L H P C V I S R E I M E N Y N I A L R W T A K Q K L Y S R T G E S V E F V
1201	C K R G Y R L S S R S H T L R T T C W D G K L E Y P T C A K R

5.85 flotillin 1 [Homo sapiens]

Protein Accession gi|5031699

Mean Expression Ratio 1.23

Median Expression Ratio 1.23

Credible Interval (0.95, 1.62)

Associated Peptides 7

Associated Spectra 9

Coverage 0.234

[0203]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.83	1.3	2	SEQ ID NO: 716	716	AQQVAVQEQEIAR
1	0.88	1.2	1.8	SEQ ID NO: 717	717	DIHDDQDYLHSLGK
1	0.85	1.2	1.8	SEQ ID NO: 718	718	LPQVAEEISGPLTSANK
3	0.9	1.2	1.7	SEQ ID NO: 719	719	TEAEIAHIALETLEGHQR
1	0.87	1.3	1.8	SEQ ID NO: 720	720	VTGEVLDILTR
1	0.87	1.3	1.8	SEQ ID NO: 721	721	LTGVSISQVNHKPLR
1	0.83	1.2	1.7	SEQ ID NO: 722	722	VFVLPCIQQIQR
SEQ ID NO: 723						
1	M F F T C G P N E A M V V S G F C R S P P V M					
	V A G G R V F V L P C I Q Q I Q R I S L N T L					
	T L N V K S E K V Y T R H G V P I S V T G I A					
	Q V K I Q G Q N K E M					
81	L A A A C Q M F L G K T E A E I A H I A L E T					
	L E G H Q R A I M A H M T V E E I Y K D R Q K					
	F S E Q V F K V A S S D L V N M G I S V V S Y					
	T L K D I H D D Q D Y					
161	L H S L G K A R T A Q V Q K D A R I G E A E A					
	K R D A G I R E A K A K Q E K V S A Q Y L S E					
	I E M A K A Q R D Y E L K K A A Y D I E V N T					
	R R A Q A D L A Y Q L					
241	Q V A K T K Q Q I E E Q R V Q V Q V V E R A Q					
	Q V A V Q E Q E I A R R E K E L E A R V R K P					
	A E A E R Y K L E R L A E A E K S Q L I M Q A					
	E A E A A S V R M R G					
321	E A E A F A I G A R A R A E A E Q M A K K A E					
	A F Q L Y Q E A A Q L D M L L E K L P Q V A E					
	E I S G P L T S A N K I T L V S S G S G T M G					
	A A K V T G E V L D I					
401	L T R L P E S V E R L T G V S I S Q V N H K P					
	L R T A					

5.86 hypothetical protein LOC91894 [Homo sapiens]

Protein Accession gi|131889517

Mean Expression Ratio 1.23

Median Expression Ratio 1.23

Credible Interval (0.786, 1.91)

Associated Peptides 1

Associated Spectra 2

Coverage 0.122

[0204]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.83	1.3	2	SEQ ID NO: 724	724	TLKPQPQQLQQNLPK
SEQ ID NO: 725						
1	M G N R V C C G G S W S C P S T F Q K K K K T					
	G S Q T R R T L K P Q P Q Q L Q Q N L P K G H					
	E T T G H T Y E R V L Q Q Q G S Q E R S P G L					
	M S E D S N L H Y A D					
81	I Q V C S R P H A R E V K H V H L E N A T E Y					
	A T L R F P Q A T P R Y D S K N G T L V					

5.87 ring finger protein 152 [Homo sapiens]

Protein Accession gi|27734873

Mean Expression Ratio 0.815

Median Expression Ratio 0.814

Credible Interval (0.506, 1.31)

Associated Peptides 1

Associated Spectra 1

Coverage 0.143

[0205]

Sequence						
A	2.5	50	97.5	ID No.	Sequence	
1	0.46	0.77	1.3	SEQ ID NO: 726	726	SVTVVTIPAEQQPLQGAPQEAVEEEE
SEQ ID NO: 727						
1	M E T L S Q D S L L E C Q I C F N Y Y S P R R					
	R P K L L D C K H T C C S V C L Q Q M R T S Q					
	K D V R C P W C R G V T K L P P G F S V S Q L					
	P D D P E V L A V I A					
81	I P H T S E H T P V F I K L P S N G C Y M L P					
	L P I S K E R A L L P G D M G C R L L P G S Q					
	Q K S V T V V T I P A E Q Q P L Q G G A P Q E					
	A V E E E Q D R R G V					
161	V K S S T W S G V C T V I L V A C V L V F L L					
	G I V L H N M S C I S K R F T V I S C G					

5.88 WIRE protein [*Homo sapiens*]
Protein Accession gi18959210

Mean Expression Ratio 1.22

Median Expression Ratio 1.23

Credible Interval (0.829, 1.8)

Associated Peptides 2

Associated Spectra 3

Coverage 0.0841

[0206]

Sequence				
A	2.5	50	97.5	Sequence ID No.
2	0.83	1.3	1.9	SEQ ID NO: 728
QPPGVPNPSSPTNESAPQLPQR				
1	0.8	1.2	1.9	SEQ ID NO: 729
TPAGPPPPPPPLR				
SEQ ID NO: 730				
1 M P I P P P P P P P P G P P P P T F H Q A N				
T E Q P K L S R D E Q R G R G A L L Q D I C K				
G T K L K K V T N I N D R S A P I L E K P K G				
S S G G Y G S G G A A				
81 L Q P K G G L F Q G G V L K L R P V G A K D G				
S E N L A G K P A L Q I P S S R A A A P R P P				
V S A A S G R P Q D D T D S S R A S L P E L P				
R M Q R P S L P D L S				

-continued

161	R P N T T S S T G M K H S S S A P P P P P P G
	R R A N A P P T P L P M H S S K A P A Y N R E
	K P L P P T P G Q R L H P G R E G P P A P P P
	V K P P P S P V N I R
241	T G P S G Q S L A P P P P P Y R Q P P G V P N
	G P S S P T N E S A P E L P Q R H N S L H R K
	T P G P V R G L A P P P P T S A S P S L L S N
	R P P P P A R D P P S
321	R G A A P P P P P P V I R N G A R D A P P P P
	P P Y R M H G S E P P S R G K P P P P S R T
	P A G P P P P P P P L R N G H R D S I T T V
	R S F L D D F E S K Y
401	S F H P V E D F P A P E E Y K H F Q R I Y P S
	K T N R A A R G A P P L P P I L R

5.89 putative MAPK activating protein PM28 [*Homo sapiens*]
Protein Accession gi41281489

Mean Expression Ratio 1.22

Median Expression Ratio 1.22

Credible Interval (0.829, 1.77)

Associated Peptides 3

Associated Spectra 3

Coverage 0.0833

[0207]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.79	1.2	1.9	SEQ ID NO: 731	LQSEVAELK
1	0.79	1.2	1.9	SEQ ID NO: 732	YLIEIAK
1	0.81	1.3	1.9	SEQ ID NO: 733	KEIADYLAAGKDER
SEQ ID NO: 734					
1 M L G S G F K A E R L R V N L R L V I N R L K L L E K K K T E L A Q K A R K E I					
A D Y L A A G K D E R A R I R V E H I I R E D Y L V E A M E I L E L Y C D L L L					
81 A R F G L I Q S M K E L D S G L A E S V S T L I W A A P R L Q S E V A E L K I V A					
D Q L C A K Y S K E Y G K L C R T N Q I G T V N D R L M H K L S V E A P P K I					
161 L V E R Y L I E I A K N Y N V P Y E P D S V V M A E A P P G V E T D L I D V G F					
T D D V K K G G P G R G G S G G F T A P V G G P D G T V P M P M P M P M P S					
241 A N T P F S Y P L P K G P S D F N G L P M G T Y Q A F P N I H P P Q I P A T P P S					
Y E S M T L M L I R I S L L H R L L V L D P S Q K P L Q S F L P D L Q I T M T					
321 T L S Y Q S C H L C Q T H Y Q L H L L V P A P Q H L K T L T L M I F P G G L K S					

5.90 flotillin 2 [*Homo sapiens*]

Protein Accession gi|94538362

Mean Expression Ratio 1.22

Median Expression Ratio 1.22

Credible Interval (0.969, 1.55)

Associated Peptides 8

Associated Spectra 15

Coverage 0.238

[0208]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.87	1.2	1.7	SEQ ID NO: 735	735	ELLAVACEQFLGK
1	0.87	1.2	1.7	SEQ ID NO: 736	736	IGEAEEAAVIEAMGK
7	1.0	1.3	1.7	SEQ ID NO: 737	737	NVVLQTLLEGHLR
1	0.85	1.2	1.7	SEQ ID NO: 738	738	QIAVEAQEILR
1	0.89	1.2	1.7	SEQ ID NO: 739	739	SILGTLTVEQIYQDR
1	0.87	1.2	1.7	SEQ ID NO: 740	740	TAEAQLAYELQGAR
2	0.88	1.2	1.7	SEQ ID NO: 741	741	MALVLEALPQIAAK
1	0.84	1.2	1.7	SEQ ID NO: 742	742	RPAAEAEHR
SEQ ID NO: 743						
1	M G N C H T V G P N E A L V V S G G C C G S D Y K Q Y V F G G W A W A W C I S D T Q R I S L E I M T L Q P R C E D V E T A E G V A L T V T G V A Q V K I M T E					
81	K E L L A V A C E Q F L G K N V Q D I K N V V L Q T L E G H L R S I L G T L T V E Q I Y Q D R D Q F A K L V R E V A A P D V G R M G I E I L S F T I K D V Y D K					
161	V D Y L S S L G K T Q T A V V Q R D A D I G V A E A E R D A G I R E A E C K K E M L D V K F M A D T K I A D S K R A F E L Q K S A F S E E V N I K T A E A Q L A					
241	Y E L Q G A R E Q Q K I R Q E E I E I E V V Q R K K Q I A V E A Q E I L R T D K E L I A T V R R P A E A E A H R I Q Q I A E G E K V K Q V L L A Q A E A E K I R					
321	K I G E A E A A V I E A M G K A E A E R M K L K A E A Y Q K Y G D A A K M A L V L E A L P Q I A A K I A A P L T K V D E I V V L S G D N S K V T S E V N R L L A					
401	E L P A S V H A L T G V D L S K I P L I K K A T G V Q V					

5.91 ephrin receptor EphA1 [*Homo sapiens*]

Protein Accession gi|56119207

Mean Expression Ratio 0.819

Median Expression Ratio 0.821

Credible Interval (0.508, 1.33)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0184

[0209]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.46	0.78	1.3	SEQ ID NO: 744	744	APGEGPQVACTGPPSAPR
SEQ ID NO: 745						
1	M E R R W P L G L G L V L L L C A P L P P G A R A K E V T L M D T S K A Q G E L G W L L D P P K D G W S E Q Q Q I L N G T P L Y M Y Q D C P M Q G R R D T D H W					
81	L R S N W I Y R G E E A S R V H V E L Q F T V R D C K S F P G G A G P L G C K E T F N L L Y M E S D Q D V G I Q L R R P L F Q K V T T V A A D Q S F T I R D L A					
161	S G S V K L N V E R C S L G R L T R R G L Y L A F H N P G A C V A L V S V R V F Y Q R C P E T L N G L A Q F P D T L P G P A G L V E V A G T C L P H A R A S P R					
241	P S G A P R M H C S P D G E W L V P V G R C H C E P G Y E E G G S G E A C V A C P S G S Y R M D M D T P H C L T C P Q Q S T A E S E G A T I C T C E S G H Y R A					
321	P G E G P Q V A C T G P P S A P R N L S F S A S G T Q L S L R W E P P A D T G G R Q D V R Y S V R C S Q C Q G T A Q D G G P C Q P C G V G V H F S P G A R G L T					
401	T P A V H V N G L E P Y A N Y T F N V E A Q N G V S G L G S S G H A S T S V S I S M G H A E S L S G L S L R L V K K E P R Q L E L T W A G S R P R S P G A N L T					
481	Y E L H V L N Q D E E R Y Q M V L E P R V L L T E L Q P D T T Y I V R V R M L T P L G P G P F S P D H E F R T S P P V S R G L T G G E I V A V I F G L L L G A A					
561	L L L G I L V F R S R R A Q R Q R Q R Q R D R A T D V D R E D K L W L K P Y V D L Q A Y E D P A Q G A L D F T R E L D P A W L M V D T V I G E G E F G E V Y R					
641	G T L R L P S Q D C K T V A I K T L K D T S P G G Q W N F L R E A T I M G Q F S H P H I L H L E G V V T K R K P I M I I T E F M E N G A L D A F L R E R E D Q					
721	L V P G Q L V A M L Q G I A S G M N Y L S N H N Y V H R D L A A R N I L V N Q N L C C K V S D F G L T R L L D D F D G T Y E T Q G G K I P I R W T A P E A I A H					

-continued

801	R	I	F	T	T	A	S	D	V	W	S	F	G	I	V	M	W	E	V	L	S	F	G
	D	K	P	Y	G	E	M	S	N	Q	E	V	M	K	S	I	E	D	G	Y	R	L	P
	P	P	V	D	C	P	A	P	L	Y	E	L	M	K	N	C	W	A	Y	D	R	A	R
	R	P	H	F	Q	K	L	Q	A	H	L												
881	E	Q	L	L	A	N	P	H	S	L	R	T	I	A	N	F	D	P	R	M	T	L	R
	L	P	S	L	S	G	S	D	G	I	P	Y	R	T	V	S	E	W	L	E	S	I	R
	M	K	R	Y	I	L	H	F	H	S	A	G	L	D	T	M	E	C	V	L	E	L	T
	A	E	D	L	T	Q	M	G	I	T	L												
961	P	G	H	Q	K	R	I	L	C	S	I	Q	G	F	K	D							

5.92 proteasome beta 3 subunit [*Homo sapiens*]

Protein Accession gil22538465

Mean Expression Ratio 1.22

Median Expression Ratio 1.22

Credible Interval (0.756, 1.98)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0878

[0210]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.77	1.3	2.2	SEQ ID NO: 746	LYIGLAGLATDVQTVQQR	
SEQ ID NO: 747						
1	M	S	I	M	S	Y
	N	G	G	A	V	M
	A	M	K	G	K	N
	C	V	A	I	A	
	A	D	R	R	F	G
	I	Q	A	Q	M	V
	T	T	D	F	Q	K
	I	F	P	M	G	
	D	R	L	Y	I	G
	L	A	G	L	A	T
	D	V	Q	T	V	A
	Q	R	L	K	F	
	R	L	N	L	Y	E
	L	K	E	G	R	
81	Q	I	K	P	Y	T
	L	M	S	M	V	A
	N	L	L	Y	E	K
	R	F	G	P	Y	
	Y	T	E	P	V	I
	A	G	L	D	P	K
	T	F	K	P	F	I
	C	S	L	D	L	
	I	G	C	P	M	V
	T	D	D	F	V	S
	G	T	C	A	E	Q
	M	Y	G	M		
	C	E	S	L	W	E
	P	N	M	D	P	
161	D	H	L	F	E	T
	I	S	Q	A	M	L
	N	A	V	D	R	D
	A	V	S	G	M	
	G	V	I	V	H	I
	I	E	K	D	K	I
	T	T	R	T	L	K
	A	R	M	D		

5.93 cathepsin D preproprotein [*Homo sapiens*]

Protein Accession gil4503143

Mean Expression Ratio 0.826

Median Expression Ratio 0.824

Credible Interval (0.69, 0.984)

Associated Peptides 15

Associated Spectra 29

Coverage 0.456

[0211]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.61	0.83	1.1	SEQ ID NO: 748	AIGAVPLIQGEYMIPCEK	
1	0.61	0.83	1.1	SEQ ID NO: 749	AYWQVHLDQVEVASGL	
4	0.63	0.82	1.1	SEQ ID NO: 750	DPDAQPGGELMLGGTDSK	
5	0.6	0.78	1	SEQ ID NO: 751	EGCEAIVDTGTSLMVGPDVEVR	
4	0.63	0.83	1.1	SEQ ID NO: 752	ISVNNVLPVFDNLMQOK	
1	0.62	0.85	1.2	SEQ ID NO: 753	LLDIACWIHHK	
1	0.6	0.82	1.1	SEQ ID NO: 754	MVGPVDEVR	
1	0.61	0.84	1.2	SEQ ID NO: 755	QVFGAATK	
2	0.65	0.87	1.2	SEQ ID NO: 756	TVVFDTGSSNLWVPSIHCK	
1	0.6	0.83	1.1	SEQ ID NO: 757	VSTLPAITLK	
2	0.6	0.8	1.1	SEQ ID NO: 758	WILGDVFIGR	
3	0.6	0.8	1.1	SEQ ID NO: 759	FDGILGMAYPR	
1	0.6	0.82	1.1	SEQ ID NO: 760	AYWQVHLDQVEVASGLTLCK	
1	0.6	0.82	1.1	SEQ ID NO: 761	VSQAGK	
1	0.6	0.83	1.1	SEQ ID NO: 762	YSQAVPAVTEGPIPEVLK	
SEQ ID NO: 763						
1	M	Q	P	S	S	L
	L	P	L	A	L	C
	L	L	A	A	P	A
	S	A	S	A	L	V
	R	I	P	L	H	K
	F	T	S	I	R	R
	T	M	S	E	V	G
	G	S	V	E	D	L
	I	A	K	G	P	V
	S	K	Y	S	Q	A
	V	P	A	V	T	E
	G	P	I	P	E	
	V	L	K	N	Y	M
	D	A	Q	Y	Y	
81	G	E	I	G	I	G
	T	P	P	Q	C	F
	T	V	V	F	D	T
	G	S	S	N	L	
	W	V	P	S	I	H
	C	K	L	L	D	I
	A	C	W	I	H	H
	K	Y	N	S	D	
	K	S	T	Y	V	K
	N	G	T	S	F	D
	I	H	Y	G	S	G
	S	L	S	G		
	Y	L	S	Q	D	T
	V	S	V	P	C	
161	Q	S	A	S	S	A
	S	A	S	A	L	G
	G	V	K	V	E	R
	Q	V	F	G	E	A
	T	K	Q	P	G	I
	T	F	I	A	A	K
	F	D	G	I	L	G
	M	A	Y	P	R	I
	S	V	N	N	V	L
	P	V	F	D	N	L
	M	Q	Q	K	L	V
	D	Q	N	I	F	S
	F	Y	L	S	R	D
	P	D	A	Q		
241	P	G	G	E	L	M
	L	M	L	G	G	T
	D	S	K	Y	Y	K
	G	S	L	S	Y	L
	N	V	T	R	K	A
	Y	W	Q	V	H	L
	D	Q	V	E	V	A
	S	G	L	T	L	C
	K	E	G	C	E	A
	I	V	D	T	G	T
	S	L	M	V	G	P
	V	D	E	V	R	
	E	L	Q	K	A	I
	G	A	V	P	L	
321	I	Q	G	E	Y	M
	I	P	C	E	K	V
	S	T	L	P	A	I
	T	L	K	V	S	Q
	A	G	K	T	L	C
	L	S	G	F	M	G
	M	D	I	P	P	S
	G	P	L	W	I	L
	G	D	V	F	I	G
	R	Y	T	V	F	D
	R	D				
401	N	N	R	V	G	F
	A	E	A	A	R	L

5.94 hypothetical protein LOC58527 [*Homo sapiens*]
Protein Accession gi|24308273

Mean Expression Ratio 0.824

Median Expression Ratio 0.827

Credible Interval (0.557, 1.22)

Associated Peptides 2

Associated Spectra 3

Coverage 0.358

[0212]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.53	0.82	1.3	SEQ ID NO: 764	CANLFEALVGTLK
2	0.52	0.78	1.2	SEQ ID NO: 765	MNVDHEVNLLVEEIH
SEQ ID NO: 766					
1 M N V D H E V N L L V E E I H R L G S K N A D G					
K L S V K F G V L F R D D K C A N L F E A L V G					
T L K A A K R R K I V T Y P G E L L Q G V H D					
D V D I I L L Q					
81 D					

5.95 annexin 5 [*Homo sapiens*]
Protein Accession gi|4502107

Mean Expression Ratio 1.21

Median Expression Ratio 1.21

Credible Interval (0.82, 1.80)

Associated Peptides 3

Associated Spectra 3

Coverage 0.141

[0213]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.78	1.2	1.8	SEQ ID NO: 767	GTVTDFPGFDER
1	0.78	1.2	1.9	SEQ ID NO: 768	QEISAAPK
1	0.83	1.3	2	SEQ ID NO: 769	QVYEEYGSLEDDVVGDTSGYYQR
SEQ ID NO: 770					
1 M A Q V L R G T V T D F P G F D E R A D A E T					
L R K A M K G L G T D E E S I L T L L T S R S					
N A Q R Q E I S A A F K T L F G R D L L D D L					
K S E L T G K F E K L					
81 I V A L M K P S R L Y D A Y E L K H A L K G A					
G T N E K V L T E I I A S R T P E E L R A I K					
Q V Y E E E Y G S L E D D V V G D T S G Y Y					
Q R M L V V L L Q A N					

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161	R D P D A G I D E A Q V E Q D A Q A L F Q A G
	E L K W G T D E E K F I T I F G T R S V S H L
	R K V F D K Y M T I S G F Q I E E T I D R E T
	S G N L E Q L L L A V
241	V K S I R S I P A Y L A E T L Y Y A M K G A G
	T D D H T L I R V M V S R S E I D L F N I R K
	E F R K N F A T S L Y S M I K G D T S G D Y K
	K A L L L L C G E D D

5.96 carboxypeptidase M precursor [*Homo sapiens*]; carboxypeptidase M precursor [*Homo sapiens*]; carboxypeptidase M precursor [*Homo sapiens*]
Protein Accession gi|6631081 gi|53832021 gi|38327526

Mean Expression Ratio 0.83

Median Expression Ratio 0.829

Credible Interval (0.535, 1.28)

Associated Peptides 1

Associated Spectra 2

Coverage NaN

[0214]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.51	0.79	1.2	SEQ ID NO: 771	GQVFDQNGNPLPNVIVEVQDR

5.97 profilin 1 [*Homo sapiens*]
Protein Accession gi|4826898

Mean Expression Ratio 0.829

Median Expression Ratio 0.83

Credible Interval (0.563, 1.23)

Associated Peptides 3

Associated Spectra 3

Coverage 0.293

[0215]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.52	0.8	1.2	SEQ ID NO: 772	DSLLQDGEFSMDLR
1	0.52	0.83	1.3	SEQ ID NO: 773	EGVHGGLINKK
1	0.53	0.82	1.3	SEQ ID NO: 774	TFVNITPAEVGVLVGK
SEQ ID NO: 775					
1 M A G W N A Y I D N L M A D G T C Q D A A I V G					
Y K D S P S V W A A V P G K T F V N I T P A E V					
G V L V G K D R S S F Y V N G L T L G G Q K C S					
V I R D S L L Q					

-continued

81	D	G	E	F	S	M	D	L	R	T	K	S	T	G	A	P	T	F	N	V	T	V	T
	K	T	D	K	T	L	V	L	L	M	G	K	E	G	V	H	G	L	I	N	K	K	C
	Y	E	M	A	S	H	L	R	R	S	Q	Y											

5.98 cortactin isoform b [*Homo sapiens*]; cortactin isoform a [*Homo sapiens*]
Protein Accession gi|20357556 gi|20357552

Mean Expression Ratio 1.2
Median Expression Ratio 1.20
Credible Interval (0.78, 1.81)
Associated Peptides 2
Associated Spectra 2
Coverage NaN

[0216]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.76	1.2	1.9	SEQ ID NO: 776	GPVSGTEPEPVYSMEAADYR	
1	0.77	1.2	2.0	SEQ ID NO: 777	TQTPPVSPAPQPTTEER	

5.99 solute carrier family 3, member 1 [*Homo sapiens*]
Protein Accession gi|187423904

Mean Expression Ratio 0.833
Median Expression Ratio 0.832
Credible Interval (0.642, 1.09)
Associated Peptides 8
Associated Spectra 10
Coverage NaN

[0217]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.56	0.8	1.1	SEQ ID NO: 778	CLDWWQEGPMYQIYPR	
3	0.63	0.84	1.1	SEQ ID NO: 779	EVDPIFGTMEDFENLVAAIHDK	
1	0.6	0.85	1.2	SEQ ID NO: 780	FMGTEAYAESIDR	
1	0.58	0.82	1.2	SEQ ID NO: 781	LIIDFIPNHTSDK	
1	0.59	0.84	1.2	SEQ ID NO: 782	LYQDLSLLHANELLNLR	
1	0.57	0.81	1.2	SEQ ID NO: 783	TQIPDVTVTQYSELYHDFTTTQVGMHD IVR	

-continued

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.58	0.82	1.2	SEQ ID NO: 784	WPNWMIGGPDSSR	
1	0.59	0.84	1.2	SEQ ID NO: 785	FLLEAK	

5.100 cell division cycle 42 isoform 1 [*Homo sapiens*]; cell division cycle 42 isoform 1 [*Homo sapiens*]
Protein Accession gi|89903012 gi|4757952

Mean Expression Ratio 1.20
Median Expression Ratio 1.20
Credible Interval (0.894, 1.62)

Associated Peptides 5
Associated Spectra 7

Coverage NaN

[0218]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.8	1.2	1.7	SEQ ID NO: 786	NVFDEAILAALPEPEPK	
3	0.95	1.3	1.8	SEQ ID NO: 787	QKPITPETAEK	
1	0.8	1.2	1.7	SEQ ID NO: 788	TLGLFDTAGQEDYDR	
1	0.79	1.2	1.7	SEQ ID NO: 789	PYTLGLFDTAGQEDYDR	
1	0.85	1.2	1.8	SEQ ID NO: 790	TPFLLVGTQIDLR	

5.101 CD59 antigen preproprotein [*Homo sapiens*]; CD59 antigen preproprotein 15 [*Homo sapiens*]; CD59 antigen preproprotein [*Homo sapiens*]; CD59 antigen preproprotein [*Homo sapiens*]; CD59 antigen preproprotein [*Homo sapiens*]; CD59 antigen preproprotein [*Homo sapiens*]; CD59 antigen preproprotein [*Homo sapiens*]; CD59 antigen preproprotein [*Homo sapiens*]
Protein Accession gi|42761474 gi|42716302 gi|42716299 gi|187829185 gi|187829183 gi|187829070 gi|187828910

Mean Expression Ratio 1.20
Median Expression Ratio 1.2
Credible Interval (0.832, 1.72)

Associated Peptides 1
Associated Spectra 5

Coverage NaN

[0219]

A	2.5	50	97.5	Sequence ID No.	Sequence
5	0.9	1.3	1.7	SEQ ID NO: 791	FEHCNFDVTTR

5.102 amnionless protein precursor [*Homo sapiens*]
Protein Accession gi|110611172

Mean Expression Ratio 1.2

Median Expression Ratio 1.20

Credible Interval (0.807, 1.81)

Associated Peptides 1

Associated Spectra 3

Coverage 0.0353

[0220]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.85	1.3	1.8	SEQ ID NO: 792	NPVFDVTASEELPLPR

SEQ ID NO: 793

1	M	G	V	L	G	R	V	L	L	W	L	Q	L	C	A	L	T	Q	A	V	S	K	L
	W	V	P	N	T	D	F	D	V	A	A	N	W	S	Q	N	R	T	P	C	A	G	G
	A	V	E	F	P	A	D	K	M	V	S	V	L	V	Q	E	G	H	A	V	S	D	M
	L	L	P	L	D	G	E	L	V	L	A												
81	S	G	A	G	F	G	V	S	D	V	G	S	H	L	D	C	G	A	G	E	P	A	V
	F	R	D	S	D	R	F	S	W	H	D	P	H	L	W	R	S	G	D	E	A	P	G
	L	F	F	V	D	A	E	R	V	P	C	R	H	D	D	V	F	F	P	P	S	A	S
	F	R	V	G	L	G	P	G	A	S	P												
161	V	R	V	R	S	I	S	A	L	G	R	T	F	T	R	D	E	D	L	A	V	F	L
	A	S	R	A	G	R	L	R	F	H	G	P	G	A	L	S	V	G	P	E	D	C	A
	D	P	S	G	C	V	C	G	N	A	E	A	Q	P	W	I	C	A	A	L	L	Q	P
	L	G	G	R	C	P	Q	A	A	C	H												
241	S	A	L	R	P	Q	G	Q	C	C	D	L	C	G	A	V	V	L	L	T	H	G	P
	A	F	D	L	E	R	Y	R	A	R	I	L	D	T	F	L	G	L	P	Q	Y	H	G
	L	Q	V	A	V	S	K	V	P	R	S	S	R	L	R	E	A	D	T	E	I	Q	V
	V	L	V	E	N	G	P	E	T	G	G												
321	A	G	R	L	A	R	A	L	L	A	D	V	A	E	N	G	E	A	L	G	V	L	E
	A	T	M	R	E	S	G	A	H	V	W	G	S	S	A	A	G	L	A	G	G	V	A
	A	A	V	L	L	A	L	L	V	L	L	V	A	P	P	L	L	R	R	A	G	R	L
	R	W	R	R	H	E	A	A	A	P	A												
401	G	A	P	L	G	F	R	N	P	V	F	D	V	T	A	S	E	E	L	P	L	P	R
	R	L	S	L	V	P	K	A	A	A	D	S	T	S	H	S	Y	F	V	N	P	L	F
	A	G	A	E	A	E	A																

5.103 von Willebrand factor A domain containing 1 isoform 1 [*Homo sapiens*]
Protein Accession gi|40068485

Mean Expression Ratio 0.834

Median Expression Ratio 0.836

Credible Interval (0.511, 1.35)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0404

[0221]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.48	0.8	1.3	SEQ ID NO: 794	EFVGQLVAPLPLGTGALR

SEQ ID NO: 795

1	M	L	P	W	T	A	L	G	L	A	L	S	L	R	L	A	L	A	R	S	G	A	E
	R	G	P	P	A	S	A	P	R	G	D	L	M	F	L	L	D	S	S	A	S	V	S
	H	Y	E	F	S	R	V	R	E	F	V	G	Q	L	V	A	P	L	P	L	G	T	G
	A	L	R	A	S	L	V	H	V	G	S												
81	R	P	Y	T	E	F	P	F	G	Q	H	S	S	G	E	A	A	Q	D	A	V	R	A
	S	A	Q	R	M	G	D	T	H	T	G	L	A	L	V	Y	A	K	E	Q	L	F	A
	E	A	S	G	A	R	P	G	V	P	K	V	L	V	W	V	T	D	G	G	S	S	D
	P	V	G	P	P	M	Q	E	L	K	D												
161	L	G	V	T	V	F	I	V	S	T	G	R	G	N	F	L	E	L	S	A	A	A	S
	A	P	A	E	K	H	L	H	F	V	D	V	D	D	L	H	I	I	V	Q	E	L	R
	G	S	I	L	D	A	M	R	P	Q	Q	L	H	A	T	E	I	T	S	S	G	F	R
	L	A	W	P	P	L	L	T	A	D	S												
241	G	Y	Y	V	L	E	L	V	P	S	A	Q	P	G	A	A	R	R	Q	Q	L	P	G
	N	A	T	D	W	I	W	A	G	L	D	P	D	T	D	Y	D	V	A	L	V	P	E
	S	N	V	R	L	L	R	P	Q	I	L	R	V	R	T	R	P	G	E	A	G	P	G
	A	S	G	P	E	S	G	A	G	P	A												
321	P	T	Q	L	A	A	L	P	A	P	E	E	A	G	P	E	R	I	V	I	S	H	A
	R	P	R	S	L	R	V	S	W	A	P	A	L	G	S	A	A	A	L	G	Y	H	V
	Q	F	G	P	L	R	G	G	E	A	Q	R	V	E	V	P	A	G	R	N	C	T	T
	L	Q	G	L	A	P	G	T	A	Y	L												
401	V	T	V	T	A	A	F	R	S	G	R	E	S	A	L	S	A	K	A	C	T	P	D
	G	P	R	P	R	P	R	P	V	P	R	A	P	T	P	G	T	A	S	R	E	P	

5.104 vacuolar protein sorting 28 isoform 1 [*Homo sapiens*]
Protein Accession gi|7705885

Mean Expression Ratio 1.20

Median Expression Ratio 1.19

Credible Interval (0.815, 1.77)

Associated Peptides 3

Associated Spectra 3

Coverage 0.249

[0222]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.79	1.2	1.9	SEQ ID NO: 796	QMLFDLESAYNAFNR
1	0.82	1.3	2.0	SEQ ID NO: 797	QTVSQWLQTLSGMSASDELDDSQVR

-continued				
1	0.76	1.2	1.8	SEQ ID NO: 798
QVQGSEISSIDEFCR				
SEQ ID NO: 799				
1	M	F	H	G I P A T P G I G A P G N K P E L Y E E
	V	K	L	Y K N A R E R E K Y D N M A E L F A V V
	K	T	M	Q A L E K A Y I K D C V S P S E Y T A A
	C	S	R	L L V Q Y K A A
81	F	R	Q	V Q G S E I S S I D E F C R K F R L D C
	P	L	A	M E R I K E D R P I T I K D D K G N L N
	R	C	I	A D V V S L F I T V M D K L R L E I R A
	M	D	E	I Q P D L R E L
161	M	E	T	M H R M S H L P P D F E G R Q T V S Q W
	L	Q	T	L S G M S A S D E L D D S Q V R Q M L F
	D	L	E	S A Y N A F N R F L H A

5.105 mannosidase, alpha, class 2B, member 1 precursor
[Homo sapiens]

Protein Accession gi|51873064

Mean Expression Ratio 1.19

Median Expression Ratio 1.19

Credible Interval (0.812, 1.76)

Associated Peptides 3

Associated Spectra 3

Coverage 0.0415

[0223]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.79	1.2	1.9	SEQ ID NO: 800	ELVDYFLNVATAQGR
1	0.78	1.2	1.9	SEQ ID NO: 801	FQVIVYNPLGR
1	0.76	1.2	1.9	SEQ ID NO: 802	HLVLDDTAQAAAAGHR
SEQ ID NO: 803					
1	M	G	A	Y A R A S G V C A R G C L D S A G P W T	
	M	S	R	A L R P P L P P L C F F L L L L A A A G	
	A	R	A	G G Y E T C P T V Q P N M L N V H L L P	
	H	T	H	D D V G W L K T	
81	V	D	Q	Y F Y G I K N D I Q H A G V Q V I L D S	
	V	I	S	A L L A D P T R R F I Y V E I A F F S R	
	W	H	Q	Q T N A T Q E V V R D L V R Q G R L E	
	F	A	N	G G W V M N D E	
161	A	A	T	H Y G A I V D Q M T L G L R F L E D T F	
	G	N	D	G R P R V A W H I D P F G H S R E Q A S	
	L	F	A	Q M G F D G F F F G R L D Y Q D K W V R	
	M	Q	K	L E M E Q V W R	
241	A	S	T	S L K P P T A D L F T G V L P N G Y N P	
	P	R	N	L C W D V L C V D Q P L V E D P R S P E	
	Y	N	A	K E L V D Y F L N V A T A Q G R Y Y R T	
	N	H	T	V M T M G S D F	
321	Q	Y	E	N A N M W F K N L D K L I R L V N A Q Q	
	A	K	G	S S V H V L Y S T P A C Y L W E L N K A	
	N	L	T	W S V K H D D F F P Y A D G P H Q F W T	
	G	Y	F	S S R P A L K R	

-continued				
401	Y	E	R	L S Y N F L Q V C N Q L E A L V G L A A
	N	V	G	P Y G S G D S A P L N E A M A V L Q H H
	D	A	V	S G T S R Q H V A N D Y A R Q L A A G W
	G	P	C	E V L L S N A L
481	A	R	L	R G F K D H F T F C Q Q L N I S I C P L
	S	Q	T	A A R F Q V I V Y N P L G R K V N W M V
	R	L	P	V S E G V F V V K D P N G R T V P S D V
	V	I	F	P S S D S Q A H
561	P	P	E	L L F S A S L P A L G F S T Y S V A Q V
	P	R	W	K P Q A R A P Q P I P R R S W S P A L T
	I	E	N	E H I R A T F D P D T G L L M E I M N M
	N	Q	Q	L L L P V R Q T
641	F	F	W	Y N A S I G D N E S D Q A S G A Y I F R
	P	N	Q	Q K P L P V S R W A Q I H L V K T P L V
	Q	E	V	H Q N F S A W C S Q V V R L Y P G Q R H
	L	E	L	E W S V G P I P
721	V	G	D	T W G K E V I S R F D T P L E T K G R F
	Y	T	D	S N G R E I L E R R R D Y R P T W K L N
	Q	T	E	P V A G N Y Y P V N T R I Y I T D G N M
	Q	L	T	V L T D R S Q G
801	G	S	S	L R D G S L E L M V H R R L L K D D G R
	G	V	S	E P L M E N G S G A W V R G R H L V L L
	D	T	A	Q A A A A G H R L L A E Q E V L A P Q V
	V	L	A	P G G G A A Y N
881	L	G	A	P P R T Q F S G L R R D L P P S V H L L
	T	L	A	S W G P E M V L L R L E H Q F A V G E D
	S	G	R	N L S A P V T L N L R D L F S T F T I T
	R	L	Q	E T T L V A N Q
961	L	R	E	A A S R L K W T T N T G P T P H Q T P Y
	Q	L	D	P A N I T L E P M E I R T F L A S V Q W
	K	E	V	D G

5.106 chloride intracellular channel 1 [Homo sapiens]

Protein Accession gi|14251209

Mean Expression Ratio 1.19

Median Expression Ratio 1.19

Credible Interval (0.876, 1.62)

Associated Peptides 4

Associated Spectra 7

Coverage 0.224

[0224]

A	2.5	50	97.5	Se- quence ID No.	Sequence
1	0.82	1.2	1.8	SEQ ID NO: 804	LAALNPESNTAGLDIFAK
2	0.83	1.2	1.7	SEQ ID NO: 805	LHIVQVVCK

-continued				
1 0.8	1.2	1.7	SEQ ID NO: 806	LTSPLPPEEVDETSAEDEGVSQR
3 0.9	1.3	1.8	SEQ ID NO: 807	VLDNYLTSPLPPEEVDETSAEDEGVSQR
SEQ ID NO: 808				
1	M	A	E	E
	Q	P	Q	V
	E	L	F	V
	K	A	G	S
	D	G	A	K
	I	G	N	
	C	P	F	S
	Q	R	L	F
	M	V	L	W
	L	K	G	V
	T	F	N	V
	T	T	V	
	D	T	K	R
	R	T	E	T
	V	Q	K	L
	C	P	G	G
	Q	L	P	F
	L	L	Y	
	G	T	E	V
	H	T	D	T
	N	K	I	
81	E	E	F	L
	E	A	V	L
	C	P	P	R
	Y	P	K	L
	A	A	L	N
	P	E	S	
	N	T	A	G
	L	D	I	F
	A	K	F	S
	A	Y	I	K
	N	S	N	P
	A	L	N	
	D	N	L	E
	K	G	L	L
	K	A	L	K
	V	L	D	N
	Y	L	T	S
	P	L	P	
	E	E	V	D
	E	T	S	A
	E	D	E	
161	G	V	S	Q
	R	K	F	L
	D	G	N	E
	L	T	L	A
	D	C	N	L
	L	P	K	
	L	H	I	V
	Q	V	V	C
	K	K	Y	R
	G	F	T	I
	P	E	A	F
	R	G	V	
	H	R	Y	L
	S	N	A	Y
	A	R	E	E
	F	A	S	T
	C	P	D	D
	E	E	I	
	E	L	A	Y
	E	Q	V	A
	K	A	L	
241	K			

5.107 complement factor D preproprotein [*Homo sapiens*]
Protein Accession gi|42544239

Mean Expression Ratio 0.84
Median Expression Ratio 0.84
Credible Interval (0.568, 1.24)

Associated Peptides 3
Associated Spectra 3

Coverage 0.241
[0225]

Sequence				
A 2.5	50	97.5	ID No.	Sequence
1 0.54	0.85	1.3	SEQ ID NO: 809	AVPHPDSPQPDITDHDLLLLQLSEK
1 0.53	0.83	1.3	SEQ ID NO: 810	RPDSLQHVLLPVLDR
1 0.51	0.81	1.3	SEQ ID NO: 811	GDGGGPLVCGGVLEGVVTSGSR
SEQ ID NO: 812				
1	M	H	S	W
	E	R	L	A
	V	L	V	L
	L	G	A	A
	A	C	A	A
	P	P	R	
	G	R	I	L
	G	R	E	A
	E	A	H	A
	R	P	Y	M
	A	S	V	Q
	L	N		
	G	A	H	L
	C	G	G	V
	L	V	A	E
	Q	W	V	L
	S	A	A	H
	C	L	E	
	D	A	A	D
	G	K	V	Q
	V	L	L	
81	G	A	H	S
	L	S	Q	P
	E	P	S	K
	R	L	Y	D
	V	L	R	A
	V	P	H	
	P	D	S	Q
	P	D	T	I
	D	H	D	L
	L	L	L	Q
	L	S	E	K
	A	T	L	
	G	P	A	V
	R	P	L	P
	W	Q	R	V
	D	R	D	V
	A	P	G	T
	L	C	D	
	V	A	G	W
	G	I	V	N
	H	A	G	
161	R	R	P	D
	S	L	Q	H
	V	L	L	P
	V	L	D	R
	A	T	C	N
	R	R	T	
	H	H	D	G
	A	I	T	E
	R	L	M	C
	A	E	S	N
	R	R	D	S
	C	K	G	

-continued				
	D	S	G	G
	P	L	V	C
	G	G	V	L
	E	G	V	V
	T	S	G	S
	R	V	C	
241	V	A	S	Y
	A	A	W	I
	D	S	V	L
	A			

5.108 scavenger receptor class B, member 2 [*Homo sapiens*]
Protein Accession gi|5031631

Mean Expression Ratio 0.842
Median Expression Ratio 0.841
Credible Interval (0.677, 1.04)

Associated Peptides 11
Associated Spectra 17

Coverage 0.247
[0226]

Sequence				
A 2.5	50	97.5	ID No.	Sequence
1 0.64	0.89	1.2	SEQ ID NO: 813	DEVLYVFPSPDFCR
1 0.59	0.83	1.2	SEQ ID NO: 814	EIIEAMLK
1 0.58	0.81	1.1	SEQ ID NO: 815	FVSAIEGMHPNQEDHETFDIN
				PLTGIIILK
2 0.6	0.82	1.1	SEQ ID NO: 816	ITFSDYESVQGLPAFR
1 0.58	0.8	1.1	SEQ ID NO: 817	IVEWNGK
3 0.59	0.79	1.1	SEQ ID NO: 818	KLDDFVETGDIR
1 0.62	0.86	1.2	SEQ ID NO: 819	LDDFVETGDIR
1 0.6	0.83	1.2	SEQ ID NO: 820	SDYESVQGLPAFR
4 0.69	0.91	1.2	SEQ ID NO: 821	SVYITFSDYESVQGLPAFR
1 0.61	0.85	1.2	SEQ ID NO: 822	TLNIPVLTVIEWSQVHFLR
1 0.61	0.84	1.2	SEQ ID NO: 823	TSLDWWITDK

SEQ ID NO: 824				
1	M	G	R	C
	C	F	Y	T
	A	G	T	L
	S	L	L	L
	L	L	V	T
	S	V	T	L
	L	V	A	R
	V	F	Q	K
	A	V	D	Q
	S	I	E	K
	K	I	V	L
	R	N	G	
	T	E	A	F
	D	S	W	E
	K	P	P	L
	P	V	Y	T
	Q	F	Y	F
	F	P	N	V
	T	N	P	E
	E	I	L	R
	G	E	T	
81	P	R	V	E
	E	V	G	P
	Y	T	Y	R
	E	L	R	N
	K	A	N	I
	Q	F	G	
	D	N	G	T
	T	I	S	A
	V	S	N	K
	A	Y	V	F
	E	R	D	Q
	S	V	G	
	D	P	K	I
	D	L	I	R
	T	L	N	I
	P	V	L	T
	V	I	E	W
	S	Q	V	
	H	F	L	R
	E	I	I	E
	A	M	L	
161	K	A	Y	Q
	Q	K	L	F
	V	T	H	T
	V	D	E	L
	L	W	G	Y
	K	D	E	
	I	L	S	L
	I	H	V	F
	R	P	D	I
	S	P	Y	F
	G	L	F	Y
	E	K	N	
	G	T	N	D
	G	D	Y	V
	F	L	T	G
	E	D	S	Y
	L	N	F	T
	K	I	V	
	E	W	N	G
	K	T	S	L
	D	W	W	

-continued

241	I	T	D	K	C	N	M	I	N	G	T	D	G	D	S	F	H	P	L	I	T	K	D
	E	V	L	Y	V	F	P	S	D	F	C	R	S	V	Y	I	T	F	S	D	Y	E	S
	V	Q	G	L	P	A	F	R	Y	K	V	P	A	E	I	L	A	N	T	S	D	N	A
	G	F	C	I	P	E	G	N	C	L	G												
321	S	G	V	L	N	V	S	I	C	K	N	G	A	P	I	I	M	S	F	P	H	F	Y
	Q	A	D	E	R	F	V	S	A	I	E	G	M	H	P	N	Q	E	D	H	E	T	F
	V	D	I	N	P	L	T	G	I	I	L	K	A	A	K	R	F	Q	I	N	I	Y	V
	K	K	L	D	D	F	V	E	T	G	D												
401	I	R	T	M	V	F	P	V	M	Y	L	N	E	S	V	H	I	D	K	E	T	A	S
	R	L	K	S	M	I	N	T	T	L	I	I	T	N	I	P	Y	I	I	M	A	L	G
	V	F	F	G	L	V	F	T	W	L	A	C	K	G	Q	G	S	M	D	E	G	T	A
	D	E	R	A	P	L	I	R	T														

5.109 plasminogen [*Homo sapiens*]
Protein Accession gi|4505881

Mean Expression Ratio 0.845

Median Expression Ratio 0.844

Credible Interval (0.519, 1.39)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0272

[0227]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.49	0.81	1.4	SEQ ID NO: 825	VILGAHQEVNLEPHVQEIEVSR
SEQ ID NO: 826					
1MEHK EVV L L L L L F L K S G Q G E P L D D Y V N T Q G A S L F S V T K K Q					
L G A G S I E E C A A K C E E D E E F T C R A F Q Y H S K E Q Q C V I M A E N R					
81K S S I I I R M R D V V L F E K K V Y L S E C K T G N G K N Y R G T M S K T K N					
G I T C Q K W S S T S P H R P R F S P A T H P S E G L E E N Y C R N P D N D P Q					
161G P W C Y T T D P E K R Y D Y C D I L E C E E E C M H C S G E N Y D G K I S K					
T M S G L E C Q A W D S Q S P H A H G Y I P S K F P N K N L K K N Y C R N P D R E					
241L R P W C F T T D P N K R W E L C D I P R C T T P P P S S G P T Y Q C L K G T G					
E N Y R G N V A V T V S G H T C Q H W S A Q T P H T H N R T P E N F P C K N L D					
321E N Y C R N P D G K R A P W C H T T N S Q V R W E Y C K I P S C D S S P V S T					
E Q L A P T A P P E L T P V V Q D C Y H G D G Q S Y R G T S S T T T T G K K C Q S					
401W S S M T P H R H Q K T P E N Y P N A G L T M N Y C R N P D A D K G P W C F					
T T D P S V R W E Y C N L K K C S G T E A S V V A P P P V V L L P D V E T P S E E D					
481C M F G N G K G Y R G K R A T T V T G T P C Q D W A A Q E P H R H S I F T P E					
T N P R A G L E K N Y C R N P D G D V G G P W C Y T T N P R K L Y D Y C D V P Q C					
561A A P S F D C G K P Q V E P K K C P G R V V G G C V A H P H S W P W Q V S L					
R T R F G M H F C G G T L I S P E W V L T A A H C L E K S P R P S S Y K V I L G A H					
641Q E V N L E P H V Q E I E V S R L F L E P T R K D I A L L K L S S P A V I T D K V					
I P A C L P S P N Y V V A D R T E C F I T G W G E T Q G T F G A G L L K E A Q					
721L P V I E N K V C N R Y E F L N G R V Q S T E L C A G H L A G G T D S C Q G D					
S G G P L V C F E K D K Y I L Q G V T S W G L G C A R P N K P G V Y V R V S R F V					
801T W I E G V M R N N					

5.110 ficolin 2 isoform a precursor [*Homo sapiens*]
Protein Accession gi|61744445

Mean Expression Ratio 0.842

Median Expression Ratio 0.844

Credible Interval (0.539, 1.31)

Associated Peptides 1

Associated Spectra 2

Coverage 0.0671

[0228]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.52	0.81	1.2	SEQ ID NO: 827	AGPPGPNGAPGEPQPCLTGPR
SEQ ID NO: 828					
1ME L D R A V G V L G A A T L L L S F L G M A W A L Q A A D T C P E V K M V G					
L E G S D K L T I L R G C P G L P G A P G P K G E A G T N G K R G E R G P P G P P					
81G K A G P P G P N G A P G E P Q P C L T G P R T C K D L L D R G H F L S G W H T					
I Y L P D C R P L T V L C D M D T D G G G W T V F Q R R V D G S V D F Y R D W A					
161T Y K Q G F G S R L G E F W L G N D N I H A L T A Q G T S E L R V D L V D F E					
D N Y Q F A K Y R S F K V A D E A E K Y N L V L G A F V E G S A G D S L T F H N N					
241Q S F S T K D Q D N D L N T G N C A V M F Q G A W W Y K N C H V S N L N G R					
Y L R G T H G S F A N G I N W K S G K G Y N Y S Y K V S E M K V R P A					

5.111 glycoporphin C isoform 2 [*Homo sapiens*]; glycoporphin C isoform 1 [*Homo sapiens*]
Protein Accession gil8051605 gil4504229

Mean Expression Ratio 1.18

Median Expression Ratio 1.18

Credible Interval (0.727, 1.93)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0229]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.72	1.2	2.1	SEQ ID NO: 829	GTEFAESADAALQGDPALQ DAGDSSR

5.112 prolylcarboxypeptidase isoform 1 preproprotein [*Homo sapiens*]; prolylcarboxypeptidase isoform 2 preproprotein [*Homo sapiens*]
Protein Accession gil4826940 gil117306169

Mean Expression Ratio 0.846

Median Expression Ratio 0.847

Credible Interval (0.677, 1.06)

Associated Peptides 9

Associated Spectra 15

Coverage NaN

[0230]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.6	0.84	1.2	SEQ ID NO: 830	AMLVFAEHR
1	0.59	0.83	1.2	SEQ ID NO: 831	DITDTLVAVTISEGAH
1	0.59	0.83	1.2	SEQ ID NO: 832	DITDTLVAVTISEGAHHL
4	0.65	0.86	1.1	SEQ ID NO: 833	DITDTLVAVTISEGAHH LDLR
2	0.61	0.84	1.2	SEQ ID NO: 834	FLTSEQALADFAELIK
3	0.63	0.84	1.1	SEQ ID NO: 835	HLNFLTSEQALADFA ELIK
1	0.6	0.83	1.2	SEQ ID NO: 836	VDHFGFNTVK
1	0.59	0.82	1.2	SEQ ID NO: 837	YYGESLPFGDNSFK
1	0.62	0.87	1.2	SEQ ID NO: 838	NALDPMSVLLAR

5.113 collagen, type VI, alpha 1 precursor [*Homo sapiens*]
Protein Accession gil87196339

Mean Expression Ratio 0.85

Median Expression Ratio 0.848

Credible Interval (0.525, 1.37)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0175

[0231]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.5	0.82	1.3	SEQ ID NO: 839	DAEEAISQTIDTIVDMIK
SEQ ID NO: 840					
1MRAARALLPLLLQACWTAQAQDEPETPRAVAFQDCPVDLFF					
VLDTSESVALRLKPYGALVDKVKSF TKRFIDNLRDRYYRC					
81DRNLVWNAGALHYSDEVEI IQGLTRMPGGRDALKSSVDA					
VKYFGKGT YTDCAIKKGLEQLLVGGSHLKENKYLI VVT DGH					
161PLEGYKEPCGGLED AVNEAKHLGVKVF SVAITPDHLEPR					
LSIIATDHTYRRNFTAADWQGSRDAEEAISQTIDTIVDMIK					
241NNVEQVCCSFECQPARGPPGLRGDPGFEGERGKPGLPGE					
KGEAGDPPGRPGDLGPVGYQGMKGEKGSRGEEKGSRGPKGYKG					
321EKGKRGIDGVDGVKGEMGYPLPGCKGSPGF DGIQGP PG					
PKGDPGAFGLKGEKGEPGA DGEAGRPGSSGPSGDEGQPGEP					
401GPPGEKGEAGDEGNPGPDGAPGERGGPGERGPRGTPGTR					
GPRGDPGEAGPQGDQGREGPVGVPGDPGEAGPIGPKGYRGD					
481EGPPGSEGARGAPGPAGPPGDPGLMGERGEDGPAGNGTE					
GFPGFPGYPGNRGAPGINGTKGYPLKGDDEGEAGDPGD DNN					
561DIAPRGVKGAKGYRGPPEGPPQGP PGHQGP GPDECEILDII					
MKMCCSCCECKCGPIDLLFVLDSSESIGLQNF EIAKDFVVK					
641VIDRLSRDELVKFEPGQSYAGVVQYSHSQMQEHVSLRSP					
SIRNVQELKEAIKSLQWMAGGTFTGEALQYTRDQLLPPSPN					
721NRIALVITDGRSDTQRDTTPLNLCS PGIQVVS VGIKDV F					
DFIPGSDQLNVI SCQGLAPSQGRPGLSLVKENYAE LLEDA					
801FLKNVTAQICIDKKCPDYTCPI TFS SPADITILLDGSASVG					
SHNFDTTKRFAKRLAERFLTAGR TDPAHDV RVAVVQYSG					
881TGQQRPERASLQFLQNYTALASAVDAMDFINDATDVNDA					
LGYVTRFYREASSGA AKKRLLLFS DGNSQGATPAAIEKAVQ					
961EAQRAGIEIFVVVVGRQVNEPHIRVLVTGKTAEYDVAYG					
ESHLFRVP SYQALLRGV FHQTVSRKV ALG					

5.114 calmodulin 1 [Homo sapiens]; calmodulin 3 [Homo sapiens]; calmodulin 2 [Homo sapiens]

Protein Accession gi|5901912 gi|58218968 gi|4502549

Mean Expression Ratio 1.18

Median Expression Ratio 1.18

Credible Interval (0.728, 1.92)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0232]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.74	1.2	2.1	SEQ ID NO: 841	VFDKDGNGYISAAELR

5.115 annexin I [Homo sapiens]

Protein Accession gi|4502101

Mean Expression Ratio 1.17

Median Expression Ratio 1.17

Credible Interval (0.795, 1.74)

Associated Peptides 2

Associated Spectra 3

Coverage 0.078

[0233]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.8	1.2	1.8	SEQ ID NO: 842	GLGTDEDTLIEILASR
1	0.76	1.2	1.8	SEQ ID NO: 843	TPAQFDADELRL

SEQ ID NO: 844

1MAMVSEFLKQAWFIENEEQEYVQTVKSSKGGPGSAVSPYP
TFNPSSDVAALHKAIMVKGVDEATIIDILTKRNNNAQRQI

81KAAAYLQETGKPLDETLKKALTGHLEEVVLALLKTPAQFDA
DELRAAMKGLGTDEDTLIEILASRTNKEIRDINRVYREEEL

161KRDLAKDITSDTSGDFRNALLSLAKGDRSEDFGVNEDLA
DS DARALYEAGERRKGTDVNVFNTILTTTSYPQLRRVFQKY

241TKYSKHDMMNKVLDLELKGDI EKCLTAIVKCATSKPAFFA
EKLHQAMKGVGTRHKALIRIMVSRSEIDMNDIKAFYQKMYG

321ISLCQAILDETKGDYEKILVALLCGGN

5.116 ras homolog gene family, member G [*Homo sapiens*]
Protein Accession gi|46249393

Mean Expression Ratio 1.17

Median Expression Ratio 1.17

Credible Interval (0.723, 1.92)

Associated Peptides 1

Associated Spectra 1

Coverage 0.089

[0234]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.73	1.2	2	SEQ ID NO: 845	TVNLNLWDTAGQEEYDR

SEQ ID NO: 846

1MQSIKCVVVG DGAVGKTCLLICYTTNAFPKEYIPTVFDNYS
AQSAVDGRTVNLNLWDTAGQEEYDRRLRTLSYPQTNVFVI

81CF S I A S P P S Y E N V R H K W H P E V C H H C P D V P I L L V G T K K D L R
A Q P D T L R R L K E Q G Q A P I T P Q Q G Q A L A K Q I H A V R Y L E C S A L

161Q Q D G V K E V F A E A V R A V L N P T P I K R G R S C I L L

5.117 immunoglobulin superfamily, member 8 [*Homo sapiens*]

Protein Accession gi 16445029

Mean Expression Ratio 0.849

Median Expression Ratio 0.853

Credible Interval (0.548, 1.29)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0440

[0235]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.52	0.84	1.3	SEQ ID NO: 847	VLPDVLQVSAAPPGPR
1	0.52	0.83	1.3	SEQ ID NO: 848	EVLVPEGPLYR

SEQ ID NO: 849

1MGA LRPTLLPPLPLLLMLLGMGCW AREVLVPEGPLYRV
AGTAVSISCNVTGYEGPAQQNF EWFLYRPEAPDTALGIVS

-continued

81	T	K	D	T	Q	F	S	Y	A	V	F	K	S	R	V	V	A	G	E	V	Q	V	Q	R	L	Q	G	D	A	V	V	L	K	I	A	R	L	Q	A			
	Q	D	A	G	I	Y	E	C	H	T	P	S	T	D	T	R	Y	L	G	S	Y	S	G	K	V	E	L	R	V	L	P	D	V	L	Q	V	S	A	A	P	P	
161	G	P	R	G	R	Q	A	P	T	S	P	P	R	M	T	V	H	E	G	Q	E	L	A	L	G	C	L	A	R	T	S	T	Q	K	H	T	H	L	A			
	V	S	F	G	R	S	V	P	E	A	P	V	G	R	S	T	L	Q	E	V	V	G	I	R	S	D	L	A	V	E	A	G	A	P	Y	A	E	R	L	A	A	
241	G	E	L	R	L	G	K	E	G	T	D	R	Y	R	M	V	V	G	G	A	Q	A	G	D	A	G	T	Y	H	C	T	A	A	E	W	I	Q	D				
	P	D	G	S	W	A	Q	I	A	E	K	R	A	V	L	A	H	V	D	V	Q	T	L	S	S	Q	L	A	V	T	V	G	P	G	E	R	R	I	G	P	G	E
321	P	L	E	L	L	C	N	V	S	G	A	L	P	P	A	G	R	H	A	A	Y	S	V	G	W	E	M	A	P	A	G	A	P	G	P	G	R	L	V			
	A	Q	L	D	T	E	G	V	G	S	L	G	P	G	Y	E	G	R	H	I	A	M	E	K	V	A	S	R	T	Y	R	L	R	L	E	A	A	R	P	G	D	
401	A	G	T	Y	R	C	L	A	K	A	Y	V	R	G	S	G	T	R	L	R	E	A	A	S	A	R	S	R	P	L	P	V	H	V	R	E	E	G	V			
	V	L	E	A	V	A	W	L	A	G	G	T	V	Y	R	G	E	T	A	S	L	L	C	N	I	S	V	R	G	G	P	P	G	L	R	L	A	A	S	W	W	
481	V	E	R	P	E	D	G	E	L	S	S	V	P	A	Q	L	V	G	G	V	G	Q	D	G	V	A	E	L	G	V	R	P	G	G	P	V	S	V				
	E	L	V	G	P	R	S	H	R	L	R	L	H	S	L	G	P	E	D	E	G	V	Y	H	C	A	P	S	A	W	V	Q	H	A	D	Y	S	W	Y	Q	A	
561	G	S	A	R	S	G	P	V	T	V	P	Y	M	H	A	L	D	T	L	F	V	P	L	L	V	G	T	G	V	A	L	V	T	G	A	T	V	L				
	G	T	I	T	C	C	F	M	K	R	L	R	K	R																												

5.118 Fc fragment of IgG binding protein [*Homo sapiens*] Associated Peptides 3
Protein Accession gill154146262

Mean Expression Ratio 1.17 Associated Spectra 6

Median Expression Ratio 1.17 Coverage 0.00833

Credible Interval (0.839, 1.62) [0236]

	A	2.5	50	97.5	Sequence ID No.	Sequence																																				
	4	0.84	1.2	1.6	SEQ ID NO: 850	VNGVLTALPVSVADGR																																				
	1	0.8	1.2	1.8	SEQ ID NO: 851	YYPLGEVFYPGPECER																																				
	1	0.8	1.2	1.8	SEQ ID NO: 852	APGWDPLCWDECR																																				
SEQ ID NO: 853																																										
1	M	G	A	L	W	S	W	I	L	W	A	G	A	T	L	L	W	G	L	T	Q	E	A	S	V	D	L	K	N	T	G	R	E	E	F	L	T	A				
	F	L	Q	N	Y	Q	L	A	Y	S	K	A	Y	P	R	L	L	I	S	S	L	S	E	S	P	A	S	V	S	I	L	S	Q	A	D	N	T	S	K	K	V	
81	T	V	R	P	G	E	S	V	M	V	N	I	S	A	K	A	E	M	I	G	S	K	I	F	Q	H	A	V	V	I	H	S	D	Y	A	I	S	V	Q	A	L	
	N	A	K	P	D	T	A	E	L	T	L	R	P	I	Q	A	L	G	T	E	Y	F	V	L	T	P	P	G	T	S	A	R	N	V	K	E	F	A				
161	V	V	A	G	A	A	G	A	S	V	S	V	T	L	K	G	S	V	T	F	N	G	K	F	Y	P	A	G	D	V	L	R	V	T	L	Q	P	Y	N			
	V	A	Q	L	Q	S	S	V	D	L	S	G	S	K	V	T	A	S	S	P	V	A	V	L	S	G	H	S	C	A	Q	K	H	T	T	C	N	H	V	V	E	
241	Q	L	L	P	T	S	A	W	G	T	H	Y	V	V	P	T	L	A	S	Q	S	R	Y	D	L	A	F	V	V	A	S	Q	A	T	K	L	T	Y	N			
	H	G	G	I	T	G	S	R	G	L	Q	A	G	D	V	E	F	E	F	E	V	R	P	S	W	P	L	Y	L	S	A	N	V	G	I	Q	V	L	L	F	G	T
321	G	A	I	R	N	E	V	T	Y	D	P	Y	L	V	L	I	P	D	V	A	A	Y	C	P	A	Y	V	V	K	S	V	P	G	C	E	G	V	A	L			
	V	V	A	Q	T	K	A	I	S	G	L	T	I	D	G	H	A	V	G	A	K	L	T	W	E	A	V	P	G	S	E	F	S	Y	A	E	V	E	L	G	T	
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	V	E	P	S	C	E	G	M	Q	C	A	A	G	Q	R	C	Q	V	V	G	G	K	A	G	C	V	A	E	S	T	A	V	C	R	A	Q	G	D	P	H	Y	
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	R	G	S	R	R	V	S	Y	V	G	L	V	T	V	R	A	Y	S	H	S	V	S	L	T	R	G	E	V	G	F	V	L	V	D	N	Q	R	S	R	L	P	
561	V	S	L	S	E	G	R	L	R	V	Y	Q	S	G	P	R	A	V	V	E	L	V	F	G	L	V	V	T	Y	D	W	D	C	Q	L	A	L	S	L			
	P	A	R	F	Q	D	Q	V	C	G	L	C	G	N	Y	N	G	D	P	A	D	D	F	L	T	P	D	G	A	L	A	P	D	A	V	E	F	A	S	S	W	
641	K	L	D	D	G	D	Y	L	C	E	D	G	C	Q	N	N	C	P	A	C	T	P	G	Q	A	Q	H	Y	E	G	D	R	L	C	G	M	L	T				
	K	L	D	G	P	F	A	V	C	H	D	T	L	D	P	R	P	F	L	E	Q	C	V	Y	D	L	C	V	V	G	G	E	R	L	S	L	C	R	G	L	S	A
721	Y	A	Q	A	C	L	E	L	G	I	S	V	G	D	W	R	S	P	A	N	C	P	L	S	C	P	A	N	S	R	Y	E	L	C	G	P	A	C	P	T		
	S	C	N	G	A	A	A	P	S	N	C	S	G	R	P	C	V	E	G	C	V	C	L	P	G	F	V	A	S	G	G	A	C	V	P	A	S	S	C	G		
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	Q	S	C	P	A	G	E	R	C	S	V	Q	N	G	L	L	G	C	Y	P	D	R	F	G	T	C	Q	G	S	G	D	P	H	Y	V	S	F	D	G	R	R	F

-continued

881 D F M G T C T Y L L V G S C G Q N A A L P A F R V L V E N E H R G S Q T V S Y
T R A V R V E A R G V K V A V R R E Y P G Q V L V D D V L Q Y L P F Q A A D G Q V

961 Q V F R Q G R D A V V R T D F G L T V T Y D W N A R V T A K V P S S Y A E A
L C G L C G N F N G D P A D D L A L R G G G Q A A N A L A F G N S W Q E E T R P
G C

1041 G A T E P G D C P K L D S L V A Q Q L Q S K N E C G I L A D P K G P F R E C H
S K L D P Q G A V R D C V Y D R C L L P G Q S G P L C D A L A T Y A A A C Q A A G

1121 A T V H P W R S E E L C P L S C P P H S H Y E A C S Y G C P L S C G D L P V P
G G C G S E C H E G C V C D E G F A L S G E S C L P L A S C G C V H Q G T Y H P P

1201 G Q T F Y P G P G C D S L C H C Q E G G L V S C E S S S C G P H E A C Q P S G
G S L G C V A V G S S T C Q A S G D P H Y T T F D G R R F D F M G T C V Y V L A Q

1281 T C G T R P G L H R F A V L Q E N V A W G N G R V S V T R V I T V Q V A N F
T L R L E Q R Q W K V T V N G V D M K L P V V L A N G Q I R A S Q H G S D V V I
E T

1361 D F G L R V A Y D L V Y Y V R V T V P G N Y Y Q Q M C G L C G N Y N G D P
K D D F Q K P N G S Q A G N A N E F G N S W E E V V P D S P C L P P T P C P P G S
E D

1441 C I P S H K C P P E L E K K Y Q K E E F C G L L S S P T G P L S S C H K L V D P
Q G P L K D C I F D L C L G G G N L S I L C S N I H A Y V S A C Q A A G G H V E

1521 P W R T E T F C P M E C P P N S H Y E L C A D T C S L G C S A L S A P P Q C Q
D G C A E G C Q C D S G F L Y N G Q A C V P I Q Q C G C Y H N G V Y Y E P E Q T V

1601 L I D N C R Q Q C T C H A G K G M V C Q E H S C K P G Q V C Q P S G G I L S C
V T K D P C H G V T C R P Q E T C K E Q G G Q G V C L P N Y E A T C W L W G D P H

1681 Y H S F D G R K F D F Q G T C N Y V L A T T G C P G V S T Q G L T P F T V T T
K N Q N R G N P A V S Y V R V T V A A L G T N I S I H K D E I G K V R V N G V L

1761 T A L P V S V A D G R I S V T Q G A S K A L L V A D F G L Q V S Y D W N W R
V D V T L P S S Y H G A V C G L C G N M D R N P N N D Q V F P N G T L A P S I P I W

1841 G G S W R A P G W D P L C W D E C R G S C P T C P E D R L E Q Y E G P G F C
G P L A P G T G G P F T T C H A H V P P E S F F K G C V L D V C M G G G D R D I L C

1921 K A L A S Y V A A C Q A A G V V I E D W R A Q V G C E I T C P E N S H Y E V
C G S P C P A S C P S P A P L T T P A V C E G P C V E G C Q C D A G F V L S A D R C

2001 V P L N N G C G C W A N G T Y H E A G S E F W A D G T C S Q W C R C G P G
G G S L V C T P A S C G L G E V C G L L P S G Q H G C Q P V S T A E C Q A W G D P
H Y

2081 V T L D G H R F N F Q G T C E Y L L S A P C H G P P L G A E N F T V T V A N E
H R G S Q A V S Y T R S V T L Q I Y N H S L T L S A R W P R K L Q V D G V F V T L

2161 P F Q L D S L L H A H L S G A D V V V T T T S G L S L A F D G D S F V R L R V
P A A Y A G S L C G L C G N Y N Q D P A D D L K A V G G K P A G W Q V G G A Q
G C

2241 G E C V S K P C P S P C T P E Q Q E S F G G P D A C G V I S A T D G P L A P C H
G L V P P A Q Y F Q G C L L D A C Q V Q G H P G G L C P A V A T Y V A A C Q A A

2321 G A Q L R E W R R P D F C P F Q C P A H S H Y E L C G D S C P G S C P S L S A
P E G C E S A C R E G C V C D A G F V L S G D T C V P V G Q C G C L H D D R Y Y P

2401 L G Q T F Y P G P G C D S L C R C R E G G E V S C E P S S C G P H E T C R P S
G G S L G C V A V G S T T C Q A S G D P H Y T T F D G R R F D F M G T C V Y V L A

2481 Q T C G T R P G L H R F A V L Q E N V A W G N G R V S V T R V I T V Q V A N
F T L R L E Q R Q W K V T V N G V D M K L P V V L A N G Q I R A S Q H G S D V V I E

2561 T D F G L R V A Y D L V Y Y V R V T V P G N Y Y Q L M C G L C G N Y N G D
P K D D F Q K P N G S Q A G N A N E F G N S W E E V V P D S P C L P P P T C P P G
S E

2641 G C I P S E E C P P E L E K K Y Q K E E F C G L L S S P T G P L S S C H K L V D
P Q G P L K D C I F D L C L G G G N L S I L C S N I H A Y V S A C Q A A G G Q V

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2721 E P W R N E T F C P M E C P Q N S H Y E L C A D T C S L G C S A L S A P L Q C
P D G C A E G C Q C D S G F L Y N G Q A C V P I Q Q C G C Y H N G A Y Y E P E Q T

2801 V L I D N C R Q Q C T C H V G K V V V C Q E H S C K P G Q V C Q P S G G I L S
C V N K D P C H G V T C R P Q E T C K E Q G G Q G V C L P N Y E A T C W L W G D P

2881 H Y H S F D G R K F D F Q G T C N Y V L A T T G C P G V S T Q G L T P F T V T
T K N Q N R G N P A V S Y V R V V T V A A L G T N I S I H K D E I G K V R V N G V

2961 L T A L P V S V A D G R I S V T Q G A S K A L L V A D F G L Q V S Y D W N W
R V D V T L P S S Y H G A V C G L C G N M D R N P N N D Q V F P N G T L A P S I P I

3041 W G G S W R A P G W D P L C W D E C R G S C P T C P E D R L E Q Y E G P G F
C G P L A P G T G G P F T T C H A H V P P E S F F K G C V L D V C M G G G D R D I L

3121 C K A L A S Y V A A C Q A A G V V I E D W R A Q V G C E I T C P E N S H Y E
V C G P P C P A S C P S P A P L T T P A V C E G P C V E G C Q C D A G F V L S A D R

3201 C V P L N N G C G C W A N G T Y H E A G S E F W A D G T C S Q W C R C G P
G G S L V C T P A S C G L G E V C G L L P S G Q H G C Q P V S T A E C Q A W G D
P H

3281 Y V T L D G H R F D F Q G T C E Y L L S A P C H G P P L G A E N F T V T V A N
E H R G S Q A V S Y T R S V T L Q I Y N H S L T L S A R W P R K L Q V D G V F V T

3361 L P F Q L D S L L H A H L S G A D V V V T T T S G L S L A F D G D S F V R L R
V P A A Y A G S L C G L C G N Y N Q D P A D D L K A V G G K P A G W Q V G G A
Q G

3441 C G E C V S K P C P S P C T P E Q Q E S F G G P D A C G V I S A T D G P L A P C
H G L V P P A Q Y F Q G C L L D A C Q V Q G H P G G L C P A V A T Y V A A C Q A

3521 A G A Q L R E W R R P D F C P F Q C P A H S H Y E L C G D S C P G S C P S L S
A P E G C E S A C R E G C V C D A G F V L S G D T C V P V G Q C G C L H D D R Y Y

3601 P L G Q T F Y P G P G C D S L C R C R E G G E V S C E P S S C G P H E T C R P S
G G S L G C V A V G S T T C Q A S G D P H Y T T F D G H R F D F M G T C V Y V L

3681 A Q T C G T R P G L H R F A V L Q E N V A W G N G R V S V T R V I T V Q V A
N F T L R L E Q R Q W K V T V N G V D M K L P V V L A N G Q I R A S Q H G S D V
V I

3761 E T D F G L R V A Y D L V Y Y V R V T V P G N Y Y Q L M C G L C G N Y N G
D P K D D F Q K P N G S Q A G N A N E F G N S W E E V V P D S P C L P P P T C P P
G S

3841 A G C I P S D K C P P E L E K K Y Q K E E F C G L L S S P T G P L S S C H K L V
D P Q G P L K D C I F D L C L G G G N L S I L C S N I H A Y V S A C Q A A G G H

3921 V E P W R N E T F C P M E C P Q N S H Y E L C A D T C S L G C S A L S A P L Q
C P D G C A E G C Q C D S G F L Y N G Q A C V P I Q Q C G C Y H N G V Y Y E P E Q

4001 T V L I D N C R Q Q C T C H V G K V V V C Q E H S C K P G Q V C Q P S G G I L
S C V T K D P C H G V T C R P Q E T C K E Q G G Q G V C L P N Y E A T C W L W G D

4081 P H Y H S F D G R K F D F Q G T C N Y V L A T T G C P G V S T Q G L T P F T V
T T K N Q N R G N P A V S Y V R V V T V A A L G T N I S I H K D E I G K V R V N G

4161 V L T A L P V S V A D G R I S V A Q G A S K A L L V A D F G L Q V S Y D W N
W R V D V T L P S S Y H G A V C G L C G N M D R N P N N D Q V F P N G T L A P S I P

4241 I W G G S W R A P G W D P L C W D E C R G S C P T C P E D R L E Q Y E G P G
F C G P L S S G T G G P F T T C H A H V P P E S F F K G C V L D V C M G G G D R D I

4321 L C K A L A S Y V A A C Q A A G V V I E D W R A Q V G C E I T C P E N S H Y
E V C G P P C P A S C P S P A P L T T P A V C E G P C V E G C Q C D A G F V L S A D

4401 R C V P L N N G C G C W A N G T Y H E A G S E F W A D G T C S Q W C R C G
P G G S L V C T P A S C G L G E V C G L L P S G Q H G C Q P V S T A E C Q A W G
D P

4481 H Y V T L D G H R F D F Q G T C E Y L L S A P C H G P P L G A E N F T V T V A
N E H R G S Q A V S Y T R S V T L Q I Y N H S L T L S A R W P R K L Q V D G V F V

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4561	A L P F Q L D S L L H A H L S G A D V V V T T T S G L S L A F D G D S F V R L R V P A A Y A A S L C G L C G N Y N Q D P A D D L K A V G G K P A G W Q V G G A Q
4641	G C G E C V S K P C P S P C T P E Q Q E S F G G P D A C G V I S A T D G P L A P C H G L V P P A Q Y F Q G C L L D A C Q V Q G H P G G L C P A V A T Y V A A C Q
4721	A A G A Q L G E W R R P D F C P L Q C P A H S H Y E L C G D S C P V S C P S L S A P E G C E S A C R E G C V C D A G F V L S G D T C V P V G Q C G C L H D G R Y
4801	Y P L G E V F Y P G P E C E R R C E C G P G G H V T C Q E G A A C G P H E E C R L E D G V Q A C H A T G C G R C L A N G G I H Y I T L D G R V Y D L H G S C S Y
4881	V L A Q V C H P K P G D E D F S I V L E K N A A G D L Q R L L V T V A G Q V V S L A Q G Q Q V T V D G E A V A L P V A V G R V R V T A E G R N M V L Q T T K G L
4961	R L L F D G D A H L L M S I P S P F R G R L C G L C G N F N G N W S D D F V L P N G S A A S S V E T F G A A W R A P G S S K G C G E G C G P Q G C P V C L A E E
5041	T A P Y E S N E A C G Q L R N P Q G P F A T C Q A V L S P S E Y F R Q C V Y D L C A Q K G D K A F L C R S L A A Y T A A C Q A A G V A V K P W R T D S F C P L H
5121	C P A H S H Y S I C T R T C Q G S C A A L S G L T G C T T R C F E G C E C D D R F L L S Q G V C I P V Q D C G C T H N G R Y L P V N S S L L T S D C S E R C S C
5201	S S S S G L T C Q A A G C P P G R V C E V K A E A R N C W A T R G L C V L S V G A N L T T F D G A R G A T T S P G V Y E L S S R C P G L Q N T I P W Y R V V A E
5281	V Q I C H G K T E A V G Q V H I F F Q D G M V T L T P N K G V W V N G L R V D L P A E K L A S V S V S R T P D G S L L V R Q K A G V Q V W L G A N G K V A V I V
5361	S N D H A G K L C G A C G N F D G D Q T N D W H D S Q E K P A M E K W R A Q D F S P C Y G

5.119 hypothetical protein LOC284422 [<i>Homo sapiens</i>] Protein Accession gi 211059425																																																	
Mean Expression Ratio 1.17																																																	
Median Expression Ratio 1.17																																																	
Credible Interval (0.796, 1.74)																																																	
Associated Peptides 2																																																	
Associated Spectra 3																																																	
Coverage NaN																																																	
[0237]																																																	
<table><tr><th colspan="10">Sequence</th></tr><tr><th>A</th><th>2.5</th><th>50</th><th>97.5</th><th>ID</th><th>No.</th><th colspan="4">Sequence</th></tr><tr><td>2</td><td>0.8</td><td>1.2</td><td>1.8</td><td>SEQ</td><td>ID NO: 854</td><td colspan="4">EGESNLGLDLEEKEPGDHER</td></tr><tr><td>1</td><td>0.78</td><td>1.2</td><td>1.9</td><td>SEQ</td><td>ID NO: 855</td><td colspan="4">MESNLYQDQSEDKR</td></tr></table>										Sequence										A	2.5	50	97.5	ID	No.	Sequence				2	0.8	1.2	1.8	SEQ	ID NO: 854	EGESNLGLDLEEKEPGDHER				1	0.78	1.2	1.9	SEQ	ID NO: 855	MESNLYQDQSEDKR			
Sequence																																																	
A	2.5	50	97.5	ID	No.	Sequence																																											
2	0.8	1.2	1.8	SEQ	ID NO: 854	EGESNLGLDLEEKEPGDHER																																											
1	0.78	1.2	1.9	SEQ	ID NO: 855	MESNLYQDQSEDKR																																											

5.120 vacuolar protein sorting 37D [<i>Homo sapiens</i>]					
Protein Accession gi 117938318					
Mean Expression Ratio 1.17					
Median Expression Ratio 1.17					
Credible Interval (0.732, 1.91)					
Associated Peptides 1					
Associated Spectra 1					
Coverage 0.0558					
[0238]					

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.73	1.2	2.0	SEQ ID NO: 856	SFPAAAVLPTGAAR
SEQ ID NO: 857					
1 M Y R A R A A R A G P E P G S P G R F G I L S T G Q L R D L L Q D E P K L D R I V R L S R K F Q G L Q L E R E A C L A S N Y A L A K E N L A L R P R L E M G R A					

-continued

81	A	L	A	I	K	Y	Q	E	L	R	E	V	A	E	N	C	A	D	K	L	Q	R	L	E	E	S	M	H	R	W	S	P	H	C	A	L	G	W	L		
	Q	A	E	L	E	E	A	E	Q	E	A	E	E	Q	M	E	Q	L	L	L	G	E	Q	S	L	E	A	F	L	P	A	F	Q	R	G	R	A	L	A	H	L
161	R	R	T	Q	A	E	K	L	Q	E	L	L	R	R	R	E	R	S	A	Q	P	A	P	T	S	A	A	D	P	P	K	S	F	P	A	A	A	V	L	P	
	T	G	A	A	R	G	P	P	A	V	P	R	S	L	P	P	L	D	S	R	P	V	P	P	L	K	G	S	P	G	C	P	L	G	P	A	P	L	L	S	
241	P	R	P	S	Q	P	E	P	P	H	R																														

5.121 protease, serine, 1 preproprotein [*Homo sapiens*]
Protein Accession gi|4506145
Mean Expression Ratio 1.17
Median Expression Ratio 1.17
Credible Interval (0.811, 1.68)

Associated Peptides 1
Associated Spectra 5
Coverage 0.0324
[0239]

A	2.5	50	97.5	Sequence ID No.	Sequence																																			
5	0.88	1.2	1.7	SEQ ID NO: 858	NKPGVYTK																																			
SEQ ID NO: 859																																								
1M	N	P	L	L	I	L	T	F	V	A	A	A	L	A	A	P	F	D	D	D	D	K	I	V	G	G	Y	N	C	E	E	N	S	V	P	Y	Q	V	S	
	L	N	S	G	Y	H	F	C	G	G	S	L	I	N	E	Q	W	V	V	S	A	G	H	C	Y	K	S	R	I	Q	V	R	L	G	E	H	N	I	E	V
81L	E	G	N	E	Q	F	I	N	A	A	K	I	I	R	H	P	Q	Y	D	R	K	T	L	N	N	D	I	M	L	I	K	L	S	S	R	A	V	I	N	A
	R	V	S	T	I	S	L	P	T	A	P	P	A	T	G	T	K	C	L	I	S	G	W	G	N	T	A	S	S	G	A	D	Y	P	D	E	L	Q	C	
161L	D	A	P	V	L	S	Q	A	K	C	E	A	S	Y	P	G	K	I	T	S	N	M	F	C	V	G	F	L	E	G	G	K	D	S	C	Q	G	D		
	S	G	G	P	V	V	C	N	G	Q	L	Q	G	V	V	S	W	G	D	G	C	A	Q	K	N	K	P	G	V	Y	T	K	V	Y	N	Y	V	K	W	
	I	K																																						
241N	T	I	A	A	N	S																																		

5.122 prominin 2 [*Homo sapiens*]
Protein Accession gi|21389623
Mean Expression Ratio 1.17
Median Expression Ratio 1.17
Credible Interval (0.766, 1.82)
Associated Peptides 1
Associated Spectra 2
Coverage 0.03
[0240]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.79	1.2	1.9	SEQ ID NO: 860	TSMEQLAQELQGLAQADNSVLGQR
SEQ ID NO: 861					
1M K H T L A L L A P L L G L G L G L A L S Q L A A G A T D C K F L G P A E H L T F T P A A R A R W L A P R V R A P G L L D S L Y G T V R R F L S V V Q L N P F P					
81S E L V K A L L N E L A S V K V N E V V R Y E A G Y V V C A V I A G L Y L L L V P T A G L C F C C C R C H R R C G G R V K T E H K A L A C E R A A L M V F L L L					
161T T L L L L I G V V C A F V T N Q R T H E Q M G P S I E A M P E T L L S L W G L V S D V P Q E L Q A V A Q Q F S L P Q E Q V S E E L D G V G V S I G S A I H T Q					
241L R S S V Y P L L A A V G S L G Q V L Q V S V H H L Q T L N A T V V E L Q A G Q Q D L E P A I R E H R D R L L E L L Q E A R C Q G D C A G A L S W A R T L E L G					

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321A D F S Q V P S V D H V L H Q L K G V P E A N F S S M V Q E E N S T F N A L P
A L A A M Q T S S V V Q E L K K A V A Q Q P E G V R T L A E G F P G L E A A S R W

401A Q A L Q E V E E S S R P Y L Q E V Q R Y E T Y R W I V G C V L C S V V L F V
V L C N L L G L N L G I W G L S A R D D P S H P E A K G E A G A R F L M A G V G L

481S F L F A A P L I L L V F A T F L V G G N V Q T L V C R S W E N G E L F E F A D
T P G N L P P S M N L S Q L L G L R K N I S I H Q A Y Q Q C K E G A A L W T V L

561Q L N D S Y D L E E H L D I N Q Y T N K L R Q E L Q S L K V D T Q S L D L L S S
A A R R D L E A L Q S S G L Q R I H Y P D F L V Q I Q R P V V K T S M E Q L A Q

641E L Q G L A Q A Q D N S V L G Q R L Q E E A Q G L R N L H Q E K V V P Q Q S L
V A K L N L S V R A L E S S A P N L Q L E T S D V L A N V T Y L K G E L P A W A A

721R I L R N V S E C F L A R E M G Y F S Q Y V A W V R E E V T Q R I A T C Q P L S
G A L D N S R V I L C D M M A D P W N A F W F C L A W C T F F L I P S I I F A V

801K T S K Y F R P I R K R L S S T S S E E T Q L F H I P R V T S L K L

5.123 cathepsin B preproprotein [*Homo sapiens*]; cathepsin B preproprotein [*Homo sapiens*]; cathepsin B preproprotein [*Homo sapiens*]; cathepsin B preproprotein [*Homo sapiens*]; cathepsin B preproprotein [*Homo sapiens*]
Protein Accession gi|4503139 gi|22538437 gi|22538435 gi|22538433 gi|22538431

Mean Expression Ratio 0.858

Median Expression Ratio 0.856

Credible Interval (0.556, 1.32)

Associated Peptides 1

Associated Spectra 2

Coverage NaN

[0241]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.54	0.83	1.3	SEQ	ID NO: 862	GQDHCГИESEVVAGIPR

5.124 radixin [*Homo sapiens*]
Protein Accession gi|4506467

Mean Expression Ratio 1.16

Median Expression Ratio 1.16

Credible Interval (0.77, 1.75)

Associated Peptides 1

Associated Spectra 3

Coverage 0.0292

[0242]

SEQ ID NO: 863				
A	2.5	50	97.5	Sequence
3	0.82	1.2	1.8	FFPEDVSEELIQEITQR
SEQ ID NO: 864				
1M P K P I N V R V T T M D A E L E F A I Q P N T T G K Q L F D Q V V K T V G L R E V W F F G L Q Y V D S K G Y S T W L K L N K K V T Q Q D V K K E N P L Q F K F				
81R A K F F P E D V S E E L I Q E I T Q R L F F L Q V K E A I L N D E I Y C P P E T A V L L A S Y A V Q A K Y G D Y N K E I H K P G Y L A N D R L L P Q R V L E Q				
161H K L T K E Q W E E R I Q N W H E E H R G M L R E D S M M E Y L K I A Q D L E M Y G V N Y F E I K N K K G T E L W L G V D A L G L N I Y E H D D K L T P K I G F				
241P W S E I R N I S F N D K K F V I K P I D K K A P D F V F Y A P R L R I N K R I L A L C M G N H E L Y M R R R K P D T I E V Q Q M K A Q A R E E K H Q K Q L E R				
321A Q L E N E K K K R E I A E K E K E R I E R E K E E L M E R L K Q I E E Q T I K A Q K E L E E Q T R K A L E L D Q E R K R A K E E A E R L E K E R R A A E E A K				
401S A I A K Q A A D Q M K N Q E Q L A A E L A E F T A K I A L L E E A K K K K E E E A T E W Q H K A F A A Q E D L E K T K E E L K T V M S A P P P P P P P V I P				

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481P T E N E H D E H D E N N A E A S A E L S N E G V M N H R S E E E R V T E T Q
K N E R V K K Q L Q A L S S E L A Q A R D E T K K T Q N D V L H A E N V K A G R D
561K Y K T L R Q I R Q G N T K Q R I D E F E A M

5.125 annexin VI isoform 2 [*Homo sapiens*]; annexin VI isoform 1 [*Homo sapiens*]

[0243]

Protein Accession gi|71773415 gi|71773329

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.77	1.1	1.7	SEQ ID NO: 865	EAILDIITSR
4	0.89	1.2	1.7	SEQ ID NO: 866	GLGTDEDTIIDIITHR
1	0.78	1.2	1.7	SEQ ID NO: 867	GSIHDFPGFDPNQDAEALY

Mean Expression Ratio 1.16

Median Expression Ratio 1.16

5.126 cystatin C precursor [*Homo sapiens*]
Protein Accession gi|4503107

Mean Expression Ratio 0.859

Median Expression Ratio 0.86

Credible Interval (0.832, 1.60)

Credible Interval (0.716, 1.03)

Associated Peptides 3

Associated Peptides 9

Associated Spectra 6

Associated Spectra 37

Coverage 0.425

Coverage NaN

[0244]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	0.88	1.2	SEQ ID NO: 868	ALDFAVGEYNK
3	0.63	0.83	1.1	SEQ ID NO: 869	KQIVAGVNYFLDVELGR
1	0.64	0.87	1.2	SEQ ID NO: 870	LDNCPFHDQPHLK
8	0.66	0.83	1.0	SEQ ID NO: 871	LVGGPMDASVEEEGVR
3	0.61	0.81	1.1	SEQ ID NO: 872	LVGGPMDASVEEEGVRR
15	0.72	0.87	1.1	SEQ ID NO: 873	QIVAGVNYFLDVELGR
4	0.65	0.84	1.1	SEQ ID NO: 874	TQPNLDNCPFHDQPHLK
1	0.66	0.9	1.2	SEQ ID NO: 875	VGGPMDASVEEEGVR
1	0.63	0.86	1.2	SEQ ID NO: 876	FLDVELGR
SEQ ID NO: 877					
1 M A G P L R A P L L L A I L A V A L A V S P A A G S S P G K P P R L V G G P M D A S V E E E G V R R A L D F A V G E Y N K A S N D M Y H S R A L Q V V R A R K					
81 Q I V A G V N Y F L D V E L G R T T C T K T Q P N L D N C P F H D Q P H L K R K A F C S F Q I Y A V P W Q G T M T L S K S T C Q D A					

5.127 tweety 3 [*Homo sapiens*]
Protein Accession gi|51100978

Mean Expression Ratio 0.86

Median Expression Ratio 0.86

Credible Interval (0.702, 1.06)

Associated Peptides 8

Associated Spectra 21

Coverage 0.222

[0245]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	0.86	1.2	SEQ ID NO: 878	AANPFQOK
4	0.66	0.87	1.1	SEQ ID NO: 879	AAPWWVSLHR
7	0.64	0.82	1.0	SEQ ID NO: 880	ALVEMQDVVAELLR
2	0.65	0.9	1.2	SEQ ID NO: 881	GPDEDGEEEEAPGPR
1	0.64	0.9	1.2	SEQ ID NO: 882	MVEEYSVLSGDILQYYLACSPR
3	0.57	0.77	1.0	SEQ ID NO: 883	QLAGRPEPLR
2	0.63	0.85	1.2	SEQ ID NO: 884	TVSNAPVTEYMSQANFQNPR
1	0.65	0.9	1.3	SEQ ID NO: 885	TVPWEQPATKDPLLR

SEQ ID NO: 886

1MAGVSYAAPWWVSLHLHRLPHFDLSWEATSSQFRPEDTDYQ

QALLLLGAAALACLALLDLFLFYSFWLCCRKRKSEEHLD

81ADCCCTAWCVIIATLVCSAGIAVGFIYGNGETSDGIHRATY

SLRHANRTVAGVQDRVWDTAVGLNHTAEPQLQLERQLAG

161RPEPLRAVQRLQGLLETLLGYTAAIPFWRNTAVSLEVLA

QVDLYDWYRWLG YLGLLLLDV IICLLVLVGLIRSSKGILV

241GVCLLGVLALVISWGALGLELAVSVGSSDFCVDPDAYVT

KMVEEYSVLSGDILQYYLACSPRAANPFQQLSGSHKALVE

321MQDVVAELRLTVPWEQPATKDPLLRVQEV L NGTEVNLQ

HLTALVDCRSLHLDYVQALTGFCYDGVGLIYLALF SFVTAL

401MFS SIVCSVPHTWQQKRGPDDEDGEEEEAAPGPRQAHDSL

RVHMPSLYSCGSSYGSSETSI PAAAH TVSNAPVTEYMSQAN

481FQNP RCENTPLIGRESPPPSYTSSMRAKYLATSQPRPDSSG

SH

5.128 hypothetical protein LOC84418 [*Homo sapiens*]
Protein Accession gi|14165278

Associated Peptides 2

Mean Expression Ratio 1.16

Associated Spectra 2

Median Expression Ratio 1.16

Coverage 0.278

Credible Interval (0.761, 1.78)

[0246]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.74	1.2	1.9	SEQ ID NO: 887	QGYPQYGWQGGPQEPPK
1	0.74	1.2	1.9	SEQ ID NO: 888	TTVYVVEDQR

SEQ ID NO: 889

1M NQENPPPYPGPGPTAPYPPYP P QPMGPGPMGGPYPP PQG

YPYQGY P QYGWQGGPQEPPKTTVYVVEDQRRDELG PSTCL

81TACWTALCCCC L W D M L T

5.129 CD82 antigen isoform 2 [*Homo sapiens*]; CD82 antigen isoform 1 [*Homo sapiens*]
Protein Accession gi|67782354 gi|4504813

Mean Expression Ratio 1.16
Median Expression Ratio 1.16
Credible Interval (0.755, 1.79)

Associated Peptides 2
Associated Spectra 2

Coverage NaN
[0247]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.74	1.2	1.8	SEQ ID NO: 890	EDSLQDAWDYVQAQVK
1	0.75	1.2	1.9	SEQ ID NO: 891	QEMGGIVTELIR

5.130 napsin A preproprotein [*Homo sapiens*]
Protein Accession gi|4758754

Mean Expression Ratio 0.862
Median Expression Ratio 0.864
Credible Interval (0.674, 1.09)

Associated Peptides 6
Associated Spectra 13

Coverage 0.207

[0248]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.59	0.83	1.1	SEQ ID NO: 892	DPEEPDGGELVLGGSDPAH
5	0.57	0.76	1	SEQ ID NO: 893	GCAAILDTGTSLITGPTEEIR
2	0.61	0.85	1.2	SEQ ID NO: 894	ILDGTGTSLITGPTEEIR
1	0.65	0.92	1.3	SEQ ID NO: 895	SPGDKPIFVPLSNYR
1	0.6	0.85	1.2	SEQ ID NO: 896	TVAFDTGSSNLWVPSR
2	0.68	0.95	1.3	SEQ ID NO: 897	VDGILSEDKLTIGGIK
SEQ ID NO: 898					
1MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRILN					
LLRGWREPAELPKLKGAPSPGDKPIFVPLSNYRDVQYFG					
81EIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH					
RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIIGGI					
161KGASVIFGEALWEPSLVFAFAHFHDGILGLGFPILSVEGVR					
PPMDVLVEQGLLDKPVFSFYLNRPDEEPDGGELVLGGSDP					
241AHYIPPLTFVPVTVPAYWQIHMERVKVGPGTLTCAKGC					
AILDGTGTSLLITGPTTEEIRALHAAIGGIPLLAGEYIILCSEI					
321PKLPVSVFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQ					
ALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLAR					
401ARTRGADLGWGETAQAFPG					

5.131 acid phosphatase 2, lysosomal isoform 1 precursor [*Homo sapiens*]
Protein Accession gi|4557010

Mean Expression Ratio 0.864
Median Expression Ratio 0.864
Credible Interval (0.64, 1.17)
Associated Peptides 4
Associated Spectra 7
Coverage 0.132

[0249]

A	2.5	50	97.5	Sequence ID No.	Sequence
4	0.6	0.83	1.1	SEQ ID NO: 899	EGMLQHWELGQALR
1	0.6	0.87	1.3	SEQ ID NO: 900	FVTLLYR
1	0.59	0.87	1.3	SEQ ID NO: 901	NVYDTLFCEQTHGLR
1	0.58	0.85	1.3	SEQ ID NO: 902	TLMSAEANLAGLFPNGMQR

SEQ ID NO: 903

1MAGKRS GWSRAALLQLLLGVNLVVMPPTRARSLRFVTLLEY
RHGDRSPVKTYPKDPYQEEEWPGQFGQLTKEGMLQHWELG

81QALRQRYHGF LNTSYHRQEVYVRSTDFDRTLMSAEANLA
GLFPNGMQRFNPNISWQPIPVHTVPITEDRLLKFPLGPCP

161RYEQLQNETRQTPEYQNESSRNAQFLDMVANETGLTDLT
LETVWNVYDTLFCEQTHGLRLPPWASPQTMQRLSRLKDFS F

241RFLFGIYQQAEKARLQGGVLLAQIRKNLTLMATTSQLPKL
LVYSAHDTTLVALQMALDVYNGEQAPYASCHIFELYQEDS

321GNFSVEMYFRNESDKAPWPLSLPGCPHRCPLQDFLRLTEP
VVPKDWQQECQLASGPADTEVIVALAVCGSILFLLIIVLL L

401TVLFRMQAQPPGYRHHVADGEDHA

5.132 apolipoprotein E precursor [*Homo sapiens*]
Protein Accession gi|4557325

Mean Expression Ratio 0.863

Median Expression Ratio 0.864

Credible Interval (0.56, 1.32)

Associated Peptides 2

Associated Spectra 2

Coverage 0.110

[0250]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.55	0.87	1.4	SEQ ID NO: 904	SWFEPLVEDMQR
1	0.52	0.83	1.3	SEQ ID NO: 905	WVQTLSEQVQEELLSSQVTQELR

SEQ ID NO: 906

1MKVLWAAALLVTFLAGCQAKVEQAVETEPEPEL RQQTEWQ
SGQRWELALLGRFWDYLRWVQTLSEQVQEELLSSQVTQELRA

81LMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQ
ARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLR

161KL RKRLLRDADDDLQKR L AVYQAGAREGAERGLSAIRERL
GPLVEQGRVRAATVGS LAGQPLQERAQAWGERLRARMEEMG

241SRT RDR LDEVKEQVAEVR AKLEEQAQQIRLQAEAFQARL
KSWFEPLVEDMQRQWAGLVEKVQA AVGTS AAPVPSDNH

5.133 transmembrane protein 176B isoform b [*Homo sapiens*]; transmembrane protein 176B isoform a [*Homo sapiens*]; transmembrane protein 176B isoform a [*Homo sapiens*]; transmembrane protein 176B isoform a [*Homo sapiens*]; transmembrane protein 176B isoform a [*Homo sapiens*]; transmembrane protein 176B isoform a [*Homo sapiens*]
Protein Accession gil156416022 gil56416020 gil156416018 gil156416016 gil156416014

Mean Expression Ratio 0.864
Median Expression Ratio 0.865
Credible Interval (0.64, 1.17)
Associated Peptides 3
Associated Spectra 8

Coverage NaN

[0251]

A	2.5	50	97.5	Sequence	ID No.	Sequence
5	0.6	0.82	1.1	SEQ ID NO: 907		FLFHPGDTVVPSTAR
1	0.58	0.85	1.2	SEQ ID NO: 908		LFHPGDTVVPSTAR
2	0.62	0.89	1.3	SEQ ID NO: 909		LLGENSVPPSPSR

5.134 GM2 ganglioside activator precursor [*Homo sapiens*]
Protein Accession gil39995109

Mean Expression Ratio 1.15
Median Expression Ratio 1.16
Credible Interval (0.703, 1.88)
Associated Peptides 1
Associated Spectra 1
Coverage 0.104

[0252]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.71	1.2	2	SEQ ID NO: 910		SEFVVPDLELP SWLT TGN YR

SEQ ID NO: 911

1M Q S L M Q A P L L I A L G L L L A A P A Q A H L K K P S Q L S S F S W D N C D
E G K D P A V I R S L T L E P D P I I V P G N V T L S V M G S T S V P L S S P L

81K V D L V L E K E V A G L W I K I P C T D Y I G S C T F E H F C D V L D M L I P T
G E P C P E P L R T Y G L P C H C P F K E G T Y S L P K S E F V V P D L E L P

161S W L T T G N Y R I E S V L S S S G K R L G C I K I A A S L K G I

5.135 mercaptopyruvate sulfurtransferase isoform 2 [*Homo sapiens*]; mercaptopyruvate sulfurtransferase isoform 2 [*Homo sapiens*]; mercaptopyruvate sulfurtransferase isoform 1 [*Homo sapiens*]
Protein Accession gil61835204 gil194473681 gil194473668

Mean Expression Ratio 0.865
Median Expression Ratio 0.866
Credible Interval (0.564, 1.33)
Associated Peptides 2
Associated Spectra 2

Coverage NaN

[0253]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.53	0.85	1.4	SEQ ID NO: 912		ALVSAQWVAEALR
1	0.53	0.85	1.4	SEQ ID NO: 913		HIPGAFFDIDQCSDR

5.136 mannosidase, alpha, class 1A, member 1 [*Homo sapiens*]
Protein Accession gil24497519

Mean Expression Ratio 0.866
Median Expression Ratio 0.867
Credible Interval (0.556, 1.32)
Associated Peptides 2
Associated Spectra 2
Coverage 0.0475

[0254]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.53	0.86	1.4	SEQ ID NO: 914	GLPPVDFVPPIGVESR
1	0.53	0.85	1.3	SEQ ID NO: 915	MYFDAVQAIETHLIR

SEQ ID NO: 916

1M P V G G L L P L F S S P A G G V L G G G L G G G G R K G S G P A A L R L T E
K F V L L L V F S A F I T L C F G A I F F L P D S S K L L S G V L F H S S P A L

81Q P A A D H K P G P G A R A E D A A E G R A R R R E E G A P G D P E A A L E D
N L A R I R E N H E R A L R E A K E T L Q K L P E E I Q R D I L L E K K K V A Q D

161Q L R D K A P F R G L P P V D F V P P I G V E S R E P A D A A I R E K R A K I K
E M M K H A W N N Y K G Y A W G L N E L K P I S K G G H S S S L F G N I K G A T

241I V D A L D T L F I M E M K H E F E E A K S W V E E N L D F N V N A E I S V F E
V N I R F V G G L L S A Y Y L S G E E I F R K K A V E L G V K L L P A F H T P S

321G I P W A L L N M K S G I G R N W P W A S G G S S I L A E F G T L H L E F M H
L S H L S G N P I F A E K V M N I R T V L N K L E K P Q G L Y P N Y L N P S S G Q

401W G Q H H V S V G G L G D S F Y E Y L L K A W L M S D K T D L E A K K M Y F
D A V Q A I E T H L I R K S S S G L T Y I A E W K G G L L E H K M G H L T C F A G G

481M F A L G A D A A P E G M A Q H Y L E L G A E I A R T C H E S Y N R T F M K L
G P E A F R F D G G V E A I A T R Q N E K Y Y I L R P E V M E T Y M Y M W R L T H

561D P K Y R K W A W E A V E A L E N H C R V N G G Y S G L R D V Y L L H E S Y
D D V Q Q S F F L A E T L K Y L Y L I F S D D D L L P L E H W I F N S E A H L L P I

641L P K D K K E V E I R E E

5.137 integral membrane protein 2B [*Homo sapiens*]
Protein Accession gil11527402

Associated Peptides 2

Mean Expression Ratio 0.87

Associated Spectra 2

Median Expression Ratio 0.868

Coverage 0.109

Credible Interval (0.571, 1.35)

[0255]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.53	0.85	1.4	SEQ ID NO: 917	SGEELIIPPDAAVDCCK
1	0.54	0.86	1.4	SEQ ID NO: 918	DPDDVVPVGQR

SEQ ID NO: 919

1M V K V T F N S A L A Q K E A K K D E P K S G E E A L I I P P D A V A V D C K D
P D D V V P V G Q R R A W C W C M C F G L A F M L A G V I L G G A Y L Y K Y F A

81L Q P D D V Y Y C G I K Y I K D D V I L N E P S A D A P A A L Y Q T I E E N I K I
F E E E E V E F I S V P V P E F A D S D P A N I V H D F N K K L T A Y L D L N

161L D K C Y V I P L N T S I V M P P R N L L E L L I N I K A G T Y L P Q S Y L I H E
H M V I T D R I E N I D H L G F F I Y R L C H D K E T Y K L Q R R E T I K G I

241Q K R E A S N C F A I R H F E N K F A V E T L I C S

5.138 tetraspan 1 [*Homo sapiens*]
Protein Accession gi|21264578
Mean Expression Ratio 1.16
Median Expression Ratio 1.15
Credible Interval (0.857, 1.57)
Associated Peptides 4
Associated Spectra 8
Coverage 0.112
[0256]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.8	1.2	1.7	SEQ ID NO: 920	AHDQKVEGCFNQLLYDIR
1	0.77	1.1	1.7	SEQ ID NO: 921	QKAHDQK
5	0.92	1.2	1.7	SEQ ID NO: 922	VEGCFNQLLYDIR
1	0.77	1.1	1.7	SEQ ID NO: 923	LVVPAIK

SEQ ID NO: 924

1M Q C F S F I K T M M I L F N L L I F L C G A A L L A V G I W V S I D G A S F L K I
F G P L S S S A M Q F V N V G Y F L I A A G V V V F A L G F L G C Y G A K T

81E S K C A L V T F F F I L L I F I A E V A A A V V A L V Y T T M A E H F L T L L
V V P A I K K D Y G S Q E D F T Q V W N T T M K G L K C C G F T N Y T D F E D

161S P Y F K E N S A F P P F C C N D N V T N T A N E T C T K Q K A H D Q K V E G
C F N Q L L Y D I R T N A V T V G G V A A G I G G L E L A A M I V S M Y L Y C N L

241
Q

5.139 apolipoprotein D precursor [*Homo sapiens*]
Protein Accession gi|4502163
Mean Expression Ratio 0.869
Median Expression Ratio 0.868
Credible Interval (0.709, 1.06)

Associated Peptides 9
Associated Spectra 23
Coverage 0.344
[0257]

A	2.5	50	97.5	Sequence ID No.	Sequence
5	0.65	0.85	1.1	SEQ ID NO: 925	CPNPPVQENFDVNK
1	0.61	0.84	1.2	SEQ ID NO: 926	IPTTFENGR
4	0.73	0.97	1.3	SEQ ID NO: 927	KMTVTDQVNCPPK
2	0.63	0.86	1.2	SEQ ID NO: 928	MTVTDQVNCPPK
3	0.65	0.87	1.2	SEQ ID NO: 929	NILTSNNIDVK
2	0.62	0.83	1.1	SEQ ID NO: 930	NPNLPPETVDSLK
1	0.63	0.87	1.2	SEQ ID NO: 931	NPPVQENFDVNK
3	0.64	0.85	1.1	SEQ ID NO: 932	WYEIEK
2	0.64	0.86	1.2	SEQ ID NO: 933	WYEIEKIPTTFENGR

SEQ ID NO: 934

1 M V M L L L L L S A L A G L F G A A E G Q A F H L G K C P N P P V Q E N F D V N
K Y L G R W Y E I E K I P T T F E N G R C I Q A N Y S L M E N G K I K V L N Q E

-continued

81L R A D G T V N Q I E G E A T P V N L T E P A K L E V K F S W F M P S A P Y W I L A T D Y E N Y A L V Y S C T C I I Q L F H V D F A W I L A R N P N L P P E T V
161D S L K N I L T S N N I D V K K M T V T D Q V N C P K L S

5.140 stomatin isoform a [*Homo sapiens*]
Protein Accession gi|38016911

Mean Expression Ratio 0.87

Median Expression Ratio 0.869

Credible Interval (0.7, 1.07)

Associated Peptides 9

Associated Spectra 18

Coverage 0.417

[0258]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.67	0.92	1.3	SEQ ID NO: 935	EASMVITESPAALQLR
4	0.66	0.87	1.2	SEQ ID NO: 936	EEIAHNMQSTLDDATDAWGIK
1	0.62	0.87	1.2	SEQ ID NO: 937	FILPCTDSFIK
2	0.6	0.83	1.1	SEQ ID NO: 938	TISFDIPPQEILTK
1	0.63	0.88	1.2	SEQ ID NO: 939	VIAAEGEMNASR
4	0.6	0.8	1.1	SEQ ID NO: 940	VQNATLAVANITNADSATR
1	0.62	0.88	1.2	SEQ ID NO: 941	YLQTLTTIAAEK
2	0.65	0.89	1.2	SEQ ID NO: 942	LPVQLQR
1	0.61	0.87	1.2	SEQ ID NO: 943	LLAQTTLR
SEQ ID NO: 944					
1M A E K R H T R D S E A Q R L P D S F K D S P S K G L G P C G W I L V A F S F L F T V I T F P I S I W M C I K I I K E Y E R A I I F R L G R I L Q G G A K G P G					
81L F F I L P C T D S F I K V D M R T I S F D I P P Q E I L T K D S V T I S V D G V V Y Y R V Q N A T L A V A N I T N A D S A T R L L A Q T T L R N V L G T K N L					
161S Q I L S D R E E I A H N M Q S T L D D A T D A W G I K V E R V E I K D V K L P V Q L Q R A M A A E A E A S R E A R A K V I A A E G E M N A S R A L K E A S M V					
241I T E S P A A L Q L R Y L Q T L T T I A A E K N S T I V F P L P I D M L Q G I I G A K H S H L G					

5.141 eukaryotic translation initiation factor 6 isoform c
[*Homo sapiens*]
Protein Accession gi|31563374

Mean Expression Ratio 0.867

Median Expression Ratio 0.869

Credible Interval (0.534, 1.41)

Associated Peptides 1

Associated Spectra 1

Coverage 0.106

[0259]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.5	0.84	1.4	SEQ ID NO: 945	TSIEDQDELSSLLQVPLVAGTVNR
SEQ ID NO: 946					
1M A V R A S F E N N C E I G C F A K L T N T Y C L V A I G G S E N F Y R C G G S P					
G A Y G G G E A C A G V K S S G S G R V P A P L P R H H R V H V P T V C S R A					
81S S P I P S P W C T R L S P A A A S S G A C V W E T E E I L A D V L K V E V F R Q					
T V A D Q V L V G S Y C V F S N Q G G L V H P K T S I E D Q D E L S S L L Q V					
161P L V A G T V N R G S E V I A A G M V V N D W C A F C G L D T T S T E L S V V					
E S V F K L N E A Q P S T I A T S M R D S L I D S L T					

5.142 kininogen 1 isoform 2 [*Homo sapiens*]
Protein Accession gil4504893

Associated Peptides 3

Mean Expression Ratio 0.876

Associated Spectra 3

Median Expression Ratio 0.869

Coverage 0.0937

Credible Interval (0.603, 1.30)

[0260]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.55	0.84	1.3	SEQ ID NO: 947	DIPTNSPELEETLHTITK
1	0.55	0.86	1.3	SEQ ID NO: 948	YFIDFVAR
1	0.58	0.89	1.4	SEQ ID NO: 949	IGEIKEETTSHLR
SEQ ID NO: 950					
1M K L I T I L F L C S R L L L S L T Q E S Q S E E I D C N D K D L F K A V D A A L K					
K Y N S Q N Q S N N Q F V L Y R I T E A T K T V G S D T F Y S F K Y E I K E					
81G D C P V Q S G K T W Q D C E Y K D A A K A A T G E C T A T V G K R S S T K F					
S V A T Q T C Q I T P A E G P V V T A Q Y D C L G C V H P I S T Q S P D L E P I L					
161R H G I Q Y F N N N T Q H S S L F M L N E V K R A Q R Q V V A G L N F R I T Y					
S I V Q T N C S K E N F L F L T P D C K S L W N G D T G E C T D N A Y I D I Q L R					
241I A S F S Q N C D I Y P G K D F V Q P P T K I C V G C P R D I P T N S P E L E E T					
L T H T I T K L N A E N N A T F Y F K I D N V K K A R V Q V V A G K K Y F I D					
321F V A R E T T C S K E S N E E L T E S C E T K K L G Q S L D C N A E V Y V V P					
W E K K I Y P T V N C Q P L G M I S L M K R P P G F S P F R S S R I G E I K E E T					
401T S H L R S C E Y K G R P P K A G A E P A S E R E V S					

5.143 syntenin isoform 3 [*Homo sapiens*]; syntenin isoform 3 [*Homo sapiens*]
Protein Accession gil55749523 gil55749515

Mean Expression Ratio 1.15

Median Expression Ratio 1.15

Credible Interval (0.747, 1.77)

Associated Peptides 1

Associated Spectra 2

Coverage NaN

[0261]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.77	1.2	1.8	SEQ ID NO: 951	ANVAVVSGAPLQGLVAR

5.144 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 [*Homo sapiens*]
Protein Accession gi|4504041

Mean Expression Ratio 1.15

Median Expression Ratio 1.15

Credible Interval (0.8, 1.64)

Associated Peptides 3

Associated Spectra 4

Coverage 0.101

[0262]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.77	1.2	1.8	SEQ ID NO: 952	ALSCTAEQGVLPDDL SGVIR
1	0.78	1.2	1.8	SEQ ID NO: 953	IAQSDYIPTQQDVLR
2	0.77	1.1	1.7	SEQ ID NO: 954	SCTAEQGVLPDDL SGVIR
SEQ ID NO: 955					
1M G C T V S A E D K A A A E R S K M I D K N L R E D G E K A A R E V K L L L L G					
A G E S G K S T I V K Q M K I I H E D G Y S E E E C R Q Y R A V V Y S N T I Q S					
81I M A I V K A M G N L Q I D F A D P S R A D D A R Q L F A L S C T A E E Q G V L					
P D D L S G V I R R L W A D H G V Q A C F G R S R E Y Q L N D S A A Y Y L N D L					
161E R I A Q S D Y I P T Q Q D V L R T R V K T T G I V E T H F T F K D L H F K M F					
D V G G Q R S E R K K W I H C F E G V T A I I F C V A L S A Y D L V L A E D E E					
241M N R M H E S M K L F D S I C N N K W F T D T S I I L F L N K K D L F E E K I T					
H S P L T I C F P E Y T G A N K Y D E A A S Y I Q S K F E D L N K R K D T K E I					
321Y T H F T C A T D T K N V Q F V F D A V T D V I I K N N L K D C G L F					

5.145 guanine nucleotide binding protein, alpha z polypeptide [*Homo sapiens*]
Protein Accession gi|4504051

Mean Expression Ratio 1.15

Median Expression Ratio 1.15

Credible Interval (0.708, 1.89)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0423

[0263]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.72	1.2	2	SEQ ID NO: 956	IAAADYIPTVEDILR
SEQ ID NO: 957					
1M G C R Q S S E E K E A A R R S R R I D R H L R S E S Q R Q R R E I K L L L L G T					
S N S G K S T I V K Q M K I I H S G G F N L E A C K E Y K P L I I Y N A I D S					
81L T R I I R A L A A L R I D F H N P D R A Y D A V Q L F A L T G P A E S K G E I T					
P E L L G V M R R L W A D P G A Q A C F S R S S E Y H L E D N A A Y Y L N D L					
161E R I A A A D Y I P T V E D I L R S R D M T T G I V E N K F T F K E L T F K M V					
D V G G Q R S E R K K W I H C F E G V T A I I F C V E L S G Y D L K L Y E D N Q					
241T S R M A E S L R L F D S I C N N N W F I N T S L I L F L N K K D L L A E K I R R					
I P L T I C F P E Y K G Q N T Y E E A A V Y I Q R Q F E D L N R N K E T K E I					
321Y S H F T C A T D T S N I Q F V F D A V T D V I I Q N N L K Y I G L C					

5.146 cytochrome P450, family 4, subfamily A, polypeptide
11 [*Homo sapiens*]
Protein Accession gil158937242
Mean Expression Ratio 0.875
Median Expression Ratio 0.873
Credible Interval (0.54, 1.41)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0231
[0264]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.51	0.84	1.4	SEQ ID NO: 958	VWPNPEVFDPPR
SEQ ID NO: 959					
1M S V S V L S P S R L L G D V S G I L Q A A S L L I L L L L I K A V Q L Y L H R Q					
W L L K A L Q Q F P C P P S H W L F G H I Q E L Q Q D Q E L Q R I Q K W V E					
81T F P S A C P H W L W G G K V R V Q L Y D P D Y M K V I L G R S D P K S H G S					
Y R F L A P W I G Y G L L L L N G Q T W F Q H R R M L T P A F H Y D I L K P Y V G					
161L M A D S V R V M L D K W E E L L G Q D S P L E V F Q H V S L M T L D T I M					
K C A F S H Q G S I Q V D R N S Q S Y I Q A I S D L N N L V F S R V R N A F H Q N D					
241T I Y S L T S A G R W T H R A C Q L A H Q H T D Q V I Q L R K A Q L Q K E G E					
L E K I K R K R H L D F L D I L L L A K M E N G S I L S D K D L R A E V D T F M F					
321E G H D T T A S G I S W I L Y A L A T H P K H Q E R C R E E I H S L L G D G A S					
I T W N H L D Q M P Y T T M C I K E A L R L Y P P V P G I G R E L S T P V T F P					
401D G R S L P K G I M V L L S I Y G L H H N P K V W P N P E V F D P F R F A P G S					
A Q H S H A F L P F S G G S R N C I G K Q F A M N E L K V A T A L T L L R F E L					
481L P D P T R I P I P I A R L V L K S K N G I H L R L R R L P N P C E D K D Q L					

5.147 olfactomedin 4 precursor [*Homo sapiens*]
Protein Accession gil32313593
Mean Expression Ratio 0.876
Median Expression Ratio 0.876
Credible Interval (0.784, 0.983)

Associated Peptides 39
Associated Spectra 112
Coverage 0.657
[0265]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	0.84	1.1	SEQ ID NO: 960	DLGDVGPPIPSPGFSSFPGVDSSSSFSSSR
1	0.64	0.86	1.1	SEQ ID NO: 961	DLSVLQKPQ
1	0.66	0.88	1.2	SEQ ID NO: 962	DQNTPVVHPPPTPGSC
1	0.67	0.89	1.2	SEQ ID NO: 963	DQNTPVVHPPPTPGSCGH
3	0.68	0.9	1.2	SEQ ID NO: 964	DTISYTELDFELIK
3	0.67	0.87	1.1	SEQ ID NO: 965	DYSPQHPPNK
40	0.7	0.8	0.91	SEQ ID NO: 966	ESFGGSSEIVDQLEVEIR
1	0.65	0.87	1.2	SEQ ID NO: 967	EYVQLISVYEK
1	0.69	0.92	1.2	SEQ ID NO: 968	GFSYLYGAWGR
1	0.68	0.9	1.2	SEQ ID NO: 969	GLYWVAPLNTDGR

-continued

2	0.61	0.8	1.1	SEQ ID NO: 970	GTCQCSVSLPDTTFPVDR
1	0.65	0.86	1.1	SEQ ID NO: 971	ITYGQGS GTAVYNNNMVNMNTGN IAR
6	0.7	0.88	1.1	SEQ ID NO: 972	LDIVMHK
1	0.64	0.85	1.1	SEQ ID NO: 973	LEFTAHVL
4	0.72	0.92	1.2	SEQ ID NO: 974	LEFTAHVLSQK
1	0.67	0.89	1.2	SEQ ID NO: 975	LEFTAHVLSQKFEK
4	0.68	0.88	1.1	SEQ ID NO: 976	LETLDKNNVLAIR
2	0.67	0.88	1.1	SEQ ID NO: 977	LLEYR
4	0.72	0.94	1.2	SEQ ID NO: 978	LYNTLDDLLLYINAR
3	0.68	0.9	1.2	SEQ ID NO: 979	LYVYNDGYLLNYDLSVLQKPQ
1	0.66	0.88	1.2	SEQ ID NO: 980	QCSVSLPDTTFPVDR
1	0.66	0.87	1.2	SEQ ID NO: 981	QYKPSASNAF
4	0.65	0.83	1.1	SEQ ID NO: 982	QYKPSASNAFMVCGVLYATR
2	0.67	0.89	1.2	SEQ ID NO: 983	SVSLPDTTFPVDR
1	0.64	0.85	1.1	SEQ ID NO: 984	TIAVTQTLPNAAAYNNR
3	0.67	0.87	1.1	SEQ ID NO: 985	WVAPLNTDGR
2	0.66	0.87	1.1	SEQ ID NO: 986	TEEIFYDYDTNTGK
5	0.72	0.91	1.2	SEQ ID NO: 987	VQSINYNPFDQK
1	0.64	0.86	1.1	SEQ ID NO: 988	YYDTNTGK
1	0.67	0.9	1.2	SEQ ID NO: 989	LLNYDLSVLQKPQ
1	0.66	0.88	1.2	SEQ ID NO: 990	YYYDTNTGK
2	0.66	0.87	1.1	SEQ ID NO: 991	LKECEASK
1	0.67	0.9	1.2	SEQ ID NO: 992	EIVALK
1	0.66	0.89	1.2	SEQ ID NO: 993	IDIMEK
1	0.67	0.9	1.2	SEQ ID NO: 994	LETLDK
1	0.67	0.9	1.2	SEQ ID NO: 995	VYNDGYLLNYDLSVLQKPQ
1	0.67	0.9	1.2	SEQ ID NO: 996	YNPFDQK
1	0.66	0.87	1.2	SEQ ID NO: 997	LYNTLDDLLLY
1	0.63	0.83	1.1	SEQ ID NO: 998	VNMYNTGNIARVNLTNTTIAVTQTLP NAAAYNNR

SEQ ID NO: 999

1MRPGLSFL LALLFFLGQAAGDLGDVGPPIPSPGFS SFPGVDS
 SSSFS SSSRS GSSSSRS LGS GGSVS QLF SNFTG SVDDR

 81GTCQCSVSLPDTTFPVDR VERLEFTAHVLSQKFEKELSKV
 REYVQLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIK

 161VEVKEMEKLVIQLKESFGGSSEIVDQLEVEIRNM TLLVEK
 LETLDKNNVLAIRREIVAL KTKLKECEASKDQNTPVVHP

 241PTPGSCGHG GVVNIS KPSVVQLNWRGF SYLYGAWGRDYS
 PQHPNKG LYWVAPLNTDGRLL EYR LYN T LDDLLLYINARE

 321LRI TYGQGS GTAVYNNNMVNMNTGN IARVNLTNTTIA
 VTQTL PNAAYNNRFSYANVAWQDIDFAVDENGLWVIYSTE A

-continued

401	S	T	G	N	M	V	I	S	K	L	N	D	T	T	L	Q	V	L	N	T	W	Y	T	K	Q	Y	K	P	S	A	S	N	A	F	M	V	C	G	
	V	L	Y	A	T	R	T	M	N	T	R	T	E	E	I	F	Y	Y	D	T	N	T	G	K	E	G	K	L	D	I	V	M	H	K	M	Q	E	K	V
	Q	S																																					
481	I	N	Y	N	P	F	D	Q	K	L	Y	V	Y	N	D	G	Y	L	L	N	Y	D	L	S	V	L	Q	K	P	Q									

5.148 peptidoglycan recognition protein 2 precursor [*Homo sapiens*]
Protein Accession gil56616294
Mean Expression Ratio 0.877
Median Expression Ratio 0.876

Credible Interval (0.542, 1.41)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0226
[0266]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.52	0.85	1.4	SEQ ID NO: 1000	TDCPGDALFDLLR
SEQ ID NO: 1001					
1	M A Q G V L W I L L G L L L W S D P G T A S L P L L M D S V I Q A L A E L E Q K				
	V P A A K T R H T A S A W L M S A P N S G P H N R L Y H F L L G A W S L N A T E				
81	L D P C P L S P E L L G L T K E V A R H D V R E G K E Y G V V L A P D G S T V A				
	V E P L L A G L E A G L Q G R R V I N L P L D S M A A P W E T G D T F P D V V A				
161	I A P D V R A T S S P G L R D G S P D V T T A D I G A N T P D A T K G C P D V Q				
	A S L P D A K A K S P P T M V D S L L A V T L A G N L G L T F L R G S Q T Q S H				
241	P D L G T E G C W D Q L S A P R T F T L L D P K A S L L T M A F L N G A L D G				
	V I L G D Y L S R T P E P R P S L S H L L S Q Y Y G A G V A R D P G F R S N F R R				
321	Q N G A A L T S A S I L A Q Q V W G T L V L L Q R L E P V H L Q L Q C M S Q E				
	Q L A Q V A A N A T K E F T E A F L G C P A I H P R C R W G A A P Y R G R P K L L				
401	Q L P L G F L Y V H H T Y V P A P P C T D F T R C A A N M R S M Q R Y H Q D				
	T Q G W G D I G Y S F V V G S D G Y V Y E G R G W H W V G A H T L G H N S R G F				
	G V				
481	A I V G N Y T A A L P T E A A L R T V R D T L P S C A V R A G L L R P D Y A L				
	L G H R Q L V R T D C P G D A L F D L L R T W P H F T A T V K P R P A R S V S K R				
561	S R R E P P P R T L P A T D L Q				

5.149 SMAD family member 9 isoform b [*Homo sapiens*];
SMAD family member 9 isoform a [*Homo sapiens*]
Protein Accession gil5174519 gi 187828357
Mean Expression Ratio 1.14
Median Expression Ratio 1.14
Credible Interval (0.696, 1.84)
Associated Peptides 1
Associated Spectra 1
Coverage NaN
[0267]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.71	1.2	1.9	SEQ ID NO: 1002	VETPVLPPVLVPR

5.150 brain creatine kinase [*Homo sapiens*]
Protein Accession gi|21536286

Associated Peptides 3

Mean Expression Ratio 1.14

Associated Spectra 3

Median Expression Ratio 1.14

Coverage 0.150

Credible Interval (0.776, 1.69)

[0268]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.75	1.2	1.8	SEQ ID NO: 1003	GTGGVDTAAVGGVFDVSNADR
1	0.76	1.2	1.8	SEQ ID NO: 1004	TDLNPDNLQGGDDLDPNYVLSSR
1	0.74	1.1	1.8	SEQ ID NO: 1005	TFLVWVNEEDHLR
SEQ ID NO: 1006					
1M P F S N S H N A L K L R F P A E D E F P D L S A H N N H M A K V L T P E L Y A					
E L R A K S T P S G F T L D D V I Q T G V D N P G H P Y I M T V G C V A G D E E					
81S Y E V F K D L F D P I I E D R H G G Y K P S D E H K T D L N P D N L Q G G D D					
L D P N Y V L S S R V R T G R S I R G F C L P P H C S R G E R R A I E K L A V E					
161A L S S L D G D L A G R Y Y A L K S M T E A E Q Q Q L I D D H F L F D K P V S					
P L L L A S G M A R D W P D A R G I W H N D N K T F L V W V N E E D H L R V I S M					
241Q K G G N M K E V F T R F C T G L T Q I E T L F K S K D Y E F M W N P H L G Y					
I L T C P S N L G T G L R A G V H I K L P N L G K H E K F S E V L K R L R L Q K R					
321G T G G V D T A A V G G V F D V S N A D R L G F S E V E L V Q M V V D G V K					
L L I E M E Q R L E Q Q A I D D L M P A Q K					

5.151 chromatin modifying protein 2A [*Homo sapiens*];
chromatin modifying protein 2A [*Homo sapiens*]

Protein Accession gi|7656922 gi|38372933

Mean Expression Ratio 1.14

Median Expression Ratio 1.14

Credible Interval (0.798, 1.62)

Associated Peptides 3

Associated Spectra 4

Coverage NaN

[0269]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.76	1.2	1.8	SEQ ID NO: 1007	AEEAASALADADLEER
2	0.8	1.2	1.8	SEQ ID NO: 1008	KAEAAASALADADLEER
1	0.73	1.1	1.6	SEQ ID NO: 1009	KIIADIK

5.152 solute carrier family 4, sodium bicarbonate cotransporter, member 4 isoform 2 [*Homo sapiens*]
Protein Accession gi|4507025

Mean Expression Ratio 0.88

Median Expression Ratio 0.878

Credible Interval (0.573, 1.34)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0329

[0270]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.53	0.84	1.3	SEQ ID NO: 1010	LQQAVMLGALTEVPVPTTR
1	0.55	0.9	1.4	SEQ ID NO: 1011	ILVATDASFLVQYFTR
SEQ ID NO: 1012					
1MSTENV E G K P S N L G E R G R A R S S T F L R V V Q P M F N H S I F T S A V					
S P A A E R I R F I L G E E D D S P A P P Q L F T E L D E L L A V D G Q E M E					
81W K E T A R W I K F E E K V E Q G G E R W S K P H V A T L S L H S L F E L R T C					
M E K G S I M L D R E A S S L P Q L V E M I V D H Q I E T G L L K P E L K D K V					
161T Y T L L R K H R H Q T K K S N L R S L A D I G K T V S S A S R M F T N P D N					
G S P A M T H R N L T S S S L N D I S D K P E K D Q L K N K F M K K L P R D A E A					
241S N V L V G E V D F L D T P F I A F V R L Q Q A V M L G A L T E V P V P T R F L					
F I L L G P K G K A K S Y H E I G R A I A T L M S D E V F H D I A Y K A K D R H					
321D L I A G I D E F L D E V I V L P P G E W D P A I R I E P P K S L P S S D K R K N					
M Y S G G E N V Q M N G D T P H D G G H G G G G H G D C E E L Q R T G R F C G					
401G L I K D I K R K A P F F A S D F Y D A L N I Q A L S A I L F I Y L A T V T N A I					
T F G G L L G D A T D N M Q G V L E S F L G T A V S G A I F C L F A G Q P L T					
481I L S S T G P V L V F E R L L F N F S K D N N F D Y L E F R L W I G L W S A F L					
C L I L V A T D A S F L V Q Y F T R F T E E G F S S L I S F I F I Y D A F K K M					
561I K L A D Y Y P I N S N F K V G Y N T L F S C T C V P P D P A N I S I S N D T T L					
A P E Y L P T M S S T D M Y H N T T F D W A F L S K K E C S K Y G G N L V G N					
641N C N F V P D I T L M S F I L F L G T Y T S S M A L K K F K T S P Y F P T T A R					
K L I S D F A I I L S I L I F C V I D A L V G V D T P K L I V P S E F K P T S P					
721N R G W F V P P F G E N P W W V C L A A A I P A L L V T I L I F M D Q Q I T A V					
I V N R K E H K L K K G A G Y H L D L F W V A I L M V I C S L M A L P W Y V A A					
801T V I S I A H I D S L K M E T E T S A P G E Q P K F L G V R E Q R V T G T L V F I					
L T G L S V F M A P I L K F I P M P V L Y G V F L Y M G V A S L N G V Q F M D					
881R L K L L L M P L K H Q P D F I Y L R H V P L R R V H L F T F L Q V L C L A L L					
W I L K S T V A A I I F P V M I L A L V A V R K G M D Y L F S Q H D L S F L D D					
961V I P E K D K K K K E D E K K K K K K G S L D S D N D D S D C P Y S E K V P					
S I K I P M D I M E Q Q P F L S D S K P S D R E R S P T F L E R H T S C					

5.153 phospholipid transfer protein isoform a precursor
[*Homo sapiens*]
Protein Accession gi|5453914

Mean Expression Ratio 0.875

Median Expression Ratio 0.878

Credible Interval (0.563, 1.35)

Associated Peptides 1

Associated Spectra 2

Coverage 0.0304

[0271]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.54	0.84	1.3	SEQ ID NO: 1013	FLEQELETITIPDLR
SEQ ID NO: 1014					
1MALFGALFLALLAGAHAEFPFGCKIRVTSKALELVKQEGRLR					
FLEQELETITIPDLRGKKEGHFYYNISEVKVTELTSLTSEL					
81DFQPQQELMLQITNASLGLRFRRLQLLYWFFYDGGYINASSA					
EGVSI RTGL EL SR DPAGRMKVS NVSCQASVSRMHAAFGGT					
161FKKVYDFLSTFITSGMRFL LNQQICPVLYHAGTVLLNSLL					
DTPVVRSSVDEL VGIDYSLMKD PVASTSNLDMDFRGAFFP					
241LTERNWSLPNRAVEPQLQEEERMVYVAFSEFFFD SAMES					
YFRAGALQLLLVGDKVPHDL DMLLRATYFGSIVLLSPAVID					
321SPLKLELRVLAPP RCTIKPSGTTISVTASVTIALVPPDQPE					
VQLSSMTMDARLSAKMALRGKALRTQLDLRRFR IYSNHS					
401ALES LALIP LQAPLKTMLQIGVMPMLNERTWRGVQIPLPE					
GINFVHEVVTNHAGFLTIGADLHFAKGLREVIEKNRPADV					
481RASTAPTPTSTA AV					

5.154 ceruloplasmin precursor [*Homo sapiens*]
Protein Accession gi|4557485

Associated Peptides 20

Mean Expression Ratio 0.879

Associated Spectra 27

Median Expression Ratio 0.878

Coverage 0.232

Credible Interval (0.737, 1.05)

[0272]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.65	0.86	1.2	SEQ ID NO: 1015	AEEEHLGILGPQLHADVGDK
2	0.6	0.82	1.1	SEQ ID NO: 1016	ALYLQYTDETFR
1	0.65	0.9	1.2	SEQ ID NO: 1017	DIFTGLIGPMK
2	0.65	0.87	1.2	SEQ ID NO: 1018	DLYSGLIGPLIVCR
1	0.63	0.86	1.2	SEQ ID NO: 1019	DVDKEFYLFPTVFDENESLLEDNIR
2	0.66	0.89	1.2	SEQ ID NO: 1020	EFYLFPTVFDENESLLEDNIR
1	0.63	0.87	1.2	SEQ ID NO: 1021	GAYPLSIEPIGVR
2	0.65	0.86	1.2	SEQ ID NO: 1022	GPEEEHLGILGPVIWAEVGD TIR
1	0.62	0.86	1.2	SEQ ID NO: 1023	GVYSSDVFDIFPGTYQTLEMPFR
1	0.63	0.86	1.2	SEQ ID NO: 1024	IYHSHIDAPK
1	0.65	0.88	1.2	SEQ ID NO: 1025	KAEEEHLGILGPQLHADVGDK
1	0.65	0.88	1.2	SEQ ID NO: 1026	LFPTVFDENESLLEDNIR
1	0.63	0.86	1.2	SEQ ID NO: 1027	MFTTAPDQVDKEDEDFQESNK
1	0.67	0.9	1.2	SEQ ID NO: 1028	MLLATEEQSPGEGDGNCVTR
1	0.64	0.87	1.2	SEQ ID NO: 1029	SVPPSASHVAPTETFTY
1	0.66	0.9	1.2	SEQ ID NO: 1030	TTIEKPVLGFLGPIIK
3	0.69	0.9	1.2	SEQ ID NO: 1031	VNKDDEEFIESNK
1	0.64	0.88	1.2	SEQ ID NO: 1032	YLFPTVFDENESLLEDNIR

-continued

1	0.64	0.88	1.2	SEQ ID NO: 1033	VTFHMK
1	0.69	0.93	1.3	SEQ ID NO: 1034	GP EEEHLGILGPVIW
SEQ ID NO: 1035					
1	M	K	I	L	I
1	L	G	I	F	L
1	F	L	C	S	T
1	P	A	W	A	K
1	K	E	K	H	Y
1	I	G	I	I	E
1	T	T	W	D	Y
1	A	S	D	H	G
1	E	K			
1	K	L	I	S	V
1	D	T	E	H	S
1	N	I	Y	L	Q
1	N	G	P	D	R
1	I	G	R	L	Y
1	K	K	A	L	Y
1	L	Q	Y	T	D
1	E	T	F		
81	R	T	T	I	E
81	K	P	V	W	L
81	G	F	L	G	P
81	I	I	K	A	E
81	T	G	D	K	V
81	Y	V	H	L	K
81	N	L	A	S	R
81	P	Y	T	F	H
81	S				
81	H	G	I	T	Y
81	K	E	H	E	G
81	A	I	Y	P	D
81	N	T	T	D	F
81	Q	R	A	D	D
81	K	V	Y	P	G
81	E	Q	Y	T	Y
81	M	L	L		
161	A	T	E	E	Q
161	S	P	G	E	G
161	D	G	N	C	V
161	T	R	I	Y	H
161	S	H	I	D	A
161	P	K	D	I	A
161	S	G	L	I	G
161	P	L	I	I	C
161	K				
161	K	D	S	L	D
161	K	E	K	E	K
161	H	I	D	R	E
161	F	V	V	M	F
161	S	V	V	D	E
161	N	F	S	W	Y
161	L	E	D	N	I
161	K	T	Y	C	
241	S	E	P	E	K
241	V	D	K	D	N
241	E	D	F	Q	E
241	S	N	R	M	Y
241	S	V	N	G	Y
241	T	F	G	S	L
241	P	G	L	S	M
241	C	A	E	D	
241	R	V	K	W	Y
241	L	F	G	M	G
241	N	E	V	D	V
241	H	A	A	F	F
241	H	G	Q	A	L
241	T	N	K	N	Y
241	R	I	D	T	I
241	N	L	F	P	A
241	T				
321	L	F	D	A	Y
321	M	V	A	Q	N
321	P	G	E	W	M
321	L	S	C	Q	N
321	L	N	H	L	K
321	A	G	L	Q	A
321	F	F	Q	V	Q
321	E	C	N		
321	K	S	S	K	D
321	N	I	R	G	K
321	H	V	R	H	Y
321	I	A	A	E	E
321	I	I	W	N	Y
321	A	P	S	G	I
321	D	I	F	T	K
321	E	N	L	T	A
401	P	G	S	D	S
401	A	V	F	F	E
401	Q	G	T	T	R
401	I	G	G	S	Y
401	K	K	L	V	Y
401	R	E	Y	T	D
401	A	S	F	T	N
401	R	K	E	R	G
401	P	E	E	H	L
401	G	I	L	G	P
401	V	I	W	A	E
401	V	G	D	T	I
401	R	V	T	F	H
401	N	K	G	A	Y
401	P	L	S	I	E
401	P	I	G	V	
481	R	F	N	K	N
481	E	G	T	Y	Y
481	S	P	N	Y	N
481	P	Q	S	R	S
481	V	P	P	S	A
481	S	H	V	A	P
481	T	E	T	E	T
481	F	T	Y	E	W
481	T				
481	V	P	K	E	V
481	G	P	T	N	A
481	D	P	V	C	L
481	A	K	M	Y	Y
481	S	A	V	D	P
481	T	K	D	I	F
481	T	G	L	I	G
481	P	M	K	I	C
561	K	K	G	S	L
561	H	A	N	G	R
561	Q	K	D	V	D
561	K	E	F	Y	L
561	F	P	T	V	F
561	D	E	N	E	S
561	L	L	L	E	D
561	N	I	R	M	
561	F	T	T	A	P
561	D	Q	V	D	K
561	E	D	E	D	F
561	Q	E	S	N	K
561	M	H	S	M	N
561	G	F	M	Y	G
561	N	Q	P	G	L
561	T	M	C	K	G
561	D				
641	S	V	V	W	Y
641	L	F	S	A	G
641	N	E	A	D	V
641	H	G	I	Y	F
641	S	G	N	T	Y
641	L	W	R	G	E
641	R	R	D	T	A
641	N	L	F	P	
641	Q	T	S	L	T
641	L	H	M	W	P
641	D	T	E	G	T
641	F	N	V	E	C
641	L	T	T	D	H
641	Y	T	G	G	M
641	K	Q	K	Y	T
641	V	N	Q	C	R
641	R				
721	Q	S	E	D	S
721	T	F	Y	L	G
721	E	R	T	Y	Y
721	I	A	A	V	E
721	V	E	W	D	Y
721	S	P	Q	R	E
721	W	E	K	E	L
721	H	H	L	Q	
721	E	Q	N	V	S
721	N	A	F	L	D
721	K	G	E	F	Y
721	I	G	S	K	Y
721	K	K	V	V	Y
721	R	Q	Y	T	D
721	S	T	F	R	V
721	P	V	E	R	K
721	A				
801	E	E	E	H	L
801	G	I	L	G	P
801	Q	L	H	A	D
801	V	G	D	K	V
801	K	I	I	F	K
801	N	M	A	T	R
801	P	Y	S	I	H
801	A	H	G	V	Q
801	T	E	S	S	T
801	V	T	P	T	L
801	P	G	E	T	L
801	T	Y	V	W	K
801	I	P	E	R	S
801	G	A	G	T	E
801	D	S	A	C	I
801	P	W	A	Y	Y
881	S	T	V	D	Q
881	V	K	D	L	Y
881	S	G	L	I	G
881	P	L	I	V	C
881	R	R	P	Y	L
881	K	V	F	N	P
881	R	R	K	L	E
881	F	A	L	L	F
881	L	V	F	D	E
881	N	E	S	W	Y
881	L	D	D	N	I
881	K	T	Y	S	D
881	H	P	E	K	V
881	N	K	D	D	E
881	E	F	I	E	S
881	N	K	M	H	A
961	I	N	G	R	M
961	F	G	N	L	Q
961	G	L	T	M	H
961	V	G	D	E	V
961	N	W	Y	L	M
961	G	M	G	N	E
961	I	D	L	H	T
961	V	H	F		
961	H	G	H	S	F
961	Q	Y	K	H	R
961	G	V	Y	S	S
961	D	V	F	D	I
961	F	P	G	T	Y
961	Q	T	L	E	M
961	F	P	R	T	P
961	G	I	W	L	L
961	H	C			
1041	H	V	T	D	H
1041	I	H	A	G	M
1041	E	T	T	Y	T
1041	V	L	Q	N	E
1041	D	T	K	S	G

5.155 glycerophosphodiester phosphodiesterase domain
containing 3 [*Homo sapiens*]

Protein Accession gi146198640

Mean Expression Ratio 0.88

Median Expression Ratio 0.88

Credible Interval (0.617, 1.25)

Associated Peptides 4

Associated Spectra 4

Coverage 0.186

[0273]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.56	0.85	1.3	SEQ ID NO: 1036	GGSGELLENTMEAMENSMAQR
1	0.58	0.88	1.3	SEQ ID NO: 1037	SDLLELDCQLTR
1	0.57	0.87	1.3	SEQ ID NO: 1038	DVGSLDFEDLPLYK
1	0.58	0.9	1.4	SEQ ID NO: 1039	VVVVSHDENLCR

SEQ ID NO: 1040

1 M S L L L Y Y A L P A L G S Y A M L S I F F L R R P H L L H T P R A P T F R I R L G
A H R G G S G E L L E N T M E A M E N S M A Q R S D L L E L D C Q L T R D R

81 V V V V S H D E N L C R Q S G L N R D V G S L D F E D L P L Y K E K L E V Y F S
P G H F A H G S D R R M V R L E D L F Q R F P R T P M S V E I K G K N E E L I R

-continued

161E I A G L V R R Y D R N E I T I W A S E K S S V M K K C K A A N P E M P L S F T
I S R G F W V L L S Y Y L G L L P F I P I P E K F F F C F L P N I I N R T Y F P
241F S C S C L N Q L L A V V S K W L I M R K S L I R H L E E R G V Q V V F W C L
N E E S D F E A A F S V G A T G V I T D Y P T A L R H Y L D N H G P A A R T S

5.156 glucuronidase, beta [*Homo sapiens*]
Protein Accession gi|4504223

Mean Expression Ratio 1.14

Median Expression Ratio 1.14

Credible Interval (0.797, 1.61)

Associated Peptides 4

Associated Spectra 4

Coverage 0.0707

[0274]

5.157 solute carrier family 4, anion exchanger, member 1
[*Homo sapiens*]

Protein Accession gi|4507021

Mean Expression Ratio 1.13

Median Expression Ratio 1.14

Credible Interval (0.734, 1.73)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0329

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.74	1.1	1.7	SEQ ID NO: 1041	GFDWPLLVK
1	0.76	1.1	1.7	SEQ ID NO: 1042	NFADFMTEQSPTR
1	0.76	1.2	1.7	SEQ ID NO: 1043	YVVGELIWNFADFMTEQSPTR
1	0.75	1.1	1.7	SEQ ID NO: 1044	TSHYPYAEVQMCDR

SEQ ID NO: 1045

1M A R G S A V A W A A L G P L L W G C A L G L Q G G M L Y P Q E S P S R E C K
E L D G L W S F R A D F S D N R R R G F E E Q W Y R R P L W E S G P T V D M P V P
81S S F N D I S Q D W R L R H F V G W V W Y E R E V I L P E R W T Q D L R T R V
V L R I G S A H S Y A I V W V N G V D T L E H E G G Y L P F E A D I S N L V Q V G
161P L P S R L R I T I A I N N T L T P T T L P P G T I Q Y L T D T S K Y P K G Y F V
Q N T Y F D F F N Y A G L Q R S V L L Y T T P T T Y I D D I T V T T S V E Q D
241S G L V N Y Q I S V K G S N L F K L E V R L L D A E N K V V A N G T G T Q G Q
L K V P G V S L W W P Y L M H E R P A Y L Y S L E V Q L T A Q T S L G P V S D F Y
321T L P V G I R T V A V T K S Q F L I N G K P F Y F H G V N K H E D A D I R G K G
F D W P L L V K D F N L L R W L G A N A F R T S H Y P Y A E E V M Q M C D R Y G
401I V V I D E C P G V G L A L P Q F F N N V S L H H H M Q V M E E V V R R D K N
H P A V V M W S V A N E P A S H L E S A G Y Y L K M V I A H T K S L D P S R P V T
481F V S N S N Y A A D K G A P Y V D V I C L N S Y Y S W Y H D Y G H L E L I Q L
Q L A T Q F E N W Y K K Y Q K P I I Q S E Y G A E T I A G F H Q D P P L M F T E E
561Y Q K S L L E Q Y H L G L D Q K R R K Y V V G E L I W N F A D F M T E Q S P T
R V L G N K K G I F T R Q R Q P K S A A F L L R E R Y W K I A N E T R Y P H S V A
641K S Q C L E N S P F T

[0275]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.72	1.1	1.8	SEQ ID NO: 1046	ADFLEQPVLGfVR
1	0.73	1.2	1.8	SEQ ID NO: 1047	LQEAAELEAVELPVPIR

SEQ ID NO: 1048

1MEE L Q D D Y E D M M E E N L E Q E E Y E D P D I P E S Q M E E P A A H D T E
A T A T D Y H T T S H P G T H K V Y V E L Q E L V M D E K N Q E L R W M E A A R

81W V Q L E E N L G E N G A W G R P H L S H L T F W S L L E L R R V F T K G T V
L L D L Q E T S L A G V A N Q L L D R F I F E D Q I R P Q D R E E L L R A L L L K

161H S H A G E L E A L G G V K P A V L T R S G D P S Q P L L P Q H S S L E T Q L F
C E Q G D G G T E G H S P S G I L E K I P P D S E A T L V L V G R A D F L E Q P

241V L G F V R L Q E A A E L E A V E L P V P I R F L F V L L G P E A P H I D Y T Q
L G R A A A T L M S E R V F R I D A Y M A Q S R G E L L H S L E G F L D C S L V

321L P P T D A P S E Q A L L S L V P V Q R E L L R R R Y Q S S P A K P D S S F Y K
G L D L N G G P D D P L Q Q T G Q L F G G L V R D I R R R Y P Y Y L S D I T D A

401F S P Q V L A A V I F I Y F A A L S P A I T F G G L L G E K T R N Q M G V S E L
L I S T A V Q G I L F A L L G A Q P L L V V G F S G P L L V F E E A F F S F C E

481T N G L E Y I V G R V W I G F W L I L L V V L V V A F E G S F L V R F I S R Y T
Q E I F S F L I S L I F I Y E T F S K L I K I F Q D H P L Q K T Y N Y N V L M V

561P K P Q G P L P N T A L L S L V L M A G T F F F A M M L R K F K N S S Y F P G
K L R R V I G D F G V P I S I L I M V L V D F F I Q D T Y T Q K L S V P D G F K V

641S N S S A R G W V I H P L G L R S E F P I W M M F A S A L P A L L V F I L I F L E
S Q I T T L I V S K P E R K M V K G S G F H L D L L V V G M G G V A A L F G

721M P W L S A T T V R S V T H A N A L T V M G K A S T P G A A A Q I Q E V K E
Q R I S G L L V A V L V G L S I L M E P I L S R I P L A V L F G I F L Y M G V T S L

801S G I Q L F D R I L L L F K P P K Y H P D V P Y V K R V K T W R M H L F T G I Q
I I C L A V L W V V K S T P A S L A L P F V L I L T V P L R R V L L P L I F R N

881V E L Q C L D A D D A K A T F D E E E G R D E Y D E V A M P V

5.158 arylsulfatase A isoform a precursor [*Homo sapiens*]; arylsulfatase A isoform a precursor [*Homo sapiens*]; arylsulfatase A isoform a precursor [*Homo sapiens*]; arylsulfatase A isoform b [*Homo sapiens*]; arylsulfatase A isoform a precursor [*Homo sapiens*]
Protein Accession gil6005990 gil146229331 gil146229329 gil146229327 gil146229324

Mean Expression Ratio 1.14

Median Expression Ratio 1.14

Credible Interval (0.749, 1.77)

Associated Peptides 2

Associated Spectra 2

Coverage NaN

[0276]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.72	1.1	1.8	SEQ ID NO: 1049	GGLPLEEVTVAEVLAAAR
1	0.73	1.2	1.9	SEQ ID NO: 1050	YMAFAHDLMAQAQR

5.159 guanine nucleotide binding protein (G protein) alpha
12 [*Homo sapiens*]
Protein Accession gil42476111
Mean Expression Ratio 1.14
Median Expression Ratio 1.14
Credible Interval (0.701, 1.86)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0341
[0277]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.7	1.2	2	SEQ ID NO: 1051	ATKGIVEHDFVIK

SEQ ID NO: 1052

1M S G V V R T L S R C L L P A E A G G A R E R R A G S G A R D A E R E A R R R S
R D I D A L L A R E R R A V R R L V K I L L L G A G E S G K S T F L K Q M R I I

81H G R E F D Q K A L L E F R D T I F D N I L K G S R V L V D A R D K L G I P W Q
Y S E N E K H G M F L M A F E N K A G L P V E P A T F Q L Y V P A L S A L W R D

161S G I R E A F S R R S E F Q L G E S V K Y F L D N L D R I G Q L N Y F P S K Q D I
L L A R K A T K G I V E H D F V I K K I P F K M V D V G G Q R S Q R Q K W F Q

241C F D G I T S I L F M V S S S E Y D Q V L M E D R R T N R L V E S M N I F E T I
V N N K L F F N V S I I L F L N K M D L L V E K V K T V S I K K H F P D F R G D

321P H R L E D V Q R Y L V Q C F D R K R R N R S K P L F H H F T T A I D T E N V
R F V F H A V K D T I L Q E N L K D I M L Q

5.160 solute carrier family 1, member 1 [*Homo sapiens*]
Protein Accession gil66773030
Mean Expression Ratio 0.882
Median Expression Ratio 0.881
Credible Interval (0.541, 1.44)

Associated Peptides 1
Associated Spectra 1
Coverage 0.0344
[0278]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.51	0.86	1.4	SEQ ID NO: 1053	TGSTPEVSTVDAMLDLIR

SEQ ID NO: 1054

1M G K P A R K G C E W K R F L K N N W V L L S T V A A V V L G I T T G V L V R
E H S N L S T L E K F Y F A F P G E I L M R M L K L I I L P L I I S S M I T G V A

81A L D S N V S G K I G L R A V V Y Y F C T T L I A V I L G I V L V V S I K P G V T
Q K V G E I A R T G S T P E V S T V D A M L D L I R N M F P E N L V Q A C F Q

161Q Y K T K R E E V K P P S D P E M N M T E E S F T A V M T T A I S K N K T K E
Y K I V G M Y S D G I N V L G L I V F C L V F G L V I G K M G E K G Q I L V D F F

241N A L S D A T M K I V Q I I M C Y M P L G I L F L I A G K I I E V E D W E I F R K
L G L Y M A T V L T G L A I H S I V I L P L I Y F I V V R K N P F R F A M G M

321A Q A L L T A L M I S S S S A T L P V T F R C A E E N N Q V D K R I T R F V L P
V G A T I N M D G T A L Y E A V A A V F I A Q L N D L D L G I G Q I I T I S I T

401A T S A S I G A A G V P Q A G L V T M V I V L S A V G L P A E D V T L I I A V D
W L L D R F R T M V N V L G D A F G T G I V E K L S K K E L E Q M D V S S E V N

481I V N P F A L E S T I L D N E D S D T K K S Y V N G G F A V D K S D T I S F T Q
T S Q F

5.161 keratin 9 [*Homo sapiens*]
Protein Accession gil55956899
Mean Expression Ratio 0.881
Median Expression Ratio 0.882
Credible Interval (0.578, 1.34)
Associated Peptides 2
Associated Spectra 2
Coverage 0.0642
[0279]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.54	0.86	1.4	SEQ ID NO: 1055	HGVQELEIELQSQLSK
1	0.55	0.87	1.4	SEQ ID NO: 1056	SYGGGSGGGFSASSLGGGFGGSR

SEQ ID NO: 1057

1M S C R Q F S S S Y L S R S G G G G G G L G S G G S I R S S Y S R F S S S G G G
G G G G R F S S S S G Y G G G S S R V C G R G G G S F G Y S Y G G S S G G G

81F S A S S L G G G F G G G S R G F G G A S G G G Y S S S G G F G G G F G G G S G
G G F G G G Y G S G F G G F G G F G G A G G G D G G I L T A N E K S T M Q E L

161N S R L A S Y L D K V Q A L E E A N N D L E N K I Q D W Y D K K G P A A I Q K
N Y S P Y Y N T I D D L K D Q I V D L T V G N N K T L L D I D N T R M T L D D F R

241I K F E M E Q N L R Q G V D A D I N G L R Q V L D N L T M E K S D L E M Q Y E
T L Q E E L M A L K K N H K E E M S Q L T G Q N S G D V N V E I N V A P G K D L T

321K T L N D M R Q E Y E Q L I A K N R K D I E N Q Y E T Q I T Q I E H E V S S S G
Q E V Q S S A K E V T Q L R H G V Q E L E I E L Q S Q L S K K A A L E K S L E D

401T K N R Y C G Q L Q M I Q E Q I S N L E A Q I T D V R Q E I E C Q N Q E Y S L L
L S I K M R L E K E I E T Y H N L L E G G Q E D F E S S G A G K I G L G R G G

481S G G S Y G R G S R G G S G G S Y G G G S G G G Y G G S G S R G G S G G S
Y G G S G S G G G S G G G Y G G S G G G H S G G S G G G H S G S G G N Y G G

561G S G S G G G S G G G Y G G S G S R G G S G G S H G G G S G F G G E S G G S
Y G G G E E A S G S G G G Y G G S G K S S H S

5.162 pyruvate kinase, muscle isoform M2 [*Homo sapiens*]
Protein Accession gil33286418
Mean Expression Ratio 1.13
Median Expression Ratio 1.13
Credible Interval (0.83, 1.57)
Associated Peptides 4
Associated Spectra 6
Coverage 0.0923
[0280]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.78	1.1	1.7	SEQ ID NO: 1058	DPVQEAWAEDVDLR
1	0.78	1.2	1.7	SEQ ID NO: 1059	FDEILEASDGIMVAR
3	0.8	1.1	1.6	SEQ ID NO: 1060	HLQLFEELR
1	0.76	1.1	1.7	SEQ ID NO: 1061	LDIDSPPTAR

SEQ ID NO: 1062

1M S K P H S E A G T A F I Q T Q Q L H A A M A D T F L E H M C R L D I D S P P I T
A R N T G I I C T I G P A S R S V E T L K E M I K S G M N V A R L N F S H G T

81H E Y H A E T I K N V R T A T E S F A S D P I L Y R P V A V A L D T K G P E I R T
G L I K G S G T A E V E L K K G A T L K I T L D N A Y M E K C D E N I L W L D

-continued

161	Y K N I C K V V E V G S K I Y V D D G L I S L Q V K Q K G A D F L V T E V E N
	G G S L G S K K G V N L P G A A V D L P A V S E K D I Q D L K F G V E Q D V D M V
241	F A S F I R K A S D V H E V R K V L G E K G K N I K I I S K I E N H E G V R R F
	D E I L E A S D G I M V A R G D L G I E I P A E K V F L A Q K M M I G R C N R A
321	G K P V I C A T Q M L E S M I K K P R P T R A E G S D V A N A V L D G A D C I
	M L S G E T A K G D Y P L E A V R M Q H L I A R E A E A A I Y H L Q L F E E L R R
401	L A P I T S D P T E A T A V G A V E A S F K C C S G A I I V L T K S G R S A H Q
	V A R Y R P R A P I I A V T R N P Q T A R Q A H L Y R G I F P V L C K D P V Q E
481	A W A E D V D L R V N F A M N V G K A R G F F K K G D V V I V L T G W R P G
	S G F T N T M R V V P V P

5.163 solute carrier family 13 member 3 isoform b [*Homo sapiens*]; solute carrier family 13 member 3 isoform a [*Homo sapiens*]
Protein Accession gil58761541 gil31377715

Mean Expression Ratio 0.884

Median Expression Ratio 0.883

Credible Interval (0.572, 1.37)

Associated Peptides 1

Associated Spectra 2

Coverage NaN

[0281]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.55	0.86	1.3	SEQ ID NO: 1063	DHPGETEVPLDLPADSR

5.164 GTPase Rab14 [*Homo sapiens*]
Protein Accession gil19923483

Mean Expression Ratio 0.887

Median Expression Ratio 0.883

Credible Interval (0.541, 1.46)

Associated Peptides 1

Associated Spectra 1

Coverage 0.140

[0282]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.51	0.86	1.5	SEQ ID NO: 1064	IYQNIQDGSLLDLNAAESGVQHKPSAPQGGR
SEQ ID NO: 1065					
1M A T A P Y N Y S Y I F K Y I I I G D M G V G K S C L L H Q F T E K K F M A D C P					
H T I G V E F G T R I I E V S G Q K I K L Q I W D T A G Q E R F R A V T R S Y					
81Y R G A A G A L M V Y D I T R R S T Y N H L S S W L T D A R N L T N P N T V I I					
L I G N K A D L E A Q R D V T Y E E A K Q F A E E N G L L F L E A S A K T G E N					
161V E D A F L E A A K K I Y Q N I Q D G S L D L N A A E S G V Q H K P S A P Q G					
G R L T S E P Q P Q R E G C G C					

5.165 coagulation factor II preproprotein [*Homo sapiens*]
Protein Accession gil4503635

Mean Expression Ratio 0.887

Median Expression Ratio 0.885

Credible Interval (0.613, 1.30)

Associated Peptides 3

Associated Spectra 3

Coverage 0.0836

[0283]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.88	1.4	SEQ ID NO: 1066	HQDFNSAVQLVENFCR
1	0.57	0.87	1.3	SEQ ID NO: 1067	SEGSSVNLSPPLEQCVPDR
1	0.58	0.88	1.4	SEQ ID NO: 1068	TFGSGEADCGLRPLFEK

SEQ ID NO: 1069

1MAHVRLGLQLPGCLALAAALCSLVHSQHVFLLAPQQARSLLR
VRRANTFLEEVRLKGNLERECVEETCSYEEAFEALESSTAT

81DVFWAKYTACETARTPRDKLAAACLEGNC AEGLGTNYRGH
VNITRSGIECQLWRSRYPHKPEINSTTHPGADLQENFCRNP

161DSSSTTGPPWCYTTPDPTVRRQEC SIPVCGQDQVTVAMTPRS
EGSSVNLSPPLEQCVPDRGQQYQGR LAVTTHGLPCLAWASA

241QAKALS KKHQDFNSAVQLVENFCRNP DGDEEGVWCYVAG
KPGDFGYCDLNYCEEAEVEETGDGLDEDS DRAIEGR TATSEY

321QTFFNPRTFGSGEADCGLRPLFEKKSL EDKTERELLESYI
DGRIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRW

401VLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIE
KISMLEKIYIHPRYNWR ENLDRDIALMKLKKKPVAFSDYIHP

481VCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVGKG
QPSVLQVVNLPIVERPVCKDSTRIRITDNMF CAGYKPDEGKR

561GDACEGDSGGPFV MKSPFNNRWYQMGIVSWGEGCDRDG
KYGFYTHVFRLLKKWIQKV IDQFGE

5.166 proteasome alpha 6 subunit [*Homo sapiens*]
Protein Accession gi|23110944

Associated Peptides 2

Mean Expression Ratio 1.13

Associated Spectra 2

Median Expression Ratio 1.13

Coverage 0.122

Credible Interval (0.738, 1.76)

[0284]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.72	1.2	1.9	SEQ ID NO: 1070	AINQGGLTSVAVR
1	0.71	1.1	1.8	SEQ ID NO: 1071	ILTEAEIDAH LVALAER

SEQ ID NO: 1072

1MSRGS SAGFDRHITIFSP EGRLYQVEYAFKAINQGGLTSVA
VRGKDCAVIVTQKKVPDKLLDSSSTVTHL FKITENIGCVM

81TGMTADSR SQVQRARYEAAANWKYKYGYEIPVDM LCKRIA
DISQVYTQNAEMRPLGCCMILIGIDEEQGPQVYKCDPAGYY

161CGFKATAAGVKQTESTSFLEKKVKKKFDWTFEQTVETAI
TCLSTVLSIDFKPSEIEVG VVTVENPKFRILTEAEIDAH LV

241AL AERD

5.167 tubulin, beta, 2 [*Homo sapiens*]
Protein Accession gil5174735

Mean Expression Ratio 1.13
Median Expression Ratio 1.13
Credible Interval (0.767, 1.67)

Associated Peptides 2
Associated Spectra 3

Coverage 0.0742
[0285]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.78	1.2	1.8	SEQ ID NO: 1073	GHYTEGAELVDSVLDVVR
1	0.72	1.1	1.7	SEQ ID NO: 1074	AVLVDLEPGTMDSVR

SEQ ID NO: 1075

1MREIVHLQAGQC GNQIGAKFW EVISDEHGI DPTGT YHGDS
DLQLERIN VYYNEATG GKYPRAVLVDLEPGTMDSVRS GP

81FGQIFRPDNFVFQSGAGNNWAKGHYTEGAELVDSVLDV
VRKEAESCDCLQG FQLTHSLGGGTGSGMGTLLISKIREEYP

161DRIMNTFSVVPSPKVS DTVVEPY NATLSVHQ LVENTDET
YCIDNEALYD ICFRTLKLTPT TYGDLNHLV SATMSGVT TCL

241RFP GQLNADLRKLA VNMVPPFRLHFFMPGFAPLTSRGSQ
QYRALTVPELTQQMFDAKNMMAACDPRHGRYLTVA AVFRGR

321MSMKEVDEQMLNVQNKNS SYFVEWIPNNVKTAVCDIPPR
GLKMSATFIGNSTAIQELFKRISEQFTAMFRRKAF LHWYT G

401EGMDEMEFTEAESNMNDLVSEYQQYQDATAEEEGEFEEE
AE EEA

5.168 solute carrier family 6, member 19 [*Homo sapiens*]
Protein Accession gil51468073

Associated Peptides 4
Associated Spectra 5

Mean Expression Ratio 0.887
Median Expression Ratio 0.887
Credible Interval (0.638, 1.24)

Coverage 0.0489
[0286]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.87	1.3	SEQ ID NO: 1076	IPSLAELETIEQEEASSR
2	0.62	0.9	1.3	SEQ ID NO: 1077	IPSLAELETIEQEEASSRPK
1	0.6	0.9	1.4	SEQ ID NO: 1078	LVLPNPGLDAR
1	0.57	0.85	1.3	SEQ ID NO: 1079	VLPNPGLDAR

SEQ ID NO: 1080

1MVR LVL PNPGLDARI PSLAELETIEQEEASSRPKWDNKAQY
MLTCLGFCVGLGNVWRFPYLCQSHGGGAFMIPFLILLVL

81EGIPLLYLEFAIGQRLRRGSLGVWSS IHPALKGLGLASMLT
SFMVGLYYNTIISWIMWYLFNSFQEPLPWSDCPLNENQT

161GYVDECARSSSPVDYFWYRET LNISTSI SDSGSIQWWMLLC
LACAWSVLYMCTIRGIETTGKAVYITSTLPYVVLTI FLIR

241GLTLKGATNGIVFLFTP NVTELAQPDTWLDAGA QVFFSFS
LAFGGLISFSSYNSVHN NCEKDSVIVSIINGFTSVYVAIV

-continued

321	V	Y	S	V	I	G	F	R	A	T	Q	R	Y	D	D	C	F	S	T	N	I	L	T	L	I	N	G	F	D	L	P	E	G	N	V	T	Q	E	N	F
	V	D	M	Q	Q	R	C	N	A	S	D	P	A	A	Y	A	Q	L	V	F	Q	T	C	D	I	N	A	F	L	S	E	A	V	E	G	T	G	L	A	F
401	I	V	F	T	E	A	I	T	K	M	P	L	S	P	L	W	S	V	L	F	F	I	M	L	F	C	L	G	L	S	S	M	F	G	N	M	E	G	V	V
	V	P	L	Q	D	L	R	V	I	P	P	K	W	P	K	E	V	L	T	G	L	I	C	L	G	T	F	L	I	G	F	I	F	T	L	N	S	G	Q	Y
481	W	L	S	L	L	D	S	Y	A	G	S	I	P	L	L	I	I	A	F	C	E	M	F	S	V	V	Y	V	Y	G	V	D	R	F	N	K	D	I	E	F
	M	I	G	H	K	P	N	I	F	W	Q	V	T	W	R	V	S	P	L	L	M	L	I	I	F	L	F	F	F	V	V	E	V	S	Q	E	L	T	Y	
561	S	I	W	D	P	G	Y	E	E	F	P	K	S	Q	K	I	S	Y	P	N	W	V	Y	V	V	V	I	V	A	G	V	P	S	L	T	I	P	G	Y	
	A	I	Y	K	L	I	R	N	H	C	Q	K	P	G	D	H	Q	G	L	V	S	T	L	S	T	A	S	M	N	G	D	L	K	Y						

5.169 decay accelerating factor for complement isoform 2 precursor [*Homo sapiens*]
Protein Accession gi|168693643

Mean Expression Ratio 1.13

Median Expression Ratio 1.13

Credible Interval (0.736, 1.71)

Associated Peptides 2

Associated Spectra 2

Coverage NaN

[0287]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.7	1.2	1.8	SEQ ID NO: 1081	EIYCPAPPQIDNGIIQGER
1	0.72	1.1	1.8	SEQ ID NO: 1082	DCGLPPDVPNAQPALEGR

5.170 membrane alanine aminopeptidase precursor [*Homo sapiens*]

Protein Accession gi|157266300

Mean Expression Ratio 1.13

Median Expression Ratio 1.13

Credible Interval (1.02, 1.25)

Associated Peptides 54

Associated Spectra 111

Coverage 0.483

[0288]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.87	1.1	1.5	SEQ ID NO: 1083	AIAQGGEEEWDFAWQFR
8	1.0	1.3	1.6	SEQ ID NO: 1084	AQIINDAFNLASAHK
1	0.81	1.1	1.4	SEQ ID NO: 1085	ASSHPLSTPASEINTPAQISELFDIAISY
5	0.88	1.1	1.4	SEQ ID NO: 1086	CNAIAQGGEEEWDFAWQFR
1	0.85	1.1	1.5	SEQ ID NO: 1087	DFAWQFR
1	0.82	1.1	1.4	SEQ ID NO: 1088	DFVQSNWK
3	0.87	1.1	1.5	SEQ ID NO: 1089	DHSAIPVINR
2	0.87	1.2	1.5	SEQ ID NO: 1090	DLMVLNDVYR
1	0.86	1.1	1.5	SEQ ID NO: 1091	DLTALSNNMLPK
1	0.82	1.1	1.5	SEQ ID NO: 1092	ELQQLEQFK
1	0.83	1.1	1.5	SEQ ID NO: 1093	ELWILNR
1	0.86	1.1	1.5	SEQ ID NO: 1094	ENSLLPDPLSSSSSNK
2	0.88	1.2	1.5	SEQ ID NO: 1095	EVVLQWPTENSK
2	0.82	1.1	1.4	SEQ ID NO: 1096	FFAGHYDTPYPLPK

-continued

1	0.86	1.1	1.5	SEQ ID NO: 1097	FSTEYELQQLEQFK
2	0.84	1.1	1.5	SEQ ID NO: 1098	FSTEYELQQLEQFKK
1	0.84	1.1	1.5	SEQ ID NO: 1099	GVGGSQPPDIDKTELVEPTEY
1	0.88	1.2	1.6	SEQ ID NO: 1100	GVGGSQPPDIDKTELVEPTEYLVVHLK
1	0.84	1.1	1.5	SEQ ID NO: 1101	IVSEFDYVEK
1	0.86	1.2	1.6	SEQ ID NO: 1102	KIQTQLQR
1	0.86	1.2	1.5	SEQ ID NO: 1103	KLFNDYGGGSFSSNLIQAVTR
1	0.84	1.1	1.5	SEQ ID NO: 1104	KQVTPLFIHFR
5	0.9	1.1	1.4	SEQ ID NO: 1105	KVVATTQMQAADAR
4	0.87	1.1	1.4	SEQ ID NO: 1106	LFNDYGGGSFSSNLIQAVTR
1	0.86	1.1	1.5	SEQ ID NO: 1107	LLAFIVSEFDYVEK
1	0.85	1.1	1.5	SEQ ID NO: 1108	LPNTLKPDSYR
2	0.86	1.1	1.5	SEQ ID NO: 1109	MLSSPLSEDVFK
1	0.85	1.1	1.5	SEQ ID NO: 1110	NAIAQGGEEDWFAWEQFR
2	0.84	1.1	1.5	SEQ ID NO: 1111	NYVWIVPITSIR
2	0.88	1.2	1.5	SEQ ID NO: 1112	PSEFNWVWIVPITSIR
2	0.89	1.2	1.5	SEQ ID NO: 1113	QQQDYWLIDVR
2	0.79	1.0	1.4	SEQ ID NO: 1114	QVTPLFIHFR
1	0.83	1.1	1.5	SEQ ID NO: 1115	QWMENPNNNPIHPN
10	0.82	1	1.2	SEQ ID NO: 1116	QWMENPNNNPIHPNLR
4	0.96	1.2	1.6	SEQ ID NO: 1117	QYMPWEAALSSLSYFK
2	0.85	1.1	1.5	SEQ ID NO: 1118	RFSTEYELQQLEQFK
4	1.0	1.3	1.7	SEQ ID NO: 1119	SDQIGLPDFNAGAMENWGLVTYR
1	0.86	1.1	1.5	SEQ ID NO: 1120	SFPCFDEPAMK
2	0.81	1.1	1.4	SEQ ID NO: 1121	SFSNLIQAVTR
1	0.84	1.1	1.5	SEQ ID NO: 1122	SIQLPTTVR
3	0.82	1.1	1.4	SEQ ID NO: 1123	STVYCNAIAQGGEEDWFAWEQFR
1	0.85	1.1	1.5	SEQ ID NO: 1124	VKDSQYEMDSEFEGELADDLAGFYR
1	0.85	1.1	1.5	SEQ ID NO: 1125	VNYDEENWR
1	0.85	1.1	1.5	SEQ ID NO: 1126	VVATTQMQAADAR
1	0.81	1.1	1.4	SEQ ID NO: 1127	VWIVPITSIR
1	0.85	1.1	1.5	SEQ ID NO: 1128	YLSYTLNPDILR
8	0.91	1.1	1.4	SEQ ID NO: 1129	DSQYEMDSEFEGELADDLAGFYR
1	0.85	1.1	1.5	SEQ ID NO: 1130	AGHYDTPYPLPK
1	0.84	1.1	1.5	SEQ ID NO: 1131	EATDVIIHISK
3	0.87	1.1	1.5	SEQ ID NO: 1132	LVVHLK
1	0.86	1.1	1.5	SEQ ID NO: 1134	RFSTEYELQQLEQFKK
1	0.84	1.1	1.5	SEQ ID NO: 1135	YVWIVPITSIR

-continued

1	0.85	1.1	1.5	SEQ ID NO: 1136	GFYISK
1	0.87	1.2	1.5	SEQ ID NO: 1137	KDNEETGFGSGTR
SEQ ID NO: 1138					
1M A K G F Y I S K S L G I L G I L L G V A A V C T I I A L S V V Y S Q E K N K N A					
N S S P V A S T T P S A S A T T N P A S A T T L D Q S K A W N R Y R L P N T L					
81K P D S Y R V T L R P Y L T P N D R G L Y V F K G S S T V R F T C K E A T D V I I					
I H S K K L N Y T L S Q G H R V V L R G V G G S Q P P D I D K T E L V E P T E					
161Y L V V H L K G S L V K D S Q Y E M D S E F E G E L A D D L A G F Y R S E Y M					
E G N V R K V V A T T Q M Q A A D A R K S F P C F D E P A M K A E F N I T L I H P					
241K D L T A L S N M L P K G P S T P L P E D P N W N V T E F H T T P K M S T Y L					
L A F I V S E F D Y V E K Q A S N G V L I R I W A R P S A I A A G H G D Y A L N V					
321T G P I L N F F A G H Y D T P Y P L P K S D Q I G L P D F N A G A M E N W G L					
V T Y R E N S L L F D P L S S S S S N K E R V V T V I A H E L A H Q W F G N L V T					
401I E W W N D L W L N E G F A S Y V E Y L G A D Y A E P T W N L K D L M V L N					
D V Y R V M A V D A L A S S H P L S T P A S E I N T P A Q I S E L F D A I S Y S K G					
481A S V L R M L S S F L S E D V F K Q G L A S Y L H T F A Y Q N T I Y L N L W D					
H L Q E A V N N R S I Q L P T T V R D I M N R W T L Q M G F P V I T V D T S T G T					
561L S Q E H F L L D P D S N V T R P S E F N Y V W I V P I T S I R D G R Q Q D Y					
W L I D V R A Q N D L F S T S G N E W V L L N L N V T G Y Y R V N Y D E E N W R					
641K I Q T Q L Q R D H S A I P V I N R A Q I I N D A F N L A S A H K V P V T L A L					
N N T L F L I E E R Q Y M P W E A A L S S L S Y F K L M F D R S E V Y G P M K N					
721Y L K K Q V T P L F I H F R N N T N N W R E I P E N L M D Q Y S E V N A I S T A					
C S N G V P E C E E M V S G L F K Q W M E N P N N N P I H P N L R S T V Y C N A					
801I A Q G G E E E W D F A W E Q F R N A T L V N E A D K L R A A L A C S K E L					
W I L N R Y L S Y T L N P D L I R K Q D A T S T I I S I T N N V I G Q G L V W D F V					
881Q S N W K K L F N D Y G G G S F S F S N L I Q A V T R R F S T E Y E L Q Q L E Q					
F K K D N E E T G F G S G T R A L E Q A L E K T K A N I K W V K E N K E V V L Q					
961W F T E N S K					

5.171 transmembrane protein 9 [*Homo sapiens*]
Protein Accession gi|7705999

Associated Peptides 1

Mean Expression Ratio 0.888

Associated Spectra 1

Median Expression Ratio 0.888

Coverage 0.104

Credible Interval (0.541, 1.42)

[0289]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.52	0.87	1.4	SEQ ID NO: 1139	KPDAYTEQLHNEEENEDAR
SEQ ID NO: 1140					
1M K L L S L V A V V G C L L V P P A E A N K S S E D I R C K C I C P P Y R N I S G					
H I Y N Q N V S Q K D C N C L H V V E P M P V P G H D V E A Y C L L C E C R Y					
81E E R S T T T I K V I I V I Y L S V V G A L L L Y M A F L M L V D P L I R K P D A					
Y T E Q L H N E E E N E D A R S M A A A A A S L G G P R A N T V L E R V E G A					
161Q Q R W K L Q V Q E Q R K T V F D R H K M L S					

5.172 toll interacting protein [*Homo sapiens*]
Protein Accession gi|21361619
Mean Expression Ratio 1.13
Median Expression Ratio 1.12
Credible Interval (0.772, 1.68)
Associated Peptides 3
Associated Spectra 3
Coverage 0.106
[0290]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.72	1.1	1.7	SEQ ID NO: 1141	AIQDMFPNMDQEVIR
1	0.78	1.2	1.9	SEQ ID NO: 1142	GPVYIGELPQDFLR
1	0.72	1.1	1.7	SEQ ID NO: 1143	IGELPQDFLR

SEQ ID NO: 1144

1M A T T V S T Q R G P V Y I G E L P Q D F L R I T P T Q Q Q R Q V Q L D A Q A A
Q Q L Q Y G G A V G T V G R L N I T V V Q A K L A K N Y G M T R M D P Y C R L R

81L G Y A V Y E T P T A H N G A K N P R W N K V I H C T V P P G V D S F Y L E I F
D E R A F S M D D R I A W T H I T I P E S L R Q G K V E D K W Y S L S G R Q G D

161D K E G M I N L V M S Y A L L P A A M V M P P Q P V V L M P T V Y Q Q G V G
Y V P I T G M P A V C S P G M V P V A L P P A A V N A Q P R C S E E D L K A I Q D M

241F P N M D Q E V I R S V L E A Q R G N K D A A I N S L L Q M G E E P

5.173 arylsulfatase F precursor [*Homo sapiens*]
Protein Accession gi|31742482
Mean Expression Ratio 0.893
Median Expression Ratio 0.89
Credible Interval (0.584, 1.38)

Associated Peptides 2
Associated Spectra 2
Coverage 0.0593
[0291]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.9	1.5	SEQ ID NO: 1145	ILDAIDDFGLR
1	0.53	0.85	1.4	SEQ ID NO: 1146	EPTSLMDILPTVASVSGGSLPQDR

SEQ ID NO: 1147

1M R P R R P L V F M S L V C A L L N T C Q A H R V H D D K P N I V L I M V D D L
G I G D L G C Y G N D T M R T P H I D R L A R E G V R L T Q H I S A A S L C S P

81S R S A F L T G R Y P I R S G M V S S G N R R V I Q N L A V P A G L P L N E T T L
A A L L K K Q G Y S T G L I G K W H Q G L N C D S R S D Q C H H P Y N Y G F D

161Y Y Y G M P F T L V D S C W P D P S R N T E L A F E S Q L W L C V Q L V A I A
I L T L T F G K L S G W V S V P W L L I F S M I L F I F L L G Y A W F S S H T S P

241L Y W D C L L M R G H E I T E Q P M K A E R A G S I M V K E A I S F L E R H S
K E T F L L F F S F L H V H T P L P T T D D F T G T S K H G L Y G D N V E E M D S

321M V G K I L D A I D D F G L R N N T L V Y F T S D H G G H L E A R R G H A Q L
G G W N G I Y K G G K G M G W E G G I R V P G I V R W P G K V P A G R L I K E P

401T S L M D I L P T V A S V S G G S L P Q D R V I D G R D L M P L L Q G N V R H S
E H E F L F H Y C G S Y L H A V R W I P K D D S G S V W K A H Y V T P V F Q P P

481A S G G C Y V T S L C R C F G E Q V T Y H N P P L L F D L S R D P S E S T P L T
P A T E P L H D F V I K K V A N A L K E H Q E T I V P V T Y Q L S E L N Q G R T

561W L K P C C G V F P F C L C D K E E E V S Q P R G P N E K R

5.174 calcium binding protein 39 [*Homo sapiens*]; calcium binding protein 39 [*Homo sapiens*]; calcium binding protein 39 [*Homo sapiens*]
Protein Accession gi|7706481 gi|195927022 gi|195927020

Mean Expression Ratio 1.12

Median Expression Ratio 1.12

Credible Interval (0.693, 1.81)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0292]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.69	1.2	1.9	SEQ ID NO: 1148	LLSAEFLEQHYDR

5.175 hemicentin 1 [*Homo sapiens*]

Protein Accession gi|118572606

Mean Expression Ratio 0.889

Median Expression Ratio 0.89

Credible Interval (0.544, 1.45)

Associated Peptides 1

Associated Spectra 1

Coverage 0.00284

[0293]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.51	0.86	1.4	SEQ ID NO: 1149	LVSLPFGIATNQDLIR

SEQ ID NO: 1150

1 M I S W E V V H T V F L F A L L Y S S L A Q D A S P Q S E I R A E E I P E G A S T L
A F V F D V T G S M Y D D L V Q V I E G A S K I L E T S L K R P K R P L F N

81 F A L V P F H D P E I G P V T I T T D P K K F Q Y E L R E L Y V Q G G G D C P E
M S I G A I K I A L E I S L P G S F I Y V F T D A R S K D Y R L T H E V L Q L I

161 Q Q K Q S Q V V F V L T G D C D D R T H I G Y K V Y E E I A S T S S G Q V F H
L D K K Q V N E V L K W V E E A V Q A S K V H L L S T D H L E Q A V N T W R I P F

241 D P S L K E V T V S L S G P S P M I E I R N P L G K L I K K G F G L H E L L N I H
N S A K V V N V K E P E A G M W T V K T S S S G R H S V R I T G L S T I D F R

321 A G F S R K P T L D F K K T V S R P V Q G I P T Y V L L N T S G I S T P A R I D L
L E L L S I S G S S L K T I P V K Y Y P H R K P Y G I W N I S D F V P P N E A

401 F F L K V T G Y D K D D Y L F Q R V S S V S F S S I V P D A P K V T M P E K T P
G Y Y L Q P G Q I P C S V D S L L P F T L S F V R N G V T L G V D Q Y L K E S A

481 S V N L D I A K V T L S D E G F Y E C I A V S S A G T G R A Q T F F D V S E P P
P V I Q V P N N V T V T P G E R A V L T C L I I S A V D Y N L T W Q R N D R D V

561 R L A E P A R I R T L A N L S L E L K S V K F N D A G E Y H C M V S S E G G S S
A A S V F L T V Q E P P K V T V M P K N Q S F T G S E V S I M C S A T G Y P K

641 P K I A W T V N D M F I V G S H R Y R M T S D G T L F I K N A A P K D A G I Y
G C L A S N S A G T D K Q N S T L R Y I E A P K L M V V Q S E L L V A L G D I T V

721 M E C K T S G I P P P Q V K W F K G D L E L R P S T F L I I D P L L G L L K I Q E
T Q D L D A G D Y T C V A I N E A G R A T G K I T L D V G S P P V F I Q E P A

801 D V S M E I G S N V T L P C Y V Q G Y P E P T I K W R R L D N M P I F S R P F S
V S S I S Q L R T G A L F I L N L W A S D K G T Y I C E A E N Q F G K I Q S E T

881 T V T V T G L V A P L I G I S P S V A N V I E G Q Q L T L P C T L L A G N P I P E
R R W I K N S A M L L Q N P Y I T V R S D G S L H I E R V Q L Q D G G E Y T C

961 V A S N V A G T N N K T T S V V V H V L P T I Q H G Q Q I L S T I E G I P V T L
P C K A S G N P K P S V I W S K K G E L I S T S S A K F S A G A D G S L Y V V S

1041 P G G E E S G E Y V C T A T N T A G Y A K R K V Q L T V Y V R P R V F G D Q
R G L S Q D K P V E I S V L A G E E V T L P C E V K S L P P P I I T W A K E T Q L I

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1121 S P F S P R H T F L P S G S M K I T E T R T S D S G M Y L C V A T N I A G N V T
Q A V K L N V H V P P K I Q R G P K H L K V Q V G Q R V D I P C N A Q G T P L P

1201 V I T W S K G G S T M L V D G E H H V S N P D G T L S I D Q A T P S D A G I Y
T C V A T N I A G T D E T E I T L H V Q E P P T V E D L E P P Y N T T F Q E R V A

1281 N Q R I E F P C P A K G T P K P T I K W L H N G R E L T G R E P G I S I L E D G
T L L V I A S V T P Y D N G E Y I C V A V N E A G T T E R K Y N L K V H V P P V

1361 I K D K E Q V T N V S V L L N Q L T N L F C E V E G T P S P I I M W Y K D N V
Q V T E S S T I Q T V N N G K I L K L F R A T P E D A G R Y S C K A I N I A G T S

1441 Q K Y F N I D V L V P P T I I G T N F P N E V S V V L N R D V A L E C Q V K G
T P F P D I H W F K D G K P L F L G D P N V E L L D R G Q V L H L K N A R R N D K

1521 G R Y Q C T V S N A A G K Q A K D I K L T I Y I P P S I K G G N V T T D I S V L
I N S L I K L E C E T R G L P M P A I T W Y K D G Q P I M S S S Q A L Y I D K G

1601 Q Y L H I P R A Q V S D S A T Y T C H V A N V A G T A E K S F H V D V Y V P
P M I E G N L A T P L N K Q V V I A H S L T L E C K A A G N P S P I L T W L K D G V

1681 P V K A N D N I R I E A G G K K L E I M S A Q E I D R G Q Y I C V A T S V A G
E K E I K Y E V D V L V P P A I E G G D E T S Y F I V M V N N L L E L D C H V T G

1761 S P P P T I M W L K D G Q L I D E R D G F K I L L N G R K L V I A Q A Q V S N
T G L Y R C M A A N T A G D H K K E F E V T V H V P P T I K S S G L S E R V V V K

1841 Y K P V A L Q C I A N G I P N P S I T W L K D D Q P V N T A Q G N L K I Q S S
G R V L Q I A K T L L E D A G R Y T C V A T N A A G E T Q Q H I Q L H V H E P P S

1921 L E D A G K M L N E T V L V S N P V Q L E C K A A G N P V P V I T W Y K D N
R L L S G S T S M T F L N R G Q I I D I E S A Q I S D A G I Y K C V A I N S A G A T

2001 E L F Y S L Q V H V A P S I S G S N N M V A V V V N N P V R L E C E A R G I P
A P S L T W L K D G S P V S S F S N G L Q V L S G G R I L A L T S A Q I S D T G R

2081 Y T C V A V N A A G E K Q R D I D L R V Y V P P N I M G E E Q N V S V L I S Q
A V E L L C Q S D A I P P P T L T W L K D G H P L L K K P G L S I S E N R S V L K

2161 I E D A Q V Q D T G R Y T C E A T N V A G K T E K N Y N V N I W V P P N I G
G S D E L T Q L T V I E G N L I S L L C E S S G I P P P N L I W K K K G S P V L T D

2241 S M G R V R I L S G G R Q L Q I S I A E K S D A A L Y S C V A S N V A G T A K
K E Y N L Q V Y I R P T I T N S G S H P T E I I V T R G K S I S L E C E V Q G I P

2321 P P T V T W M K D G H P L I K A K G V E I L D E G H I L Q L K N I H V S D T G
R Y V C V A V N V A G M T D K K Y D L S V H A P P S I I G N H R S P E N I S V V E

2401 K N S V S L T C E A S P S I S I T W F K D G W P V S L S N S V R I L S G G R
M L R L M Q T T M E D A G Q Y T C V V R N A A G E E R K I F G L S V L V P P H I

2481 V G E N T L E D V K V K E K Q S V T L T C E V T G N P V P E I T W H K D G Q
P L Q E D E A H H I I S G G R F L Q I T N V Q V P H T G R Y T C L A S S P A G H K S

2561 R S F S L N V F V S P T I A G V G S D G N P E D V T V I L N S P T S L V C E A Y
S Y P P A T I T W F K D G T P L E S N R N I R I L P G G R T L Q I L N A Q E D N

2641 A G R Y S C V A T N E A G E M I K H Y E V K V Y I P P I I N K G D L W G P G L
S P K E V K I K V N N T L T L E C E A Y A I P S A S L S W Y K D G Q P L K S D D H

2721 V N I A A N G H T L Q I K E A Q I S D T G R Y T C V A S N I A G E D E L D F D
V N I Q V P P S F Q K L W E I G N M L D T G R N G E A K D V I I N N P I S L Y C E

2801 T N A A P P P T L T W Y K D G H P L T S S D K V L I L P G G R V L Q I P R A K
V E D A G R Y T C V A V N E A G E D S L Q Y D V R V L V P P I I K G A N S D L P E

2881 E V T V L V N K S A L I E C L S S G S P A P R N S W Q K D G Q P L L E D D H H
K F L S N G R I L Q I L N T Q I T D I G R Y V C V A E N T A G S A K K Y F N L N V

2961 H V P P S V I G P K S E N L T V V V N N F I S L T C E V S G F P P P D L S W L K
N E Q P I K L N T N T L I V P G G R T L Q I I R A K V S D G G E Y T C I A I N Q

3041 A G E S K K K F S L T V Y V P P S I K D H D S E S L S V V N V R E G T S V S L E
C E S N A V P P P V I T W Y K N G R M I T E S T H V E I L A D G Q M L H I K K A

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3121 EVSDTGTQYVVCRAINVAAGRDDKNFHLNVYVPPPSIEGPERE
VIVETISNPVTLTCDATGIPPTIAWLKNHKRIENS D S L E V

3201 R I L S G G S K L Q I A R S Q H S D S G N Y T C I A S N M E G K A Q K Y Y F L
S I Q V P P S V A G A E I P S D V S V L L G E N V E L V C N A N G I P T P L I Q W

3281 L K D G K P I A S G E T E R I R V S A N G S T L N I Y G A L T S D T G K Y T C V
A T N P A G E E D R I F N L N V Y V T P T I R G N K D E A E K L M T L V D T S I

3361 N I E C R A T G T P P P Q I N W L K N G L P L P L S S H I R L L A A G Q V I R I
V R A Q V S D V A V Y T C V A S N R A G V D N K H Y N L Q V F A P P N M D N S M

3441 G T E E I T V L K G S S T S M A C I T D G T P A P S M A W L R D G Q P L G L D
A H L T V S T H G M V L Q L L K A E T E D S G K Y T C I A S N E A G E V S K H F I

3521 L K V L E P P H I N G S E E H E E I S V I V N N P L E L T C I A S G I P A P K M T
W M K D G R P L P Q T D Q V Q T L G G G E V L R I S T A Q V E D T G R Y T C L

3601 A S S P A G D D D K E Y L V R V H V P P N I A G T D E P R D I T V L R N R Q V
T L E C K S D A V P P P V I T W L R N G E R L Q A T P R V R I L S G G R Y L Q I N

3681 N A D L G D T A N Y T C V A S N I A G K T T R E F I L T V N V P P N I K G G P
Q S L V I L L N K S T V L E C I A E G V P T P R I T W R K D G A V L A G N H A R Y

3761 S I L E N G F L H I Q S A H V T D T G R Y L C M A T N A A G T D R R R I D L Q
V H V P P S I A P G P T N M T V I V N V Q T T L A C E A T G I P K P S I N W R K N

3841 G H L L N V D Q N Q N S Y R L L S S G S L V I I S P S V D D T A T Y E C T V T
N G A G D D K R T V D L T V Q V P P S I A D E P T D F L V T K H A P A V I T C T A

3921 S G V P F P S I H W T K N G I R L L P R G D G Y R I L S S G A I E I L A T Q L N
H A G R Y T C V A R N A A G S A H R H V T L H V H E P P V I Q P Q P S E L H V I

4001 L N N P I L L P C E A T G T P S P F I T W Q K E G I N V N T S G R N H A V L P S
G G L Q I S R A V R E D A G T Y M C V A Q N P A G T A L G K I K L N V Q V P P V

4081 I S P H L K E Y V I A V D K P I T L S C E A D G L P P P D I T W H K D G R A I V
E S I R Q R V L S S G S L Q I A F V Q P G D A G H Y T C M A A N V A G S S S T S

4161 T K L T V H V P P R I R S T E G H Y T V N E N S Q A I L P C V A D G I P T P A I
N W K K D N V L L A N L L G K Y T A E P Y G E L I L E N V V L E D S G F Y T C V

4241 A N N A A G E D T H T V S L T V H V L P T F T E L P G D V S L N K G E Q L R L
S C K A T G I P L P K L T W T F N N N I I P A H F D S V N G H S E L V I E R V S K

4321 E D S G T Y V C T A E N S V G F V K A I G F V Y V K E P P V F K G D Y P S N
W I E P L G G N A I L N C E V K G D P T P T I Q W N R K G V D I E I S H R I R Q L G

4401 N G S L A I Y G T V N E D A G D Y T C V A T N E A G V V E R S M S L T L Q S
P P I I T L E P V E T V I N A G G K I I L N C Q A T G E P Q P T I T W S R Q G H S I

4481 S W D D R V N V L S N N S L Y I A D A Q K E D T S E F E C V A R N L M G S V
L V R V P V I V Q V H G G F S Q W S A W R A C S V T C G K G I Q K R S R L C N Q P L

4561 P A N G G K P C Q G S D L E M R N C Q N K P C P V D G S W S E W S L W E E C
T R S C G R G N Q T R T R T C N N P S V Q H G G R P C E G N A V E I I M C N I R P C

4641 P V H G A W S A W Q P W G T C S E S C G K G T Q T R A R L C N N P P P A F G
G S Y C D G A E T Q M Q V C N E R N C P I H G K W A T W A S W S A C S V S C G G
G A

4721 R Q R T R G C S D P V P Q Y G G R K C E G S D V Q S D F C N S D P C P T H G
N W S P W S G W G T C S R T C N G G Q M R R Y R T C D N P P P S N G G R A C G G
P D

4801 S Q I Q R C N T D M C P V D G S W G S W H S W S Q C S A S C G G G E K T R K
R L C D H P V P V K G G R P C P G D T T Q V T R C N V Q A C P G G P Q R A R G S V I

4881 G N I N D V E F G I A F L N A T I T D S P N S D T R I I R A K I T N V P R S L G S
A M R K I V S I L N P I Y W T T A K E I G E A V N G F T L T N A V F K R E T Q

4961 V E F A T G E I L Q M S H I A R G L D S D G S L L L D I V V S G Y V L Q L Q S P
A E V T V K D Y T E D Y I Q T G P G Q L Y A Y S T R L F T I D G I S I P Y T W N

5041 H T V F Y D Q A Q G R M P F L V E T L H A S S V E S D Y N Q I E E T L G F K I
H A S I S K G D R S N Q C P S G F T L D S V G P F C A D E D E C A A G N P C S H S

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5121	C H N A M G T Y Y C S C P K G L T I A A D G R T C Q D I D E C A L G R H T C
	H A G Q D C D N T I G S Y R C V V R C G S G F R R T S D G L S C Q D I N E C Q E S S
5201	P C H Q R C F N A I G S F H C G C E P G Y Q L K G R K C M D V N E C R Q N V
	C R P D Q H C K N T R G G Y K C I D L C P N G M T K A E N G T C I D I D E C K D G T
5281	H Q C R Y N Q I C E N T R G S Y R C V C P R G Y R S Q G V G R P C M D I N E
	C E Q V P K P C A H Q C S N T P G S F K C I C P P G Q H L L G D G K S C A G L E R L
5361	P N Y G T Q Y S S Y N L A R F S P V R N N Y Q P Q Q H Y R Q Y S H L Y S S Y S
	E Y R N S R T S L S R T R R T I R K T C P E G S E A S H D T C V D I D E C E N T D
5441	A C Q H E C K N T F G S Y Q C I C P P G Y Q L T H N G K T C Q D I D E C L E Q
	N V H C G P N R M C F N M R G S Y Q C I D T P C P P N Y Q R D P V S G F C L K N C
5521	P P N D L E C A L S P Y A L E Y K L V S L P F G I A T N Q D L I R L V A Y T Q D
	G V M H P R T T F L M V D E E Q T V P F A L R D E N L K G V V Y T T R P L R E A
5601	E T Y R M R V R A S S Y S A N G T I E Y Q T T F I V Y I A V S A Y P Y

5.176 prostate stem cell antigen preproprotein [*Homo sapi-*
ens]
Protein Accession gi|5031995

Mean Expression Ratio 1.12

Median Expression Ratio 1.12

Credible Interval (0.692, 1.81)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0813
[0294]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.7	1.2	1.9	SEQ ID NO: 1151	AVGLLTVISK
SEQ ID NO: 1152					
1 M K A V L L A L L M A G L A L Q P G T A L L C Y S C K A Q V S N E D C L Q V E					
N C T Q L G E Q C W T A R I R A V G L L T V I S K G C S L N C V D D S Q D Y Y V G					
81 K K N I T C C D T D L C N A S G A H A L Q P A A A I L A L L P A L G L L L W G P					
G Q L					

5.177 solute carrier family 47, member 1 [*Homo sapiens*]
Protein Accession gi|22907060
Mean Expression Ratio 1.12
Median Expression Ratio 1.12
Credible Interval (0.725, 1.74)
Associated Peptides 1
Associated Spectra 2
Coverage 0.0246
[0295]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.74	1.2	1.8	SEQ ID NO: 1153	QEEPLPEHPQDGAK
SEQ ID NO: 1154					
1 M E A P E E P A P V R G G P E A T L E V R G S R C L R L S A F R E E L R A L L V L					
A G P A F L V Q L M V F L I S F I S S V F C G H L G K L E L D A V T L A I A V					
81 I N V T G V S V G F G L S S A C D T L I S Q T Y G S Q N L K H V G V I L Q R S A L					
V L L L C C F P C W A L F L N T Q H I L L L F R Q D P D V S R L T Q T Y V T I					

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161F I P A L P A T F L Y M L Q V K Y L L N Q G I V L P Q I V T G V A A N L V N A L
A N Y L F L H Q L H L G V I G S A L A N L I S Q Y T L A L L L F L Y I L G K K L

241H Q A T W G G W S L E C L Q D W A S F L R L A I P S M L M L C M E W W A Y E
V G S F L S G I L G M V E L G A Q S I V Y E L A I I V Y M V P A G F S V A A S V R V

321G N A L G A G D M E Q A R K S S T V S L L I T V L F A V A F S V L L L S C K D
H V G Y I F T T D R D I I N L V A Q V V P I Y A V S H L F E A L A C T S G G V L R

401G S G N Q K V G A I V N T I G Y Y V V G L P I G I A L M F A T T L G V M G L W
S G I I I C T V F Q A V C F L G F I I Q L N W K K A C Q Q A Q V H A N L K V N N V

481P R S G N S A L P Q D P L H P G C P E N L E G I L T N D V G K T G E P Q S D Q Q
M R Q E E P L P E H P Q D G A K L S R K Q L V L R R G L L L L G V F L I L L V G

561I L V R F Y V R I Q

5.178 polymeric immunoglobulin receptor [*Homo sapiens*] Associated Peptides 16
Protein Accession gi|31377806

Mean Expression Ratio 1.12 Associated Spectra 25

Median Expression Ratio 1.12 Coverage 0.234

Credible Interval (0.926, 1.35) [0296]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.83	1.1	1.6	SEQ ID NO: 1155	DGSFSVVITGLR
2	0.78	1.0	1.4	SEQ ID NO: 1156	ILLNPQDKDGSFSVVITGLR
1	0.83	1.1	1.6	SEQ ID NO: 1157	LDIQGTGQLLFSVINQLR
1	0.8	1.1	1.5	SEQ ID NO: 1158	LVSLTLNLVTR
9	0.9	1.1	1.4	SEQ ID NO: 1159	NADLQVLKPEPELVYEDLR
1	0.83	1.2	1.6	SEQ ID NO: 1160	QLFVNEESTIPR
1	0.8	1.1	1.5	SEQ ID NO: 1161	QSSGENCDVVNTLGK
1	0.85	1.2	1.6	SEQ ID NO: 1162	TVTINCPFK
1	0.81	1.1	1.5	SEQ ID NO: 1163	VVNIAQLSQDDSGR
1	0.78	1.1	1.5	SEQ ID NO: 1164	YLCGAHSDGQLQEGSPIQAW
1	0.8	1.1	1.5	SEQ ID NO: 1165	YWCLWEGAQNGR
1	0.82	1.1	1.6	SEQ ID NO: 1166	SVVINQLR
1	0.83	1.1	1.6	SEQ ID NO: 1167	KTENAQK
1	0.79	1.1	1.5	SEQ ID NO: 1168	HCALGPEVANVAK
1	0.82	1.1	1.5	SEQ ID NO: 1169	ILLNPQDK
1	0.8	1.1	1.5	SEQ ID NO: 1170	ADAAPDEK
SEQ ID NO: 1171					
1M L L F V L T C L L A V F P A I S T K S P I F G P E E V N S V E G N S V S I T C Y Y P P T S V N R H T R K Y W C R Q G A R G G C I T L I S S E G Y V S S K Y A G					
81R A N L T N F P E N G T F V V N I A Q L S Q D D S G R Y K C G L G I N S R G L S F D V S L E V S Q G P G L L N D T K V Y T V D L G R T V T I N C P F K T E N A Q					
161K R K S L Y K Q I G L Y P V L V I D S S G Y V N P N Y T G R I R L D I Q G T G Q L L F S V V I N Q L R L S D A G Q Y L C Q A G D D S N S N K K N A D L Q V L K P					
241E P E L V Y E D L R G S V T F H C A L G P E V A N V A K F L C R Q S S G E N C D V V V N T L G K R A P A F E G R I L L N P Q D K D G S F S V V I T G L R K E D A					

-continued

321G R R Y L C G A H S D G Q L Q E G S P I Q A W Q L F V N E E S T I P R S P T V V K
G V A G G S V A V L C P Y N R K E S K S I K Y W C L W E G A Q N G R C P L L V D

401S E G W V K A Q Y E G R L S L L E E P G N G T F T V I L N Q L T S R D A G F Y
W C L T N G D T L W R T T V E I K I I E G E P N L K V P G N V T A V L G E T L K V

481P C H F P C K F S S Y E K Y W C K W N N T G C Q A L P S Q D E G P S K A F V N
C D E N S R L V S L T L N L V T R A D E G W Y W C G V K Q G H F Y G E T A A V Y V

561A V E E R K A A G S R D V S L A K A D A A P D E K V L D S G F R E I E N K A I
Q D P R L F A E E K A V A D T R D Q A D G S R A S V D S G S S E E Q G G S S R A L

641V S T L V P L G L V L A V G A V A V G V A R A R H R K N V D R V S I R S Y R T
D I S M S D F E N S R E F G A N D N M G A S S I T Q E T S L G G K E E F V A T T E

721S T T E T K E P K K A K R S S K E E A E M A Y K D F L L Q S S T V A A E A Q D
G P O E A

5.179 cathepsin C isoform a preproprotein [*Homo sapiens*]
Protein Accession gi189083844

Mean Expression Ratio 1.12

Median Expression Ratio 1.12

Credible Interval (0.874, 1.43)

Associated Peptides 6

Associated Spectra 13

Coverage NaN

[0297]

-continued

A	2.5	50	97.5	Sequence	ID No.	Sequence
3	0.83	1.1	1.6	SEQ	ID NO: 1175	NVHGINFVSPVR
1	0.8	1.1	1.6	SEQ	ID NO: 1176	WFAPFK
2	0.84	1.1	1.6	SEQ	ID NO: 1177	LELVHHGPMVAFA

5.180 biliverdin reductase B (flavin reductase (NADPH))
[*Homo sapiens*]
Protein Accession gi|4502419

Mean Expression Ratio 0.897

Median Expression Ratio 0.896

Credible Interval (0.551, 1.46)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0728

[0298]

A	2.5	50	97.5	Sequence	ID No.	Sequence
4	0.83	1.1	1.5	SEQ	ID NO: 1172	AVAFEVYDDFLHYK
2	0.78	1.1	1.5	SEQ	ID NO: 1173	EVYDDFLHYK
1	0.79	1.1	1.6	SEQ	ID NO: 1174	GTDECAIESIAVAATPIPK

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.52	0.87	1.5	SEQ ID NO: 1178	TVAGQDAVIVLLGTR

SEQ ID NO: 1179

1MAVKKKIIAIFGATGQTGLTTTLAQAVQAGYEVTVLVLRDSSRL
PSEGPRPAHV VVG DVLQAADVDKTVAGQDAVIVLLGTRND

81LSPTTVMSEGARNIVAAAMKAHGV D K V V A C T S A F L L W D P T
KVP P R L Q A V T D D H I R M H K V L R E S G L K Y V A V M P P H I G D Q P L T

161G A Y T V T L D G R G P S R V I S K H D L G H F M L R C L T T D E Y D G H S T
Y P S H Q Y Q

5.181 prostatic binding protein [*Homo sapiens*]
Protein Accession gi|4505621
Mean Expression Ratio 1.12
Median Expression Ratio 1.12
Credible Interval (0.79, 1.59)
Associated Peptides 2
Associated Spectra 5
Coverage 0.144
[0299]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.78	1.1	1.7	SEQ ID NO: 1180	LYTLVLTDPDAPSR
3	0.78	1.1	1.6	SEQ ID NO: 1181	YVWLVEQDRPLK

SEQ ID NO: 1182

1M P V D L S K W S G P L S L Q E V D E Q P Q H P L H V T Y A G A A V D E L G K V
L T P T Q V K N R P T S I S W D G L D S G K L Y T L V L T D P D A P S R K D P K

81Y R E W H H F L V V N M K G N D I S S G T V L S D Y V G S G P P K G T G L H R
Y V W L V Y E Q D R P L K C D E P I L S N R S G D H R G K F K V A S F R K K Y E L

161R A P V A G T C Y Q A E W D D Y V P K L Y E Q L S G K

5.182 proteasome alpha 4 subunit isoform 1 [*Homo sapiens*]; proteasome alpha 4 subunit isoform 1 [*Homo sapiens*]
Protein Accession gi|4506185 gi|156713442
Mean Expression Ratio 1.12
Median Expression Ratio 1.12
Credible Interval (0.696, 1.82)
Associated Peptides 1
Associated Spectra 1
Coverage NaN
[0300]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.69	1.2	1.9	SEQ ID NO: 1183	LLDEVFFSEK

5.183 palate, lung and nasal epithelium associated precursor [*Homo sapiens*]; palate, lung and nasal epithelium associated precursor [*Homo sapiens*]
Protein Accession gi|7706119 gi|18765705
Mean Expression Ratio 0.896

Median Expression Ratio 0.897
Credible Interval (0.552, 1.44)
Associated Peptides 1
Associated Spectra 1
Coverage NaN
[0301]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.52	0.87	1.5	SEQ ID NO: 1184	LQVNTPLVGASLLR

5.184 vacuolar protein sorting factor 4A [*Homo sapiens*]
Protein Accession gi|7019569
Mean Expression Ratio 1.12
Median Expression Ratio 1.12
Credible Interval (0.773, 1.59)
Associated Peptides 4
Associated Spectra 4
Coverage 0.144
[0302]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.74	1.1	1.7	SEQ ID NO: 1185	IYIPLPEEAAR
1	0.74	1.1	1.7	SEQ ID NO: 1186	LHLGSTPHNLTDAHIHELAR
1	0.75	1.1	1.7	SEQ ID NO: 1187	QHKPSIIFIDEVDSLCSGR

-continued

1	0.73	1.1	1.7	SEQ ID NO: 1188	LLEPVVCM S D M L R
SEQ ID NO: 1189					
1M T T S T L Q K A I D L V T K A T E E D K A K N Y E E A L R L Y Q H A V E Y F L					
H A I K Y E A H S D K A K E S I R A K C V Q Y L D R A E K L K D Y L R S K E K H					
81G K K P V K E N Q S E G K G S D S D S E G D N P E K K K L Q E Q L M G A V V M					
E K P N I R W N D V A G L E G A K E A L K E A V I L P I K F P H L F T G K R T P W					
161R G I L L F G P P G T G K S Y L A K A V A T E A N N S T F F S V S S S D L M S K					
W L G E S E K L V K N L F E L A R Q H K P S I I F I D E V D S L C G S R N E N E					
241S E A A R R I K T E F L V Q M Q G V G N N N D G T L V L G A T N I P W V L D S					
A I R R R F E K R I Y I P L P E E A A R A Q M F R L H L G S T P H N L T D A N I H					
321E L A R K T E G Y S G A D I S I I V R D S L M Q P V R K V Q S A T H F K K V C G					
P S R T N P S M M I D D L L T P C S P G D P G A M E M T W M D V P G D K L L E P					
401V V C M S D M L R S L A T T R P T V N A D D L L K V K K F S E D F G Q E S					

5.185 transmembrane protein 192 [*Homo sapiens*]
Protein Accession gi|154240704

Associated Peptides 2

Mean Expression Ratio 0.899

Associated Spectra 2

Median Expression Ratio 0.899

Coverage 0.0996

Credible Interval (0.586, 1.35)

[0303]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.9	1.4	SEQ ID NO: 1190	IYAYPSNITSETGFR
1	0.55	0.88	1.4	SEQ ID NO: 1191	AKPEPDILEEEK
SEQ ID NO: 1192					
1M A A G G R M E D G S L D I T Q S I E D D P L L D A Q L L P H H S L Q A H F R P R					
F H P L P T V I I V N L L W F I H L V F V V L A F L T G V L C S Y P N P N E D					
81K C P G N Y T N P L K V Q T V I I L G K V I L W I L H L L L E C Y I Q Y H H S K I					
R N R G Y N L I Y R S T R H L K R L A L M I Q S S G N T V L L L I L C M Q H S					
161F P E P G R L Y L D L I L A I L A L E L I C S L I C L L I Y T V K I R R F N K A K P					
E P D I L E E E K I Y A Y P S N I T S E T G F R T I S S L E E I V E K Q G D					
241T I E Y L K R H N A L L S K R L L A L T S S D L G C Q P S R T					

5.186 vitronectin precursor [*Homo sapiens*]
Protein Accession gi|88853069

Mean Expression Ratio 0.901

Median Expression Ratio 0.9

Credible Interval (0.619, 1.31)

Associated Peptides 3

Associated Spectra 3

Coverage 0.09

[0304]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.87	1.3	SEQ ID NO: 1193	DVWGIEGPIDAAFTR
1	0.58	0.9	1.4	SEQ ID NO: 1194	DWHGVPGQVDAAMAGR
1	0.59	0.91	1.4	SEQ ID NO: 1195	FEDGVLDPDYPR

-continued

SEQ ID NO: 1196

1

M A P L R P L L I L A L L A W V A L A D Q E S C K G R C T E G F N V D K K C Q C

D E L C S Y Y Q S C C T D Y T A E C K P Q V T R G D V F T M P E D E Y T V Y D D

81

G E E K N N A T V H E Q V G G P S L T S D L Q A Q S K G N P E Q T P V L K P E E

E A P A P E V G A S K P E G I D S R P E T L H P G R P Q P P A E E E L C S G K P

161

F D A F T D L K N G S L F A F R G Q Y C Y E L D E K A V R P G Y P K L I R D V

W G I E G P I D A A F T R I N C Q G K T Y L F K G S Q Y W R F E D G V L D P D Y P

241

R N I S D G F D G I P D N V D A A L A L P A H S Y S G R E R V Y F F K G K Q Y

W E Y Q F Q H Q P S Q E E C E G S S L S A V F E H F A M M Q R D S W E D I F E L L

321

F W G R T S A G T R Q P Q F I S R D W H G V P G Q V D A A M A G R I Y I S G M

A P R P S L A K K Q R F R H R N R K G Y R S Q R G H S R G R N Q N S R R P S R A T

401

W L 5 L F 5 S E E S N L G A N N Y D D Y R M D W L V P A T C E P I Q S V F F F S

G D K Y Y R V N L R T R R V D T V D P P Y P R S I A Q Y W L G C P A P G H L

5.187 von Willebrand factor preproprotein [*Homo sapiens*]
Protein Accession gi|89191868

Associated Peptides 7

Mean Expression Ratio 1.11

Associated Spectra 13

Median Expression Ratio 1.11

Coverage 0.0387

Credible Interval (0.866, 1.41)

[0305]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.81	1.1	1.6	SEQ ID NO: 1197	AFVLSSVDELEQQR
2	0.8	1.1	1.5	SEQ ID NO: 1198	APILIQDFETLPR
4	0.8	1.1	1.4	SEQ ID NO: 1199	AVVILVTDVSVDSVDAADAAR
1	0.78	1.1	1.6	SEQ ID NO: 1200	LLDLVFLLDGSSR
3	0.81	1.1	1.5	SEQ ID NO: 1201	LP GDIQVVPIGVGPANVQELER
1	0.81	1.1	1.6	SEQ ID NO: 1202	VIVIPVGIGPHANLK
1	0.81	1.1	1.6	SEQ ID NO: 1203	EAPDLVLQR

SEQ ID NO: 1204

1

M I P A R F A G V L L A L A L I L P G T L C A E G T R G R S S T A R C S L F G S D

F V N T F D G S M Y S F A G Y C S Y L L A G G C Q K R S F S I I G D F Q N G K

81

R V S L S V Y L G E F F D I H L F V N G T V T Q G D Q R V S M P Y A S K G L Y L

E T E A G Y Y K L S G E A Y G F V A R I D G S G N F Q V L L S D R Y F N K T C G

161

L C G N F N I F A E D D F M T Q E G T L T S D P Y D F A N S W A L S S G E Q W

C E R A S P P S S S C N I S S G E M Q K G L W E Q C Q L L K S T S V F A R C H P L

241

V D P E P F V A L C E K T L C E C A G G L E C A C P A L L E Y A R T C A Q E G

M V L Y G W T D H S A C S P V C P A G M E Y R Q C V S P C A R T C Q S L H I N E M

321

C Q E R C V D G C S C P E G Q L L D E G L C V E S T E C P C V H S G K R Y P P

G T S L S R D C N T C I C R N S Q W I C S N E E C P G E C L V T G Q S H F K S F D

401

N R Y F T F S G I C Q Y L L A R D C Q D H S F S I V I E T V Q C A D D R D A V C

T R S V T V R L P G L H N S L V K L K H G A G V A M D G Q D V Q L P L L K G D L

481

R I Q H T V T A S V R L S Y G E D L Q M D W D G R G R L L V K L S P V Y A G

K T C G L C G N Y N G N Q G D D F L T P S G L A E P R V E D F G N A W K L H G D

C Q

561

D L Q K Q H S D P C A L N P R M T R F S E E A C A V L T S P T F E A C H R A V

S P L P Y L R N C R Y D V C S C S D G R E C L C G A L A S Y A A A C A G R G V R V

641

A W R E P G R C E L N C P K G Q V Y L Q C G T P C N L T C R S L S Y P D E E C

N E A C L E G C F C P P G L Y M D E R G D C V P K A Q C P C Y Y D G E I F Q P E D

-continued

721 I F S D H H T M C Y C E D G F M H C T M S G V P G S L L P D A V L S S P L S H
R S K R S L S C R P P M V K L V C P A D N L R A E G L E C T K T C Q N Y D L E C M

801 S M G C V S G C L C P P G M V R H E N R C V A L E R C P C F H Q G K E Y A P G
E T V K I G C N T C V C R D R K W N C T D H V C D A T C S T I G M A H Y L T F D G

881 L K Y L F P G E C Q Y V L V Q D Y C G S N P G T F R I L V G N K G C S H P S V
K C K K R V T I L V E G G E I E L F D G E V N V K R P M K D E T H F E V V E S G R

961 Y I I L L L G K A L S V V W D R H L S I S V V L K Q T Y Q E K V C G L C G N F D
G I Q N N D L T S S N L Q V E E D P V D F G N S W K V S S Q C A D T R K V P L D

1041 S S P A T C H N N I M K Q T M V D S S C R I L T S D V F Q D C N K L V D P E P
Y L D V C I Y D T C S C E S I G D C A C F C D T I A A Y A H V C A Q H G K V V T W

1121 R T A T L C P Q S C E E R N L R E N G Y E C E W R Y N S C A P A C Q V T C Q
H P E P L A C P V Q C V E G C H A H C P P G K I L D E L L Q T C V D P E D C P V C E

1201 V A G R R F A S G K K V T L N P S D P E H C Q I C H C D V V N L T C E A C Q E
P G G L V V P P T D A P V S P T T L Y V E D I S E P P L H D F Y C S R L L D L V F

1281 L L D G S S R L S E A E F E V L K A F V V D M M E R L R I S Q K W V R V A V
V E Y H D G S H A Y I G L K D R K R P S E L R R I A S Q V K Y A G S Q V A S T S E V

1361 L K Y T L F Q I F S K I D R P E A S R I T L L M A S Q E P Q R M S R N F V R Y
V Q G L K K K K V I V I P V G I G P H A N L K Q I R L I E K Q A P E N K A F V L

1441 S S V D E L E Q Q R D E I V S Y L C D L A P E A P P P T L P P D M A Q V T V G
P G L L G V S T L G P K R N S M V L D V A F V L E G S D K I G E A D F N R S K E F

1521 M E E V I Q R M D V G Q D S I H V T V L Q Y S Y M V T V E Y P F S E A Q S K
G D I L Q R V R E I R Y Q G G N R T N T G L A L R Y L S D H S F L V S Q G D R E Q A

1601 P N L V Y M V T G N P A S D E I K R L P G D I Q V V P I G V G P N A N V Q E L
E R I G W P N A P I L I Q D F E T L P R E A P D L V L Q R C C S G E G L Q I P T L

1681 S P A P D C S Q P L D V I L L L D G S S S F P A S Y F D E M K S F A K A F I S K
A N I G P R L T Q V S V L Q Y G S I T T I D V P W N V V P E K A H L L S L V D V

1761 M Q R E G G P S Q I G D A L G F A V R Y L T S E M H G A R P G A S K A V V I
L V T D V S V D S V D A A A D A A R S N R V T V F P I G I G D R Y D A A Q L R I L A

1841 G P A G D S N V V K L Q R I E D L P T M V T L G N S F L H K L C S G F V R I C
M D E D G N E K R P G D V W T L P D Q C H T V T C Q P D G Q T L L K S H R V N C D

1921 R G L R P S C P N S Q S P V K V E E T C G C R W T C P C V C T G S S T R H I V
T F D G Q N F K L T G S C S Y V L F Q N K E Q D L E V I L H N G A C S P G A R Q G

2001 C M K S I E V K H S A L S V E L H S D M E V T V N G R L V S V P Y V G G N M
E V N V Y G A I M H E V R F N H L G H I F T F T P Q N N E F Q L Q L S P K T F A S K

2081 T Y G L C G I C D E N G A N D F M L R D G T V T T D W K T L V Q E W T V Q R
P G Q T C Q P I L E E Q C L V P D S S H C Q V L L L P L F A E C H K V L A P A T F Y

2161 A I C Q Q D S C H Q E Q V C E V I A S Y A H L C R T N G V C V D W R T P D F
C A M S C P P S L V Y N H C E H G C P R H C D G N V S S C G D H P S E G C F C P P D

2241 K V M L E G S C V P E E A C T Q C I G E D G V Q H Q F L E A W V P D H Q P C
Q I C T C L S G R K V N C T T Q P C P T A K A P T C G L C E V A R L R Q N A D Q C C

2321 P E Y E C V C D P V S C D L P P V P H C E R G L Q P T L T N P G E C R P N F T
C A C R K E E C K R V S P P S C P P H R L P T L R K T Q C C D E Y E C A C N C V N

2401 S T V S C P L G Y L A S T A T N D C G C T T T T C L P D K V C V H R S T I Y P
V G Q F W E E G C D V C T C T D M E D A V M G L R V A Q C S Q K P C E D S C R S G

2481 F T Y V L H E G E C C G R C L P S A C E V V T G S P R G D S Q S S W K S V G S
Q W A S P E N P C L I N E C V R V K E E V F I Q Q R N V S C P Q L E V P V C P S G

2561 F Q L S C K T S A C C P S C R C E R M E A C M L N G T V I G P G K T V M I D V
C T T C R C M V Q V G V I S G F K L E C R K T T C N P C P L G Y K E E N N T G E C

2641 C G R C L P T A C T I Q L R G G Q I M T L K R D E T L Q D G C D T H F C K V N
E R G E Y F W E K R V T G C P P F D E H K C L A E G G K I M K I P G T C C D T C E

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2721 E P E C N D I T A R L Q Y V K V G S C K S E V E V D I H Y C Q G K C A S K A
M Y S I D I N D V O D O C S C C S P T R T E P M O V A L H C T N G S V V Y H E V L N

2801 A M E C K C S P R K C S K

5.188 tripartite motif protein TRIM14 isoform alpha [*Homo sapiens*]; tripartite motif protein TRIM14 isoform alpha [*Homo sapiens*]; tripartite motif protein TRIM14 isoform alpha [*Homo sapiens*]

Protein Accession gi|15208667 gi|15208665 gi|15208663

Mean Expression Ratio 0.9

Median Expression Ratio 0.9

Credible Interval (0.61, 1.35)

Associated Peptides 2

Associated Spectra 3

Coverage NaN

[0306]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.61	0.9	1.4	SEQ ID NO: 1205	GLVEAVESTLQTPLDIR
1	0.57	0.88	1.4	SEQ ID NO: 1206	ATFOEPLYPALR

5.189 PREDICTED: similar to hCG1642538 [*Homo sapiens*]; PREDICTED: similar to hCG1642538 [*Homo sapiens*]

Protein Accession gi|169216113 gi|169215489

Mean Expression Ratio 1.11

Median Expression Ratio 1.11

Credible Interval (0.773, 1.61)

Associated Peptides 1

Associated Spectra 5

Coverage NaN

[0307]

A	2.5	50	97.5	Sequence ID No.	Sequence
5	0.82	1.1	1.6	SEQ ID NO: 1207	DIQMTQSPSSLSASVGDR

5.190 actin, alpha 1, skeletal muscle [*Homo sapiens*]

Protein Accession gi|4501881

Mean Expression Ratio 1.11

Median Expression Ratio 1.11

Credible Interval (0.691, 1.82)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0424

[0308]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.69	1.1	1.9	SEQ ID NO: 1208	YPIEHGIITNWDDMEK
SEQ ID NO: 1209					
1M C D E D E T T A L V C D N G S G L V K A G F A G D D A P R A V F F S I V G R P					
R H Q G V M V G M G Q K D S Y V G D E A Q S K R G I L T L K Y P I E H G I I T N					
81W D D M E K I W H H T F Y N E L R V A P E E H P T L L T E A P L N P K A N R E					
K M T Q I M F E T F N V P A M Y V A I Q A V L S L Y A S G R T T G I V L D S G D G					
161V T H N V P I Y E G Y A L P H A I M R L D L A G R D L T D Y L M K I L T E R G					
Y S F V T T A E R E I V R D I K E K L C Y V A L D F E N E M A T A A S S S S L E K					
241S Y E L P D G Q V I T I G N E R F R C P E T L F Q P S F I G M E S A G I H E T T Y					
N S I M K C D I D I R K D L Y A N N V M S G G T T M Y P G I A D R M Q K E I T					
321A L A P S T M K I K I I A P P E R K Y S V W I G G S I L A S L S T F Q Q M W I T K					
Q E Y D E A G P S I V H R K C F					

5.191 RAP2B, member of RAS oncogene family [*Homo sapiens*]
Protein Accession gi|38201690
Mean Expression Ratio 1.11
Median Expression Ratio 1.11
Credible Interval (0.688, 1.78)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0656
[0309]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.68	1.1	1.9	SEQ ID NO: 1210	ASVDELFAEIVR

SEQ ID NO: 1211

1MREYKV VVLGSGGVGKSALT VQFVTGSFIEKYDPTIEDFYR
KEIEVDSSPSVLEILDTAGTEQFASMRDLYIKNGQGFI L

81VYSLVNQQSFQDIKPMRDQII RVKRYERVP MILVGNKV D L
EGEREVS YGEGKALAE EWSCPFMETSAKNKASVDELFAEI

161V R Q M N Y A A Q P N G D E G C C S A C V I L

5.192 ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function) [*Homo sapiens*]
Protein Accession gi|7662358
Mean Expression Ratio 0.907
Median Expression Ratio 0.905
Credible Interval (0.622, 1.33)
Associated Peptides 3
Associated Spectra 3
Coverage 0.0486
[0310]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.9	1.4	SEQ ID NO: 1212	IDDLIGDLVQR
1	0.58	0.9	1.4	SEQ ID NO: 1213	LLLVSFDFGR
1	0.58	0.9	1.4	SEQ ID NO: 1214	KIDDLIGDLVQR

SEQ ID NO: 1215

1M K L L V I L L F S G L I T G F R S D S S S S L P P K L L L V S F D G F R A D Y L K
N Y E F P H L Q N F I K E G V L V E H V K N V F I T K T F P N H Y S I V T G

81L Y E E S H G I V A N S M Y D A V T K K H F S D S N D K D P F W W N E A V P I
W V T N Q L Q E N R S S A A A M W P G T D V P I H D T I S S Y F M N Y N S S V S F

161E E R L N N I T M W L N N S N P P V T F A T L Y W E E P D A S G H K Y G P E D
K E N M S R V L K K I D D L I G D L V Q R L K M L G L W E N L N V I I T S D H G M

241T Q C S Q D R L I N L D S C I D H S Y Y T L I D L S P V A A I L P K I N R T E V Y
N K L K N C S P H M N V Y L K E D I P N R F Y Y Q H N D R I Q P I I L V A D E

321G W T I V L N E S S Q K L G D H G Y D N S L P S M H P F L A A H G P A F H K G
Y K H S T I N I V D I Y P M M C H I L G L K P H P N N G T F G H T K C L L V D Q W

401C I N L P E A I A I V I G S L L V L T M L T C L I I I M Q N R L S V P R P F S R L Q
L Q E D D D D P L I G

5.193 transmembrane BAX inhibitor motif containing 1
[Homo sapiens]
Protein Accession gil50593008
Mean Expression Ratio 0.905
Median Expression Ratio 0.906
Credible Interval (0.645, 1.27)
Associated Peptides 1
Associated Spectra 8
Coverage 0.045
[0311]

A	2.5	50	97.5	Sequence ID No.	Sequence
8	0.67	0.88	1.2	SEQ ID NO: 1216	AVSDSFGPGEWDDR

SEQ ID NO: 1217

1M S N P S A P P P Y E D R N P L Y P G P P P P G G Y G Q P S V L P G G Y P A Y P G
Y P Q P G Y G H P A G Y P Q P M P P T H P M P M N Y G P G H G Y D G E E R A V

81S D S F G P G E W D D R K V R H T F I R K V Y S I I S V Q L L I T V A I I A I F T F
V E P V S A F V R R N V A V Y Y V S Y A V F V V T Y L I L A C C Q G P R R R

161F P W N I I L L T L F T F A M G F M T G T I S S M Y Q T K A V I I A M I I T A V V
S I S V T I F C F Q T K V D F T S C T G L F C V L G I V L L V T G I V T S I V

241L Y F Q Y V Y W L H M L Y A A L G A I C F T L F L A Y D T Q L V L G N R K H T
I S P E D Y I T G A L Q I Y T D I I Y I F T F V L Q L M G D R N

5.194 mucolipin 1 [Homo sapiens]
Protein Accession gil10092597
Mean Expression Ratio 1.1
Median Expression Ratio 1.10
Credible Interval (0.676, 1.79)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0483
[0312]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.67	1.1	1.9	SEQ ID NO: 1218	LLTPNPGYGTQAGPSPAPPTPPEEEDLR

SEQ ID NO: 1219

1M T A P A G P R G S E T E R L L T P N P G Y G T Q A G P S P A P P T P P E E E D L
R R R L K Y F F M S P C D K F R A K G R K P C K L M L Q V V K I L V V T V Q L

81I L F G L S N Q L A V T F R E E N T I A F R H L F L L G Y S D G A D D T F A A Y T
R R E Q L Y Q A I F H A V D Q Y L A L P D V S L G R Y A Y V R G G G D P W T N G

161S G L A L C Q R Y Y H R G H V D P A N D T F D I D P M V V T D C I Q V D P P E
R P P P P S D D L T L L E S S S Y K N L T L K F H K L V N V T I H F R L K T I

241N L Q S L I N N E I P D C Y T F S V L I T F D N K A H S G R I P I S L E T Q A H I Q
E C K H P S V F Q H G D N S F R L L F D V V V I L T C S L S F L L C A R S L

321L R G F L L Q N E F V G F M W R Q R G R V I S L W E R L E F V N G W Y I L L V
T S D V L T I S G T I M K I G I E A K N L A S Y D V C S I L L G T S T L L V W V G

401V I R Y L T F F H N Y N I L I A T L R V A L P S V M R F C C C V A V I Y L G Y C
F C G W I V L G P Y H V K F R S L S M V S E C L F S L I N G D D M F V T F A A M

481Q A Q Q G R S S L V W L F S Q L Y L Y S F I S L F I Y M V L S L F I A L I T G A Y
D T I K H P G G A G A E E S E L Q A Y I A Q C Q D S P T S G K F R R G S G S A

561C S L L C C C G R D P S E E H S L L V N

5.195 annexin IV [*Homo sapiens*]
Protein Accession gi|4502105
Mean Expression Ratio 1.10
Median Expression Ratio 1.10
Credible Interval (0.674, 1.81)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0343
[0313]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.67	1.1	1.9	SEQ ID NO: 1220	NHLLHVFDEYK

SEQ ID NO: 1221

1MAMATKGGTVKAAASGFNAMEDAQTLRKAMKGLGTDEDAI
ISVLA YRNTAQRQEIRTA YKSTIGRDLIDDLKSELSGNF EQ

81VIVGMMTPPTVLYDVQELRRAMKGA GTDEGC LIEILAS RTP
EEIRRI SQT YQQQ YGRSLED DIRSDT SFMFQ RVLVLSL SAG

161GRDEGN YLDDALVRQDAQDLYEAGEKKWGTDEVKFLT V
LCSRNRNHL LHVFD EYKRISQKDIEQSIKSETSGSFEDALLA

241IIVKCMRNKSA YFAEKLYKSMKGLGTDDNTLIRVMVSRAE
IDMLDIRAHFKRL YGKSLYSFIKGDTS GDYRKVLVLVLCGGD

321D

5.196 PREDICTED: similar to kappa immunoglobulin (sub-
group V kappa I) [*Homo sapiens*]
Protein Accession gi|169218204
Mean Expression Ratio 0.907
Median Expression Ratio 0.908
Credible Interval (0.615, 1.35)
Associated Peptides 2
Associated Spectra 3
Coverage NaN
[0314]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.89	1.4	SEQ ID NO: 1222	DIQLTQSPSFLSASVGDR
2	0.6	0.9	1.3	SEQ ID NO: 1223	LLIYAASTLQSGVPSR

5.197 diazepam binding inhibitor isoform 2 [*Homo sapi-
ens*]; diazepam binding inhibitor isoform 3 [*Homo sapiens*];
diazepam binding inhibitor isoform 1 [*Homo sapiens*]
Protein Accession gi|120433593 gi|120433590 gi|10140853
Mean Expression Ratio 1.1
Median Expression Ratio 1.10
Credible Interval (0.677, 1.80)
Associated Peptides 1
Associated Spectra 1
Coverage NaN
[0315]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.67	1.1	1.9	SEQ ID NO: 1224	QATVGDINTERPGMLDFTGK

5.198 CD63 antigen isoform B [*Homo sapiens*]; CD63 antigen isoform A [*Homo sapiens*]
Protein Accession gi|91199546 gi|4502679

Mean Expression Ratio 1.10
Median Expression Ratio 1.10
Credible Interval (0.871, 1.40)
Associated Peptides 8
Associated Spectra 15

Coverage NaN
[0316]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.78	1.1	1.6	SEQ ID NO: 1225	DKVMSEFNNNFR
7	0.83	1.1	1.4	SEQ ID NO: 1226	VMSEFNNNFR
2	0.84	1.2	1.6	SEQ ID NO: 1227	QQMENYPK

-continued

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.8	1.1	1.6	SEQ ID NO: 1228	MQADFK
1	0.78	1.1	1.5	SEQ ID NO: 1229	GINFNEK
1	0.78	1.1	1.5	SEQ ID NO: 1230	EGCVEK
1	0.78	1.1	1.6	SEQ ID NO: 1231	IGGWLR
1	0.77	1.1	1.5	SEQ ID NO: 1232	AIHKEGCVEK

5.199 tubulin, alpha 4a [*Homo sapiens*]
Protein Accession gi|17921989

Mean Expression Ratio 1.10
Median Expression Ratio 1.1
Credible Interval (0.715, 1.69)
Associated Peptides 1
Associated Spectra 2
Coverage 0.0335
[0317]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.71	1.1	1.7	SEQ ID NO: 1233	AVFVDLEPTVIDEIR
SEQ ID NO: 1234					
1MRECI S V H V G Q A G V Q M G N A C W E L Y C L E H G I Q P D G Q M P S D					
K T I G G G D D S F T T F F C E T G A G K H V P R A V F V D L E P T V I D E I R N					
81G P Y R Q L F H P E Q L I T G K E D A A N N Y A R G H Y T I G K E I I D P V L D R					
I R K L S D Q C T G L Q G F L V F H S F G G G T G S G F T S L L M E R L S V D					
161Y G K K S K L E F S I Y P A P Q V S T A V V E P Y N S I L T T H T T L E H S D C					
A F M V D N E A I Y D I C R R N L D I E R P T Y T N L N R L I S Q I V S S I T A					
241S L R F D G A L N V D L T E F Q T N L V P Y P R I H F P L A T Y A P V I S A E K					
A Y H E Q L S V A E I T N A C F E P A N Q M V K C D P R H G K Y M A C C L L Y R					
321G D V V P K D V N A A I A A I K T K R S I Q F V D W C P T G F K V G I N Y Q P P					
T V V P G G D L A K V Q R A V C M L S N T T A I A E A W A R L D H K F D L M Y A					
401K R A F V H W Y V G E G M E E G E F S E A R E D M A A L E K D Y E E V G I D					
S Y E D E D E G E E					

5.200 MARVEL domain containing 3 isoform 1 [*Homo sapiens*]
Protein Accession gi|65301122

Mean Expression Ratio 1.10
Median Expression Ratio 1.1
Credible Interval (0.737, 1.62)
Associated Peptides 2
Associated Spectra 3
Coverage 0.061
[0318]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.69	1.1	1.7	SEQ ID NO: 1235	EAPPEPPQQR
2	0.75	1.1	1.7	SEQ ID NO: 1236	GLTWDAAAPGPAPWEAPPEPPQQR

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SEQ ID NO: 1237
1M E D P S G A R E P R A R P R E R D P G R R P H P D Q G R T H D R P R D R P G D
  P R R K R S S D G N R R R D G D R D P E R D Q E R D G N R D R N R D R E R E
81R E R D P D R G P R R D T H R D A G P R A G E H G V W E K P R Q S R T R D G A
  R G L T W D A A A P P G P A P W E A P E P P Q P Q R K G D P G R R R P E S E P P S
161E R Y L P S T P R P G R E E V E Y Y Q S E A E G L L E C H K C K Y L C T G R G
  V V Q I V E V V L N G M V L I C I V A S Y F V L A G F S A S F S S G G G F G N N Y
241Y S P F E G T E L E Q V R Q L D Q Q Y T I L R S P L I Y G G V A V S L G L G V L
  T M G V L L Q G A K S R T M L S G K W L L T E A A F S L L A A V G Y C T G I G V
321Y L H V A L Q I N S T D T C K T R E R L Y A R K G L T W M D C Q L A G T D G
  A A A T F A C L L V I M Y G A S V V L A L R S Y R E Q K R Y K G S R E Q P G S Y S D
401A P E Y L W S G T L

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5.201 sialin [*Homo sapiens*]

Protein Accession [gi|6912666](#)

Mean Expression Ratio 0.91

Median Expression Ratio 0.91

Credible Interval (0.65, 1.25)

Associated Peptides 4

Associated Spectra 5

Coverage 0.0848

[0319]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.64	0.94	1.4	SEQ ID NO: 1238	ACPEHSAPIK
1	0.6	0.91	1.4	SEQ ID NO: 1239	ALEGLGEGVTFPAMH
1	0.58	0.87	1.3	SEQ ID NO: 1240	EYILSSLR
1	0.6	0.9	1.4	SEQ ID NO: 1241	TPLLPGAPR

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SEQ ID NO: 1242
1M R S P V R D L A R N D G E E S T D R T P L L P G A P R A E A A P V C C S A R Y
  N L A I L A F F G F F I V Y A L R V N L S V A L V D M V D S N T T L E D N R T S

81K A C P E H S A P I K V H H N Q T G K K Y Q W D A E T Q G W I L G S F F Y G Y I
  I T Q I P G G Y V A S K I G G K M L L G F G I L G T A V L T L F T P I A A D L G

161V G P L I V L R A L E G L G E G V T F P A M H A M W S S W A P P L E R S K L L
  S I S Y A G A Q L G T V I S L P L S G I I C Y Y M N W T Y V F Y F F G T I G I F W

241F L L W I W L V S D T P Q K H K R I S H Y E K E Y I L S S L R N Q L S S Q K S V
  P W V P I L K S L P L W A I V V A H F S Y N W T F Y T L L T L L P T Y M K E I L

321R F N V Q E N G F L S S L P Y L G S W L C M I L S G Q A A D N L R A K W N F S
  T L C V R R I F S L I G M I G P A V F L V A A G F I G C D Y S L A V A F L T I S T

401T L G G F C S S G F S I N H L D I A P S Y A G I L L G I T N T F A T I P G M V G P
  V I A K S L T P D N T V G E W Q T V F Y I A A A I N V F G A I F F T L F A K G

481E V O N W A L N D H H G H R H

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5.202 solute carrier family 1 (neutral amino acid transporter), member 5 [*Homo sapiens*]

Protein Accession gi|5032093

Mean Expression Ratio 0.912

Median Expression Ratio 0.91

Credible Interval (0.561, 1.48)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0203

[0320]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.54	0.89	1.5	SEQ ID NO: 1243	EVLDSFLDLAR
SEQ ID NO: 1244					
1M V A D P P R D S K G L A A A E P T A N G G L A L A S I E D Q G A A A G G Y C G					
S R D Q V R R C L R A N L L V L L T V V A V V A G V A L G L G V S G A G G A L A					
81L G P E R L S A F V F P G E L L L R L L R M I I L P L V V C S L I G G A A S L D P					
G A L G R L G A W A L L F F L V T T L L A S A L G V G L A L A L Q P G A A S A					
161A I N A S V G A A G S A E N A P S K E V L D S F L D L A R N I F P S N L V S A A					
F R S Y S T T Y E E R N I T G T R V K V P V G Q E V E G M N I L G L V V F A I V					
241F G V A L R K L G P E G E L L I R F F N S F N E A T M V L V S W I M W Y A P V					
G I M F L V A G K I V E M E D V G L L F A R L G K Y I L C C L L G H A I H G L L V					
321L P L I Y F L F T R K N P Y R F L W G I V T P L A T A F G T S S S S A T L P L M					
M K C V E E N N G V A K H I S R F I L P I G A T V N M D G A A L F Q C V A A V F					
401I A Q L S Q Q S L D F V K I I T I L V T A T A S S V G A A G I P A G G V L T L A I I					
L E A V N L P V D H I S L I L A V D W L V D R S C T V L N V E G D A L G A G					
481L L Q N Y V D R T E S R S T E P E L I Q V K S E L P L D P L P V P T E E G N P L L					
K H Y R G P A G D A T V A S E K E S V M					

5.203 claudin 2 [*Homo sapiens*]
Protein Accession gi|9966781

Mean Expression Ratio 1.10

Median Expression Ratio 1.10

Credible Interval (0.686, 1.79)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0652
[0321]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.68	1.1	1.9	SEQ ID NO: 1245	SNYYDAYQAQPLATR
SEQ ID NO: 1246					
1M A S L G L Q L V G Y I L G L L G L L G T L V A M L L P S W K T S S Y V G A S I					
V T A V G F S K G L W M E C A T H S T G I T Q C D I Y S T L L G L P A D I Q A A					
81Q A M M V T S S A I S S L A C I I S V V G M R C T V F C Q E S R A K D R V A V A					
G G V F F I L G G L L G F I P V A W N L H G I L R D F Y S P L V P D S M K F E I					
161G E A L Y L G I I S S L F S L I A G I I L C F S C S S Q R N R S N Y Y D A Y Q A Q					
P L A T R S S P R P G Q P P K V K S E F N S Y S L T G Y V					

5.204 myoferlin isoform a [*Homo sapiens*]; myoferlin iso-
form b [*Homo sapiens*]
Protein Accession gi|7305053 gi|9718759

Mean Expression Ratio 1.10
Median Expression Ratio 1.10
Credible Interval (0.677, 1.78)
Associated Peptides 1
Associated Spectra 1
Coverage NaN
[0322]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.66	1.1	1.9	SEQ ID NO: 1247	IYPLPDDPSVPAPPR

5.205 tubulin, alpha 1a [*Homo sapiens*]
Protein Accession gi|17986283
Mean Expression Ratio 1.10
Median Expression Ratio 1.10
Credible Interval (0.708, 1.68)
Associated Peptides 2
Associated Spectra 2
Coverage 0.0532
[0323]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.7	1.1	1.8	SEQ ID NO: 1248	AVFVDLEPTVIDEVR
1	0.67	1.1	1.7	SEQ ID NO: 1249	EIIDLVLR

SEQ ID NO: 1250

1MRECI SIHV GQAGV QIGNACWEL YCLEHGI QPDGQ MP S D K
T I G G D D S F N T F F S E T G A G K H V P R A V F V D L E P T V I D E V R T

81G T Y R Q L F H P E Q L I T G K E D A A N N Y A R G H Y T I G K E I I D L V L D
R I R K L A D Q C T G L Q G F L V F H S F G G G T G S G F T S L L M E R L S V D

161Y G K K S K L E F S I Y P A P Q V S T A V V E P Y N S I L T T H T T L E H S D C
A F M V D N E A I Y D I C R R N L D I E R P T Y T N L N R L I G Q I V S S I T A

241S L R F D G A L N V D L T E F Q T N L V P Y P R I H F P L A T Y A P V I S A E K
A Y H E Q L S V A E I T N A C F E P A N Q M V K C D P R H G K Y M A C C L L Y R

321G D V V P K D V N A A I A T I K T K R T I Q F V D W C P T G F K V G I N Y Q P P
T V V P G G D L A K V Q R A V C M L S N T T A I A E A W A R L D H K F D L M Y A

401K R A F V H W Y V G E G M E E G E F S E A R E D M A A L E K D Y E E V G V D
S V E G E G E E E G E E Y

5.206 PDZ domain containing 1 [*Homo sapiens*]
Protein Accession gi|21361142
Mean Expression Ratio 0.913
Median Expression Ratio 0.915
Credible Interval (0.722, 1.15)

Associated Peptides 8
Associated Spectra 14
Coverage 0.212
[0324]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.66	0.9	1.2	SEQ ID NO: 1251	AGVLADHLEI VNGENVEDASHEEVVEK
2	0.63	0.87	1.2	SEQ ID NO: 1252	EAPAPTPTSLEVSSPPDTTEEVDHKPK
5	0.66	0.87	1.2	SEQ ID NO: 1253	INGVFVDKEEHMQVVDLVR
1	0.66	0.93	1.3	SEQ ID NO: 1254	GVYMTDITPQGVAMR
1	0.66	0.93	1.3	SEQ ID NO: 1255	MTDITPQGVAMR
1	0.63	0.89	1.3	SEQ ID NO: 1256	VMFLLVDK
1	0.66	0.94	1.3	SEQ ID NO: 1257	VMFLLVDKETDKR
1	0.67	0.95	1.3	SEQ ID NO: 1258	AYDYFQAK

SEQ ID NO: 1259

1M T S T F N P R E C K L S K Q E G Q N Y G F F L R I E K D T E G H L V R V V E K
C S P A E K A G L Q D G D R V L R I N G V F V D K E E H M Q V V D L V R K S G N

81S V T L L V L D G D S Y E K A V K T R V D L K E L G Q S Q K E Q G L S D N I L S
P V M N G G V Q T W T Q P R L C Y L V K E G G S Y G F S L K T V Q G K K G V Y M

-continued

161T D I T P Q G V A M R A G V L A D D H L I E V N G E N V E D A S H E E V V E K
V K K S G S R V M F L L V D K E T D K R H V E Q K I Q F K R E T A S L K L L P H Q

241P R I V E M K K G S N G Y G F Y L R A G S E Q K G Q I I K D I D S G S P A E E A
G L K N N D L V V A V N G E S V E T L D H D S V V E M I R K G G D Q T S L L V V

321D K E T D N M Y R L A H F S P F L Y Y Q S Q E L P N G S V K E A P A P T P T S L
E V S S P P D T T E E V D H K P K L C R L A K G E N G Y G F H L N A I R G L P G

401S F I K E V Q K G G P A D L A G L E D E D V I I E V N G V N V L D E P Y E K V V
D R I Q S S G K N V T L L V C G K K A Y D Y F Q A K K I P I V S S L A D P L D T

481P P D S K E G I V V E S N H D S H M A K E R A H S T A S H S S S N S E D T E M

5.207 deleted in malignant brain tumors 1 isoform c precursor [*Homo sapiens*]; deleted in malignant brain tumors 1 isoform b precursor [*Homo sapiens*]

Protein Accession gil148539844 gil148539842

Mean Expression Ratio 1.09

Median Expression Ratio 1.09

Credible Interval (0.668, 1.80)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0325]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.67	1.1	1.9	SEQ ID NO: 1260	FGQGS GPIVLD D V R

5.208 galactosylceramidase isoform a precursor [*Homo sapiens*]

Protein Accession gil83281450

Mean Expression Ratio 0.915

Median Expression Ratio 0.916

Credible Interval (0.556, 1.50)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0234

[0326]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.53	0.9	1.5	SEQ ID NO: 1261	EFDGIGAVSGGATSR
SEQ ID NO: 1262					
1M A E W L L S A S W Q R R A K A M T A A A G S A G R A A V P L L L C A L L A P					
G G A Y V L D D S D G L G R E F D G I G A V S G G G A T S R L L V N Y P E P Y R S					
81Q I L D Y L F K P N F G A S L H I L K V E I G G D G Q T T D G T E P S H M H Y A					
L D E N Y F R G Y E W W L M K E A K K R N P N I T L I G L P W S F P G W L G K G					
161F D W P Y V N L Q L T A Y Y V V T W I V G A K R Y H D L D I D Y I G I W N E R					
S Y N A N Y I K I L R K M L N Y Q G L Q R V K I I A S D N L W E S I S A S M L L D					
241A E L F K V V D V I G A H Y P G T H S A K D A K L T G K K L W S S E D F S T L					
N S D M G A G C W G R I L N Q N Y I N G Y M T S T I A W N L V A S Y Y E Q L P Y G					
321R C G L M T A Q E P W S G H Y V V E S P V W V S A H T T Q F T Q P G W Y Y L					
K T V G H L E K G G S Y V A L T D G L G N L T I I I E T M S H K H S K C I R P F L P					
401Y F N V S Q Q F A T F V L K G S F S E I P E L Q V W Y T K L G K T S E R F L F K					
Q L D S L W L L D S D G S F T L S L H E D E L F T L T T L T T G R K G S Y P L P					
481P K S Q P F P S T Y K D D F N V D Y P F F S E A P N F A D Q T G V F E Y F T N I					
E D P G E H H F T L R Q V L N Q R P I T W A A D A S N T I S I I G D Y N W T N L					
561T I K C D V Y I E T P D T G G V F I A G R V N K G G I L I R S A R G I F F W I F A					
N G S Y R V T G D L A G W I I Y A L G R V E V T A K K W Y T L T L T I K G H F					
641T S G M L N D K S L W T D I P V N F P K N G W A A I G T H S F E F A Q F D N F					
L V E A T R					

5.209 target of myb1 isoform 1 [*Homo sapiens*]; target of myb1 isoform 2 [*Homo sapiens*]
Protein Accession gil4885637 gil209180457

Mean Expression Ratio 0.916
Median Expression Ratio 0.917
Credible Interval (0.615, 1.34)

Associated Peptides 2
Associated Spectra 3

Coverage NaN
[0327]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.58	0.89	1.3	SEQ ID NO: 1263	LPNLSSPSAEGPPGPPSG PAPR	
1	0.6	0.93	1.5	SEQ ID NO: 1264	SSPDLTGVVTIYEDLR	

5.210 hypothetical protein LOC55194 [*Homo sapiens*];
PREDICTED: hypothetical protein [*Homo sapiens*]
Protein Accession gil8922567 gil169160626

Mean Expression Ratio 1.09
Median Expression Ratio 1.09

Credible Interval (0.666, 1.81)
Associated Peptides 1

Associated Spectra 1
Coverage NaN
[0328]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.67	1.1	1.9	SEQ ID NO: 1265	TGQPDLLGTGTGSPSTAT GTLGR	

5.211 cystin 1 [*Homo sapiens*]
Protein Accession gil81158080

Mean Expression Ratio 1.09
Median Expression Ratio 1.09
Credible Interval (0.737, 1.62)

Associated Peptides 2
Associated Spectra 3

Coverage 0.241
[0329]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.71	1.1	1.7	SEQ ID NO: 1266	SPESLPAGPGAAALEGGTR	
2	0.73	1.1	1.7	SEQ ID NO: 1267	VPVAAAEVPGAAAEAPGR	
SEQ ID NO: 1268						
1 M G S G S S R S S R T L R R R R S P E S L P A G P G A A A L E G G T R R R V P V A						
A A E V P G A A A E E A P G R D P S P V A P P D G R D E T L R L L D E L L A E						
81 S A A W G P P E P A P R R P A R L R P T A V A G S A V C A E Q S T E G H P G S G						
N V S E A P G S G R K K P E R P A A I S Y D H S E E G L M A S I E R E Y C R						

5.212 CD151 antigen [*Homo sapiens*]; CD151 antigen [*Homo sapiens*]; CD151 antigen [*Homo sapiens*]; CD151 antigen [*Homo sapiens*]
Protein Accession gil87159824 gil87159822 gil21237751
gil21237748

Mean Expression Ratio 1.09
Median Expression Ratio 1.09
Credible Interval (0.733, 1.62)
Associated Peptides 1
Associated Spectra 3
Coverage NaN
[0330]

A	2.5	50	97.5	Sequence	ID No.	Sequence
3	0.76	1.1	1.6	SEQ ID NO: 1269	LETPIQEHLR	

5.213 RAB2A, member RAS oncogene family [*Homo sapi-*
ens]
Protein Accession gi|4506365
Mean Expression Ratio 0.921
Median Expression Ratio 0.921
Credible Interval (0.596, 1.43)
Associated Peptides 1
Associated Spectra 2
Coverage 0.066
[0331]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.58	0.9	1.4	SEQ ID NO: 1270	DTFNHLTTWLEDAR
SEQ ID NO: 1271					
1MAYAYLFKYIIIGD TG V GK S C L L L Q F T D K R F Q P V H D L T I G V					
E F G A R M I T I D G K Q I K L Q I W D T A G Q E S F R S I T R S Y Y R G A A					
81G A L L V Y D I T R R D T F N H L T T W L E D A R Q H S N S N M V I M L I G N K					
S D L E S R R E V K K E E G E A F A R E H G L I F M E T S A K T A S N V E E A F					
161I N T A K E I Y E K I Q E G V F D I N N E A N G I K I G P Q H A A T N A T H A G					
N Q G G Q Q A G G G C C					

5.214 CNDP dipeptidase 2 [*Homo sapiens*]
Protein Accession gi|8922699
Mean Expression Ratio 1.08
Median Expression Ratio 1.09
Credible Interval (0.811, 1.46)

Associated Peptides 5
Associated Spectra 8
Coverage 0.135
[0332]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.75	1.1	1.6	SEQ ID NO: 1272	GNILIPGINEAVAAVTEEEHK
3	0.77	1.1	1.5	SEQ ID NO: 1273	LPDGSEIPLPPILLGR
1	0.74	1.1	1.6	SEQ ID NO: 1274	LYDDIDFDIEEFAK
2	0.77	1.1	1.6	SEQ ID NO: 1275	QKLPDGSEIPLPPILLGR
1	0.76	1.1	1.6	SEQ ID NO: 1276	TVFGVEPDLTR
SEQ ID NO: 1277					
1MAA L T T L F K Y I D E N Q D R Y I K K L A K W V A I Q S V S A W P E K R G E					
I R R M M E V A A A D V K Q L G G S V E L V D I G K Q K L P D G S E I P L P P I					
81L L G R L G S D P Q K K T V C I Y G H L D V Q P A A L E D G W D S E P F T L V E					
R D G K L Y G G S T D D K G P V A G W I N A L E A Y Q K T G Q E I P V N V R F					
161C L E G M E E S G S E G L D E L I F A R K D T F F K D V D Y V C I S D N Y W L					
G K K K P C I T Y G L R G I C Y F F I E V E C S N K D L H S G V Y G G S V H E A M					
241T D L I L L M G S L V D K R G N I L I P G I N E A V A A V T E E E H K L Y D D I					
D F D I E E F A K D V G A Q I L L H S H K K D I L M H R W R Y P S L S L H G I E					
321G A F S G S G A K T V I P R K V V G K F S I R L V P N M T P E V V G E Q V T S Y					
L T K K F A E L R S P N E F K V Y M G H G G K P W V S D F S H P H Y L A G R R A					
401M K T V F G V E P D L T R E G G S I P V T L T F Q E A T G K N V M L L P V G S					
A D D G A H S Q N E K L N R Y N Y I E G T K M L A A Y L Y E V S Q L K D					

5.215 syntaxin binding protein 2 isoform b [*Homo sapiens*];
syntaxin binding protein 2 isoform a [*Homo sapiens*]
Protein Accession gi|188528901 gi|188528689

Mean Expression Ratio 1.09
Median Expression Ratio 1.09
Credible Interval (0.709, 1.67)
Associated Peptides 2
Associated Spectra 2
Coverage NaN

[0333]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.7	1.1	1.8	SEQ ID NO: 1278	NLEQLGGTVTNPGGSGT SSR
1	0.67	1.1	1.7	SEQ ID NO: 1279	VLLLYILLR

5.216 actinin, alpha 4 [*Homo sapiens*]
Protein Accession gi|12025678

Mean Expression Ratio 1.09
Median Expression Ratio 1.08
Credible Interval (0.672, 1.74)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0132

[0334]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.1	1.8	SEQ ID NO: 1280	VGWEQLTTIAR

SEQ ID NO: 1281

1M V D Y H A A N Q S Y Q Y G P S S A G N G A G G G G S M G D Y M A Q E D D W
D R D L L L D P A W E K Q Q R K T F T A W C N S H L R K A G T Q I E N I D E D F R D

81G L K L M L L L E V I S G E R L P K P E R G K M R V H K I N N V N K A L D F I A
S K G V K L V S I G A E E I V D G N A K M T L G M I W T I I L R F A I Q D I S V

161E E T S A K E G L L L W C Q R K T A P Y K N V N V Q N F H I S W K D G L A F N
A L I H R H R P E L I E Y D K L R K D D P V T N L N N A F E V A E K Y L D I P K M

241L D A E D I V N T A R P D E K A I M T Y V S S F Y H A F S G A Q K A E T A A N
R I C K V L A V N Q E N E H L M E D Y E K L A S D L L E W I R R T I P W L E D R V

321P Q K T I Q E M Q Q K L E D F R D Y R R V H K P P K V Q E K C Q L E I N F N T
L Q T K L R L S N R P A F M P S E G K M V S D I N N G W Q H L E Q A E K G Y E E W

401L L N E I R R L E R L D H L A E K F R Q K A S I H E A W T D G K E A M L K H R
D Y E T A T L S D I K A L I R K H E A F E S D L A A H Q D R V E Q I A A I A Q E L

481N E L D Y Y D S H N V N T R C Q K I C D Q W D A L G S L T H S R R E A L E K T
E K Q L E A I D Q L H L E Y A K R A A P F N N W M E S A M E D L Q D M F I V H T I

561E E I E G L I S A H D Q F K S T L P D A D R E R E A I L A I H K E A Q R I A E S N
H I K L S G S N P Y T T V T P Q I I N S K W E K V Q Q L V P K R D H A L L E E

641Q S K Q Q S N E H L R R Q F A S Q A N V V G P W I Q T K M E E I G R I S I E M N
G T L E D Q L S H L K Q Y E R S I V D Y K P N L D L L E Q Q H Q L I Q E A L I F

721D N K H T N Y T M E H I R V G W E Q L L T T I A R T I N E V E N Q I L T R D A K
G I S Q E Q M Q E F R A S F N H F D K D H G G A L G P E E F K A C L I S L G Y D

801V E N D R Q G E A E F N R I M S L V D P N H S G L V T F Q A F I D F M S R E T T
D T D T A D Q V I A S F K V L A G D K N F I T A E E L R R E L P P D Q A E Y C I

881A R M A P Y Q G P D A V P G A L D Y K S F S T A L Y G E S D L

5.217 matrix metalloproteinase 7 preproprotein [*Homo sapi-*
ens]
Protein Accession gil4505219
Mean Expression Ratio 0.919
Median Expression Ratio 0.923
Credible Interval (0.603, 1.41)
Associated Peptides 2
Associated Spectra 2
Coverage 0.120
[0335]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.9	1.4	SEQ ID NO: 1282	AFAPGTGLGGDAHFD EDER
1	0.57	0.91	1.5	SEQ ID NO: 1283	FFGLPITGMLNSR

SEQ ID NO: 1284

1M R L T V L C A V C L L P G S L A L P L P Q E A G G M S E L Q W E Q A Q D Y L K
R F Y L Y D S E T K N A N S L E A K L K E M Q K F F G L P I T G M L N S R V I E

81I M Q K P R C G V P D V A E Y S L F P N S P K W T S K V V T Y R I V S Y T R D L
P H I T V D R L V S K A L N M W G K E I P L H F R K V V W G T A D I M I G F A R

161G A H G D S Y P F D G P G N T L A H A F A P G T G L G G D A H F D E D E R W
T D G S S L G I N F L Y A A T H E L G H S L G M G H S S D P N A V M Y P T Y G N G D

241P Q N F K L S Q D D I K G I Q K L Y G K R S N S R K K

5.218 keratin 1 [*Homo sapiens*]
Protein Accession gil119395750
Mean Expression Ratio 0.923
Median Expression Ratio 0.923
Credible Interval (0.668, 1.28)

Associated Peptides 3
Associated Spectra 6
Coverage 0.0637
[0336]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.6	0.9	1.3	SEQ ID NO: 1285	QISNLQQSISDAEQR
4	0.68	0.94	1.3	SEQ ID NO: 1286	THNLEPYFESFINNLR
1	0.62	0.91	1.4	SEQ ID NO: 1287	NKYEDEINKR

SEQ ID NO: 1288

1M S R Q F S S R S G Y R S G G G F S S G S A G I I N Y Q R R T T S S S T R R S G G
G G G R F S S C G G G G S F G A G G G F G S R S L V N L G G S K S I S I S V

81A R G G G R G S G F G G G Y G G G F G G G G F G G G G I G G G G F
G G F G S G G G G F G G G G F G G G Y G G G Y G P V C P P G G I Q E V T I N Q S

161L L Q P L N V E I D P E I Q K V K S R E R E Q I K S L N N Q F A S F I D K V R F L
E Q Q N Q V L Q T K W E L L Q Q V D T S T R T H N L E P Y F E S F I N N L R R

241R V D Q L K S D Q S R L D S E L K N M Q D M V E D Y R N K Y E D E I N K R T
N A E N E F V T I K K D V D G A Y M T K V D L Q A K L D N L Q Q E I D F L T A L Y Q

321A E L S Q M Q T Q I S E T N V I L S M D N N R S L D L D S I I A E V K A Q Y E D
I A Q K S K A E A E S L Y Q S K Y E E L Q I T A G R H G D S V R N S K I E I S E

401L N R V I Q R L R S E I D N V K K Q I S N L Q Q S I S D A E Q R G E N A L K D A
K N K L N D L E D A L Q Q A K E D L A R L L R D Y Q E L M N T K L A L D L E I A

481T Y R T L L E G E E S R M S G E C A P N V S V S V S T S H T T I S G G G S R G G
G G G Y G S G S S Y G S G G G S Y G S G G G G G G R G S Y G S G G S S Y G

-continued

561S G G G S Y G S G G G G G H G S Y G S G S S S G G Y R G S G G G G G S S
G G R G S G G G S S G G S I G R G S S S G G V K S S G G S S S V K F V S T T Y S

641G V T R

5.219 lactotransferrin precursor [*Homo sapiens*]
Protein Accession gil54607120

Mean Expression Ratio 0.925

Median Expression Ratio 0.924

Credible Interval (0.744, 1.15)

Associated Peptides 12

Associated Spectra 16

Coverage 0.217

[0337]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.66	0.9	1.2	SEQ ID NO: 1289	CSTSPLLEACEFLR
2	0.69	0.94	1.3	SEQ ID NO: 1290	DEYELLCPDNTR
1	0.67	0.94	1.3	SEQ ID NO: 1291	DSPIQCIQAIENR
1	0.65	0.92	1.3	SEQ ID NO: 1292	DVTVLQNTDGNNEAWAK
1	0.68	0.95	1.3	SEQ ID NO: 1293	ESTVFEDLSDEAER
2	0.63	0.85	1.2	SEQ ID NO: 1294	ESTVFEDLSDEAERDEYELLCPDNTR
1	0.66	0.93	1.3	SEQ ID NO: 1295	FDEYFSQSCAPGSDPR
1	0.68	0.95	1.3	SEQ ID NO: 1296	FQLFGSPSGQK
1	0.66	0.93	1.3	SEQ ID NO: 1297	GGSFQLNELQGLK
1	0.65	0.91	1.3	SEQ ID NO: 1298	IDSGLYLGSFYTAIQNLR
2	0.69	0.94	1.3	SEQ ID NO: 1299	QVLLHQQAK
1	0.67	0.93	1.3	SEQ ID NO: 1300	YLG PQYVAGITNLK
SEQ ID NO: 1301					
1M K L V F L V L L F L G A L G L C L A G R R R S V Q W C A V S Q P E A T K C F Q W Q R N M R K V R G P P V S C I K R D S P I Q C I Q A I A E N R A D A V T L D G					
81G F I Y E A G L A P Y K L R P V A A E V Y G T E R Q P R T H Y Y A V A V V K K G G S F Q L N E L Q G L K S C H T G L R R T A G W N V P I G T L R P F L N W T G P					
161P E P I E A A V A R F F S A S C V P G A D K G Q F P N L C R L C A G T G E N K C A F S S Q E P Y F S Y S G A F K C L R D G A G D V A F I R E S T V F E D L S D E					
241A E R D E Y E L L C P D N T R K P V D K F K D C H L A R V P S H A V V A R S V N G K E D A I W N L L R Q A Q E K F G K D K S P K F Q L F G S P S G Q K D L L F K					
321D S A I G F S R V P P R I D S G L Y L G S G Y F T A I Q N L R K S E E E V A A R R A R V V W C A V G E Q E L R K C N Q W S G L S E G S V T C S S A S T T E D C I					
401A L V L K G E A D A M S L D G G Y V Y T A G K C G L V P V L A E N Y K S Q Q S S D P D P N C V D R P V E G Y L A V A V V R R S D T S L T W N S V K G K K S C H T					
481A V D R T A G W N I P M G L L F N Q T G S C K F D E Y F S Q S C A P G S D P R S N L C A L C I G D E Q G E N K C V P N S N E R Y Y G Y T G A F R C L A E N A G D					
561V A F V K D V T V L Q N T D G N N N E A W A K D L K L A D F A L L C L D G K R K P V T E A R S C H L A M A P N H A V V S R M D K V E R L K Q V L L H Q Q A K F G					
641R N G S D C P D K F C L F Q S E T K N L L F N D N T E C L A R L H G K T T Y E K Y L G P Q Y V A G I T N L K K C S T S P L L E A C E F L R K					

5.220 tumor differentially expressed protein 1 [*Homo sapiens*]; tumor differentially expressed protein 1 [*Homo sapiens*]

Protein Accession gi|5803193 gi|39812106

Mean Expression Ratio 0.926

Median Expression Ratio 0.926

Credible Interval (0.567, 1.51)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0338]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.54	0.9	1.5	SEQ ID NO: 1302	LTLSGSDSVILGDTTSG ASDEEDGQPR

5.221 phosphodiesterase 8A isoform 2 [*Homo sapiens*]; phosphodiesterase 8A isoform 1 [*Homo sapiens*]

Protein Accession gi|47132537 gi|27734721

Mean Expression Ratio 1.08

Median Expression Ratio 1.08

Credible Interval (0.667, 1.74)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0339]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.66	1.1	1.8	SEQ ID NO: 1303	LVAEDAPSPAAPPLSSGG PR

5.222 SH3 domain and tetratricopeptide repeats 1 [*Homo sapiens*]

Protein Accession gi|1145386551

Mean Expression Ratio 0.928

Median Expression Ratio 0.927

Credible Interval (0.572, 1.50)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0112

[0340]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.54	0.9	1.5	SEQ ID NO: 1304	QALASLTPTGTQALR

SEQ ID NO: 1305					
1	M	E	N	L	P
	V	S	W	E	K
	A	G	P	E	E
	A	K	A	P	V
	R	G	D	E	A
	P	P	A	R	V
	A	G	P	A	A
	G	T	P	P	C
	Q	M	G	V	Y
81	P	T	D	L	T
	A	R	V	L	G
	E	L	S	A	R
	L	L	S	I	H
	S	D	Q	D	R
	I	V	V	T	F
	K	T	F	E	E
	I	W	K	F	S
	T	Y	H	A	L
161	G	F	T	H	H
	C	L	A	N	L
	L	M	D	Q	A
	F	W	L	L	P
	S	E	E	E	E
	T	A	I	Q	V
	H	V	D	E	N
	A	L	R		
241	S	G	A	P	Q
	G	E	A	A	P
	E	T	D	S	S
	P	P	S	P	S
	V	S	S	E	E
	V	A	V	A	A
	A	A	P	E	P
	L	I	P	F	H
	Q	G	S	G	
321	P	E	E	M	T
	F	R	G	D	L
	I	E	I	L	G
	A	Q	V	P	S
	L	P	W	C	V
	G	R	H	A	A
	S	G	R	V	G
	F	V	R	S	
401	R	R	M	S	G
	T	D	V	C	S
	V	Y	S	L	D
	S	V	E	E	A
	E	T	E	Q	P
	Q	E	K	E	I
	P	P	P	C	L
	S	P	E	P	Q
481	E	E	P	S	F
	C	L	E	A	E
	D	D	W	E	D
	P	E	A	L	S
	S	S	L	L	L
	F	L	N	A	P
	G	Y	K	A	S
	F	R	G	L	Y
	D				
561	R	L	C	F	L
	L	G	R	L	C
	S	R	R	L	K
	L	S	Q	A	R
	V	Y	F	E	E
	A	L	G	A	L
	E	G	S	F	G
	D	L	F	L	V
	V	A	V	A	N
	L	A	S	I	Y
	R	K	Q	K	N
	R	E	K	C	A
	Q	V	V	P	K
	A	M	A	L	L
	L	G	T	P	D
	H	I	C	S	
641	T	E	A	E	G
	E	L	L	Q	L
	A	L	R	R	A
	V	G	G	Q	S
	L	Q	A	E	A
	R	A	C	F	L
	L	A	R	H	H
	V	H	L	K	
	Q	P	E	E	A
	L	P	F	L	E
	R	L	L	L	H
	R	D	S	G	A
	P	E	A	A	W
	L	S	D	C	Y
	L	L	L	A	D
	I	Y	S	R	K
721	C	L	P	H	L
	V	L	S	C	V
	K	V	A	S	L
	R	T	R	G	S
	L	A	G	S	L
	R	S	V	N	L
	V	L	Q	N	A
	P	Q	P	H	S
	L	P	A	Q	T
	S	H	Y	L	R
	Q	A	L	A	S
	L	T	P	G	T
	G	Q	A	L	R
	G	P	L	Y	T
	S	L	A	Q	L
	Y	S	H	H	G
801	C	H	G	P	A
	I	T	F	M	T
	Q	A	V	E	A
	S	A	I	A	G
	V	R	A	I	V
	D	H	L	V	A
	L	A	L	A	W
	L	H	V	L	H
	G				
	Q	S	P	V	A
	L	D	I	L	Q
	S	V	R	D	A
	V	V	A	S	E
	D	Q	E	G	V
	I	A	N	M	V
	A	V	A	L	K
	R	T	G	R	T
	R				

-continued

881	Q A A E S Y Y R A L R V A R D L G Q Q R N Q A V G L A N F G A L C L H A G A
	S R L A Q H Y L L E A V R L F S R L P L G E C G R D F T H V L L Q L G H L C T R Q G
961	P A Q Q G K G Y Y E W A L L V A V E M G H V E S Q L R A V Q R L C H F Y S A
	V M P S E A Q C V I Y H E L Q L S L A C K V A D K V L E G Q L L E T I S Q L Y L S L
1041	G T E R A Y K S A L D Y T K R S L G I F I D L Q K K E K E A H A W L Q A G K I
	Y Y I L R Q S E L V D L Y I Q V A Q N V A L Y T G D P N L G L E L F E A A G D I F
1121	F D G A W E R E K A V S F Y R D R A L P L A V T T G N R K A E L R L C N K L
	V A L L A T L E E P Q E G L E F A H M A L A L S I T L G D R L N E R V A Y H R L A A
1201	L Q H R L G H G E L A E H F Y L K A L S L C N S P L E F D E E T L Y Y V K V Y
	L V L G D I I F Y D L K D P F D A A G Y Y Q L A L A A A V D L G N K K A Q L K I Y
1281	T R L A T I Y H N F L L D R E K S L F F Y Q K A R T F A T E L N V R R V N L P
	P L P L C G W A P W L A P S H P R

5.223 aminoacylase 1 [*Homo sapiens*]
Protein Accession gi|4501901

Associated Peptides 3

Mean Expression Ratio 0.926

Associated Spectra 4

Median Expression Ratio 0.927

Coverage 0.125

Credible Interval (0.649, 1.32)

[0341]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.59	0.91	1.4	SEQ ID NO: 1306	DMNLTLEPEIMPAATDNR
1	0.61	0.92	1.4	SEQ ID NO: 1307	GPREEHPSVTLFR
2	0.63	0.93	1.4	SEQ ID NO: 1308	TVQPKPDYGAAVAFFEETAR
SEQ ID NO: 1309					
1M T S K G P E E E H P S V T L F R Q Y L R I R T V Q P K P D Y G A A V A F F E E T					
A R Q L G L G C Q K V E V A P G Y V V T V L T W P G T N P T L S S I L L N S H					
81T D V V P V F K E H W S H D P F E A F K D S E G Y I Y A R G A Q D M K C V S I Q					
Y L E A V R R L K V E G H R F P R T I H M T F V P D E E V G G H Q G M E L F V Q					
161R P E F H A L R A G F A L D E G I A N P T D A F T V F Y S E R S P W W V R V T					
S T G R P G H A S R F M E D T A A E K L H K V V N S I L A F R E K E W Q R L Q S N					
241P H L K E G S V T S V N L T K L E G G V A Y N V I P A T M S A S F D F R V A P					
D V D F K A F E E Q L Q S W C Q A A G E G V T L E F A Q K W M H P Q V T P T D D S					
321N P W W A A F S R V C K D M N L T L E P E I M P A A T D N R Y I R A V G V P A					
L G F S P M N R T P V L L H D H D E R L H E A V F L R G V D I Y T R L L P A L A S					
401V P A L P S D S					

5.224 cathepsin A isoform a precursor [*Homo sapiens*]
Protein Accession gi|119395729

Mean Expression Ratio 0.928

Median Expression Ratio 0.928

Credible Interval (0.708, 1.21)

Associated Peptides 9

Associated Spectra 9

Coverage 0.207

[0342]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.66	0.94	1.3	SEQ ID NO: 1310	CNFDNK
1	0.65	0.94	1.3	SEQ ID NO: 1311	DLECVTNLQEVAR
1	0.67	0.96	1.4	SEQ ID NO: 1312	HLHYWFVESQK
1	0.64	0.91	1.3	SEQ ID NO: 1313	NFLVNLQYR
1	0.66	0.93	1.3	SEQ ID NO: 1314	QYSGYLK
1	0.65	0.94	1.3	SEQ ID NO: 1315	YGDSGEQIAGFVK
1	0.61	0.88	1.3	SEQ ID NO: 1316	YATNDTEVAQSNFEALQDFFR
1	0.64	0.91	1.3	SEQ ID NO: 1317	ALNIPEQLPQWDMCNFLVNLQYR
1	0.63	0.9	1.3	SEQ ID NO: 1318	EFSHIAFL

SEQ ID NO: 1319

1MTSSPRAPPGEQGGRGGAEMIRAAPPPFLFLLLLLLLLVSWA
SRGEAAPDQDEIQRLPGLAKQPSFRQYSGY LKGS GSKHL

81HYWFVESQKDPENSPVVVLWLN GGP GCS SLDGLLT EHG PFL
VQPDGVTLEYNPYSWNLIANVLYLES PAGVGFSYSDDKFY

161ATNDTEVAQSNFEALQDFFRLFP EYKNNKLF LTGESYAGI
YIPTLAVLVMQDPSMNLQGLAVGNGLSSSYEQNDNSLVYFA

241Y YHGLLGNRLWSSSLQTHCCSQNKCNFYDNKDL ECVTNL
QEVARI VGN SGLNIYNLYAPCAGGVPSHF RYEKDTVVVQDLG

321NIFTRLPLKRMWHQALLRSGDKVRMDPPCTNTTAASTYL
NNPYVRKALNIPEQLPQWDMCNFLVNLQYRRLYRSMNSQYL

401KLLSSQKYQILLYNGD VDMACNFMGDEWFVDSL NQKME
VQRRPWL VKYGD SGEQIAGFVKEFSHIAFLTIKGAGHMVPTD

481KPLAAFTMF SRFLNKQPY

5.225 pleckstrin homology domain containing, family B (evectins) member 2 isoform 3 [*Homo sapiens*]; pleckstrin homology domain containing, family B (evectins) member 2 isoform 2 [*Homo sapiens*]

Protein Accession gi 154800478 gi|54800476

Mean Expression Ratio 0.93

Median Expression Ratio 0.929

Credible Interval (0.652, 1.32)

Associated Peptides 4

Associated Spectra 4

Coverage NaN

[0343]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	0.93	1.4	SEQ ID NO: 1320	AGLYGQQPANQVIIR
1	0.61	0.93	1.4	SEQ ID NO: 1321	GQQPANQVIIR

-continued

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.6	0.91	1.4	SEQ ID NO: 1322	NWFDLWSDGHLIYYD DQTR
1	0.61	0.93	1.4	SEQ ID NO: 1323	VHMPMDCINIR

5.226 BH3 interacting domain death agonist isoform 2 [*Homo sapiens*]; BH3 interacting domain death agonist isoform 3 [*Homo sapiens*]; BH3 interacting domain death agonist isoform 1 [*Homo sapiens*]

Protein Accession gi|4557361 gi|37574728 gi|37574726

Mean Expression Ratio 0.929

Median Expression Ratio 0.93

Credible Interval (0.572, 1.52)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0344]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.54	0.9	1.5	SEQ ID NO: 1324	DLATALEQLLQAYPR

5.227 enolase 1 [*Homo sapiens*]

Protein Accession gi|4503571

Mean Expression Ratio 1.08

Median Expression Ratio 1.08

Credible Interval (0.799, 1.44)

Associated Peptides 5

Associated Spectra 7

Coverage 0.184

[0345]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.75	1.1	1.5	SEQ ID NO: 1325	AAVPSGASTGIYEALRLR
2	0.75	1.1	1.5	SEQ ID NO: 1326	HIADLAGNSEVILPVPAFNIVINGGSHAGNK
1	0.76	1.1	1.6	SEQ ID NO: 1327	YISPDQLADLYK
1	0.73	1.1	1.5	SEQ ID NO: 1328	VVIGMDVAASEFFR
1	0.74	1.1	1.6	SEQ ID NO: 1329	YDLDFK

SEQ ID NO: 1330

1MSILKIHAREIFDSRGNPTVEVDLFTSKGLFRAAVPSGASTG
IYEALRLRDNDKTRYMGKGVSKAVEHINKTIAPALVSK

81KLNVTETEKKIDKLMIEMDGTENKSKFGANAILGVSLAVCK
AGAVEKGVPLRYRHIADLAGNSEVILPVPAFNIVINGGSHAG

161NKLAMQEFMILPVGAANFREAMRIGAEVYHNLKNVIKEK
YGKDATTNVGDEGGFAPNILENKEGLELLKTAIGKAGYTDK

241VIGMDVAASEFFFRSGKYDLDFKSPDDPSRYISPDQLADLY
KSFIKDYPPVVSIEDPFDQDDWGAWQKFTASAGIQVVGDDL

321TVTNPKRIAKAVNEKSCNCLLLKVNQIGSVTESLQACKLA
QANGWGVMSHRSGETEDTFIADLVVGLCTGQIKTGAPCR

401SERLAKYNQLRLRIEEELGSKAKFAGRNFNRNPLAK

5.228 hypothetical protein LOC64855 isoform 2 [*Homo sapiens*]; hypothetical protein LOC64855 isoform 1 [*Homo sapiens*]

Protein Accession gi|79750824 gi|51093863

Mean Expression Ratio 1.08

Median Expression Ratio 1.08

Credible Interval (0.708, 1.64)

Associated Peptides 2

Associated Spectra 2

Coverage NaN

[0346]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.68	1.1	1.7	SEQ ID NO: 1331	FQELIFEDFAR
1	0.68	1.1	1.7	SEQ ID NO: 1332	EASPESPPASPDPGVTEIR

5.229 ribophorin II isoform 2 precursor [*Homo sapiens*]
Protein Accession gi|209413738

Mean Expression Ratio 0.93

Median Expression Ratio 0.93

Credible Interval (0.573, 1.5)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0347]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.56	0.91	1.5	SEQ ID NO: 1333	SIVEEIEDLVAR

5.230 urate anion exchanger 1 isoform a [*Homo sapiens*]
Protein Accession gi|24497485

Mean Expression Ratio 0.93

Median Expression Ratio 0.932

Credible Interval (0.608, 1.41)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0561

[0348]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.92	1.5	SEQ ID NO: 1334	AFSELLDLVGGLGR
1	0.59	0.93	1.5	SEQ ID NO: 1335	GAVQDTLTPEVLLSAMR
SEQ ID NO: 1336					
1MAFSELLDLVGGLGRFQVLQTMALMVSI MWLCTQSMLENF					
SAAVP SHRCWAPLLDNSTAQASILGSL SPEALLAISIPPG					
81PNQRPHQCRRFRQPQWQLLDPNATATSWSEADTEPCVDG					
WVYDRSIFTSTIVAKWNLVCDSHALKPMAQSIYLAGILVGA					
161AACGPASDRFGRRLLVLTWSYLQMAVMGTAAAFAPAFPV					
YCLFRFLLAFAVAGVMMNTGTL LMEWTAARARPLVMTLNS					
LG					
241FSFGHGLTAAVAYGV RDWTL LQLVVSVPFFLCFLYSWWL					
AESARWLLTTGRLDWGLQELWRVAAINGKGAVQDTLTPEVL					
321LSAMREEELSMGQPPASLGTLLRMPGLRFRTCISTLCWFAP					
GFTFFGLALDLQALGSNIFLLQMFI GVV DIPAKMGALLLL					
401SHLGRRP TLAAASLLLAGL CILANTLVPHEMGALRSALAVL					
GLGGVGAAFTCITIYSSSELFP TVLRMTAVGLGQMAARGGA					
481ILGPLVRL LGVHGPWLPLLVYGTVPVLSGLAALLLPETQS					
LPLPDTIQDVQNQAVKKATHGTLGNSVLKSTQF					

5.231 chromatin modifying protein 4C [*Homo sapiens*]
Protein Accession gi|22748643
Mean Expression Ratio 1.07
Median Expression Ratio 1.07
Credible Interval (0.65, 1.75)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0687
[0349]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.66	1.1	1.8	SEQ ID NO: 1337	QLTQIDGTLSTIEFQR

SEQ ID NO: 1338

1M S K L G K F F K G G G S S K S R A A P S P Q E A L V R L R E T E E M L G K K Q
E Y L E N R I Q R E I A L A K K H G T Q N K R A A L Q A L K R K K R F E K Q L T

81Q I D G T L S T I E F Q R E A L E N S H T N T E V L R N M G F A A K A M K S V H
E N M D L N K I D D L M Q E I T E Q Q D I A Q E I S E A F S Q R V G F G D D F D

161E D E L M A E L E E L E Q E E L N K K M T N I R L P N V P S S S L P A Q P N R K
P G M S S T A R R S R A A S S Q R A E E E D D D I K Q L A A W A T

5.232 saccin [*Homo sapiens*]
Protein Accession gi|163659918
Mean Expression Ratio 0.932
Median Expression Ratio 0.932
Credible Interval (0.577, 1.52)
Associated Peptides 1
Associated Spectra 1
Coverage NaN
[0350]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.55	0.91	1.5	SEQ ID NO: 1339	NHPSVSWLK

5.233 lumican precursor [*Homo sapiens*]
Protein Accession gi|4505047
Mean Expression Ratio 0.936
Median Expression Ratio 0.932
Credible Interval (0.577, 1.53)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0444

[0351]

SEQ ID NO: 1340				
A	2.5	50	97.5	Sequence
1	0.55	0.92	1.5	ISSETSLPPDMYECLR

SEQ ID NO: 1341

1M S L S A F T L F L A L I G G T S G Q Y Y D Y D F P L S I Y G Q S S P N C A P E C
N C P E S Y P S A M Y C D E L K L K S V P M V P P G I K Y L Y L R N N Q I D H
81I D E K A F E N V T D L Q W L I L D H N L L E N S K I K G R V F S K L K Q L K K
L H I N H N N L T E S V G P L P K S L E D L Q L T H N K I T K L G S F E G L V N

161L T F I H L Q H N R L K E D A V S A A F K G L K S L E Y L D L S F N Q I A R L P
S G L P V S L L T L Y L D N N K I S N I P D E Y F K R F N A L Q Y L R L S H N E

241L A D S G I P G N S F N V S S L V E L D L S Y N K L K N I P T V N E N L E N Y Y
L E V N Q L E K F D I K S F C K I L G P L S Y S K I K H L R L D G N R I S E T S

321L P P D M Y E C L R V A N E V T L N

5.234 chromatin modifying protein 1B [*Homo sapiens*]
Protein Accession gi|31542306
Mean Expression Ratio 1.07
Median Expression Ratio 1.07
Credible Interval (0.662, 1.73)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0302
[0352]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.1	1.8	SEQ ID NO: 1342	HLFNLK

SEQ ID NO: 1343

1M S N M E K H L F N L K F A A K E L S R S A K K C D K E E K A E K A K I K K A I
Q K G N M E V A R I H A E N A I R Q K N Q A V N F L R M S A R V D A V A A R V Q

81T A V T M G K V T K S M A G V V K S M D A T L K T M N L E K I S A L M D K F E
H Q F E T L D V Q T Q Q M E D T M S S T T T L T T P Q N Q V D M L L Q E M A D E A

161G L D L N M E L P Q G Q T G S V G T S V A S A E Q D E L S Q R L A R L R D Q V

5.235 SHC (Src homology 2 domain containing) transform-
ing protein 1 isoform 2 [*Homo sapiens*]; SHC (Src homol-
ogy 2 domain containing) transforming protein 1 isoform 3
[*Homo sapiens*]
Protein Accession gi|32261324 gi|194239664

Mean Expression Ratio 0.933
Median Expression Ratio 0.936
Credible Interval (0.571, 1.50)
Associated Peptides 1
Associated Spectra 1
Coverage NaN

[0353]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.55	0.92	1.5	SEQ ID NO: 1344	QAVGGAGPPNPAINGSA PR

5.236 hypothetical protein LOC28970 [*Homo sapiens*]
Protein Accession gi|21361495
Mean Expression Ratio 1.07
Median Expression Ratio 1.07
Credible Interval (0.755, 1.53)
Associated Peptides 3
Associated Spectra 4
Coverage 0.109
[0354]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.7	1.0	1.5	SEQ ID NO: 1345	APLVCLPVFVSR
1	0.73	1.1	1.7	SEQ ID NO: 1346	FLPAEFLYR
1	0.71	1.1	1.6	SEQ ID NO: 1347	WLHFYEMK

SEQ ID NO: 1348

1M A C A E F S F H V P S L E E L A G V M Q K G L K D N F A D V Q V S V V D C P D
L T K E P F T F P V K G I C G K T R I A E V G G V P Y L L P L V N Q K K V Y D L

81N K I A K E I K L P G A F I L G A G A G P P Q T L G F N S E F M P V I Q T E S E H
K P P V N G S Y F A H V N P A D G G C L L E K Y S E K C H D F Q C A L L A N L

-continued

161	F	A	S	E	G	Q	P	G	K	P	A	E	F	S	S	C	P	L	N	S	D	E	E	V	N	K	W	L	H	F	Y	E	M	K	A	P	L	V	C			
	L	P	V	F	V	S	R	D	P	G	F	D	L	R	L	E	H	T	H	F	F	S	R	H	G	E	G	G	H	Y	H	Y	D	T	T	P	D	I	V	E	Y	
241	L	G	Y	F	L	P	A	E	F	L	Y	R	I	D	Q	P	K	E	T	H	S	I	G	R	D																	

5.237 ATPase, H+ transporting, lysosomal V0 subunit a4 [*Homo sapiens*]; ATPase, H+ transporting, lysosomal V0 subunit a4 [*Homo sapiens*]; ATPase, H+ transporting, lysosomal V0 subunit a4 [*Homo sapiens*]
Protein Accession gil85386547 gil85386056 gil85386053

Mean Expression Ratio 1.07

Median Expression Ratio 1.07

Credible Interval (0.659, 1.76)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0355]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.1	1.8	SEQ ID NO: 1349	LEDLITVITQTESHR

5.238 chloride channel 7 isoform b [*Homo sapiens*]; chloride channel 7 isoform a [*Homo sapiens*]
Protein Accession gil167466160 gil14149607

Mean Expression Ratio 0.934

Median Expression Ratio 0.937

Credible Interval (0.616, 1.43)

Associated Peptides 2

Associated Spectra 2

Coverage NaN

[0356]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.59	0.93	1.5	SEQ ID NO: 1350	IFEYFR
1	0.58	0.92	1.4	SEQ ID NO: 1351	YESLDYDENSEQLFLEER

5.239 solute carrier family 34 (sodium phosphate), member 2 [*Homo sapiens*]
Protein Accession gil110611906

Mean Expression Ratio 1.07

Median Expression Ratio 1.07

Credible Interval (0.785, 1.44)

Associated Peptides 5

Associated Spectra 7

Coverage 0.058

[0357]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.72	1.1	1.5	SEQ ID NO: 1352	APETFDNITISR
3	0.86	1.2	1.7	SEQ ID NO: 1353	KLQNNWFLPLWMR
1	0.71	1.0	1.5	SEQ ID NO: 1354	YLEGAAGQQPTAPDK
1	0.72	1.1	1.5	SEQ ID NO: 1355	LQNNWFLPLWMR
1	0.7	1	1.5	SEQ ID NO: 1356	NFLPLWMR

SEQ ID NO: 1357					
1	M	A	P	W	P
2	E	L	G	D	A
3	Q	P	N	P	D
4	K	Y	L	E	G
5	A	A	G	Q	Q
6	P	T	A	P	D
7	K	S	K	E	T
8	N	K	T	D	
9	N	T	E	A	P
10	V	T	K	I	E
11	L	L	P	S	Y
12	S	T	A	T	L
13	I	D	E	P	T
14	E	V	D	D	P
15	W	N	L	P	T
16	L	Q	D	S	G
17	I				
18	81	K	W	S	E
19	R	D	T	K	G
20	K	I	L	C	F
21	F	Q	G	I	G
22	R	L	I	L	L
23	L	G	F	L	Y
24	F	F	V	F	V
25	C	S	L	D	I
26	L	S	S	A	F
27	Q	L	V	G	G
28	K	M	A	G	Q
29	F	F	S	N	S
30	S	I	M	S	N
31	P	L	L	G	L
32	V	I	G	V	L
33	V	T	V	L	V
34	Q	S	S		
35	161	S	T	S	T
36	S	I	V	V	S
37	M	V	S	S	S
38	L	L	T	V	R
39	A	A	I	P	I
40	I	M	G	A	N
41	I	G	T	S	I
42	T	N	T	I	V
43	A	L	M		
44	Q	V	G	D	R
45	S	E	F	R	R
46	A	F	A	G	A
47	T	V	H	D	F
48	F	N	W	L	S
49	V	L	V	L	L
50	P	V	E	V	A
51	T	H	Y		
52	241	L	E	I	I
53	T	Q	L	I	V
54	E	S	F	H	F
55	K	N	G	E	D
56	A	P	D	L	L
57	K	V	I	T	K
58	P	F	T	K	L
59	I	V	Q	L	D
60	K	K			
61	V	I	S	Q	I
62	A	M	N	D	E
63	K	A	K	N	K
64	S	L	V	K	I
65	W	C	K	T	F
66	T	N	K	T	Q
67	I	N	V	T	V
68	P	S	T	A	
69	321	N	C	T	S
70	P	S	L	C	W
71	T	D	G	I	Q
72	N	W	T	M	K
73	N	V	T	Y	K
74	E	N	I	A	K
75	C	Q	H	I	F
76	V	N	F	H	L
77	P	D	L	A	V
78	G	T	I	L	L
79	I	L	S	L	V
80	L	C	G	C	L
81	I	M	I	V	K
82	I	L	G	S	V
83	L	K	G	Q	V
84	A	T	V	I	K

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401	K	T	I	N	T	D	F	P	F	P	F	A	W	L	T	G	Y	L	A	I	L	V	G	A	G	M	T	F	I	V	Q	S	S	S	V	F	T	S	A	L		
	T	P	L	I	G	I	G	V	I	T	I	E	R	A	Y	P	L	T	L	G	S	N	I	G	T	T	T	T	A	I	L	A	A	L	A	S	P	G	N	A		
481	L	R	S	S	L	Q	I	A	L	C	H	F	F	F	N	I	S	G	I	L	L	W	Y	P	I	P	F	T	R	L	P	I	R	M	A	K	G	L	G	N	I	S
	A	K	Y	R	W	F	A	V	F	Y	L	I	I	F	F	F	L	I	P	L	T	V	F	G	L	S	L	A	G	W	R	V	L	V	G	V	G	V				
561	P	V	V	F	I	I	I	L	V	L	C	L	R	L	L	Q	S	R	C	P	R	V	L	P	K	K	L	Q	N	W	N	F	L	P	L	W	M	R	S	L		
	K	P	W	D	A	V	V	S	K	F	T	G	C	F	Q	M	R	C	C	C	C	R	V	C	C	R	A	C	C	L	L	C	G	C	P	K	C	C	R			
641	C	S	K	C	C	E	D	L	E	E	A	Q	E	G	Q	D	V	P	V	K	A	P	E	T	F	D	N	I	T	I	S	R	E	A	Q	G	E	V	P	A		
	S	D	S	K	T	E	C	T	A	L																																

5.240 UBX domain protein 6 [*Homo sapiens*]
Protein Accession gi|13376854

Mean Expression Ratio 1.07
Median Expression Ratio 1.07
Credible Interval (0.666, 1.74)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0544
[0358]

A	2.5	50	97.5	Sequence ID No.	Sequence																																				
1	0.66	1.1	1.8	SEQ ID NO: 1358	ELQAEATVSGSPEAPGTNVVSEPR																																				
SEQ ID NO: 1359																																									
1	M	K	K	F	Q	E	F	K	A	D	I	K	F	K	S	A	G	P	G	Q	K	L	K	E	S	V	G	E	K	A	H	K	E	K	P	N	Q	P	A		
	P	R	P	P	R	Q	G	P	T	N	E	A	Q	M	A	A	A	A	A	L	A	R	L	E	Q	K	Q	S	R	A	W	G	P	T	S	Q	D	T	I	R	
81	N	Q	V	R	K	E	L	Q	A	E	A	T	V	S	G	S	P	E	A	P	G	T	N	V	V	S	E	P	R	E	E	G	S	A	H	L	A	V	P	G	
	V	Y	F	T	C	P	L	T	G	A	T	L	R	K	D	Q	R	D	A	C	I	K	E	A	I	L	L	H	F	S	T	D	P	V	A	A	S	I	M	K	
161	I	Y	T	F	N	K	D	Q	D	R	V	K	L	G	V	D	T	I	A	K	Y	L	D	N	I	H	L	H	P	E	E	E	K	Y	R	K	I	K	L	Q	
	N	K	V	F	Q	E	R	I	N	C	L	E	G	T	H	E	F	F	E	A	I	G	F	Q	K	V	L	L	P	A	Q	D	Q	E	D	P	E	E	F	Y	
241	V	L	S	E	T	T	L	A	Q	P	Q	S	L	E	R	H	K	E	Q	L	L	A	A	E	P	V	R	A	K	L	D	R	Q	R	R	V	F	Q	P	S	
	P	L	A	S	Q	F	E	L	P	G	D	F	F	N	L	T	A	E	E	I	K	R	E	Q	R	L	R	S	E	A	V	E	R	L	S	V	L	R	T	K	
321	A	M	R	E	K	E	E	Q	R	G	L	R	K	Y	N	Y	T	L	L	R	V	R	L	P	D	G	C	L	L	Q	G	T	F	Y	A	R	E	R	L		
	G	A	V	Y	G	F	V	R	E	A	L	Q	S	D	W	L	P	F	E	L	L	A	S	G	G	Q	K	L	S	E	D	E	N	L	A	L	N	E	C	G	L
401	V	P	S	A	L	L	T	F	S	W	D	M	A	V	L	E	D	I	K	A	A	G	A	E	P	D	S	I	L	K	P	E	L	L	S	A	I	E	K	L	L

5.241 tetratricopeptide repeat domain 38 [*Homo sapiens*]
Protein Accession gi 116812608
Mean Expression Ratio 0.935
Median Expression Ratio 0.938

Credible Interval (0.577, 1.50)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0192
[0359]

A	2.5	50	97.5	Sequence ID No.	Sequence																																			
1	0.55	0.92	1.5	SEQ ID NO: 1360	VLELLLPPIR																																			
SEQ ID NO: 1361																																								
1	M	A	A	A	S	P	L	R	D	C	Q	A	W	K	D	A	R	L	P	L	S	T	T	S	N	E	A	C	K	L	F	D	A	T	L	T	Q	Y	V	K
	W	T	N	D	K	S	L	G	I	E	G	C	L	S	K	L	K	A	A	D	P	T	F	V	M	G	H	A	M	A	T	G	L	V	L	I	G	T	G	
81	S	S	V	K	L	D	K	E	L	D	L	A	V	K	T	M	V	E	I	S	R	T	Q	P	L	T	R	R	E	Q	L	H	V	S	A	V	E	T	F	A
	N	G	N	F	P	K	A	C	E	L	W	E	Q	I	L	Q	D	H	P	T	D	M	L	A	L	K	F	S	H	D	A	Y	F	Y	L	G	Y	Q	E	Q

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161	M R D S V A R I Y P F W T P D I P L S S Y V K G I Y S F G L M E T N F Y D Q A E
	K L A K E A L S I N P T D A W S V H T V A H I H E M K A E I K D G L E F M Q H S
241	E T L W K D S D M L A C H N Y W H W A L Y L I E K G E Y E A A L T I Y D T H I
	L P S L Q A N D A M L D V V D S C S M L Y R L Q M E G V S V G Q R W Q D V L P V A
321	R K H S R D H I L L F N D A H F L M A S L G A H D P Q T T Q E L L T T L R D A
	S E S P G E N C Q H L L A R D V G L P L C Q A L V E A E D G N P D R V L E L L L P

5.242 crystallin, alpha B [*Homo sapiens*]
Protein Accession gi|4503057

Mean Expression Ratio 1.06
Median Expression Ratio 1.07
Credible Interval (0.686, 1.63)
Associated Peptides 1
Associated Spectra 2
Coverage 0.0629
[0360]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.69	1.1	1.7	SEQ ID NO: 1362	VLGDVIEVHGK

SEQ ID NO: 1363

1	M D I A I H H P W I R R P F F P F H S P S R L F D Q F F G E H L L E S D L F P T S T
	S L S P F Y L R P P S F L R A P S W F D T G L S E M R L E K D R F S V N L D
81	V K H F S P E E L K V K V L G D V I E V H G K H E E R Q D E H G F I S R E F H R
	K Y R I P A D V D P L T I T S S L S S D G V L T V N G P R K Q V S G P E R T I P
161	I T R E E K P A V T A A P K K

5.243 dual oxidase 2 precursor [*Homo sapiens*]
Protein Accession gi|132566532

Mean Expression Ratio 1.07
Median Expression Ratio 1.07
Credible Interval (0.658, 1.73)

Associated Peptides 1
Associated Spectra 1
Coverage 0.00775
[0361]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.1	1.8	SEQ ID NO: 1364	AQLAEVVESMFR

SEQ ID NO: 1365

1	M L R A R P E A L M L L G A L L T G S L G P S G N Q D A L S L P W E V Q R Y D G
	W F N N L R H H E R G A V G C R L Q R R V P A N Y A D G V Y Q A L E E P Q L P N
81	P R R L S N A A T R G I A G L P S L H N R T V L G V F F G Y H V L S D V V S V E
	T P G C P A E F L N I R I P P G D P V F D P D Q R G D V V L P F Q R S R W D P E
161	T G R S P S N P R D L A N Q V T G W L D G S A I Y G S S H S W S D A L R S F S
	G G Q L A S G P D P A F P R D S Q N P L L M W A A P D P A T G Q N G P R G L Y A F
241	G A E R G N R E P F L Q A L G L L W F R Y H N L W A Q R L A R Q H P D W E D
	E E L F Q H A R K R V I A T Y Q N I A V Y E W L P S F L Q K T L P E Y T G Y R P F L
321	D P S I S P E F V V A S E Q F F S T M V P P G V Y M R N A S C H F R K V L N K G
	F Q S S Q A L R V C N N Y W I R E N P N L N S T Q E V N E L L L G M A S Q I S E

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401L	E D N I V V E D L R D Y W P G P G K F S R T D Y V A S S I Q R G R D M G L P S Y S Q A L L A F G L D I P R N W S D L N P N V D P Q V L E A T A A L Y N Q D L S
481Q	L E L L L G G L L E S H G D P G P L F S A I V L D Q F V R L R D G D R Y W F E N T R N G L F S K K E I E D I R N T T L R D V L V A V I N I D P S A L Q P N V F
561V	W H K G A P C P Q P K Q L T T D G L P Q C A P L T V L D F F E G S S P G F A I T I I A L C C L P L V S L L L S G V V A Y F R G R E H K K L Q K K L K E S V K K
641E	A A K D G V P A M E W P G P K E R S S P I I I Q L L S D R C L Q V L N R H L T V L R V V Q L Q P L Q Q V N L I L S N N R G C R T L L L K I P K E Y D L V L L F
721S	S E E E R G A F V Q Q L W D F C V R W A L G L H V A E M S E K E L F R K A V T K Q Q R E R I L E I F F R H L F A Q V L D I N Q A D A G T L P L D S S Q K V R E
801A	L T C E L S R A E F A E S L G L K P Q D M F V E S M F S L A D K D G N G Y L S F R E F L D I L V V F M K G S P E D K S R L M F T M Y D L D E N G F L S K D E F
881F	T M M R S F I E I S N N C L S K A Q L A E V V E S M F R E S G F Q D K E E L T W E D F H F M L R D H D S E L R F T Q L C V K G G G G G G N G I R D I F K Q N I
961S	C R V S F I T R T P G E R S H P Q G L G P P A P E A P E L G G P G L K K R F G K K A A V P T P R L Y T E A L Q E K M Q R G F L A Q K L Q Q Y K R F V E N Y R R
1041H	I V C V A I F S A I C V G V F A D R A Y Y Y G F A S P P S D I A Q T T L V G I I L S R G T A A S V S F M F S Y I L L T M C R N L I T F L R E T F L N R Y V P F
1121D	A A V D F H R W I A M A A V V L A I L H S A G H A V N V Y I F S V S P L S L L A C I F P N V F V N D G S K L P Q K F Y W W F F Q T V P G M T G V L L L L V L A
1201I	M Y V F A S H H F R R R S F R G F W L T H H L Y I L L Y A L L I I H G S Y A L I Q L P T F H I Y F L V P A I I Y G G D K L V S L S R K K V E I S V V K A E L L
1281P	S G V T Y L Q F Q R P Q G F E Y K S G Q W V R I A C L A L G T T E Y H P F T L T S A P H E D T L S L H I R A V G P W T T R L R E I Y S S P K G N G C A G Y P K
1361L	Y L D G P F G E G H Q E W H K F E V S V L V G G G I G V T P F A S I L K D L V F K S S L G S Q M L C K K I Y F I W V T R T Q R Q F E W L A D I I Q E V E E N D
1441H	Q D L V S V H I Y V T Q L A E K F D L R T T M L Y I C E R H F Q K V L N R S L F T G L R S I T H F G R P P F E P F F N S L Q E V H P Q V R K I G V F S C G P P

5.244 DnaJ (Hsp40) homolog, subfamily C, member 5
[Homo sapiens]
Protein Accession gi|45504382
Mean Expression Ratio 0.938
Median Expression Ratio 0.938

Credible Interval (0.626, 1.41)
Associated Peptides 1
Associated Spectra 3
Coverage 0.126
[0362]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.62	0.92	1.4	SEQ ID NO: 1366	APEGEETEFYVSPEDLEAQLQSDER
SEQ ID NO: 1367					
1M A D Q R Q R S L S T S G E S L Y H V L G L D K N A T S D D I K K S Y R K L A L K Y H P D K N P D N P E A A D K F K E I N N A H A I L T D A T K R N I Y D K Y G					
81S L G L Y V A E Q F G E E N V N T Y F V L S S W W A K A L F V F C G L L T C C Y C C C C L C C C F N C C C G K C K P K A P E G E E T E F Y V S P E D L E A Q L Q					
161S D E R E A T D T P I V I Q P A S A T E T T Q L T A D S H P S Y H T D G F N					

5.245 vacuolar H+ATPase B2 [*Homo sapiens*]
Protein Accession gil19913428
Mean Expression Ratio 0.939
Median Expression Ratio 0.939
Credible Interval (0.652, 1.36)
Associated Peptides 3
Associated Spectra 4
Coverage 0.110
[0363]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.62	0.9	1.3	SEQ ID NO: 1368	GIVNGAAPELPVPTGGPAVGAR
1	0.63	0.95	1.5	SEQ ID NO: 1369	IPIFSAAGLPHNEIAAQICR
1	0.61	0.94	1.4	SEQ ID NO: 1370	QIYPPINVLP SLSR

SEQ ID NO: 1371

1MALRAMRGIVNGAAPPELPVPTGGPAVGAREQALAVSRNYL
SQPRLTYKTVSGVNGPLVILDHVKFPRYAEIVHLLTLPDGT

81KRSGQVLEVS GSKAVVQVFEGTSGIDAKKTSCEFTGDI LR
TPVSEDM LGRVFN GSGKPIDRGPVVLAEDFLDIMGQPINP

161QCR IYPEEMIQTGIS AIDGMNSIARGQKIP IFS AAGLPHNE
IAAQICRQAGLVKKSKD VVDYSEENFAIVFAAMGVN MET

241ARFFKSDFEENGSM DNVCLFLNLANDPTIERIITPRLALT T
AEFLAYQCEKHVLVIL TDMSSYAEALREVSAAREEEVPGR

321RGFPGYMYTDLATIYERAGRVEGRNGSITQIPILTMPNDD
ITHPIPDLTGYITEGQIYVDRQLHNRQIYPPINVLP SLSR

401LMKSAIGEGMTRKDHADVSNQLYACYAIGKDVQAMKAV
VGEEALTSDDL LYLEFLQKFERNFIAAQGPYENRTVFETL D I G

481WQLLRIFPK EMLKRIPQSTLSEFYPRDS AKH

5.246 angiotensin I converting enzyme 2 precursor [*Homo sapiens*]
Protein Accession gil11225609
Mean Expression Ratio 0.939
Median Expression Ratio 0.939
Credible Interval (0.697, 1.27)
Associated Peptides 5
Associated Spectra 7
Coverage 0.0745
[0364]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	0.92	1.3	SEQ ID NO: 1372	GQKPNIDVTDAMVDQAWDAQR
2	0.66	0.93	1.3	SEQ ID NO: 1373	LWAWESWR
1	0.66	0.97	1.4	SEQ ID NO: 1374	NQMILFG EEDVR
2	0.68	0.98	1.4	SEQ ID NO: 1375	QLRPLYEEYVVLK
1	0.6	0.88	1.3	SEQ ID NO: 1376	WSAFLK

SEQ ID NO: 1377

1MS S S S W L L L S L V A V T A A Q S T I E E Q A K T F L D K F N H E A E D L F Y
Q S S L A S W N Y N T N I T E E N V Q N M N N A G D K W S A F L K E Q S T L A

81QMYPLQEIQNLTVK LQLQALQQNGSSVLS EDKSKRLNTIL
NTMSTIYSTGKVCNP DNPQECLLLEPGLNEIMANSLDYNE

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161R L W A W E S W R S E V G K Q L R P L Y E E Y V V L K N E M A R A N H Y E D
Y G D Y W R G D Y E V N G V D G Y D Y S R G Q L I E D V E H T F E E I K P L Y E H L

241H A Y V R A K L M N A Y P S Y I S P I G C L P A H L L G D M W G R F W T N L Y
S L T V P F G Q K P N I D V T D A M V D Q A W D A Q R I F K E A E K F F V S V G L

321P N M T Q G F W E N S M L T D P G N V Q K A V C H P T A W D L G K G D F R I
L M C T K V T M D D F L T A H H E M G H I Q Y D M A Y A A Q P F L L R N G A N E
G F

401H E A V G E I M S L S A A T P K H L K S I G L L S P D F Q E D N E T E I N F L L K
Q A L T I V G T L P F T Y M L E K W R W M V F K G E I P K D Q W M K K W W E M

481K R E I V G V V E P V P H D E T Y C D P A S L F H V S N D Y S F I R Y Y T R T L
Y Q F Q F Q E A L C Q A A K H E G P L H K C D I S N S T E A G Q K L F N M L R L

561G K S E P W T L A L E N V V G A K N M N V R P L L N Y F E P L F T W L K D Q
N K N S F V G W S T D W S P Y A D Q S I K V R I S L K S A L G D K A Y E W N D N E M

641Y L F R S S V A Y A M R Q Y F L K V K N Q M I L F G E E D V R V A N L K P R I
S F N F F V T A P K N V S D I I P R T E V E K A I R M S R S R I N D A F R L N D N

721S L E F L G I Q P T L G P P N Q P P V S I W L I V F G V V M G V I V V G I V I L I F
T G I R D R K K K N K A R S G E N P Y A S I D I S K G E N N P G F Q N T D D

801V Q T S F

5.247 aquaporin 1 [*Homo sapiens*]
Protein Accession gi|37694062

Associated Peptides 3

Mean Expression Ratio 1.07

Associated Spectra 10

Median Expression Ratio 1.07

Coverage 0.145

Credible Interval (0.791, 1.44)

[0365]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.75	1.1	1.6	SEQ ID NO: 1378	DLGGSAPLAIGLSVALGHL
1	0.71	1.1	1.5	SEQ ID NO: 1379	TSGQVEEYDL DADDINSR
8	0.83	1.1	1.4	SEQ ID NO: 1380	VWTSGQVEEYDL DADDINSR
SEQ ID NO: 1381					
1MASEFKKKLFWRVVAEFLATTLFVFISIGSALGFKYPVGN					
NQTA VQDNV KVS LAFGLS IATLAQSVGHISGAHLNPAVT					
81LGLLLSCQISIFRALMVIIAQCVGAIVATAILSGITSSSLTGN					
SLGRNDLADGVNSGQGLGIEIIGTLQLVLCVLATTD RR					
161RRDLGGSAPLAIGLSVALGHL LAIDYTGCGINPARSFGSA					
VITHNFSNHWIFWVGPF IGGALAVLIYDFILAPRSSDLTD					
241RVKVWTS GQVEEYDL DADDINSRVEMKPK					

5.248 secretoglobin, family 1A, member 1 (uteroglobin)
[*Homo sapiens*]
Protein Accession gi|4507809
Mean Expression Ratio 0.938
Median Expression Ratio 0.939
Credible Interval (0.586, 1.51)
Associated Peptides 1
Associated Spectra 1
Coverage 0.11
[0366]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.56	0.92	1.5	SEQ ID NO: 1382	LVDTLPQKPR

SEQ ID NO: 1383

1 M K L A V T L T L V T L A L C C S S A S A E I C P S F Q R V I E T L L M D T P S S Y
E A A M E L F S P D Q D M R E A G A Q L K K L V D T L P Q K P R E S I I K L

81 M E K I A Q S S L C N

5.249 structural maintenance of chromosomes 2 [*Homo sapiens*]; structural maintenance of chromosomes 2 [*Homo sapiens*]; structural maintenance of chromosomes 2 [*Homo sapiens*]
Protein Accession gi 110347425 gi 110347420
gil110347418
Mean Expression Ratio 1.06
Median Expression Ratio 1.06
Credible Interval (0.654, 1.72)
Associated Peptides 1
Associated Spectra 1
Coverage NaN

[0367]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.64	1.1	1.8	SEQ ID NO: 1384	LGRNVNMRAMNVLTEAER

5.250 superoxide dismutase 1, soluble [*Homo sapiens*]
Protein Accession gi|4507149
Mean Expression Ratio 1.07
Median Expression Ratio 1.06
Credible Interval (0.661, 1.73)
Associated Peptides 1
Associated Spectra 1
Coverage 0.091
[0368]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.1	1.8	SEQ ID NO: 1385	GDGPVQGIINFEQK

SEQ ID NO: 1386

1 M A T K A V C V L K G D G P V Q G I I N F E Q K E S N G P V K V W G S I K G L T
E G L H G F H V H E F G D N T A G C T S A G P H F N P L S R K H G G P K D E E R

81 H V G D L G N V T A D K D G V A D V S I E D S V I S L S G D H C I I G R T L V V
H E K A D D L G K G G N E E S T K T G N A G S R L A C G V I G I A Q

5.251 phospholipid scramblase 1 [*Homo sapiens*]
Protein Accession gi|10863877

Mean Expression Ratio 1.06
Median Expression Ratio 1.06
Credible Interval (0.774, 1.46)

Associated Peptides 4
Associated Spectra 6

Coverage 0.170
[0369]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.72	1.1	1.6	SEQ ID NO: 1387	EAFTDADNFGIQFPLDLVK
3	0.76	1.1	1.5	SEQ ID NO: 1388	IIDNMGQEVITLER
1	0.71	1.0	1.5	SEQ ID NO: 1389	SGYPGPQVSYPFPPAGH
1	0.74	1.1	1.6	SEQ ID NO: 1390	IIDNMGQEVITLERPLR

SEQ ID NO: 1391

1M D K Q N S Q M N A S H P E T N L P V G Y P P Q Y P P T A F Q G P P G Y S G Y P
G P Q V S Y P P P P A G H S G P G P A G F P V P N Q P V Y N Q P V Y N Q P V G A

81A G V P W M P A P Q P P L N C P P G L E Y L S Q I D Q I L I H Q Q I E L L E V L T
G F E T N N K Y E I K N S F G Q R V Y F A A E D T D C C T R N C C G P S R P F

161T L R I I D N M G Q E V I T L E R P L R C S S C C C P C C L Q E I E I Q A P P G V
P I G Y V I Q T W H P C L P K F T I Q N E K R E D V L K I S G P C V V C S C C

241G D V D F E I K S L D E Q C V V G K I S K H W T G I L R E A F T D A D N F G I Q
F P L D L D V K M K A V M I G A C F L I D F M F F E S T G S Q E Q K S G V W

5.252 ATPase, H+ transporting, lysosomal V0 subunit al isoform c [*Homo sapiens*]; ATPase, H+ transporting, lysosomal V0 subunit al isoform b [*Homo sapiens*]; ATPase, H+ transporting, lysosomal V0 subunit al isoform a [*Homo sapiens*]

Protein Accession gi|19913418 gi|194097403 gi|194097401

Mean Expression Ratio 0.94
Median Expression Ratio 0.94
Credible Interval (0.663, 1.34)

Associated Peptides 4
Associated Spectra 4

Coverage NaN
[0370]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	0.94	1.4	SEQ ID NO: 1392	ANIPIMDTGENPEVPFPR
1	0.62	0.94	1.4	SEQ ID NO: 1393	ASLYPCPETPQER

-continued

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	0.92	1.4	SEQ ID NO: 1394	IDDLQMVLNQTEDHR
1	0.63	0.95	1.5	SEQ ID NO: 1395	KANIPIMDTGENPEVPFPR

5.253 solute carrier family 44, member 2 [*Homo sapiens*]
Protein Accession gi|31377727

Mean Expression Ratio 1.06
Median Expression Ratio 1.06
Credible Interval (0.646, 1.73)

Associated Peptides 1
Associated Spectra 1

Coverage 0.0227

[0371]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.1	1.8	SEQ ID NO: 1396	DGDCPAVLIPSKPLAR
SEQ ID NO: 1397					
1M G D E R P H Y Y G K H G T P Q K Y D P T F K G P I Y N R G C T D I I C C V F L L L A I V G Y V A V G I I A W T H G D P R K V I Y P T D S R G E F C G Q K G T K					
81N E N K P Y L F V F N I V K C A S P L V L L E F Q C P T P Q I C V E K C P D R Y L T Y L N A R S S R D F E Y Y K Q F C V P G F K N N K G V A E V L R D G D C P A					
161V L I P S K P L A R R C F P A I H A Y K G V L M V G N E T T Y E D G H G S R K N I T D L V E G A K K A N G V L E A R Q L A M R I F E D Y T V S W Y W I I I G L V					
241I A M A M S L L F I I L L R F L A G I M V W V M I I M V I L V L G Y G I F H C Y M E Y S R L R G E A G S D V S L V D L G F Q T D F R V Y L H L R Q T W L A F M I					
321I L S I L E V I I I L L L I F L R K R I L I A I A L I K E A S R A V G Y V M C S L L Y P L V T F F L L C L C I A Y W A S T A V F L S T S N E A V Y K I F D D S P					
401C P F T A K T C N P E T F P S S N E S R Q C P N A R C Q F A F Y G G E S G Y H R A L L G L Q I F N A F M F F W L A N F V L A L G Q V T L A G A F A S Y Y W A L R					
481K P D D L P A F P L F S A F G R A L R Y H T G S L A F G A L I L A I V Q I I R V I L E Y L D Q R L K A A E N K F A K C L M T C L K C C F W C L E K F I K F L N R					
561N A Y I M I A I Y G T N F C T S A R N A F F L L M R N I I R V A V L D K V T D F L F L L G K L L I V G S V G I L A F F F F T H R I R I V Q D T A P P L N Y Y W V					
641P I L T V I V G S Y L I A H G F F S V Y G M C V D T L F L C F L E D L E R N D G S A E R P Y F M S S T L K K P L N K T N K K A A E S					

5.254 guanine nucleotide binding protein (G protein), alpha
inhibiting activity polypeptide 3 [*Homo sapiens*]
Protein Accession gil5729850

Credible Interval (0.702, 1.63)

Associated Peptides 2

Associated Spectra 2

Mean Expression Ratio 1.07

Coverage 0.0763

Median Expression Ratio 1.06

[0372]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.66	1.1	1.7	SEQ ID NO: 1398	ISQSNYIPTQQDVLRL
1	0.68	1.1	1.7	SEQ ID NO: 1399	SNTIQSIIAIIR
SEQ ID NO: 1400					
1M G C T L S A E D K A A V E R S K M I D R N L R E D G E K A A K E V K L L L L G A G E S G K S T I V K Q M K I I H E D G Y S E D E C K Q Y K V V V Y S N T I Q S					
81I I A I I R A M G R L K I D F G E A A R A D D A R Q L F V L A G S A E E G V M T P E L A G V I K R L W R D G G V Q A C F S R S R E Y Q L N D S A S Y Y L N D L D					
161R I S Q S N Y I P T Q Q D V L R T R V K T T G I V E T H F T F K D L Y F K M F D V G G Q R S E R K K W I H C F E G V T A I I F C V A L S D Y D L V L A E D E E M					
241N R M H E S M K L F D S I C N N K W F T E T S I I L F L N K K D L F E E K I K R S P L T I C Y P E Y T G S N T Y E E A A Y I Q C Q F E D L N R R K D T K E I Y					
321T H F T C A T D T K N V Q F V F D A V T D V I I K N N L K E C G L Y					

5.255 PREDICTED: hypothetical protein [*Homo sapiens*]

[0373]

Protein Accession gi|1169217813

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.69	1.1	1.7	SEQ ID NO: 1401	YNRITLNNDIMLIK

Mean Expression Ratio 1.06

Median Expression Ratio 1.06

Credible Interval (0.685, 1.62)

Associated Peptides 1

Associated Spectra 2

Coverage NaN

5.256 dipeptidyl peptidase 7 preproprotein [*Homo sapiens*]
Protein Accession gi|62420888

Mean Expression Ratio 0.94
Median Expression Ratio 0.943
Credible Interval (0.655, 1.34)

Associated Peptides 2

Associated Spectra 4

Coverage 0.065

[0374]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.63	0.92	1.3	SEQ ID NO: 1402	GHTELLTVEQALADFAELLR
1	0.62	0.95	1.4	SEQ ID NO: 1403	DLFLQGAYDTVR

SEQ ID NO: 1404

1M G S A P W A P V L L L A L G L R G L Q A G A R R A P D P G F Q E R F F Q Q R L
D H F N F E R F G N K T F P Q R F L V S D R F W V R G E G P I F F Y T G N E G D

81V W A F A N N S A F V A E L A A E R G A L L V F A E H R Y Y G K S L P F G A Q
S T Q R G H T E L L T V E Q A L A D F A E L L R A L R R D L G A Q D A P A I A F G

161G S Y G G M L S A Y L R M K Y P H L V A G A L A A S A P V L A V A G L G D S
N Q F F R D V T A D F E G Q S P K C T Q G V R E A F R Q I K D L F L Q G A Y D T V R

241W E F G T C Q P L S D E K D L T Q L F M F A R N A F T V L A M M D Y P Y P T D
F L G P L P A N P V K V G C D R L L S E A Q R I T G L R A L A G L V Y N A S G S E

321H C Y D I Y R L Y H S C A D P T G C G T G P D A R A W D Y Q A C T E I N L T F
A S N N V T D M F P D L P F T D E L R Q R Y C L D T W G V W P R P D W L L T S F W

401G G D L R A A S N I I F S N G N L D P W A G G G I R R N L S A S V I A V T I Q G
G A H H L D L R A S H P E D P A S V V E A R K L E A T I I G E W V K A A R R E Q

481Q P A L R G G P R L S L

5.257 tropomyosin 4 [*Homo sapiens*]
Protein Accession gi|4507651

Mean Expression Ratio 1.06
Median Expression Ratio 1.06
Credible Interval (0.66, 1.71)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0403

[0375]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.1	1.8	SEQ ID NO: 1405	IQLVEEELDR

SEQ ID NO: 1406

1 M A G L N S L E A V K R K I Q A L Q Q Q A D E A E D R A Q G L Q R E L D G E R E
R R E K A E G D V A A L N R R I Q L V E E E L D R A Q E R L A T A L Q K L E E A

-continued

81	E	K	A	A	D	E	S	E	R	G	M	K	V	I	E	N	R	A	M	K	D	E	E	K	M	E	I	Q	E	M	Q	L	K	E	A	K	H	I	A		
	E	E	A	D	R	K	Y	E	E	V	A	R	K	L	V	I	L	E	G	E	L	E	R	A	E	E	R	A	E	V	S	E	L	K	C	G	D	L	E	E	E
161	L	K	N	V	T	N	N	L	K	S	L	E	A	A	S	E	K	Y	S	E	K	E	D	K	Y	E	E	E	I	K	L	L	S	D	K	L	K	E	A	E	
	T	R	A	E	F	A	E	R	T	V	A	K	L	E	K	T	I	D	D	L	E	E	K	L	A	Q	A	K	E	E	N	V	G	L	H	Q	T	L	D	Q	
241	T	L	N	E	L	N	C	I																																	

5.258 keratin 10 [*Homo sapiens*]
Protein Accession gi|195972866

Mean Expression Ratio 0.945

Median Expression Ratio 0.944

Credible Interval (0.663, 1.35)

Associated Peptides 3

Associated Spectra 4

Coverage NaN

[0376]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.65	0.95	1.4	SEQ ID NO: 1407	NQILNLTTDNANILLQIDNAR

-continued

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	0.92	1.4	SEQ ID NO: 1408	SQYEQLAEQNRK
1	0.63	0.95	1.4	SEQ ID NO: 1409	SQYEQLAEQNR

5.259 myosin VI [*Homo sapiens*]
Protein Accession gi|92859701

Mean Expression Ratio 1.05

Median Expression Ratio 1.06

Credible Interval (0.647, 1.72)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0101

[0377]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.64	1.1	1.8	SEQ ID NO: 1410	LVGILDILDEENR

SEQ ID NO: 1411
1 M E D G K P V W A P H P T D G F Q M G N I V D I G P D S L T I E P L N Q K G K T
F L A L I N Q V F P A E E D S K K D V E D N C S L M Y L N E A T L L H N I K V R
81 Y S K D R I Y T Y V A N I L I A V N P Y F D I P K I Y S S E A I K S Y Q G K S L G T
R P P H V F A I A D K A F R D M K V L K M S Q S I I V S G E S G A G K T E N
161 T K F V L R Y L T E S Y G T G Q D I D D R I V E A N P L L E A F G N A K T V R N
N N S S R F G K F V E I H F N E K S S V V G G F V S H Y L L E K S R I C V Q G K
241 E E R N Y H I F Y R L C A G A S E D I R E K L H L S S P D N F R Y L N R G C T R
Y F A N K E T D K Q I L Q N R K S P E Y L K A G S M K D P L L D D H G D F I R M
321 C T A M K K I G L D D E E K L D L F R V V A G V L H L G N I D F E E A G S T S
G G C N L K N K S A Q S L E Y C A E L L G L D Q D D L R V S L T T R V M L T T A G
401 G T K G T V I K V P L K V E Q A N N A R D A L A K T V Y S H L F D H V V N R
V N Q C F P F E T S S Y F I G V L D I A G F E Y F E H N S F E Q F C I N Y C N E K L
481 Q Q F F N E R I L K E E Q E L Y Q K E G L G V N E V H Y V D N Q D C I D L I E A
K L V G I L D I L D E E N R L P Q P S D Q H F T S A V H Q K H K D H F R L T I P
561 R K S K L A V H R N I R D D E G F I I R H F A G A V C Y E T T Q F V E K N N D A
L H M S L E S L I C E S R D K F I R E L F E S S T N N N K D T K Q K A G K L S F
641 I S V G N K F K T Q L N L L L D K L R S T G A S F I R C I K P N L K M T S H H F
E G A Q I L S Q L Q C S G M V S V L D L M Q G G Y P S R A S F H E L Y N M Y K K
721 Y M P D K L A R L D P R L F C K A L F K A L G L N E N D Y K F G L T K V F F R
P G K F A E F D Q I M K S D P D H L A E L V K R V N H W L T C S R W K K V Q W C S

-continued

801	L S V I K L K N K I K Y R A E A C I K M Q K T I R M W L C K R R H K P R I D G L
	V K V G T L K K R L D K F N E V V S V L K D G K P E M N K Q I K N L E I S I D T
881	L M A K I K S T M M T Q E Q I Q K E Y D A L V K S S E E L L S A L Q K K K Q Q
	E E E A E R L R R I Q E E M E K E R K R R E E D E K R R R K E E E E R R M K L E M
961	E A K R K Q E E E E R K K R E D D E K R I Q A E V E A Q L A R Q K E E E S Q Q
	Q A V L E Q E R R D R E L A L R I A Q S E A E L I S D E A Q A D L A L R R N D G T
1041	R P K M T P E Q M A K E M S E F L S R G P A V L A T K A A A G T K K Y D L S
	K W K Y A E L R D T I N T S C D I E L L A A C R E E F H R R L K V Y H A W K S K N K
1121	K R N T E T E Q R A P K S V T D Y D F A P F L N N S P Q Q N P A A Q I P A R Q
	R E I E M N R Q Q R F F R I P F I R P A D Q Y K D P Q S K K K G W W Y A H F D G P
1201	W I A R Q M E L H P D K P P I L L V A G K D D M E M C E L N L E E T G L T R
	K R G A E I L P R Q F E E I W E R C G G I Q Y L Q N A I E S R Q A R P T Y A T A M L
1281	Q S L L K

5.260 heat shock protein 90 kDa alpha (cytosolic), class A member 1 isoform 1 [*Homo sapiens*]
Protein Accession gil153792590

Mean Expression Ratio 1.06

Median Expression Ratio 1.06

Credible Interval (0.65, 1.72)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0176

[0378]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.1	1.8	SEQ ID NO: 1412	HLEINPDHSIIETLR

SEQ ID NO: 1413

1M P P C S G G D G S T P P G P S L R D R D C P A Q S A E Y P R D R L D P R P G S P
S E A S S P P F L R S R A P V N W Y Q E K A Q V F L W H L M V S G S T T L L C

81L W K Q P F H V S A F P V T A S L A F R Q S Q G A G Q H L Y K D L Q P F I L L R
L L M P E E T Q T Q D Q P M E E E E V E T F A F Q A E I A Q L M S L I I N T F Y

161S N K E I F L R E L I S N S S D A L D K I R Y E S L T D P S K L D S G K E L H I N
L I P N K Q D R T L T I V D T G I G M T K A D L I N N L G T I A K S G T K A F

241M E A L Q A G A D I S M I G Q F G V G F Y S A Y L V A E K V T V I T K H N D D
E Q Y A W E S S A G G S F T V R T D T G E P M G R G T K V I L H L K E D Q T E Y L

321E E R R I K E I V K K H S Q F I G Y P I T L F V E K E R D K E V S D D E A E E K E
D K E E E K E K E E K E S E D K P E I E D V G S D E E E E K K D G D K K K K K

401K I K E K V I D Q E E L N K T K P I W T R N P D D I T N E E Y G E F Y K S L T N
D W E D H L A V K H F S V E G Q L E F R A L L F V P R R A P F D L F E N R K K K

481N N I K L Y V R R V F I M D N C E E L I P E Y L N F I R G V V D S E D L P L N I S
R E M L Q Q S K I L K V I R K N L V K K C L E L F T E L A E D K E N Y K K F Y

561E Q F S K N I K L G I H E D S Q N R K K L S E L L R Y Y T S A S G D E M V S L K
D Y C T R M K E N Q K H I Y Y I T G E T K D Q V A N S A F V E R L R K H G L E V

-continued

641	I	Y	M	I	E	P	I	D	E	Y	C	V	Q	Q	L	K	E	F	E	G	K	T	L	V	S	V	T	K	E	G	L	E	L	P	E	D	E	E	E	K		
	K	K	Q	E	E	K	K	T	K	F	E	N	L	C	K	I	M	K	D	I	L	E	K	K	V	E	K	V	V	V	S	N	R	L	V	T	S	P	C	C		
721	I	V	T	S	T	Y	G	W	T	A	N	M	E	R	I	M	K	A	Q	A	L	R	D	N	S	T	M	G	Y	M	A	A	K	K	H	L	E	I				
	N	P	D	H	S	I	I	E	T	L	R	Q	K	A	E	A	D	K	N	D	K	S	V	K	D	L	V	I	L	L	Y	E	T	A	L	L	S	S	G	F	S	L
801	E	D	P	Q	T	H	A	N	R	I	Y	R	M	I	K	L	G	L	G	I	D	E	D	D	P	T	A	D	D	T	S	A	A	V	T	E	E	M	P	P		
	L	E	G	D	D	D	T	S	R	M	E	E	V	D																												

5.261 RAB1A, member RAS oncogene family isoform 1
[*Homo sapiens*]; RAB1B, member RAS oncogene family
[*Homo sapiens*]
Protein Accession gil4758988 gi 13569962

Mean Expression Ratio 1.06
Median Expression Ratio 1.06
Credible Interval (0.65, 1.70)
Associated Peptides 1
Associated Spectra 1
Coverage NaN

[0379]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.64	1.1	1.8	SEQ ID NO: 1414		EFADSLGIPFLETSK

5.262 villin 1 [*Homo sapiens*]
Protein Accession gil194394237

Mean Expression Ratio 1.05
Median Expression Ratio 1.05
Credible Interval (0.685, 1.62)
Associated Peptides 2
Associated Spectra 2
Coverage NaN

[0380]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.65	1.0	1.7	SEQ ID NO: 1415		LMEVMNHVLGK
1	0.66	1.1	1.7	SEQ ID NO: 1416		LQEENLVITPR

5.263 PREDICTED: similar to hCG1992647, partial [*Homo sapiens*]
Protein Accession gil169217452

Mean Expression Ratio 0.95
Median Expression Ratio 0.95
Credible Interval (0.604, 1.47)
Associated Peptides 1
Associated Spectra 2

Coverage NaN

[0381]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.6	0.94	1.5	SEQ ID NO: 1417		AVTELGRPDAEYWNSQK

5.264 aldehyde dehydrogenase 1A1 [*Homo sapiens*]
Protein Accession gil21361176

Mean Expression Ratio 1.05
Median Expression Ratio 1.05
Credible Interval (0.723, 1.55)

Associated Peptides 2
Associated Spectra 3

Coverage 0.0439

[0382]

A	2.5	50	97.5	Sequence	ID No.	Sequence
2	0.7	1.0	1.6	SEQ ID NO: 1418		IFVEESIYDEFVR
1	0.69	1.1	1.7	SEQ ID NO: 1419		ILDLIESGK

-continued

SEQ ID NO: 1420
1MSSSGT PDL PVL L TDL KIQYTKIFINNEWHD S VSGKKFPVF
NPATEEEELCQVEEGDKEDVDKAVKAARQAFQIGSPWRMTM

81DASERGRLLYKLLADLIERDRLLLATMESMNGGKLYSNAY
LNDLAGCICKTLRYCAGWADKIQGRTIPIIDGNFFT YTRHEPI

161GVCGQIIPWNFPPLVMLIWKIGPALSCGNTVVVKPAEQTPL
TALHVASLIKEAGFPFGVVNI VPGYGPTAGAAISSHMDID

241KVAF TGST EVGKLIK EAAAGKSNLKRVTLELG GKS PCIVLA
DADLDNAVEFAHHGVFYHQGCCIAASRI FVEESIYDEFV

321RRSVERAKKYILGNPLTPGV TQGPQIDKEQYDKILDLIES
GKKEGAKLECGGGPWGNKG YFVQPTVF SNVTDEMRIA KEE

401IFGPVQQIMKFKSLDDVIKRANNTFYGLSAGVFTKDI DKA
ITISSALQAGTVWVNCYGVVSAQC PFGGFKMSGNGRELGE

481YGFHEYTEVKT VTVKISQKNS

5.265 phosphoglycerate kinase 1 [*Homo sapiens*]
Protein Accession gi|4505763

Mean Expression Ratio 1.05

Median Expression Ratio 1.05

Credible Interval (0.758, 1.47)

Associated Peptides 4

Associated Spectra 5

Coverage 0.161

[0383]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.72	1.0	1.5	SEQ ID NO: 1421	ACANPAAGSVILLENLR
1	0.72	1.1	1.6	SEQ ID NO: 1422	ALESPERPFLAILGGAK
1	0.74	1.1	1.6	SEQ ID NO: 1423	ITLPVDFVTADKFDENAK
1	0.68	1.0	1.5	SEQ ID NO: 1424	LGDVYVNDAPGTAHR

SEQ ID NO: 1425

1MSLSNKL TLDKLDVKGKRVVMRVDFNVPMKNNQITNNQRI
KAAVPSIKFCLDNGAKSVVLM SHLGRPDGVPMPDKYSLEP

81VAVELKSL LGKDVLFLKDCVGPEVEKACANPAAGSVILLE
NLRPHVEEEGKGKDASGNKVKAEPAKIEAFRASLSKLGDV

161YVNDAFGT AHRHSSMVGVNLPQKAGGFLMKKELNYFA
KALESERPFLAILGGAKVADKIQLINNMLDKVNEMIIGGGM

241AFTFLKVLNNMEIGTSLFDEEGAKIVKDLMSKAEKNGVKI
TLPVDFVTADKFDENAKTGQATVASGIPAGWMGLDCGPES

321SKKYAEAVTRAKQIVWNGPVG VFEWEAFARGTKALMDE
VVKATSRGCITIIIGGGDTATCCA KWNTEDKVS HVSTGGGASL

401ELLEGKVLPGVDALSN I

5.266 eukaryotic translation initiation factor 5A isoform A [*Homo sapiens*]

Protein Accession gi|219555707

Mean Expression Ratio 1.05

Median Expression Ratio 1.05

Credible Interval (0.636, 1.73)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0384]

		Sequence				Sequence	
A	2.5	50	97.5	ID No.		Sequence	
1	0.65	1.1	1.8	SEQ ID NO: 1426		NDFQLIGIQDGYLSLLQDSGEVR	

5.267 heat shock 70 kDa protein 1A [*Homo sapiens*]; heat shock 70 kDa protein 1B [*Homo sapiens*]

Protein Accession gi 194248072 gi|167466173

Mean Expression Ratio 1.05

Median Expression Ratio 1.05

Credible Interval (0.861, 1.29)

Associated Peptides 12

Associated Spectra 21

Coverage NaN

[0385]

		Sequence				Sequence	
A	2.5	50	97.5	ID No.		Sequence	
2	0.74	1.0	1.4	SEQ ID NO: 1427		AQIHDLVLVGGSTR	
2	0.77	1.1	1.4	SEQ ID NO: 1428		ATAGDTHLGGEDFDNR	
1	0.74	1.0	1.4	SEQ ID NO: 1429		AVITVPAYFNDSQR	
2	0.79	1.1	1.4	SEQ ID NO: 1430		EIAEAYLGYPVTNAVITVP AYFNDSQR	
3	0.78	1.1	1.4	SEQ ID NO: 1431		FEELCSDLFR	
1	0.76	1.1	1.5	SEQ ID NO: 1432		FELSGIPPAPR	
1	0.77	1.1	1.5	SEQ ID NO: 1433		HWPFQVINDGDKPK	

-continued

		Sequence				Sequence	
A	2.5	50	97.5	ID No.		Sequence	
3	0.77	1.0	1.4	SEQ ID NO: 1434		LLQDFFNGR	
3	0.78	1.0	1.4	SEQ ID NO: 1435		LVNHFVVEEFK	
1	0.79	1.1	1.5	SEQ ID NO: 1436		LVNHFVVEEFKR	
1	0.75	1.0	1.4	SEQ ID NO: 1437		NQVALNPQNTVFDAK	
1	0.77	1.1	1.5	SEQ ID NO: 1438		QTQIFTTYSQNPQGVLIQV YEGER	

5.268 hypothetical protein LOC126321 isoform b [*Homo sapiens*]; hypothetical protein LOC126321 isoform c [*Homo sapiens*]; hypothetical protein LOC126321 isoform a [*Homo sapiens*]

Protein Accession gi|111378395 gi|111378391
gi|111378386

Mean Expression Ratio 0.954

Median Expression Ratio 0.952

Credible Interval (0.647, 1.41)

Associated Peptides 2

Associated Spectra 3

Coverage NaN

[0386]

		Sequence				Sequence	
A	2.5	50	97.5	ID No.		Sequence	
1	0.62	0.96	1.5	SEQ ID NO: 1439		GPGPPAAGAAPSFR	
2	0.63	0.94	1.4	SEQ ID NO: 1440		VEPTQDISISDQLGGQD VPVFR	

5.269 PDZK1 interacting protein 1 [*Homo sapiens*]

Protein Accession gi|5031657

Mean Expression Ratio 0.954

Median Expression Ratio 0.954

Credible Interval (0.637, 1.43)

Associated Peptides 1

Associated Spectra 3

Coverage 0.149

[0387]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.64	0.94	1.4	SEQ ID NO: 1441	SSEHENAYENVPEEGK

SEQ ID NO: 1442

1 M S A L S L L I L G L L T A V P P A S C Q Q G L G N L Q P W M Q G L I A V A V F
L V L V A I A F A V N H F W C Q E E P E P A H M I L T V G N K A D G V L V G T D

81 G R Y S S M A A S F R S S E H E N A Y E N V P E E E G K V R S T P M

5.270 hexosaminidase A preproprotein [*Homo sapiens*]
Protein Accession gil189181666

Mean Expression Ratio 0.954

Median Expression Ratio 0.954

Credible Interval (0.589, 1.53)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0388]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.95	1.6	SEQ ID NO: 1443	IQPDTHIQVWR

5.271 paralemmin isoform 1 [*Homo sapiens*]

Protein Accession gil93141031

Mean Expression Ratio 1.05

Median Expression Ratio 1.05

Credible Interval (0.637, 1.73)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0491

[0389]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	1.1	1.8	SEQ ID NO: 1444	EPAPPNGSAAEPPTAAASR

SEQ ID NO: 1445

1 M E V L A A E T T S Q Q E R L Q A I A E K R K R Q A E I E N K R R Q L E D E R R
Q L Q H L K S K A L R E R W L L E G T P S S A S E G D E D L R R Q M Q D D E Q K

81 T R L L E D S V S R L E K E I E V L E R G D S A P A T A K E N A A A P S P V R A P
A P S P A K E E R K T E V V M N S Q Q T P V G T P K D K R V S N T P L R T V D

161 G S P M M K A A M Y S V E I T V E K D K V T G E T R V L S S T T L L P R Q P L
P L G I K V Y E D E T K V V H A V D G T A E N G I H P L S S S E V D E L I H K A D

241 E V T L S E A G S T A G A A E T R G A V E G A A R T T P S R R E I T G V Q A Q P
G E A T S G P P G I Q P G Q E P P V T M I F M G Y Q N V E D E A E T K K V L G L

321 Q D T I T A E L V V I E D A A E P K E P A P P N G S A A E P P T E A A S R E E N
Q A G P E A T T S D P Q D L D M K K H R C K C C S I M

5.272 mannosidase, alpha, class 2B, member 2 [*Homo sapiens*]
Protein Accession gi|50659093

Mean Expression Ratio 1.04

Median Expression Ratio 1.05

Credible Interval (0.676, 1.62)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0238

[0390]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.66	1.1	1.7	SEQ ID NO: 1446	FIAVEQEFFR
1	0.65	1.0	1.7	SEQ ID NO: 1447	IEQEYQAGPLELNR

SEQ ID NO: 1448

1M G Q L C W L P L L A P L L L R P P G V Q S A G P I R A F V V P H S H M D V G
W V Y T V Q E S M R A Y A A N V Y T S V V E E L A R G Q Q R R F I A V E Q E F F

81R L W W D G V A S D Q Q K Y Q V R Q L L E E G R L E F V I G G Q V M H D E A
V T H L D D Q I L Q L T E G H G F L Y E T F G I R P Q F S W H V D P F G A S A T T P

161T L F A L A G F N A H L G S R I D Y D L K A A M Q E A R G L Q F V W R G S P S
L S E R Q E I F T H I M D Q Y S Y C T P S H I P F S N R S G F Y W N G V A V F P K

241P P Q D G V Y P N M S E P V T P A N I N L Y A E A L V A N V K Q R A A W F R T
P H V L W P W G C D K Q F F N A S V Q F A N M D P L L D H I N S H A A E L G V S V

321Q Y A T L G D Y F R A L H A L N V T W R V R D H H D F L P Y S T E P F Q A W
T G F Y T S R S S L K G L A R R A S A L L Y A G E S M F T R Y L W P A P R G H L D P

401T W A L Q Q L Q Q L R W A V S E V Q H H D A I T G T E S P K V R D M Y A T H
L A S G M L G M R K L M A S I V L D E L Q P Q A P M A A S S D A G P A G H F A S
V Y

481N P L A W T V T T I V T L T V G F P G V R V T D E A G H P V P S Q I Q N S T E T
P S A Y D L L I L T T I P G L S Y R H Y N I R P T A G A Q E G T Q E P A A T V A

561S T L Q F G R R L R R R T S H A G R Y L V P V A N D C Y I V L L D Q D T N L M
H S I W E R Q S N R T V R V T Q E F L E Y H V N G D V K Q G P I S D N Y L F T P G

641K A A V P A W E A V E M E I V A G Q L V T E I R Q Y F Y R N M T A Q N Y T Y
A I R S R L T H V P Q G H D G E L L C H R I E Q E Y Q A G P L E L N R E A V L R T S

721T N L N S Q Q V I Y S D N N G Y Q M Q R R P Y V S Y V N N S I A R N Y Y P M V
Q S A F M E D G K S R L V L L S E R A H G I S S Q G N G Q V E V M L H R R L W N N

801F D W D L G Y N L T L N D T S V V H P V L W L L L G S W S L T T A L R Q R S A
L A L Q H R P V V L F G D L A G T A P K L P G P Q Q Q E A V T L P P N L H L Q I L

881S I P G W R Y S S N H T E H S Q N L R K G H R G E A Q A D L R R V L L R L Y H
L Y E V G E D P V L S Q P V T V N L E A V L Q A L G S V V A V E E R S L T G T W D

961L S M L H R W S W R T G P G R H R G D T T S P S R P P G G P I I T V H P K E I R
T F F I H F Q Q Q

[0391]

A	2.5	50	97.5	Sequence	ID No.	Sequence
1	0.65	1.1	1.7	SEQ	ID NO: 1449	DLISNNEQLPMLGFR
1	0.66	1.1	1.7	SEQ	ID NO: 1450	RPGAPESK

5.274 dipeptidylpeptidase IV [*Homo sapiens*]Protein Accession [gi|18765694](#)

Mean Expression Ratio 0.958

Median Expression Ratio 0.957

Credible Interval (0.749, 1.22)

Associated Peptides 9

Associated Spectra 12

Coverage 0.141

[0392]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.68	0.96	1.4	SEQ ID NO: 1451	CGIAVAPVSR
1	0.71	0.98	1.4	SEQ ID NO: 1452	FRPSEPHTLDGNSFYK
1	0.66	0.94	1.3	SEQ ID NO: 1453	ISLQWLR
2	0.63	0.87	1.2	SEQ ID NO: 1454	LGTFEVEDQIEAAR
1	0.67	0.95	1.4	SEQ ID NO: 1455	SFYSDSLQYPK
1	0.7	0.98	1.4	SEQ ID NO: 1456	VWNNDIYVK
1	0.68	0.97	1.4	SEQ ID NO: 1457	WEYYDSVYTER
2	0.71	0.99	1.4	SEQ ID NO: 1458	YMGLPTPEDNLDHYR
2	0.7	0.97	1.3	SEQ ID NO: 1459	FWYQMILPPHFDK

SEO ID NO: 1460

SEQ ID NO: 1400

1M K T P W K V V L L G L L G A A A L V T I I T V P V V L L N K G T D D A T A D S R
K T Y T L T D Y L K N T Y R L K L Y S L R W I S D H E Y L Y K Q E N N I L V F N

81A E Y G N S S V F L E N S T F D E F G H S I N D Y S I S P D G Q F I L L E Y N Y V
K Q W R H S Y T A S Y D I Y D L N K R Q L I T E E R I P N N T Q W V T W S P V

161G H K L A Y V W N N D I Y V K I E P N L P S Y R I T W T G K E D I I Y N G I T D
W V Y E E E V F S A Y S A L W W S P N G T F L A Y A Q F N D T E V P L I E Y S F

241Y S D E S L Q Y P K T V R V P Y P K A G A V N P T V K K F F V V N T D S L S S V
T N A T S I Q I T A P A S M L I G D H Y L C D V T W A T Q E R I S L Q W L R R I Q

321N Y S V M D I C D Y D E S S G R W N C L V A R Q H I E M S T T G W V G R F R P
S E P H F T L D G N S F Y K I I S N E E G Y R H I C Y F Q I D K K D C T F I T K G

401T W E V I G I E A L T S D Y L Y I S N E Y K G M P G G R N L Y K I Q L S D Y T
K V T C L S C E L N P E R C Q Y Y S V S F S K E A K Y Y Q L R C S G P G L P L Y

481T L H S S V N D K G L R V L E D N S A L D K M L Q N V Q M P S K K L D F I I L
N E T K F W Y Q M I L P P H F D K S K K Y P L L L D V Y A G P C S Q K A D T V F R

561L N W A T Y L A S T E N I I V A S F D G R G S G Y Q G D K I M H A I N R R L G T
F E V E D Q I E A A R Q F S K M G F V D N K R I A I W G W S Y G G Y V T S M V L

641G S G S G V F K C G I A V A P V S R W E Y Y D S V Y T E R Y M G L P T P E D N
L D H Y R N S T V M S R A E N F K Q V E Y L L I H G T A D D N V H F Q Q S A Q I S

721K A L V D V G V D F Q A M W Y T D E D H G I A S S T A H Q H I Y T H M S H F I
K O C F S I P

5.275 lipocalin 2 [*Homo sapiens*]
Protein Accession gi|38455402
Mean Expression Ratio 0.955
Median Expression Ratio 0.959
Credible Interval (0.658, 1.37)
Associated Peptides 3
Associated Spectra 4
Coverage 0.247
[0393]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.63	0.93	1.4	SEQ ID NO: 1461	SLGLPENHIVFPVPIDQCIDG
1	0.64	0.96	1.5	SEQ ID NO: 1462	VPLQQNFQDNQFQ GK
1	0.63	0.97	1.5	SEQ ID NO: 1463	WYVVGLAGNAILR

SEQ ID NO: 1464

1M P L G L L W L G L A L L G A L H A Q A Q D S T S D L I P A P P L S K V P L Q Q
N F Q D N Q F Q G K W Y V V G L A G N A I L R E D K D P Q K M Y A T I Y E L K E

81D K S Y N V T S V L F R K K K C D Y W I R T F V P G C Q P G E F T L G N I K S Y
P G L T S Y L V R V V S T N Y N Q H A M V F F K K V S Q N R E Y F K I T L Y G R

161T K E L T S E L K E N F I R F S K S L G L P E N H I V F P V P I D Q C I D G

5.276 zinc finger protein 262 [*Homo sapiens*]
Protein Accession gi|44890068
Mean Expression Ratio 0.956
Median Expression Ratio 0.959
Credible Interval (0.585, 1.54)

Associated Peptides 1
Associated Spectra 1
Coverage 0.00904
[0394]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.95	1.6	SEQ ID NO: 1465	SSAEMIENTNSLGK

SEQ ID NO: 1466

1M A E R E V E S G P R K R F E Q K S G A V F D E I V E N C G G I M D T E M S E D I
D H N L T P T L D S M S Y G M P N Q T G S E N S L L D E D D Y F L N S G D L A

81G I P V V G S D N E D E Q D F S S K D N L V S S I H T D D S L E V E R R V T Q H
E S D N E N E I Q I Q N K L K K D F P K Q F D Q V S V F K S I R K D F S L V R E

161N S K E T F S G K E K N R D L T Y E R E K R L D K P H K D L D S R L K S S F F D
K A A N Q V E E T L H T H L P Q T P E T N F R D S S Y P F A N K E S I G S E L G

241N S F A S N I R I K E E P L D D E Y D K A M A P Q Q G L L D K I K D E P D N A Q
E Y S H G Q Q Q K T Q E G E L K I S A V F S V S G S P L A P Q L T T G F Q P S L

321A S S G M N K M L P S V P A T A V R V S C S G C K K I L Q K G Q T A Y Q R K G
S T Q L F C S T L C L T G Y T V P P A R P P P P L T K K T C S S C S K D I L N P K

401D V I S A Q F E N T T T S K D F C S Q S C L S T Y E L K K K P I V T I N T N S I S
T K C S M C Q K N A V I R H E V N Y Q N V V H K L C S D A C F S K F R S A N N

481L T M N C C E N C G G Y C Y S G S G Q C H M L Q I E G Q S K K F C S S S C I T
A Y K Q K S A K I T P C A L C K S L R S S A E M I E N T N S L G K T E L F C S V N

561C L S A Y R V K M V T S A G V Q V Q C N S C K T S A I P Q Y H L A M S D G S I
R N F C S Y S C V V A F Q N L F N K P T G M N S S V V P L S Q G Q V I V S I P T G

641S T V S A G G G S T S A V S P T S I S S S A A A G L Q R L A A Q S Q H V G F A R
S V V K L K C Q H C N R L F A T K P E L L D Y K G K M F Q F C G K N C S D E Y K

-continued

721	K I N N V M A M C E Y C K I E K I V K E T V R F S G A D K S F C S E G C K L L
	Y K H D L A K R W G N H C K M C S Y C L Q T S P K L V Q N N L G G K V E E F C C E
801	E C M S K Y T V L F Y Q M A K C D A C K R Q G K L S E S L K W R G E M K H F
	C N L L C I L M F C N Q Q S V C D P P S Q N N A A N I S M V Q A A S A G P P S L R K
881	D S T P V I A N V V S L A S A P A A Q P T V N S N S V L Q G A V P T V T A K I I
	G D A S T Q T D A L K L P P S Q P P R L L K N K A L L C K P I T Q T K A T S C K
961	P H T Q N K E C Q T E D T P S Q P Q I I V V P V P V P V F V P I P L H L Y T Q Y A
	P V P F G I P V P M P V P M L I P S S M D S E D K V T E S I E D I K E K L P T
1041	H P F E A D L L E M A E M I A E D E E K K T L S Q G E S Q T S E H E L F L D T
	K I F E K D Q G S T Y S G D L E S E A V S T P H S W E E E L N H Y A L K S N A V Q
1121	E A D S E L K Q F S K G E T E Q D L E A D F P S D S F D P L N K G Q G I Q A R
	S R T R R R H R D G F P Q P R R R G R K K S I V A V E P R S L I Q G A F Q G C S V
1201	S G M T L K Y M Y G V N A W K N W V Q W K N A K E E Q G D L K C G G V E
	Q A S S S P R S D P L G S T Q D H A L S Q E S S E P G C R V R S I K L K E D I L S C T F
1281	A E L S L G L C Q F I Q E V R R P N G E K Y D P D S I L Y L C L G I Q Q Y L F E
	N G R I D N I F T E P Y S R F M I E L T K L L K I W E P T I L P N G Y M F S R I
1361	E E E H L W E C K Q L G A Y S P I V L L N T L L F F N T K Y F Q L K N V T E H
	L K L S F A H V M R R T R T L K Y S T K M T Y L R F F P P L Q K Q E S E P D K L T
1441	V G K R K R N E D D E V P V G V E M A E N T D N P L R C P V R L Y E F Y L S
	K C S E S V K Q R N D V F Y L Q P E R S C V P N S P M W Y S T F P I D P G T L D T M
1521	L T R I L M V R E V H E E L A K A K S E D S D V E L S D

5.277 angiotensin I converting enzyme isoform 1 precursor
[Homo sapiens]
Protein Accession gi|4503273

Mean Expression Ratio 1.04

Median Expression Ratio 1.04

Credible Interval (0.681, 1.59)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0253
[0395]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.0	1.7	SEQ ID NO: 1467	SMYETPSLEQDLER
1	0.65	1.1	1.7	SEQ ID NO: 1468	RQEEAALLSQEFAEAWGQK
SEQ ID NO: 1469					
1	M G A A S G R R G P G L L L P L P L L L L L P P Q P A L A L D P G L Q P G N F S A				
	D E A G A Q L F A Q S Y N S S A E Q V L F Q S V A A S W A H D T N I T A E N A				
81	R R Q E E A A L L S Q E F A E A W G Q K A K E L Y E P I W Q N F T D P Q L R R I				
	I G A V R T L G S A N L P L A K R Q Q Y N A L L S N M S R I Y S T A K V C L P N				
161	K T A T C W S L D P D L T N I L A S S R S Y A M L L F A W E G W H N A A G I P				
	L K P L Y E D F T A L S N E A Y K Q D G F T D T G A Y W R S W Y N S P T F E D D L				
241	E H L Y Q Q L E P L Y L N L H A F V R R A L H R R Y G D R Y I N L R G P I P A H				
	L L G D M W A Q S W E N I Y D M V V P F P D K P N L D V T S T M L Q Q G W N A T				
321	H M F R V A E E F F T S L E L S P M P P E F W E G S M L E K P A D G R E V V C				
	H A S A W D F Y N R K D F R I K Q C T R V T M D Q L S T V H H E M G H I Q Y Y L Q				
401	Y K D L P V S L R R G A N P G F H E A I G D V L A L S V S T P E H L H K I G L L				
	D R V T N D T E S D I N Y L L K M A L E K I A P L P F G Y L V D Q W R W G V F S				
481	G R T P P S R Y N F D W W Y L R T K Y Q G I C P P V T R N E T H F D A G A K F				
	H V P N V T P Y I R Y F V S F V L Q F Q F H E A L C K E A G Y E G P L H Q C D I Y				
561	R S T K A G A K L R K V L Q A G S S R P W Q E V L K D M V G L D A L D A Q P				
	L L K Y F Q P V T Q W L Q E Q N Q Q N G E V L G W P E Y Q W H P P L P D N Y P E				
	G I				

-continued

641	D L V T D E A E A S K F V E E Y D R T S Q V V W N E Y A E A N W N Y N T N I T T E T S K I L L Q K N M Q I A N H T L K Y G T Q A R K F D V N Q L Q N T T I K R I
721	I K K V Q D L E R A A L P A Q E L E E Y N K I L L D M E T T Y S V A T V C H P N G S C L Q L E P D L T N V M A T S R K Y E D L L W A W E G W R D K A G R A I L Q
801	F Y P K Y V E L I N Q A A R L N G Y V D A G D S W R S M Y E T P S L E Q D L E R L F Q E L Q P L Y L N L H A Y V R R A L H R H Y G A Q H I N L E G P I P A H L L
881	G N M W A Q T W S N I Y D L V V P F P S A P S M D T T E A M L K Q G W T P R R M F K E A D D F F T S L G L L P V P P E F W N K S M L E K P T D G R E V V C H A S
961	A W D F Y N G K D F R I K Q C T T V N L E D L V V A H H E M G H I Q Y F M Q Y K D L P V A L R E G A N P G F H E A I G D V L A L S V S T P K H L H S L N L L S S
1041	E G G S D E H D I N F L M K M A L D K I A F I P F S Y L V D Q W R W R V F D G S I T K E N Y N Q E W W S L R L K Y Q G L C P P V P R T Q G D F D P G A K F H I P
1121	S S V P Y I R Y F V S F I I Q F Q F H E A L C Q A A G H T G P L H K C D I Y Q S K E A G Q R L A T A M K L G F S R P W P E A M Q L I T G Q P N M S A S A M L S Y
1201	F K P L L D W L R T E N E L H G E K L G W P Q Y N W T P N S A R S E G P L P D S G R V S F L G L D L D A Q Q A R V G Q W L L L F L G I A L L V A T L G L S Q R L
1281	F S I R H R S L H R H S H G P Q F G S E V E L R H S

5.278 skeletal muscle receptor tyrosine kinase [*Homo sapi-*
ens]
Protein Accession gi|5031927

Mean Expression Ratio 0.956

Median Expression Ratio 0.96

Credible Interval (0.579, 1.54)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0196

[0396]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.56	0.94	1.6	SEQ ID NO: 1470	CIARQVAAGMAYLSERK
SEQ ID NO: 1471					
1MREL VNIPLVHILTLVAFSGTEKLPKAPVITTPLETVDALVE EVATFMCAVESYPQPEISWTRNKILIKLFDTRYSIREN					
81GQLLTILSVEDSDDGIYCCCTANNGVGGAVESCGALQVKM KPKITRPPINVKIIIEGLKAVLPCTTMGNPKPSVSWIKGDS P					
161LRENSRIAVLESGLSRIHNVQKEDAGQYRCVAKNSLGTA YSKVVKLEVEVFARILRAPESHNVTFGSFVTLHCTATGIPV					
241PTITWIEENGNAVSSGSIQESVKDRVIDSRLLQLFITKPGLYT CIATNKHGEKFSTAKAAATISIAEWSKPQKDNKG YCAQY					
321RGEV CNAVLA KDALVFLNTSYADPEEAQELLVHTAWNEL KVVS P VCRPA AEA L LCNHIFQECS PGV VPTPIPICREYCLA					
401VKELFCAKEWLVMEEKTHRGLYRSEMHLLSVPECSKLPS MHWDP TACARLP HLDY NKENLKTFFPMTSSSKPSVDIPNLPS					
481SSSSSFVSPTYSMTV IISIMSSFAIFVLLTITTL YCCR R R K QWK NK KRESAAVTLTTLPS ELLLDRLHPNPMYQRMP L L					
561LNPKLLSLEYPRNNIEYVRDIGEGAFGRV FQARAPGLLPY EPFTMVAVKMLKEEASADMQA D FQREAA LMAEF DNPNI V K					
641LLGVCAVGKPMCLLFEY MAYGD LNEFLRSMS PHTVCSLS HSDLSMRAQVSSPGPPPLSCAEQLC IARQVAAGMAYLSERK					
721FVHRDLATRNC LVGENMVVKIADFGLSRN IYSADYYKAN ENDAIPIRWMPPESIFYNRYTTESDVWAYGVVLWEIFSYGL					

-continued

801Q P Y Y G M A H E E V I Y Y V R D G N I L S C P E N C P V E L Y N L M R L C W
S K L P A D R P S F T S I H R I L E R M C E R A E G T V S V

5.279 spastin isoform 2 [*Homo sapiens*]; spastin isoform 1
[*Homo sapiens*]

[0397]

Protein Accession gi|40806170 gi|11875211

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.64	1.0	1.8	SEQ ID NO: 1472	SSGAAPAPASASAPAPVPG GEAER

Mean Expression Ratio 1.04

5.280 allograft inflammatory factor 1 isoform 3 [*Homo sapiens*]

Median Expression Ratio 1.04

Protein Accession gi|14574568

Credible Interval (0.638, 1.69)

Mean Expression Ratio 1.05

Median Expression Ratio 1.04

Associated Peptides 1

Credible Interval (0.698, 1.57)

Associated Peptides 1

Associated Spectra 1

Associated Spectra 3

Coverage 0.0748

Coverage NaN

[0398]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.71	1.1	1.6	SEQ ID NO: 1473	MSQTRDLQGGK

SEQ ID NO: 1474

1 M S Q T R D L Q G G K A F G L L K A Q Q E E R L D E I N K Q F L D D P K Y S S D
E D L P S K L E G F K E K Y M E F D L N G N G D I D I M S L K R M L E K L G V P
81 K T H L E L K K L I G E V S S G S G E T F S Y P D F L R M M L G K R S A I L K M I
L M Y E E K A R E K E K P T G P P A K K A I S E L P

5.281 carbonyl reductase 1 [*Homo sapiens*]

Protein Accession gi|4502599

Mean Expression Ratio 1.05

Median Expression Ratio 1.04

Credible Interval (0.726, 1.51)

Associated Peptides 2

Associated Spectra 4

Coverage 0.105

[0399]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.73	1.0	1.5	SEQ ID NO: 1475	FHQLDIDDLQSIR
1	0.68	1.1	1.6	SEQ ID NO: 1476	GQAAVQQQLQAEGLSPR

SEQ ID NO: 1477

1 M S S G I H V A L V T G G N K G I G L A I V R D L C R L F S G D V V L T A R D V T
R G Q A A V Q Q L Q A E G L S P R F H Q L D I D D L Q S I R A L R D F L R K E
81 Y G G L D V L V N N A G I A F K V A D P T P F H I Q A E V T M K T N F F G T R D
V C T E L L P L I K P Q G R V V N V S S I M S V R A L K S C S P E L Q Q K F R S

-continued

161	E	T	I	T	E	E	L	V	G	L	M	N	K	F	V	E	D	T	K	K	G	V	H	Q	K	E	G	W	P	S	S	A	Y	G	V	T	K	I			
	G	V	T	V	L	S	R	I	H	A	R	K	L	S	E	Q	R	K	G	D	K	I	L	L	N	A	C	C	P	G	W	V	R	T	D	M	A	G	P	K	A
241	T	K	S	P	E	E	G	A	E	T	P	V	Y	L	A	L	L	P	P	D	A	E	G	P	H	G	Q	F	V	S	E	K	R	V	E	Q	W				

5.282 sodium/hydrogen exchanger regulatory factor 1
[Homo sapiens]
Protein Accession gil4759140
Mean Expression Ratio 0.961
Median Expression Ratio 0.96

Credible Interval (0.78, 1.19)
Associated Peptides 10
Associated Spectra 19
Coverage 0.26
[0400]

A	2.5	50	97.5	Sequence ID NO.	Sequence
6	0.75	0.97	1.2	SEQ ID NO: 1478	AQEAPGQAEPPAAAEVQGAGNENEPR
1	0.72	1	1.4	SEQ ID NO: 1479	EADKSHPEQR
1	0.69	0.96	1.4	SEQ ID NO: 1480	EALAEAALESPR
1	0.65	0.9	1.2	SEQ ID NO: 1481	EAPGQAEPPAAAEVQGAGNENEPR
3	0.75	1	1.4	SEQ ID NO: 1482	EPPAAAEVQGAGNENEPR
1	0.68	0.93	1.3	SEQ ID NO: 1483	QEAPGQAEPPAAAEVQGAGNENEPR
1	0.73	1.0	1.4	SEQ ID NO: 1484	SKPGQFIR
3	0.68	0.9	1.2	SEQ ID NO: 1485	VIPSQEHLNGPLPVPF
1	0.7	0.97	1.3	SEQ ID NO: 1486	ETDEFFK
1	0.69	0.97	1.3	SEQ ID NO: 1487	SVDPDSPAEASGLR
SEQ ID NO: 1488					
1MSADAAAGAPLPRLCCLEKGPNGYG FHLHGEK GKLGQYIR					
LVEPGSPA EKAGLLAGDRLVEVNGENVEKET HQQVVSRI R					
81AALNAVRLLVDPETDEQLQKLG VQVREEL LRAQEAPGQ					
AEPPAAAEVQGAGNENEPREADKSHPEQREL RPRLCTMKKG					
161PSGYGFNLHSDKSKPGQFIRSVDPDSPAEASGLRAQDRIV					
EVNGVCM EGKQHGDVVS AIRAGDETKLLVVDRETDEFFK					
241KCRVIPSQEHLNGPLPV PFTNGEI QKENSREALAEAALES					
PRPALVRSASSDTS EELNSQDSPPKQDSTAPSSTSSSDPI					
321LDFNISLAMAKERAHQKRSSKRAPQMDWSKKNELFSNL					

5.283 argininosuccinate synthetase 1 [*Homo sapiens*];
argininosuccinate synthetase 1 [*Homo sapiens*]
Protein Accession gi|53759107 gi|16950633

Mean Expression Ratio 1.04

Median Expression Ratio 1.04

Credible Interval (0.682, 1.58)

Associated Peptides 2

Associated Spectra 2

Coverage NaN

[0401]

A	2.5	50	97.5	Sequence ID NO.	Sequence
1	0.65	1.1	1.7	SEQ ID NO: 1489	EFVEEFIWPAIQSSALYED R
1	0.64	1.0	1.7	SEQ ID NO: 1490	APNTPDILEIEFK

5.284 spinster homolog 1 isoform 1 [*Homo sapiens*]; spin-
ster homolog 1 isoform 1 [*Homo sapiens*]
Protein Accession gi|215490096 gi|14042968

Mean Expression Ratio 1.04

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	1.0	1.7	SEQ ID NO: 1493	CSGIASAAAAVEAAR
SEQ ID NO: 1494					
1M D A E G L A L L P P V T L A A L V D S W L R E D C P G L N Y A A L V S G A G					
P S Q A A L W A K S P G V L A G Q P F F D A I F T Q L N C Q V S W F L P E G S K					
81L V P V A R V A E V R G P A H C L L L G E R V A L N T L A R C S G I A S A A A A					
A V E A A R G A G W T G H V A G T R K T T P G F R L V E K Y G L L V G G A A S H					
161R Y D L G G L V M V K D N H V V A A G G V E K A V R A A R Q A A D F A L K					
V E V E C S S L Q E A V Q A A E A G A D L V L L D N F K P E E L H P T A T V L K A					
Q F					
241P S V A V E A S G G I T L D N L P Q F C G P H I D V I S M G M L T Q A A P A L D					
F S L K L F A K E V A P V P K I H					

Median Expression Ratio 1.04

Credible Interval (0.707, 1.55)

Associated Peptides 2

Associated Spectra 3

Coverage NaN

[0402]

A	2.5	50	97.5	Sequence ID NO.	Sequence
1	0.66	1.0	1.6	SEQ ID NO: 1491	AQLHVQGLLHEAGSTDDR
2	0.7	1.1	1.6	SEQ ID NO: 1492	SEEPEVPDQEGLR

5.285 quinolinate phosphoribosyltransferase [*Homo sapi-
ens*]
Protein Accession gi|45269149

Mean Expression Ratio 1.04

Median Expression Ratio 1.04

Credible Interval (0.64, 1.67)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0539

[0403]

5.286 transmembrane protein 106A [*Homo sapiens*]; PRE-
DICTED: similar to Transmembrane protein 106A [*Homo
sapiens*]; PREDICTED: similar to Transmembrane protein
106A isoform 3 [*Homo sapiens*]
Protein Accession gi|21450796 gi|169211133 gi 113427131

Mean Expression Ratio 0.97

Median Expression Ratio 0.965

Credible Interval (0.601, 1.58)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0404]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.96	1.6	SEQ ID NO: 1495	QLVALIPYGDQR

5.287 uroplakin 1A [*Homo sapiens*]
Protein Accession gi|5902148

Mean Expression Ratio 1.04

Median Expression Ratio 1.04

Credible Interval (0.64, 1.70)

Associated Peptides 1

Associated Spectra 1

Coverage 0.062

[0405]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	1.1	1.8	SEQ ID NO: 1496	AATPEVVPWPPLCCR
SEQ ID NO: 1497					
1M A S A A A A E A E K G S P V V V G L L V V G N I I I L L S G L S L F A E T I W V					
T A D Q Y R V Y P L M G V S G K D D V F A G A W I A I F C G F S F F M V A S F					
81G V G A A L C R R R S M V L T Y L V L M L I V Y I F E C A S C I T S Y T H R D Y					
M V S N P S L I T K Q M L T F Y S A D T D Q G Q E L T R L W D R V M I E Q E C C					
161G T S G P M D W V N F T S A F R A A T P E V V F P W P P L C C R R T G N F I P L					
N E E G C R L G H M D Y L F T K G C F E H I G H A I D S Y T W G I S W F G F A I					
241L M W T L P V M L I A M Y F Y T M L					

5.288 secretory carrier membrane protein 3 isoform 1
[*Homo sapiens*]
Protein Accession gi|16445419

Mean Expression Ratio 0.964

Median Expression Ratio 0.965

Credible Interval (0.593, 1.56)

Associated Peptides 1

Associated Spectra 1

Coverage 0.075

[0406]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.95	1.6	SEQ ID NO: 1498	EPPPAYEPPAPAPLPSPSAPSLQPSR
SEQ ID NO: 1499					
1M A Q S R D G G N P F A E P S E L D N P F Q D P A V I Q H R P S R Q Y A T L D V					
Y N P F E T R E P P P A Y E P P A P A P L P P P S A P S L Q P S R K L S P T E P					
81K N Y G S Y S T Q A S A A A A T A E L L K K Q E E L N R K A E E L D R R E R E L					
Q H A A L G G T A T R Q N N W P P L P S F C P V Q P C F F Q D I S M E I P Q E F					
161Q K T V S T M Y Y L W M C S T L A L L L N F L A C L A S F C V E T N N G A G F					
G L S I L W V L L F T P C S F V C W Y R P M Y K A F R S D S S F N F V F F F I F					
241F V Q D V L F V L Q A I G I P G W G F S G W I S A L V V P K G N T A V S V L M					
L L V A L L F T G I A V L G I V M L K R I H S L Y R R T G A S F Q K A Q Q E F A A					
321G V F S N P A V R T A A A N A A G A A E N A F R A P					

5.289 guanine nucleotide binding protein (G protein),
gamma 2 [*Homo sapiens*]
Protein Accession gil54114974
Mean Expression Ratio 1.04
Median Expression Ratio 1.04
Credible Interval (0.635, 1.69)
Associated Peptides 1
Associated Spectra 1
Coverage 0.225
[0407]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	1.0	1.8	SEQ ID NO: 1500	EDPLLTPVPASENPFR

SEQ ID NO: 1501

1M A S N N T A S I A Q A R K L V E Q L K M E A N I D R I K V S K A A A D L M A Y
C E A H A K E D P L L T P V P A S E N P F R E K K F F C A I L

5.290 sorbitol dehydrogenase [*Homo sapiens*]
Protein Accession gil156627571
Mean Expression Ratio 0.967
Median Expression Ratio 0.967
Credible Interval (0.601, 1.58)

Associated Peptides 1
Associated Spectra 1
Coverage 0.0476
[0408]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.95	1.6	SEQ ID NO: 1502	LENYPIPEPGPNEVLLR

SEQ ID NO: 1503

1M A A A A K P N N L S L V V H G P G D L R L E N Y P I P E P G P N E V L L R M H
S V G I C G S D V H Y W E Y G R I G N F I V K K P M V L G H E A S G T V E K V G

81S S V K H L K P G D R V A I E P G A P R E N D E F C K M G R Y N L S P S I F F C A
T P P D D G N L C R F Y K H N A A F C Y K L P D N V T F E E G A L I E P L S V

161G I H A C R R G G V T L G H K V L V C G A G P I G M V T L L V A K A M G A A
Q V V V T D L S A T R L S K A K E I G A D L V L Q I S K E S P Q E I A R K V E G Q
L

241G C K P E V T I E C T G A E A S I Q A G I Y A T R S G G N L V L V G L G S E M T
T V P L L H A A I R E V D I K G V F R Y C N T W P V A I S M L A S K S V N V K P

321L V T H R F P L E K A L E A F E T F K K G L G L K I M L K C D P S D Q N P

5.291 major facilitator superfamily domain containing 1
[Homo sapiens]
Protein Accession gil112232393
Mean Expression Ratio 0.97
Median Expression Ratio 0.967
Credible Interval (0.601, 1.6)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0258
[0409]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.56	0.96	1.6	SEQ ID NO: 1504	ALLAGGPDEADR
SEQ ID NO: 1505					
1M E E E D E E A R A L L A G G P D E A D R G A P A A P G A L P A L C D P S R L A					
H R L L V L L L M C F L G F G S Y F C Y D N P A A L Q T Q V K R D M Q V N T T K					
81F M L L Y A W Y S W P N V V L C F F G G F L I D R V F G I R W G T I I F S C F V					
C I G Q V V F A L G G I F N A F W L M E F G R F V F G I G G E S L A V A Q N T Y					
161A V S W F K G K E L N L V F G L Q L S M A R I G S T V N M N L M G W L Y S K					
I E A L L G S A G H T T L G I T L M I G G V T C I L S L I C A L A L A Y L D Q R A E					
241R I L H K E Q G K T G E V I K L T D V K D F S L P L W L I F I I C V C Y Y V A V					
F P F I G L G K V F F T E K F G F S S Q A A S A I N S V V Y V I S A P M S P V F					
321G L L V D K T G K N I I W V L C A V A A T L V S H M M L A F T M W N P W I A					
M C L L G L S Y S L L A C A L W P M V A F V V P E H Q L G T A Y G F M Q S I Q N L G					
401L A I I S I I A G M I L D S R G Y L F L E V F F I A C V S L S L L S V V L L Y L V N					
R A Q G G N L N Y S A R Q R E E I K F S H T E					

5.292 superoxide dismutase 3, extracellular precursor
[Homo sapiens]
Protein Accession gil118582275
Mean Expression Ratio 1.03
Median Expression Ratio 1.03

Credible Interval (0.669, 1.6)
Associated Peptides 2
Associated Spectra 2
Coverage 0.1
[0410]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1.1	1.7	SEQ ID NO: 1506	VTEIWQEVMQR
1	0.64	1.0	1.7	SEQ ID NO: 1507	AVVVHAGEDDLGR
SEQ ID NO: 1508					
1M L A L L C S C L L L A A G A S D A W T G E D S A E P N S D S A E W I R D M Y A					
K V T E I W Q E V M Q R R D D D G A L H A A C Q V Q P S A T L D A A Q P R V T G					
81V V L F R Q L A P R A K L D A F F A L E G F P T E P N S S S R A I H V H Q F G D L					
S Q G C E S T G P H Y N P L A V P H P Q H P G D F G N F A V R D G S L W R Y R					
161A G L A A S L A G P H S I V G R A V V V H A G E D D L G R G G N Q A S V E N					
G N A G R R L A C C V V G V C G P G L W E R Q A R E H S E R K K R R R E S E C K					
A A					

5.293 nuclear transport factor 2 [*Homo sapiens*]
Protein Accession gi|5031985
Mean Expression Ratio 0.967
Median Expression Ratio 0.967
Credible Interval (0.599, 1.58)
Associated Peptides 1
Associated Spectra 1
Coverage 0.110
[0411]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.96	1.6	SEQ ID NO: 1509	NINDAWVCTNDMFR

SEQ ID NO: 1510

1 M G D K P I W E Q I G S S F I Q H Y Y Q L F D N D R T Q L G A I Y I D A S C L T W
E G Q Q F Q G K A A I V E K L S S L P F Q K I Q H S I T A Q D H Q P T P D S C

81 I I S M V V G Q L K A D E D P I M G F H Q M F L L K N I N D A W V C T N D M F
R L A L H N F G

5.294 hexosaminidase B preproprotein [*Homo sapiens*]
Protein Accession gi|4504373
Mean Expression Ratio 0.967
Median Expression Ratio 0.967
Credible Interval (0.686, 1.36)

Associated Peptides 4
Associated Spectra 4
Coverage 0.0971
[0412]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.64	0.97	1.4	SEQ ID NO: 1511	EISEVFPDQFIHLGGDEVEFK
1	0.63	0.96	1.5	SEQ ID NO: 1512	LAPGTIVEVWK
1	0.64	0.97	1.5	SEQ ID NO: 1513	VLDIIATINK
1	0.63	0.96	1.4	SEQ ID NO: 1514	YLDLISYGQDWR

SEQ ID NO: 1515

1 M E L C G L G L P R P P M L L A L L L A T L L A A M L A L L T Q V A L V V Q V A
E A A R A P S V S A K P G P A L W P L P L S V K M T P N L L H L A P E N F Y I S

81 H S P N S T A G P S C T L L E E A F R R Y H G Y I F G F Y K W H H E P A E F Q A
K T Q V Q Q L L V S I T L Q S E C D A F P N I S S D E S Y T L L V K E P V A V L

161 K A N R V W G A L R G L E T F S Q L V Y Q D S Y G T F T I N E S T I I D S P R F
S H R G I L I D T S R H Y L P V K I I L K T L D A M A F N K F N V L H W H I V D

241 D Q S F P Y Q S I T F P E L S N K G S Y S L S H V Y T P N D V R M V I E Y A R L
R G I R V L P E F D T P G H T L S W G K G Q K D L L T P C Y S R Q N K L D S F G

321 P I N P T L N T T Y S F L T T F F K E I S E V F P D Q F I H L G G D E V E F K C W
E S N P K I Q D F M R Q K G F G T D F K K L E S F Y I Q K V L D I I A T I N K

401 G S I V W Q E V F D D K A K L A P G T I V E V W K D S A Y P E E L S R V T A S
G F P V I L S A P W Y L D L I S Y G Q D W R K Y Y K V E P L D F G G T Q K Q K Q L

481 F I G G E A C L W G E Y V D A T N L T P R L W P R A S A V G E R L W S S K D V
R D M D D A Y D R L T R H R C R M V E R G I A A Q P L Y A G Y C N H E N M

5.295 nucleoporin 188 kDa [*Homo sapiens*]
Protein Accession gi|62955803

Associated Peptides 1

Mean Expression Ratio 0.967

Associated Spectra 4

Median Expression Ratio 0.967

Coverage 0.00515

Credible Interval (0.665, 1.41)

[0413]

A	2.5	50	97.5	Sequence ID No.	Sequence
4	0.67	0.96	1.4	SEQ ID NO: 1516	MLQHYLQNK
SEQ ID NO: 1517					
1M A A A A G G P C V R S S R E L W T I L L G R S A L R E L S Q I E A E L N K H W					
R R L L E G L S Y Y K P P S P S S A E K V K A N K D V A S P L K E L G L R I S K					
81F L G L D E E Q S V Q L L Q C Y L Q E D Y R G T R D S V K T V L Q D E R Q S Q					
A L I L K I A D Y Y Y E E R T C I L R C V L H L L T Y F Q D E R H P Y R V E Y A D					
161C V D K L E K E L V S K Y R Q Q F E E L Y K T E A P T W E T H G N L M T E R Q					
V S R W F V Q C L R E Q S M L L E I I F L Y Y A Y F E M A P S D L L V L T K M F K					
241E Q G F G S R Q T N R H L V D E T M D P F V D R I G Y F S A L I L V E G M D I E					
S L H K C A L D D R R E L H Q F A Q D G L I C Q D M D C L M L T F G D I P H H A					
321P V L L A W A L L R H T L N P E E T S S V V R K I G G T A I Q L N V F Q Y L T R					
L L Q S L A S G G N D C T T S T A C M C V Y G L L S F V L T S L E L H T L G N Q					
401Q D I I D T A C E V L A D P S L P E L F W G T E P T S G L G I I L D S V C G M F P					
H L L S P L L Q L L R A L V S G K S T A K K V Y S F L D K M S F Y N E L Y K H					
481K P H D V I S H E D G T L W R R Q T P K L L Y P L G G Q T N L R I P Q G T V G					
Q V M L D D R A Y L V R W E Y S Y S S W T L F T C E I E M L L H V V S T A D V I Q					
561H C Q R V K P I I D L V H K V I S T D L S I A D C L L P I T S R I Y M L L Q R L T					
T V I S P P V D V I A S C V N C L T V L A A R N P A K V W T D L R H T G F L P					
641F V A H P V S S L S Q M I S A E G M N A G G Y G N L L M N S E Q P Q G E Y G V					
T I A F L R L I T T L V K G Q L G S T Q S Q G L V P C V M F V L K E M L P S Y H K					
721W R Y N S H G V R E Q I G C L I L E L I H A I L N L C H E T D L H S S H T P S L					
Q F L C I C S L A Y T E A G Q T V I N I M G I G V D T I D M V M A A Q P R S D G					
801A E G Q G Q G Q L L I K T V K L A F S V T N N V I R L K P P S N V V S P L E Q A					
L S Q H G A H G N N L I A V L A K Y I Y H K H D P A L P R L A I Q L L K R L A T					
881V A P M S V Y A C L G N D A A A I R D A F L T R L Q S K I E D M R I K V M I L					
E F L T V A V E T Q P G L I E L F L N L E V K D G S D G S K E F S L G M W S C L H					
961A V L E L I D S Q Q Q D R Y W C P P L L H R A A I A F L H A L W Q D R R D S A					
M L V L R T K P K F W E N L T S P L F G T L S P P S E T S E P S I L E T C A L I M					
1041K I I C L E I Y Y V V K G S L D Q S L K D T L K K F S I E K R F A Y W S G Y V					
K S L A V H V A E T E G S S C T S L L E Y Q M L V S A W R M L L I I A T T H A D I					
1121M H L T D S V V R R Q L F L D V L D G T K A L L L V P A S V N C L R L G S M					
K C T L L L I L L R Q W K R E L G S V D E I L G P L T E I L E G V L Q A D Q Q L M E					
1201K T K A K V F S A F I T V L Q M K E M K V S D I P Q Y S Q L V L N V C E T L Q					
E E V I A L F D Q T R H S L A L G S A T E D K D S M E T D D C S R S R H R D Q R D					
1281G V C V L G L H L A K E L C E V D E D G D S W L Q V T R R L P I L P T L L T T					
L E V S L R M K Q N L H F T E A T L H L L L T L A R T Q Q G A T A V A G A G I T Q					
1361S I C L P L L S V Y Q L S T N G T A Q T P S A S R K S L D A P S W P G V Y R L S					
M S L M E Q L L K T L R Y N F L P E A L D F V G V H Q E R T L Q C L N A V R T V					
1441Q S L A C L E E A D H T V G F I L Q L S N F M K E W H F H L P Q L M R D I Q V					
N L G Y L C Q A C T S L L H S R K M L Q H Y L Q N K N G D G L P S A V A Q R V Q R					
1521P P S A A S A A P S S S K Q P A A D T E A S E Q Q A L H T V Q Y G L L K I L S					
K T L A A L R H F T P D V C Q I L L D Q S L D L A E Y N F L F A L S F T T T P T F D					
1601S E V A P S F G T L L A T V N V A L N M L G E L D K K K E P L T Q A V G L S T					
Q A E G T R T L K S L L M F T M E N C F Y L L I S Q A M R Y L R D P A V H P R D K					

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1681	Q R M K Q E L S S E L S T L L S S L S R Y F R R G A P S S P A T G V L P S P Q G
	K S T S L S K A S P E S Q E P L I Q L V Q A F V R H M Q R

5.296 hypothetical protein LOC54978 [*Homo sapiens*]
Protein Accession gi|31542711

Mean Expression Ratio 0.965
Median Expression Ratio 0.967
Credible Interval (0.589, 1.58)

Associated Peptides 1
Associated Spectra 1

Coverage 0.0323
[0414]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.95	1.6	SEQ ID NO: 1518	GRPLAESEQER

SEQ ID NO: 1519

1MAWTKYQLFLAGLMLVTGSINTLSAKWADNFM AEGCGGS
KEHSFQH PFLQAVGMFLGEFSC LA AFYLLRCRAAGQSDSSV

81DPQQPFNP LFLP PALCDMTGTSLMYVALNMTSASSFQML
RGAVIIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVG L

161ADLLSKHDSQHKLSEVITGDLLII MAQII VAIQMVL EEKFV
YKHNVHPLRAVGTEGLFGFVILSLLLVPMYYIPAGSFSG

241NPRGTLEDALDAFCQVGGQQPLIAVAL LGNISSIAFFNFAGI
SVTKELSATTRMVLDSLRTVVIWALS LALGW EAFHALQI

321LGFLILLIGTALYNGLHRP L LGR LSRGRPLAE ESEQERLLG
GTRTPINDAS

5.297 disrupted in renal carcinoma 2 [*Homo sapiens*]
Protein Accession gi|14249552

Associated Peptides 2
Associated Spectra 3

Mean Expression Ratio 1.03
Median Expression Ratio 1.03
Credible Interval (0.705, 1.52)

Coverage 0.069
[0415]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.7	1.0	1.6	SEQ ID NO: 1520	EAAAAALPAAVPGPGR
1	0.66	1.0	1.6	SEQ ID NO: 1521	QPLLGPGLGPGLGASWR

SEQ ID NO: 1522

1MGSRWSS E EERQPL L GPGLGPGLGASWRSREAAAAALPAA
VPGPGRVYGRRWLVLLFSL LA FVQGLVWNTWGP IQNSAR

81QAYGFSSWDIALLV LWGP IGF L P CFAFMWLLDKRGLRITV
LLTSFLMV L GTGLRCIPISDLILKRRLIHGGQMLNGLAGP

161TVMNAAPFLSTTWFSADERATATAIASMLSYLGGACAF L
VGPLVVPA PNGTSP L LA AES SRAHIKDRIEAVLYAEFGVV C

241LIFSATLAYFP PRPPLPPSVAAA SQR LSYRRSVCRLLSNFR
FLMIALAYAIPLGVFAGWSGVLDLILTPAHVSQVDAGWI

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321	G F W S I V G G C V V G I A M A R F A D F I R G M L K L I L L L L F S G A T L S
	S T W F T L T C L N S I T H L P L T T V T L Y A S C I L L G V F L N S S V P I F
401	F E L F V E T V Y P V P E G I T C G V V T F L S N M F M G V L L F F L T F Y H T
	E L S W F N W C L P G S C L L S L L L I L C F R E S Y D R L Y L D V V V S V

5.298 adenine phosphoribosyltransferase isoform b [*Homo sapiens*]

Protein Accession gil71773201

Mean Expression Ratio 1.03

Median Expression Ratio 1.03

Credible Interval (0.636, 1.69)

Associated Peptides 1

Associated Spectra 1

Coverage 0.097

[0416]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	1.0	1.7	SEQ ID NO: 1523	SFPDFPTPGVVFR

SEQ ID NO: 1524

1	M A D S E L Q L V E Q R I R S F P D F P T P G V V F R D I S P V L K D P A S F R A
	A I G L L A R H L K A T H G G R I D Y I A G L D S R G F L F G P S L A Q E L G
81	L G C V L I R K R G K L P G P T L W A S Y S L E Y G K A E L E I Q K D A L E P G
	Q R V V V V D D L L A T G V

5.299 GNAS complex locus XLas [*Homo sapiens*]

Protein Accession gil117938759

Mean Expression Ratio 1.03

Median Expression Ratio 1.03

Credible Interval (0.755, 1.40)

Associated Peptides 4

Associated Spectra 7

Coverage 0.0501

[0417]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.7	0.98	1.4	SEQ ID NO: 1525	IEDYFPEFAR
1	0.69	1.0	1.5	SEQ ID NO: 1526	SNLVPPVELANPENQFR
2	0.8	1.1	1.6	SEQ ID NO: 1527	YTPEDATPEPGEDPR
1	0.7	1.0	1.5	SEQ ID NO: 1528	LQEALNLFK

SEQ ID NO: 1529

1	M G V R N C L Y G N N M S G Q R D I P P E I G E Q P E Q P P L E A P G A A A P G
	A G P S P A E E M E T E P P H N E P I P V E N D G E A C G P P E V S R P N F Q V
81	L N P A F R E A G A H G S Y S P P P E E A M P F E A E Q P S L G G F W P T L E Q
	P G F P S G V H A G L E A F G P A L M E P G A F S G A R P G L G G Y S P P P E E
161	A M P F E F D Q P A Q R G C S Q L L L Q V P D L A P G G P G A A G V P G A P P
	E E P Q A L R P A K A G S R G G Y S P P P E E T M P F E L D G E G F G D D S P P P
241	G L S R V I A Q V D G S S Q F A A V A A S S A V R L T P A A N A P P L W V P G
	A I G S P S Q E A V R P P S N F T G S S P W M E I S G P P F E I G S A P A G V D D
321	T P V N M D S P P I A L D G P P I K V S G A P D K R E R A E R P P V E E E A A E
	M E G A A D A A E G G K V P S P G Y G S P A A G A A S A D T A A R A A P A A P A

-continued

401D P D S G A T P E D P D S G T A P A D P D S G A F A A D P D S G A A P A A P A
D P D S G A A P D A P A D P D S G A A P D A P A D P D A G A A P E A P A A P A A A

481E T R A A H V A P A A P D A G A P T A P A A S A T R A A Q V R R A A S A A P A
S G A R R K I H L R P P S P E I Q A A D P P T P R P T R A S A W R G K S E S S R G

561R R V Y Y D E G V A S S D D D S S G D E S D D G T S G C L R W F Q H R R N R R
R R K P Q R N L L R N F L V Q A F G G C F G R S E S P Q P K A S R S L K V K K V P

641L A E K R R Q M R K E A L E K R A Q K R A E K K R S K L I D K Q L Q D E K M
G Y M C T H R L L L L G A G E S G K S T I V K Q M R I L H V N G F N G E G G E E D P

721Q A A R S N S D G E K A T K V Q D I K N N L K E A I E T I V A A M S N L V P P
V E L A N P E N Q F R V D Y I L S V M N V P D F D F P P E F Y E H A K A L W E D E

801G V R A C Y E R S N E Y Q L I D C A Q Y F L D K I D V I K Q A D Y V P S D Q D
L L R C R V L T S G I F E T K F Q V D K V N F H M F D V G G Q R D E R R K W I Q C

881F N D V T A I I F V V A S S S Y N M V I R E D N Q T N R L Q E A L N L F K S I W
N N R W L R T I S V I L F L N K Q D L L A E K V L A G K S K I E D Y F P E F A R

961Y T T P E D A T P E P G E D P R V T R A K Y F I R D E F L R I S T A S G D G R H
Y C Y P H F T C A V D T E N I R R V F N D C R D I I Q R M H L R Q Y E L L

5.300 A kinase (PRKA) anchor protein 12 isoform 2 [*Homo sapiens*]

Protein Accession gil21493024

Mean Expression Ratio 1.03

Median Expression Ratio 1.03

Credible Interval (0.673, 1.58)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0232

[0418]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.64	1.0	1.6	SEQ ID NO: 1530	EESQLPGTGGPEDVLQPVQR
1	0.65	1.0	1.7	SEQ ID NO: 1531	EVIAEEEEPTVTEPLPENR
SEQ ID NO: 1532					
1	M L G T I T I T V G Q R D S E D V S K R D S D K E M A T K S A V V H D I T D D G Q E E T P E I I E Q I P S S E S N L E E L T Q P T E S Q A N D I G F K K V F K F				
81	V G F K F T V K K D K T E K P D T V Q L L T V K K D E G E G A A G A G D H K D P S L G A G E A A S K E S E P K Q S T E K P E E T L K R E Q S H A E I S P P A E S				
161	G Q A V E E C K E E G E E K Q E K E P S K S A E S P T S P V T S E T G S T F K K F F T Q G W A G W R K K T S F R K P K E D E V E A S E K K K E Q E P E K V D T E				
241	E D G K A E V A S E K L T A S E Q A H P Q E P A E S A H E P R L S A E Y E K V E L P S E E Q V S G S Q G P S E E K P A P L A T E V F D E K I E V H Q E E V V A E				
321	V H V S T V E E R T E E Q K T E V E E T A G S V P A E E L V E M D A E P Q E A E P A K E L V K L K E T C V S G E D P T Q G A D L S P D E K V L S K P P E G V V S				
401	E V E M L S S Q E R M K V Q G S P L K K L F T S T G L K K L S G K K Q K G K R G G D E E S G E H T Q V P A D S P D S Q E E Q K G E S S A S S P E E P E E I T C				
481	L E K G L A E V Q Q D G E A E E G A T S D G E K K R E G V T P W A S F K K M V T P K K R V R R P S E S D K E D E L D K V K S A T L S S T E S T A S E M Q E E M K				
561	G S V E E P K P E E P K R K V D T S V S W E A L I C V G S S K K R A R R G S S S D E E G G P K A M G G D H Q K A D E A G K D K E T G T D G I L A G S Q E H D P G				
641	Q G S S S P E Q A G S P T E G E G V S T W E S F K R L V T P R K K S K S K L E E K S E D S I A G S G V E H S T P D T E P G K E E S W V S I K K F I P G R R K K R				
721	P D G K Q E Q A P V E D A G P T G A N E D D S D V P A V V P L S E Y D A V E R E K M E A Q Q A Q K S A E Q P E Q K A A T E V S K E L S E S Q V H M M A A A V A D				

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801	G T R A A T I I E E R S P S W I S A S V T E P L E Q V E A E A A L L T E E V L E R
	E V I A E E E P P T V T E P L P E N R E A R G D T V V S E A E L T P E A V T A
881	A E T A G P L G A E E G T E A S A A E E T T E M V S A V S Q L T D S P D T T E E
	A T P V Q E V E G G V P D I E E Q E R R T Q E V L Q A V A E K V K E E S Q L P G
961	T G G P E D V L Q P V Q R A E A E R P E E Q A E A S G L K K E T D V V L K V D
	A Q E A K T E P F T Q G K V V G Q T T P E S F E K A P Q V T E S I E S S E L V T T
1041	C Q A E T L A G V K S Q E M V M E Q A I P P D S V E T P T D S E T D G S T P V
	A D F D A P G T T Q K D E I V E I H E E N E V A S G T Q S G G T E A E A V P A Q K
1121	E R P P A P S S F V F Q E E T K E Q S K M E D T L E H T D K E V S V E T V S I L
	S K T E G T Q E A D Q Y A D E K T K D V P F F E G L E G S I D T G I T V S R E K
1201	V T E V A L K G E G T E E A E C K K D D A L E L Q S H A K S P P S P V E R E M
	V V Q V E R E K T E A E P T H V N E E K L E H E T A V T V S E E V S K Q L L Q T V
1281	N V P I I D G A K E V S S L E G S P P P C L G Q E E A V C T K I Q V Q S S E A S
	F T L T A A A E E E K V L G E T A N I L E T G E T L E P A G A H L V L E E K S S
1361	E K N E D F A A H P G E D A V P T G P D C Q A K S T P V I V S A T T K K G L S
	S D L E G E K T T S L K W K S D E V D E Q V A C Q E V K V S V A I E D L E P E N G
1441	I L E L E T K S S K L V Q N I I Q T A V D Q F V R T E E T A T E M L T S E L Q T
	Q A H V I K A D S Q D A G Q E T E K E G E E P Q A S A Q D E T P I T S A K E E S
1521	E S T A V G Q A H S D I S K D M S E A S E K T M T V E V E G S T V N D Q Q L
	E E V V L P S E E E G G A G T K S V P E D D G H A L L A E R I E K S L V E P K E D
1601	E K G D D V D D P E N Q N S A L A D T D A S G G L T K E S P D T N G P K Q K
	E K E D A Q E V E L Q E G K V H S E S D K A I T P Q A Q E E L Q K Q E R E S A K S E
1681	L T E S

5.301 orosomucoid 1 precursor [*Homo sapiens*]

Protein Accession gil167857790

Mean Expression Ratio 0.97

Median Expression Ratio 0.97

Credible Interval (0.666, 1.44)

Associated Peptides 3

Associated Spectra 3

Coverage NaN

[0419]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	0.97	1.5	SEQ ID NO: 1533	WFYIASAFR
1	0.64	0.99	1.5	SEQ ID NO: 1534	EQLGEFYEALDCLR
1	0.61	0.95	1.5	SEQ ID NO: 1535	YVGQQEHAHLILR

5.302 lysozyme precursor [*Homo sapiens*]
Protein Accession gi|4557894
Mean Expression Ratio 0.969
Median Expression Ratio 0.97
Credible Interval (0.6, 1.57)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0811
[0420]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.96	1.6	SEQ ID NO: 1536	STDYGIFQINSR

SEQ ID NO: 1537

1 M K A L I V L G L V L L S V T V Q G K V F E R C E L A R T L K R L G M D G Y R G
I S L A N W M C L A K W E S G Y N T R A T N Y N A G D R S T D Y G I F Q I N S R

81 Y W C N D G K T P G A V N A C H L S C S A L L Q D N I A D A V A C A K R V V R
D P Q G I R A W V A W R N R C Q N R D V R Q Y V Q G C G V

5.303 vacuolar protein sorting 37C [*Homo sapiens*]
Protein Accession gi|57863314
Mean Expression Ratio 0.972
Median Expression Ratio 0.97
Credible Interval (0.658, 1.44)
Associated Peptides 3
Associated Spectra 3
Coverage 0.177
[0421]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	0.97	1.5	SEQ ID NO: 1538	FLEGEVPLETFLENFSSMR
1	0.64	1	1.6	SEQ ID NO: 1539	NLEFQGPLEISR
1	0.6	0.93	1.4	SEQ ID NO: 1540	TLQELEELQNDSEIDQLALESPE VQDLQLER

SEQ ID NO: 1541

1 M E T L K D K T L Q E L E E L Q N D S E A I D Q L A L E S P E V Q D L Q L E R E
M A L A T N R S L A E R N L E F Q G P L E I S R S N L S D R Y Q E L R K L V E R

81 C Q E Q K A K L E K F S S A L Q P G T L L D L L Q V E G M K I E E E S E A M A E
K F L E G E V P L E T F L E N F S S M R M L S H L R R V R V E K L Q E V V R K P

161 R A S Q E L A G D A P P P R P P P P V R P V P Q G T P P V V E E Q P Q P P L A M
P P Y P L P Y S P S P S L P V G P T A H G A L P P A P F P V V S Q P S F Y S G P

241 L G P T Y P A A Q L G P R G A A G Y S W S P Q R S M P P R P G Y P G T P M G A
S G P G Y P L R G G R A P S P G Y P Q Q S P Y P A T G G K P P Y P I Q P Q L P S F

321 P G Q P Q P S V P L Q P P Y P P G P A P P Y G F P P P P G P A W P G Y

5.304 NAD(P)H dehydrogenase, quinone 2 [*Homo sapiens*]
Protein Accession gi|156564357
Mean Expression Ratio 0.972
Median Expression Ratio 0.97
Credible Interval (0.596, 1.58)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0779
[0422]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.97	1.6	SEQ ID NO: 1542	VLAPQISFAPEIASSEER
SEQ ID NO: 1543					
1MAGKKVLIVYAHQEPKSFNGSLKNVAVDELSRQGCTVTVS					
DLYAMNLEPRATDKDITGTLSPNEVFNYGVETHEAYKQRS					
81LASDITDEQKKVREADLVIQFPPLYWFSVPAILKGMMDRV					
LCQGFAFDIPGFYDSGLLQGGKLLSVTTGGTAEMYTKTG					
161VNGDSRYFLWPLQHGTTLHFCCGFKVLA PQISFAPEIASSEER					
RKGMMVAAWSQRLQTIWKKEEPIPCTAHWHFGQ					

5.305 cystatin B [*Homo sapiens*]
Protein Accession gi|4503117
Mean Expression Ratio 0.97
Median Expression Ratio 0.97
Credible Interval (0.603, 1.59)

Associated Peptides 1
Associated Spectra 1
Coverage 0.122
[0423]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.96	1.6	SEQ ID NO: 1544	VHVGDEDFVHLR
SEQ ID NO: 1545					
1MMCGAPSA TQPA TAE TQH IADQVRSQLEEKENKKFPVFKA					
VSFKSQVVAGTNYFIKVHVGDEDFVHLRVFQSLPHENKPL					
81TLSNYQTNKAKHDELT YF					

5.306 triosephosphate isomerase 1 [*Homo sapiens*]
Protein Accession gi|4507645
Mean Expression Ratio 1.03
Median Expression Ratio 1.03
Credible Interval (0.635, 1.68)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0522
[0424]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	1.0	1.7	SEQ ID NO: 1546	TATPQQAQEVHEK
SEQ ID NO: 1547					
1MAPSRKFFVGGNWKMN GRKQSLGELIGTLNAAKVPADTE					
VVCA PPTAYIDFARQKLDPKIAVAAQNCYKV TNGAFTGEIS					

[0425]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	0.93	1.4	SEQ ID NO: 1553	IIHGQDFDQR
1	0.63	0.96	1.5	SEQ ID NO: 1554	LGEPDYIPSQQDILLAR
1	0.65	0.98	1.5	SEQ ID NO: 1555	LTESLNIFETIVNNR
1	0.66	1	1.5	SEQ ID NO: 1556	VFLQYLP AIR

-continued

SEQ ID NO: 1557					
1	M	A	D	F	L
2	P	S	R	S	V
3	L	S	V	C	F
4	P	G	C	L	L
5	T	S	G	E	A
6	E	Q	Q	R	K
7	S	K	E	I	D
8	K	C	L	S	R
9	E	K	T	Y	V
10	K	R	L	V	K
11	I	L	L	L	G
12	A	G	E	S	G
13	K	S	T	F	L
14	K	Q	M	R	I
15	I	H	G	Q	D
16	F	D	Q	R	A
17	8	1	R	E	E
18	F	R	P	T	I
19	V	S	N	V	I
20	K	G	M	R	V
21	L	V	D	A	R
22	E	K	L	H	I
23	P	W	G	D	N
24	S	N	Q	Q	H
25	G	D	K	M	M
26	S	F	D	T	R
27	A	P	M	A	A
28	Q	G	M	V	E
29	T	R	V	F	L
30	Q	Y	L	P	A
31	I	R	A	L	W
32	A	D	S	G	I
33	Q	N	1	6	1
34	A	Y	D	R	R
35	R	E	F	Q	L
36	G	E	S	V	K
37	Y	F	L	D	N
38	L	D	K	L	G
39	E	P	D	Y	I
40	P	S	Q	Q	D
41	I	L	L	A	R
42	R	P	T	K	G
43	I	H	E	Y	D
44	F	E	I	K	N
45	V	P	F	K	M
46	V	D	V	G	G
47	Q	R	S	E	R
48	K	R	W	F	E
49	C	F	D	S	V
50	2	4	1	T	S
51	I	L	F	L	V
52	S	S	S	E	F
53	D	Q	V	L	M
54	E	D	R	L	T
55	N	R	L	T	E
56	S	L	N	I	F
57	E	T	I	V	N
58	N	R	V	F	S
59	N	V	S	I	I
60	L	F	L	N	K
61	T	D	L	L	E
62	E	E	K	V	Q
63	I	V	S	I	K
64	D	Y	F	L	E
65	F	E	G	D	P
66	H	C	L	R	3
67	2	1	D	V	Q
68	K	F	L	V	E
69	C	F	R	N	K
70	R	R	D	Q	Q
71	Q	K	P	L	Y
72	H	H	F	T	T
73	A	I	N	T	E
74	N	I	R	L	V
75	F	R	D	V	K
76	D	T	I	L	H
77	D	N	L	K	Q
78	L	M	L	Q	

5.309 phospholipid scramblase 3 [*Homo sapiens*]
Protein Accession gi|31543417

Associated Peptides 1

Associated Spectra 3

Mean Expression Ratio 1.03

Median Expression Ratio 1.03

Coverage 0.0678

Credible Interval (0.687, 1.54)

[0427]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.7	1.0	1.5	SEQ ID NO: 1558	EALTDADDFGLQFPLDLVDVR
SEQ ID NO: 1559					
1	M	A	G	Y	L
2	P	P	K	G	Y
3	A	P	S	P	P
4	P	P	P	P	P
5	P	P	P	P	P
6	P	P	P	P	P
7	P	P	P	P	P
8	P	P	P	P	P
9	P	P	P	P	P
10	P	P	P	P	P
11	P	P	P	P	P
12	P	P	P	P	P
13	P	P	P	P	P
14	P	P	P	P	P
15	P	P	P	P	P
16	P	P	P	P	P
17	P	P	P	P	P
18	P	P	P	P	P
19	P	P	P	P	P
20	P	P	P	P	P
21	P	P	P	P	P
22	P	P	P	P	P
23	P	P	P	P	P
24	P	P	P	P	P
25	P	P	P	P	P
26	P	P	P	P	P
27	P	P	P	P	P
28	P	P	P	P	P
29	P	P	P	P	P
30	P	P	P	P	P
31	P	P	P	P	P
32	P	P	P	P	P
33	P	P	P	P	P
34	P	P	P	P	P
35	P	P	P	P	P
36	P	P	P	P	P
37	P	P	P	P	P
38	P	P	P	P	P
39	P	P	P	P	P
40	P	P	P	P	P
41	P	P	P	P	P
42	P	P	P	P	P
43	P	P	P	P	P
44	P	P	P	P	P
45	P	P	P	P	P
46	P	P	P	P	P
47	P	P	P	P	P
48	P	P	P	P	P
49	P	P	P	P	P
50	P	P	P	P	P
51	P	P	P	P	P
52	P	P	P	P	P
53	P	P	P	P	P
54	P	P	P	P	P
55	P	P	P	P	P
56	P	P	P	P	P
57	P	P	P	P	P
58	P	P	P	P	P
59	P	P	P	P	P
60	P	P	P	P	P
61	P	P	P	P	P
62	P	P	P	P	P
63	P	P	P	P	P
64	P	P	P	P	P
65	P	P	P	P	P
66	P	P	P	P	P
67	P	P	P	P	P
68	P	P	P	P	P
69	P	P	P	P	P
70	P	P	P	P	P
71	P	P	P	P	P
72	P	P	P	P	P
73	P	P	P	P	P
74	P	P	P	P	P
75	P	P	P	P	P
76	P	P	P	P	P
77	P	P	P	P	P
78	P	P	P	P	P
79	P	P	P	P	P
80	P	P	P	P	P
81	P	P	P	P	P
82	P	P	P	P	P
83	P	P	P	P	P
84	P	P	P	P	P
85	P	P	P	P	P
86	P	P	P	P	P
87	P	P	P	P	P
88	P	P	P	P	P
89	P	P	P	P	P
90	P	P	P	P	P
91	P	P	P	P	P
92	P	P	P	P	P
93	P	P	P	P	P
94	P	P	P	P	P
95	P	P	P	P	P
96	P	P	P	P	P
97	P	P	P	P	P
98	P	P	P	P	P
99	P	P	P	P	P
100	P	P	P	P	P

5.310 plasma glutamate carboxypeptidase [*Homo sapiens*]
Protein Accession gi|7706387

Mean Expression Ratio 0.974

Median Expression Ratio 0.972

Credible Interval (0.602, 1.57)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0233

[0428]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.59	0.96	1.6	SEQ ID NO: 1560	LALLVDTVGPRLSG
SEQ ID NO: 1561					
1	M	K	F	L	I
2	F	A	F	F	G
3	G	V	H	L	L
4	S	L	C	S	G
5	K	A	I	C	K
6	N	G	I	S	K
7	R	T	F	E	E
8	I	K	E	E	I
9	A	S	C	G	D
10	V	A	K	A	I
11	I	N	L	A	V
12	Y	G	K	A	Q
13	N	R	S	Y	E
14	R	L	A	L	L
15	V	D	T	V	G
16	P	R	L	S	G
17	8	1	S	K	N
18	L	E	K	A	I
19	Q	I	M	Y	Q
20	N	L	Q	Q	D
21	G	L	E	K	V
22	H	L	E	P	V
23	R	I	P	H	W
24	E	R	G	E	E
25	S	A	V	M	L
26	E	P	R	I	H
27	K	I	A	I	L
28	G	L	G	S	S
29	I	G	T	P	P
30	E	G	I	T	A
31	E	V	L	V	V
32	T	S	F	D	E
33	L	Q			

-continued

161	R R A S E A R G K I V V Y N Q P Y I N Y S R T V Q Y R T Q G A V E A A K V G A
	L A S L I R S V A S F S I Y S P H T G I Q E Y Q D G V P K I P T A C I T V E D A E
241	M M S R M A S H G I K I V I Q L K M G A K T Y P D T D S F N T V A E I T G S K
	Y P E Q V V L V S G H L D S W D V G Q G A M D D G G G A F I S W E A L S L I K D L
321	G L R P K R T L R L V L W T A E E Q G G V G A F Q Y Y Q L H K V N I S N Y S L
	V M E S D A G T F L P T G L Q F T G S E K A R A I M E E V M S L L Q P L N I T Q V
401	L S H G E G T D I N F W I Q A G V P G A S L L D D L Y K Y F F F H H S H G D T
	M T V M D P K Q M N V A A A V W A V V S Y V V A D M E E M L P R S

5.311 bone marrow stromal cell antigen 1 precursor [*Homo sapiens*]
Protein Accession gi|168229159

Mean Expression Ratio 1.02

Median Expression Ratio 1.03

Credible Interval (0.626, 1.66)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0429]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	1.0	1.7	SEQ ID NO: 1562	SLFWENSHLLVNSFADNTR

5.312 solute carrier organic anion transporter family, member 4C1 [*Homo sapiens*]

Protein Accession gi|38679890

Mean Expression Ratio 0.974

Median Expression Ratio 0.973

Credible Interval (0.595, 1.57)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0221

[0430]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.97	1.6	SEQ ID NO: 1563	GIENLAFVPSSPDILR
SEQ ID NO: 1564					
1M K S A K G I E N L A F V P S S P D I L R R L S A S P S Q I E V S A L S S D P Q R E					
N S Q P Q E L Q K P Q E P Q K S P E P S L P S A P P N V S E E K L R S L S L					
81S E F E E G S Y G W R N F H P Q C L Q R C N T P G G F L L H Y C L L A V T Q G I					
V V N G L V N I S I S T V E K R Y E M K S S L T G L I S S S Y D I S F C L L S L					
161F V S F F G E R G H K P R W L A F A A F M I G L G A L V F S L P Q F F S G E Y K					
L G S L F E D T C V T T R N S T S C T S S T S S L S N Y L Y V F I L G Q L L L G					
241A G G T P L Y T L G T A F L D D S V P T H K S S L Y I G T G Y A M S I L G P A I					
G Y V L G G Q L L T I Y I D V A M G E S T D V T E D D P R W L G A W W I G F L L					
321S W I F A W S L I I P F S C F P K H L P G T A E I Q A G K T S Q A H Q S N S N A					
D V K F G K S I K D F P A A L K N L M K N A V F M C L V L S T S S E A L I T T G					
401F A T F L P K F I E N Q F G L T S S F A A T L G G A V L I P G A A L G Q I L G G F					
L V S K F R M T C K N T M K F A L F T S G V A L T L S F V F M Y A K C E N E P					
481F A G V S E S Y N G T G E L G N L I A P C N A N C N C S R S Y Y Y P V C G D G					
V Q Y F S P C F A G C S N P V A H R K P K V Y Y N C S C I E R K T E I T S T A E T					
561F G F E A K A G K C E T H C A K L P I F L C I F F I V I I F T F M A G T P I T V S I					
L R C V N H R Q R S L A L G I Q F M V L R L L G T I P G P I I F G F T I D S					
641T C I L W D I N D C G I K G A C W I Y D N I K M A H M L V A I S V T C K V I T					
M F F N G F A I F L Y K P P P S A T D V S F H K E N A V V T N V L A E Q D L N K I					
721V K E G					

5.313 glucose transporter 14 [*Homo sapiens*]
Protein Accession gi|23592238
Mean Expression Ratio 1.03
Median Expression Ratio 1.03
Credible Interval (0.626, 1.68)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0173
[0431]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	1.0	1.7	SEQ ID NO: 1565	QVTVLELFR

SEQ ID NO: 1566

1MEFHNGGHHVSGIGGFLVSLTSRMKPHHTLAVTPALIFAITVA
TIGSFQFGYNTGVINAPETIIKEEFINKTLTDKANAPPSE

81VLLTNLWSLSVAIFSVMIGSFSVGLFVNRFGRRNSMLI
VNLAAATGGCLMGLCKIAESVEMLIILGRLLVIGLFCGLCTG

161FVPMYIGEISPTALRGAFGTNLQGLGIVIGILVAQIFGLEELIL
GSEELWPPVLLGFTIILPAIILQSAALPCCPESPRFLLINR

241KKEENATRIQLRWGTQDVSQDIQEMKDESARMSQEKQV
TVLEELFRVSSSYRQPIIISIVLQLSQQLSGINAVFYYSTGIF

321KDAQVQQPIIYATISAGVVNTIFTLLSLFLVERAGRRTLHM
IGLGGMAFCSTLMTVSLLLKNHYNGMSFVCIGAILVFVAC

401FEIGPGPIPWFIVAELFSQGP RPAAAMAVAGCSNWT SNFLV
GLLFPSSAAYYLGA YVFIIFTGFLLITFLAFTFFKVPETRGR

481TFEDITRAFEGQAHGADRSGKDGVMGMNSIEPAKETTTNV

5.314 PREDICTED: hypothetical protein [*Homo sapiens*]
Protein Accession gi|169218200
Mean Expression Ratio 1.03
Median Expression Ratio 1.03
Credible Interval (0.79, 1.35)
Associated Peptides 4
Associated Spectra 13
Coverage NaN
[0432]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.78	1.1	1.5	SEQ ID NO: 1567	ESNGQPENNYK
9	0.83	1.1	1.3	SEQ ID NO: 1568	GFYPSDIAVEWESNGQP ENNYK
1	0.7	1	1.4	SEQ ID NO: 1569	NQVSLTCLVK
1	0.68	0.98	1.4	SEQ ID NO: 1570	TTPPMLDSGDSFFLYSK

5.315 serine hydroxymethyltransferase 1 (soluble) isoform 2 [*Homo sapiens*]; serine hydroxymethyltransferase 1 (soluble) isoform 1 [*Homo sapiens*]
Protein Accession gi|22547189 gi|22547186
Mean Expression Ratio 0.972
Median Expression Ratio 0.974
Credible Interval (0.599, 1.56)
Associated Peptides 1
Associated Spectra 1
Coverage NaN
[0433]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.97	1.6	SEQ ID NO: 1571	VNPDTGYINYDQLEENAR

5.316 calcium binding protein P22 [*Homo sapiens*]
Protein Accession gi|6005731
Mean Expression Ratio 1.02
Median Expression Ratio 1.03
Credible Interval (0.625, 1.65)
Associated Peptides 1
Associated Spectra 1
Coverage 0.082

[0434]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	1.0	1.7	SEQ ID NO: 1572	IINAFFPEGEDQVNFR

SEQ ID NO: 1573

1M G S R A S T L L R D E E L E E I K K E T G F S H S Q I T R L Y S R F T S L D K G E
N G T L S R E D F Q R I P E L A I N P L G D R I I N A F F P E G E D Q V N F

81R G F M R T L A H F R P I E D N E K S K D V N G P E P L N S R S N K L H F A F R
L Y D L D K D E K I S R D E L L Q V L R M M V G V N I S D E Q L G S I A D R T I

161Q E A D Q D G D S A I S F T E F V K V L E K V D V E Q K M S I R F L H

5.317 sushi domain containing 2 [*Homo sapiens*]
Protein Accession gi|10092665

Associated Peptides 1

Mean Expression Ratio 0.975

Associated Spectra 1

Median Expression Ratio 0.975

Coverage 0.0170

Credible Interval (0.594, 1.57)

[0435]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.57	0.97	1.6	SEQ ID NO: 1574	GEYVLLAALTDLR

SEQ ID NO: 1575

1M K P A L L P W A L L L L A T A L G P G P G P T A D A Q E S C S M R C G A L D G
P C S C H P T C S G L G T C C L D F R D F C L E I L P Y S G S M M G G K D F V V

81R H F K M S S P T D A S V I C R F K D S I Q T L G H V D S S G Q V H C V S P L L
Y E S G R I P F T V S L D N G H S F P R A G T W L A V H P N K V S M M E K S E L

161V N E T R W Q Y Y G T A N T S G N L S L T W H V K S L P T Q T I T I E L W G Y
E E T G M P Y S Q E W T A K W S Y L Y P L A T H I P N S G S F T F T P K P A P P S

241Y Q R W R V G A L R I I D S K N Y A G Q K D V Q A L W T N D H A L A W H L S
D D F R E D P V A W A R T Q C Q A W E E L E D Q L P N F L E E L P D C P C T L T Q A

321R A D S G R F F T D Y G C D M E Q G S V C T Y H P G A V H C V R S V Q A S L R
Y G S G Q Q C C Y T A D G T Q L L T A D S S G G S T P D R G H D W G A P P F R T P

401P R V P S M S H W L Y D V L S F Y Y C C L W A P D C P R Y M Q R R P S N D C
R N Y R P P R L A S A F G D P H F V T F D G T N F T F N G R G E Y V L L E A A L T D

481L R V Q A R A Q P G T M S N G T E T R G T G L T A V A V Q E G N S D V V E V
R L A N R T G G L E V L L N Q E V L S F T E Q S W M D L K G M F L S V A A G D R
V S

561I M L A S G A G L E V S V Q G P F L S V S V L L P E K F L T H T H G L L G T L N
N D P T D D F T L H S G R V L P P G T S P Q E L F L F G A N W T V H N A S S L L

641T Y D S W F L V H N F L Y Q P K H D P T F E P L F P S E T T L N P S L A Q E A A
K L C G D D H F C N F D V A A T G S L S T G T A T R V A H Q L H Q R R M Q S L Q

721P V V S C G W L A P P P N G Q K E G N R Y L A G S T I Y F H C D N G Y S L A G
A E T S T C Q A D G T W S S P T P K C Q P G R S Y A V L L G I I F G G L A V V A A

801V A L V Y V L L R R R K G N T H V W G A Q P

5.318 occludin [*Homo sapiens*]
Protein Accession gi|4505487
Mean Expression Ratio 1.03
Median Expression Ratio 1.03
Credible Interval (0.708, 1.48)
Associated Peptides 2
Associated Spectra 4
Coverage 0.0766
[0436]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.71	1.1	1.6	SEQ ID NO: 1576	NVSAGTQDVPSPPSDYVER
2	0.67	1.1	5	SEQ ID NO: 1577	STPVPEVVQELPLTSPVDDFR

SEQ ID NO: 1578

1MSSSRPLESPPPYRPDEFKPNHYAPSNDIYGGEMHVRLPMLSQ
PAYSFYPEDEILHFYKWTSPPGVIRILSMLIIVMCIAIF

81ACVASTLAWDRGYGTSLLLGGSVGYPYGGSGFGSYGSGYGY
YGYGYGYGYGGYTDPRAAKGFMLAMAAFCFIAALLVIFVTSV

161IRSEMSTRTRRYL SVIIVSAI L GIMVFIATIVYIMGVNPTA
QSSGSLYGSQIYALCNQFYTPAATGLYVDQYLYHYCVVD

241PQEAIAIVLGFMIIVAFALIIFFAVKTRRKMDRYDKSNILW
DKHEIYDEQPPNVEEWVKNVSA GTQDVPSPPSDYVERVD

321SPMAYSSNGKVN DKRFY PESSYKSTPVPEVVQELPLTSPV
DDFRQPRYSSSGGNFETPSKRAPAKGRAGRSKRTEQDHYET

401DYTTGGESCDELEEDWIREYPPITSDQQRQLYKRNFD TGL
QEYKSLQSELD EINKELSR LDKELDDYREES E EYMAA ADE

481YNRLKQVKGSADYKSKKNHCKQLKSKLSHIKKMVGDYD
RQKT

5.319 CD81 antigen [*Homo sapiens*]
Protein Accession gi|4757944
Mean Expression Ratio 1.03
Median Expression Ratio 1.03
Credible Interval (0.623, 1.68)

Associated Peptides 1
Associated Spectra 1
Coverage 0.0847
[0437]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	1.0	1.7	SEQ ID NO: 1579	QFYDQALQQAVVDDDDANNAK

SEQ ID NO: 1580

1MGVEGCTKCKIKYLLFVFN FVFWLAGGVILGVALLRLRHD PQ
TTNLLYLELGDKPAPNTFYVGIIYILIAVGAVMMFVGF LGC

81YGAIQESQCLLGTFFTCLVILFACEVAAGI WGFVNKDQIA
KDV KQFYDQALQQAVVDDDDANNAKAVVKTFHETLDCCGSS

161TLTALTTSVLKNNLCPSGSNIISNLFKEDCHQKIDDLFS GK
LYLIGIAAIVVAVIMIFEMI L SMVLCCGIRNSSVY

5.320 ectonucleotide pyrophosphatase/phosphodiesterase 6
[Homo sapiens]
Protein Accession gi|23503267
Mean Expression Ratio 0.977
Median Expression Ratio 0.976
Credible Interval (0.745, 1.27)
Associated Peptides 8
Associated Spectra 9
Coverage 0.225
[0438]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.72	1.0	1.5	SEQ ID NO: 1581	FVSPLTLVADEGWFITENR
1	0.69	0.99	1.4	SEQ ID NO: 1582	GIFLAFGPDFK
1	0.69	0.98	1.4	SEQ ID NO: 1583	IDVEGHHYGASPQR
2	0.7	0.99	1.4	SEQ ID NO: 1584	LLVFLLDGFR
1	0.68	0.97	1.4	SEQ ID NO: 1585	NVPTDINFANAVSDALDSFK
1	0.66	0.97	1.4	SEQ ID NO: 1586	YISLNDLQQVK
1	0.68	0.96	1.4	SEQ ID NO: 1587	GWHGYDNELMDMR
1	0.64	0.92	1.3	SEQ ID NO: 1588	AFGPDFK

SEQ ID NO: 1589

1MAVKLGTL L L L A L A L G L A Q P A S A R R K L L V F L L D G F R S D Y I S
D E A L E S L P G F K E I V S R G V K V D Y L T P D F P S L S Y P N Y Y T L M T

81G R H C E V H Q M I G N Y M W D P T T N K S F D I G V N K D S L M P L W W N
G S E P L W V T L T K A K R K V Y M Y Y W P G C E V E I L G V R P T Y C L E Y K
N V

161P T D I N F A N A V S D A L D S F K S G R A D L A A I Y H E R I D V E G H H Y G
P A S P Q R K D A L K A V D T V L K Y M T K W I Q E R G L Q D R L N V I I F S D

241H G M T D I F W M D K V I E L N K Y I S L N D L Q Q V K D R G P V V S L W P A
P G K H S E I Y N K L S T V E H M T V Y E K E A I P S R F Y Y K K G K F V S P L T

321L V A D E G W F I T E N R E M L P F W M N S T G R R E G W Q R G W H G Y D N
E L M D M R G I F L A F G P D F K S N F R A A P I R S V D V Y N V M C N V V G I T P

401L P N N G S W S R V M C M L K G R A S T A P P V W P S H C A L A L I L L F L L A

5.321 solute carrier family 5 (sodium/glucose cotrans-
porter), member 2 [Homo sapiens]
Protein Accession gi|4507033
Mean Expression Ratio 1.02
Median Expression Ratio 1.02

Credible Interval (0.661, 1.58)
Associated Peptides 1
Associated Spectra 2
Coverage 0.0283
[0439]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.66	1.0	1.6	SEQ ID NO: 1590	GGVGSPPLTQEEAAAAAR

SEQ ID NO: 1591

1MEEHTEAGSAPEMGAQKALIDNPADILVIAAYFLLVIGVGL
W S M C R T N R G T V G G Y F L A G R S M V W W P V G A S L F A S N I G S G H

81F V G L A G T G A A S G L A V A G F E W N A L F V V L L L G W L F A P V Y L T
A G V I T M P Q Y L R K R F G G R R I R L Y L S V L S L F L Y I F T K I S V D M F

-continued

161	S	G	A	V	F	I	Q	Q	A	L	G	W	N	I	Y	A	S	V	I	A	L	L	G	I	T	M	I	Y	T	V	T	G	G	L	A	A	L	M	Y	T	
	D	T	V	Q	T	F	V	I	L	G	G	A	C	I	L	M	G	Y	A	F	H	E	V	G	G	Y	S	G	L	F	D	K	Y	L	G	A	A	T	S	L	
241	T	V	S	E	D	P	A	V	G	N	I	S	S	F	C	Y	R	P	R	P	D	S	Y	H	L	L	R	H	P	V	T	G	D	L	P	W	P	A	L	L	
	L	G	L	T	I	V	S	G	W	Y	W	C	S	D	Q	V	I	V	Q	R	C	L	A	G	K	S	L	T	H	I	K	A	G	C	I	L	C	G	Y	L	
321	K	L	T	P	M	F	L	M	V	M	P	G	M	I	S	R	I	L	Y	P	D	E	V	A	C	V	V	P	E	V	C	R	R	V	C	G	T	E	V		
	G	C	S	N	I	A	Y	P	R	L	V	V	K	L	M	P	N	G	L	R	G	L	M	L	A	V	M	L	A	A	L	M	S	S	L	A	S	I	F	N	S
401	S	S	T	L	F	T	M	D	I	Y	T	R	L	R	P	R	A	G	D	R	E	L	L	V	G	R	L	W	V	V	F	I	V	V	S	V	A				
	W	L	P	V	V	Q	A	A	Q	G	G	Q	L	F	D	Y	I	Q	A	V	S	S	Y	L	A	P	P	V	S	A	V	F	V	L	A	L	F	V	P	R	V
481	N	E	Q	G	A	F	W	G	L	I	G	G	L	M	G	L	A	R	L	I	P	E	F	S	F	G	S	G	S	C	V	Q	P	S	A	C	P	A	F		
	L	C	G	V	H	Y	L	Y	F	A	I	V	L	F	F	C	S	G	L	L	T	L	T	V	S	L	C	T	A	P	I	P	R	K	H	L	H	R	L	V	
561	F	S	L	R	H	S	K	E	E	R	E	D	L	D	A	D	E	Q	Q	G	S	S	L	P	V	Q	N	G	C	P	E	S	A	M	E	M	N	E	P		
	Q	A	P	A	P	S	L	F	R	Q	C	L	L	W	F	C	G	M	S	R	G	V	G	S	P	P	P	L	T	Q	E	E	A	A	A	A	A	R	R	L	
641	E	D	I	S	E	D	P	S	W	A	R	V	V	N	L	N	A	L	L	M	M	A	V	A	V	F	L	W	G	F	Y	A									

5.322 MIT, microtubule interacting and transport, domain containing 1 [*Homo sapiens*]
Protein Accession gi|20270349

Mean Expression Ratio 1.03

Median Expression Ratio 1.02

Credible Interval (0.627, 1.65)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0723
[0440]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	1.0	1.7	SEQ ID NO: 1592	EYLNETHVTEVWIEDPYIR
SEQ ID NO: 1593					
1MAKSGLRQDPQSTAAATV LKRAVELDSESRYPQALVCYQE					
GIDL L LQVLKGT KDNTKRCNLREKISKYMDRAENIKKYLD					
81QEKEDGKYHKQIKIEENATGFSYESLFREYLNETHVTEVWI					
EDPYIRHTHQLYNFLRFCEMLIKRPCKVKTIHLLTSLDEG					
161IEQVQQSRGLQEIEESLRSHGV LLEVQYSSSIHSDREIRFNN					
GWMIKIGRGLDYFKKPKQSRFSLGYCDFDLRPCHETTVDI					
241FHKKHTKNI					

5.323 ring finger protein 167 [*Homo sapiens*]
Protein Accession gi|14149702
Mean Expression Ratio 0.976
Median Expression Ratio 0.98
Credible Interval (0.67, 1.40)
Associated Peptides 2
Associated Spectra 4
Coverage 0.0657
[0441]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	0.97	1.5	SEQ ID NO: 1594	GDEDQEEETQGQEEGDEGEPR
3	0.67	0.97	1.4	SEQ ID NO: 1595	GPGDEDQEEETQGQEEGDEGEPR
SEQ ID NO: 1596					
1MHPA A F P L P V V V A A V L W G A A P T R G L I R A T S D H N A S M D F A D					
L P A L F G A T L S Q E G L Q G F L V E A H P D N A C S P I A P P P P A P V N G					

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81	S	V	F	I	A	L	L	R	R	F	D	C	N	F	D	L	K	V	L	N	A	Q	K	A	G	Y	G	A	A	V	V	H	N	V	N	S	N	E	L		
	L	N	M	V	W	N	S	E	E	I	Q	Q	Q	I	W	I	P	S	V	F	I	G	E	R	S	S	E	Y	L	R	A	L	F	V	Y	E	K	G	A	R	V
161	L	L	V	P	D	N	T	F	P	L	G	Y	Y	L	I	P	F	T	G	I	V	G	L	L	V	L	A	M	G	A	V	M	I	A	R	C	I	Q	H	R	
	K	R	L	Q	R	N	R	L	T	K	E	Q	L	K	Q	I	P	T	H	D	Y	Q	K	G	D	Q	Y	D	V	C	A	I	C	L	D	E	Y	E	D	G	
241	D	K	L	R	V	L	P	C	A	H	A	Y	H	S	R	C	V	D	P	W	L	T	Q	T	R	K	T	C	P	I	C	K	Q	P	V	H	R	G	P		
	G	D	E	D	Q	E	E	E	T	Q	G	Q	E	E	G	D	E	G	E	P	R	D	H	P	A	S	E	R	T	P	L	L	G	S	S	P	T	L	P	T	S
321	F	G	S	L	A	P	A	P	L	V	F	P	G	P	S	T	D	P	P	L	S	P	P	S	S	P	V	I	L	V											

5.324 ubiquitin protein ligase E3C [*Homo sapiens*]
Protein Accession gi|187960100

Mean Expression Ratio 0.98

Median Expression Ratio 0.98

Credible Interval (0.6, 1.59)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0442]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.58	0.98	1.6	SEQ ID NO: 1597	LNQRQIRQHCLAFR

5.325 syntaxin 8 [*Homo sapiens*]
Protein Accession gi|4759188

Mean Expression Ratio 0.98

Median Expression Ratio 0.98

Credible Interval (0.609, 1.57)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0763

[0443]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.59	0.98	1.6	SEQ ID NO: 1598	IIQEQDAGLDALSSIISR
SEQ ID NO: 1599					
1	M	A	P	D	P
	W	F	S	T	Y
	D	S	T	C	Q
	I	A	Q	E	I
	A	E	K	I	Q
	Q	R	N	Q	Y
	E	R	K	G	E
	K	A	P	K	L
	T	V	T	I	R
	A	L	L	Q	N
	L	K	E	K	I
	A	L	L	K	D
	L	L	L	R	A
	V	S	T	H	Q
	I	T	Q	L	E
	G	D	R	R	Q
81	N	L	L	D	D
	L	V	T	R	E
	R	L	L	L	A
	S	F	K	N	E
	G	A	E	P	D
	L	I	R	S	S
	L	M	S	E	E
	A	K	R	G	A
	P	N	P	W	L
	F	E	E	P	E
	E	T	R	G	L
	G	F	D	E	I
	R	Q	Q	Q	K
	I	I	Q	E	Q
	D	A	G	L	D
	A	L	S	S	
161	I	I	S	R	Q
	K	Q	M	G	Q
	E	I	G	N	E
	L	D	E	Q	N
	E	I	I	D	D
	L	A	N	L	V
	E	N	T	D	E
	K	L	R	N	E
	T	R	R	V	N
	M	V	D	R	K
	S	A	S	C	G
	M	I	M	V	I
	L	L	L	L	V
	A	I	V	V	V
	A	V	W	P	T
	N				

5.326 sorting nexin 3 [*Homo sapiens*]
Protein Accession gi|4507143

Mean Expression Ratio 0.981

Median Expression Ratio 0.98

Credible Interval (0.603, 1.60)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0494

[0444]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.59	0.98	1.6	SEQ ID NO: 1600	YSDFEWLR
SEQ ID NO: 1601					
1	M	A	E	T	V
	A	D	T	R	R
	L	I	T	K	P
	Q	N	L	N	D
	A	Y	G	P	P
	S	N	F	L	E
	I	D	V	S	N
	P	Q	T	V	G
	V				
	G	R	G	R	F
	T	T	Y	E	I
	R	V	K	T	N
	L	P	I	F	K
	L	K	E	S	T
	V	R	R	R	Y
	S	D	F	E	W
	L	R	S	E	

-continued

81	L	E	R	E	S	K	V	V	V	P	P	L	P	G	K	A	F	L	R	Q	L	P	F	R	G	D	D	G	I	F	D	D	N	F	I	E	E	R	K	Q	G	
	L	E	Q	F	I	N	K	V	A	G	H	P	L	A	Q	N	E	R	C	L	H	M	F	L	Q	D	E	I	I	D	K	S	Y	T	P	S	K	I	R			
161	H	A																																								

5.327 RAB7, member RAS oncogene family [*Homo sapi-*
ens]
Protein Accession gil34147513
Mean Expression Ratio 1.02
Median Expression Ratio 1.02
Credible Interval (0.798, 1.3)
Associated Peptides 9
Associated Spectra 12
Coverage 0.483
[0445]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.74	1	1.4	SEQ ID NO: 1602	DEFLIQASPR
1	0.72	1.0	1.5	SEQ ID NO: 1603	DPENFPFVVLGNK
2	0.77	1.1	1.5	SEQ ID NO: 1604	EAINVEQAFQTAR
1	0.71	1.0	1.4	SEQ ID NO: 1605	FQSLGVAFYR
1	0.72	1.0	1.4	SEQ ID NO: 1606	LVTMQIWDTAGQER
2	0.72	1	1.4	SEQ ID NO: 1607	QETEVELYNEFPEPIK
1	0.71	1	1.4	SEQ ID NO: 1608	TLDSWRDEFLIQASPR
1	0.71	1	1.4	SEQ ID NO: 1609	FSNQYK
1	0.71	1.0	1.4	SEQ ID NO: 1610	NNIPYFETSAK

SEQ ID NO: 1611
1M T S R K K V L L K V I I L G D S G V G K T S L M N Q Y V N K K F S N Q Y K A T
I G A D F L T K E V M V D D R L V T M Q I W D T A G Q E R F Q S L G V A F Y R G
81A D C C V L V F D V T A P N T F K T L D S W R D E F L I Q A S P R D P E N F P F
V V L G N K I D L E N R Q V A T K R A Q A W C Y S K N N I P Y F E T S A K E A I
161N V E Q A F Q T I A R N A L K Q E T E V E L Y N E F P E P I K L D K N D R A K A
S A E S C S C

5.328 prenylcysteine oxidase 1 [*Homo sapiens*]
Protein Accession gil166795301

[0446]

Mean Expression Ratio 1.02
Median Expression Ratio 1.02
Credible Interval (0.714, 1.44)
Associated Peptides 4
Associated Spectra 4
Coverage NaN

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.65	1	1.5	SEQ ID NO: 1612	FGLNTVLTTDNS DLFINSIGIVPSVR
1	0.66	1	1.5	SEQ ID NO: 1613	FLNEMIAPVMR
1	0.66	1.0	1.5	SEQ ID NO: 1614	MHMWVEDVLDK
1	0.7	1.1	1.6	SEQ ID NO: 1615	SDFYDIVLVATPLNR

5.329 glucose phosphate isomerase [*Homo sapiens*]
Protein Accession gil18201905
Mean Expression Ratio 1.02
Median Expression Ratio 1.02
Credible Interval (0.62, 1.63)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0305
[0447]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	1.0	1.7	SEQ ID NO: 1616	MIPCDFLIPVQTQHP
SEQ ID NO: 1617					
1M A A L T R D P Q F Q K L Q Q W Y R E H R S E L N L R R L F D A N K D R F N H F					
S L T L N T N H G H I L V D Y S K N L V T E D V M R M L V D L A K S R G V E A A					
81R E R M F N G E K I N Y T E G R A V L H V A L R N R S N T P I L V D G K D V M P					
E V N K V L D K M K S F C Q R V R S G D W K G Y T G K T I T D V I N I G I G G S					
161D L G P L M V T E A L K P Y S S G G P R V W Y V S N I D G T H I A K T L A Q L					
N P E S S L F I I A S K T F T T Q E T I T N A E T A K E W F L Q A A K D P S A V A					
241K H F V A L S T N T T K V K E F G I D P Q N M F E F W D W V G G R Y S L W S					
A I G L S I A L H V G F D N F E Q L L S G A H W M D Q H F R T T P L E K N A P V L L					
321A L L G I W Y I N C F G C E T H A M L P Y D Q Y L H R F A A Y F Q Q G D M E S					
N G K Y I T K S G T R V D H Q T G P I V W G E P G T N G Q H A F Y Q L I H Q G T K					
401M I P C D F L I P V Q T Q H P I R K G L H H K I L L A N F L A Q T E A L M R G K					
S T E E A R K E L Q A A G K S P E D L E R L L P H K V F E G N R P T N S I V F T					
481K L T P F M L G A L V A M Y E H K I F V Q G I I W D I N S F D Q W G V E L G K					
Q L A K K I E P E L D G S A Q V T S H D A S T N G L I N F I K Q Q R E A R V Q					

5.330 galactosidase, beta 1 isoform a preproprotein [*Homo sapiens*]
Protein Accession gil119372308
Mean Expression Ratio 0.981
Median Expression Ratio 0.982

Credible Interval (0.798, 1.20)
Associated Peptides 12
Associated Spectra 17
Coverage 0.183
[0448]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.74	1	1.4	SEQ ID NO: 1618	AGATLDLLVENMGR
2	0.73	0.99	1.3	SEQ ID NO: 1619	AYVAVDGIPQGVLER
2	0.79	1.1	1.5	SEQ ID NO: 1620	GQVWINGFNLGR
1	0.71	0.99	1.4	SEQ ID NO: 1621	LAHELGLLVILRPGPY
1	0.71	0.98	1.3	SEQ ID NO: 1622	TEAVASSLYDILAR
1	0.72	1	1.4	SEQ ID NO: 1623	TVGAALDILCPSPGIK
1	0.71	0.98	1.4	SEQ ID NO: 1624	VAVDGIPQGVLER
1	0.7	0.98	1.4	SEQ ID NO: 1625	WLGVLPLPK
2	0.69	0.92	1.3	SEQ ID NO: 1626	HHLGDDVVLF
1	0.7	0.97	1.3	SEQ ID NO: 1627	ACDFDYLR

-continued

1	0.71	0.98	1.4	SEQ ID NO: 1628	VNYGAYINDFK
2	0.67	0.9	1.2	SEQ ID NO: 1629	LAHELGLLVILR
SEQ ID NO: 1630					
1M P G F L V R I L P L L L V L L L L G P T R G L R N A T Q R M F E I D Y S R D S F					
L K D G Q P P R Y I S G S I H Y S R V P R P Y W K D R L L K M K M A G L N A I					
81Q T Y V P W N F H E P W P G Q Y Q F S E D H D V E Y F L R L A H E L G L L V I L					
R P G P Y I C A E W E M G G L P A W L L E K E S I L L R S S D P D Y L A A V D K					
161W L G V L L P K M K P L L Y Q N G G P V I T V Q V E N E Y G S Y F A C D F D Y					
L R F L Q K R F R H H L G D D V V L F T T D G A H K T F L K C G A L Q G L Y T T V					
241D F G T G S N I T D A F L S Q R K C E P K G P L I N S E F Y T G W L D H W G Q P					
H S T I K T E A V A S S L Y D I L A R G A S V N L Y M F I G G T N F A Y W N G A					
321N S P Y A A Q P T S Y D Y D A P L S E A G D L T E K Y F A L R N I I Q K F E K V					
P E G P I P P S T P K F A Y G K V T L E K L K T V G A A L D I L C P S G P I K S					
401L Y P L T F I Q V K Q H Y G F V L Y R T T L P Q D C S N P A P L S S P L N G V H					
D R A Y V A V D G I P Q G V L E R N N V I T L N I T G K A G A T L D L L V E N M					
481G R V N Y G A Y I N D F K G L V S N L T L S S N I L T D W T I F P L D T E D A V					
R S H L G G W G H R D S G H H D E A W A H N S S N Y T L P A F Y M G N F S I P S					
561G I P D L P Q D T F I Q F P G W T K G Q V W I N G F N L G R Y W P A R G P Q L					
T L F V P Q H I L M T S A P N T I T V L E L E W A P C S S D D P E L C A V T F V D					
641R P V I G S S V T Y D H P S K P V E K R L M P P P P Q K N K D S W L D H V					

5.331 GDP dissociation inhibitor 2 isoform 1 [Homo sapi-
ens]
Protein Accession gil6598323
Mean Expression Ratio 0.986
Median Expression Ratio 0.983

Credible Interval (0.61, 1.63)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0337
[0449]

A	2.5	50	97.5	Sequence ID No. 1631	Sequence
1	0.59	0.98	1.6	SEQ ID NO: 1632	TDDYLDQPCYETINR
SEQ ID NO: 1633					
1M N E E Y D V I V L G T G L T E C I L S G I M S V N G K K V L H M D R N P Y Y G					
G E S A S I T P L E D L Y K R F K I P G S P P E S M G R G R D W N V D L I P K F					
81L M A N G Q L V K M L L Y T E V T R Y L D F K V T E G S F V Y K G G K I Y K V					
P S T E A E A L A S S L M G L F E K R R F R K F L V Y V A N F D E K D P R T F E G					
161I D P K K T T M R D V Y K K F D L G Q D V I D F T G H A L A L Y R T D D Y L D					
Q P C Y E T I N R I K L Y S E S L A R Y G K S P Y L Y P L Y G L G E L P Q G F A R					
241L S A I Y G G T Y M L N K P I E E I I V Q N G K V I G V K S E G E I A R C K Q L I					
C D P S Y V K D R V E K V G Q V I R V I C I L S H P I K N T N D A N S C Q I I					
321I P Q N Q V N R K S D I Y V C M I S F A H N V A A Q G K Y I A I V S T T V E T K					
E P E K E I R P A L E L L E P I E Q K F V S I S D L L V P K D L G T E S Q I F I					
401S R T Y D A T T H F E T T C D D I K N I Y K R M T G S E F D F E E M K R K K N					
D I Y G E D					

5.332 solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform c [*Homo sapiens*]; solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform f [*Homo sapiens*]; solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform e [*Homo sapiens*]; solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform d [*Homo sapiens*]; solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform b [*Homo sapiens*]; solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform a [*Homo sapiens*]
Protein Accession gil65506891 gil61744483 gil61744481 gil61744479 gil61744477 gil61744475

Mean Expression Ratio 1.02
Median Expression Ratio 1.02
Credible Interval (0.627, 1.64)
Associated Peptides 1
Associated Spectra 1
Coverage NaN

[0450]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	1.0	1.7	SEQ ID NO: 1634	LLTSFLPAQLLR

5.333 heat shock 70 kDa protein 8 isoform 1 [*Homo sapiens*]
Protein Accession gil5729877
Mean Expression Ratio 1.02
Median Expression Ratio 1.02
Credible Interval (0.866, 1.20)
Associated Peptides 18
Associated Spectra 36
Coverage 0.302

[0451]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.75	1.0	1.4	SEQ ID NO: 1635	AVVTVPAYFNDSQR
2	0.74	0.98	1.3	SEQ ID NO: 1636	CNEIINWLDK
1	0.75	1.0	1.4	SEQ ID NO: 1637	DAGTIAGLNVLR
1	0.74	1.0	1.4	SEQ ID NO: 1638	FDDAVVQSDMK
5	0.8	1.0	1.3	SEQ ID NO: 1639	FEELNADLFR
1	0.75	1.0	1.4	SEQ ID NO: 1640	FELTGIPPAPR
2	0.76	1.0	1.4	SEQ ID NO: 1641	LLQDFFNGK
2	0.78	1.0	1.4	SEQ ID NO: 1642	MVNHFIAEFK
1	0.74	1.0	1.4	SEQ ID NO: 1643	NQTAEKEEFEHQQK
1	0.74	1	1.4	SEQ ID NO: 1644	NQVAMNPTNTVFDAK
1	0.75	1.0	1.4	SEQ ID NO: 1645	QTQTFTTYSQNPQGVLIQVYEGER
2	0.77	1.0	1.4	SEQ ID NO: 1646	RFDDAVVQSDMK
2	0.78	1.0	1.4	SEQ ID NO: 1647	SQIHDIIVLVGGSTR
5	0.76	0.98	1.3	SEQ ID NO: 1648	STAGDTHLGGEDFDNR
6	0.77	0.98	1.2	SEQ ID NO: 1649	TVTNAVVTVPAYFNDSQR
1	0.77	1.0	1.4	SEQ ID NO: 1650	MVVNDAGRPK
1	0.76	1.0	1.4	SEQ ID NO: 1651	VQVEYK
1	0.77	1.0	1.4	SEQ ID NO: 1652	HWPFMVVNDAGRPK

SEQ ID NO: 1653
1 M S K G P A V G I D L G T T Y S C V G V F Q H G K V E I I A N D Q G N R T T P S Y
V A F T D T E R L I G D A A K N Q V A M N P T N T V F D A K R L I G R R F D D

-continued

81A	V	V	Q	S	D	M	K	H	W	P	F	M	V	V	N	D	A	G	R	P	K	V	Q	V	E	Y	K	G	E	T	K	S	F	Y	P	E	E				
	V	S	S	M	V	L	T	K	M	K	E	I	A	E	A	Y	L	G	K	T	V	T	N	A	V	V	T	V	P	A	Y	F	N	D	S	Q	R	Q	A	T	
	K	D																																							
161A	G	T	I	A	G	L	N	V	L	R	I	I	N	E	P	T	A	A	A	I	A	Y	G	L	D	K	K	V	G	A	E	R	N	V	L	I	F	D	L		
	G	G	G	T	F	D	V	S	I	L	T	I	E	D	G	I	F	E	V	K	S	T	A	G	D	T	H	L	G	G	E	D	F	D	N	R	M	V	N	H	
241F	I	A	E	F	K	R	K	H	K	K	D	I	S	E	N	K	R	A	V	R	R	L	R	T	A	C	E	R	A	K	R	T	L	S	S	S	T	Q	A		
	S	I	E	I	D	S	L	Y	E	G	I	D	F	Y	T	S	I	T	R	A	R	F	E	E	L	N	A	D	L	F	R	G	T	L	D	P	V	E	K	A	
321L	R	D	A	K	L	D	K	S	Q	I	H	D	I	V	L	V	G	G	S	T	R	I	P	K	I	Q	K	L	L	Q	D	F	F	N	G	K	E	L	N		
	K	S	I	N	P	D	E	A	V	A	Y	G	A	A	V	Q	A	A	I	L	S	G	D	K	S	E	N	V	Q	D	L	L	L	L	D	V	T	P	L	S	
401L	G	I	E	T	A	G	G	V	M	T	V	L	I	K	R	N	T	T	I	P	T	K	Q	T	Q	T	F	T	T	Y	S	D	N	Q	P	G	V	L	I		
	Q	V	Y	E	G	E	R	A	M	T	K	D	N	N	L	L	G	K	F	E	L	T	G	I	P	P	A	P	R	G	V	P	Q	I	E	V	T	F	D	I	
481D	A	N	G	I	L	N	V	S	A	V	D	K	S	T	G	K	E	N	K	I	T	I	T	N	D	K	G	R	L	S	K	E	D	I	E	R	M	V	Q		
	E	A	E	K	Y	K	A	E	D	E	K	Q	R	D	K	V	S	S	K	N	S	L	E	S	Y	A	F	N	M	K	A	T	V	E	D	E	K	L	Q	G	
561K	I	N	D	E	D	K	Q	K	I	L	D	K	C	N	E	I	I	N	W	L	D	K	N	Q	T	A	E	K	E	E	F	E	H	Q	Q	K	E	L	E		
	K	V	C	N	P	I	I	T	K	L	Y	Q	S	A	G	G	M	P	G	G	M	P	G	G	F	P	G	G	G	A	P	P	S	G	G	A	S	S	G	P	
641T	I	E	E	V	D																																				

5.334 RAB9A, member RAS oncogene family [*Homo sapi-*
ens]

Protein Accession gi|4759012

Mean Expression Ratio 1.02

Median Expression Ratio 1.02

Credible Interval (0.627, 1.66)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0697

[0452]

A	2.5	50	97.5	Sequence ID No.	Sequence																																			
1	0.61	1.0	1.7	SEQ ID NO: 1654	DATNVAAAFEEAVR																																			
SEQ ID NO: 1655																																								
1M	A	G	K	S	S	L	F	K	V	I	L	L	G	D	G	G	V	G	K	S	S	L	M	N	R	Y	V	T	N	K	F	D	T	Q	L	F	H	T	I	
	G	V	E	F	L	N	K	D	L	E	V	D	G	H	F	V	T	M	Q	I	W	D	T	A	G	Q	E	R	F	R	S	L	R	T	P	F	Y	R	G	S
81D	C	C	L	L	T	F	S	V	D	D	S	Q	S	F	Q	N	L	S	N	W	K	K	E	F	I	V	Y	A	D	V	K	E	P	E	S	F	P	F	V	I
	L	G	N	K	I	D	I	S	E	R	Q	V	S	T	E	E	A	Q	A	W	C	R	D	N	G	D	Y	P	Y	F	E	T	S	A	K	D	A	T	N	
161V	A	A	A	F	E	E	A	V	R	R	V	L	A	T	E	D	R	S	D	H	L	I	Q	T	D	T	V	N	L	H	R	K	P	K	P	S	S	S	C	C

5.335 complement component 8, gamma polypeptide
[*Homo sapiens*]

Protein Accession gi|166197660

Mean Expression Ratio 1.02

Median Expression Ratio 1.02

Credible Interval (0.627, 1.65)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0453]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	1.0	1.7	SEQ ID NO: 1656	SLPVSDSVLSGFQR

5.336 MAPK scaffold protein 1 [*Homo sapiens*]

Protein Accession gi|11496277

Mean Expression Ratio 0.986

Median Expression Ratio 0.985

Credible Interval (0.667, 1.45)

Associated Peptides 2

Associated Spectra 3

Coverage 0.210

[0454]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.64	0.97	1.5	SEQ ID NO: 1657	ELAPLFEELR
1	0.64	1	1.6	SEQ ID NO: 1658	KLPSVEGLHAIVVSDR

SEQ ID NO: 1659

1 M A D D L K R F L Y K K L P S V E G L H A I V V S D R D G V P V I K V A N D N A
P E H A L R P G F L S T F A L A T D Q G S K L G L S K N K S I I C Y Y N T Y Q V

81 V Q F N R L P L V V S F I A S S S A N T G L I V S L E K E L A P L F E E L R Q V V
E V S

5.337 transketolase isoform 1 [*Homo sapiens*]; transketolase isoform 2 [*Homo sapiens*]; transketolase isoform 1 [*Homo sapiens*]

Protein Accession gi|4507521 gi|205277465 gi|205277463

Mean Expression Ratio 1.01

Median Expression Ratio 1.01

Credible Interval (0.618, 1.61)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0455]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	1	1.7	SEQ ID NO: 1660	LDNLVAILDINR

5.338 complement factor B preproprotein [*Homo sapiens*]
Protein Accession gi|67782358

Mean Expression Ratio 0.989

Median Expression Ratio 0.988

Credible Interval (0.646, 1.52)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0314

[0456]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	0.99	1.6	SEQ ID NO: 1661	LLQEGQALEYVCPSGFYPPVQTR
1	0.62	1	1.6	SEQ ID NO: 1662	VCPSGFYPPVQTR

SEQ ID NO: 1663

1 M G S N L S P Q L C L M P F I L G L L S G G V T T T P W S L A R P Q G S C S L E G
V E I K G G S F R L L Q E G Q A L E Y V C P S G F Y P Y P V Q T R T C R S T G

81 S W S T L K T Q D Q K T V R K A E C R A I H C P R P H D F E N G E Y W P R S P Y
Y N V S D E I S F H C Y D G Y T L R G S A N R T C Q V N G R W S G Q T A I C D N

161 G A G Y C S N P G I P I G T R K V G S Q Y R L E D S V T Y H C S R G L T L R G S
Q R R T C Q E G G S W S G T E P S C Q D S F M Y D T P Q E V A E A F L S S L T E

241 T I E G V D A E D G H G P G E Q Q K R K I V L D P S G S M N I Y L V L D G S D S
I G A S N F T G A K K C L V N L I E K V A S Y G V K P R Y G L V T Y A T Y P K I

321 W V K V S E A D S S N A D W V T K Q L N E I N Y E D H K L K S G T N T K K A
L Q A V Y S M M S W P D D V P P E G W N R T R H V I I L M T D G L H N M G G D P
I T

401 V I D E I R D L L Y I G K D R K N P R E D Y L D V Y V F G V G P L V N Q V N I N
A L A S K K D N E Q H V F K V K D M E N L E D V F Y Q M I D E S Q S L S L C G M

481 V W E H R K G T D Y H K Q P W Q A K I S V I R P S K G H E S C M G A V V S E
Y F V L T A A H C F T V D D K E H S I K V S V G G E K R D L E I E V V L F H P N Y N

561 I N G K K E A G I P E F Y D Y D V A L I K L K N K L K Y G Q T I R P I C L P C T E
G T T R A L R L P P T T T C Q Q Q K E E L L P A Q D I K A L F V S E E E K K L

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641	T R K E V Y I K N G D K K G S C E R D A Q Y A P G Y D K V K D I S E V V T P R
	F L C T G G V S P Y A D P N T C R G D S G G P L I V H K R S R F I Q V G V I S W G
721	V V D V C K N Q K R Q K Q V P A H A R D F H I N L F Q V L P W L K E K L Q D
	E D L G F L

5.339 cyclin M3 isoform 1 [*Homo sapiens*]; cyclin M3 isoform 2 [*Homo sapiens*]
Protein Accession gi|40068049 gi|40068047

Median Expression Ratio 0.989

Credible Interval (0.608, 1.62)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0458]

Mean Expression Ratio 0.987

Median Expression Ratio 0.989

Credible Interval (0.601, 1.59)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0457]

Sequence					
A	2.5	50	97.5	ID No.	Sequence
1	0.58	0.98	1.6	SEQ ID NO: 1664	AQNLPQSPENTDLQVIPGSQTR

5.341 solute carrier family 12 (potassium/chloride transporters), member 9 [*Homo sapiens*]
Protein Accession gi|31881740

Mean Expression Ratio 0.989

Median Expression Ratio 0.99

Credible Interval (0.652, 1.51)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0438

[0459]

5.340 solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 [*Homo sapiens*]
Protein Accession gi|194239733

Mean Expression Ratio 0.993

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.62	0.99	1.6	SEQ ID NO: 1666	AEVQEVVWGEAGAGEPEAEEEG DFVNSGR
1	0.62	1	1.6	SEQ ID NO: 1667	YLALLETLTR

SEQ ID NO: 1668

1 M A S E S S P L L A Y R L L G E E G V A L P A N G A G G P G G A S A R K L S T F
L G V V V P T V L S M F S I V V F L R I G F V V G H A G L L Q A L A M L L V A Y

81 F I L A L T V L S V C A I A T N G A V Q G G G A Y F M I S R T L G P E V G G S I G
L M F Y L A N V C G C A V S L L G L V E S V L D V F G A D A T G P S G L R V L

161 P Q G Y G W N L L Y G S L L L G L V G G V C T L G A G L Y A R A S F L T F L L
V S G S L A S V L I S F V A V G P R D I R L T P R P G P N G S S L P P R F G H F T

241 G F N S S T L K D N L G A G Y A E D Y T T G A V M N F A S V F A V L F N G C T
G I M A G A N M S G E L K D P S R A I P L G T I V A V A Y T F F V Y V L L F F L S

321 S F T C D R T L L Q E D Y G F F R A I S L W P P L V L I G I Y A T A L S A S M S S
L I G A S R I L H A L A R D D L F G V I L A P A K V V S R G N P W A A V L Y

401 S W G L V Q L V L L A G K L N T L A A V V T V F Y L V A Y A A V D L S C L S L
E W A S A P N F R P T F S L F S W H T C L L G V A S C L L M M F L I S P G A A G G

-continued

481	S L L L M G L L A A L L T A R G G P S S W G Y V S Q A L L F H Q V R K Y L L R
	L D V R K D H V K F W R P Q L L L L V G N P R G A L P L L R L A N Q L K K G G L Y
561	V L G H V T L G D L D S L P S D P V Q P Q Y G A W L S L V D R A Q V K A F V
	D L T L S P S V R Q G A Q H L L R I S G L G G M K P N T L V L G F Y D D A P P Q D H
641	F L T D P A F S E P A D S T R E G S S P A L S T L F P P P R A P G S P R A L N P Q
	D Y V A T V A D A L K M N K N V V L A R A S G A L P P E R L S R G S G G T S Q
721	L H H V D V W P L N L L R P R G G P G Y V D V C G L F L L Q M A T I L G M V P
	A W H S A R L R I F L C L G P R E A P G A A E G R L R A L L S Q L R I R A E V Q E
801	V V W G E G A G A G E P E A E E E G D F V N S G R G D A E A E A L A R S A N
	A L V R A Q Q G R G T G G G P G G P E G G D A E G P I T A L T F L Y L P R P P A D P
881	A R Y P R Y L A L L E T L T R D L G P T L L V H G V T P V T C T D L

5.342 RAB5C, member RAS oncogene family isoform a [*Homo sapiens*]; RAB5C, member RAS oncogene family isoform b [*Homo sapiens*]

Protein Accession gi|41393614 gi|41393545

Mean Expression Ratio 1.01

Median Expression Ratio 1.01

Credible Interval (0.624, 1.64)

Associated Peptides 1

Associated Spectra 1

Coverage NaN

[0460]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.6	1	1.7	SEQ ID NO: 1669	FEIWDTAGQER

5.343 pyruvate kinase, liver and RBC isoform 1 [*Homo sapiens*]
Protein Accession gi|10835121

Mean Expression Ratio 1.01

Median Expression Ratio 1.01

Credible Interval (0.63, 1.67)

Associated Peptides 1

Associated Spectra 1

Coverage 0.0348

[0461]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	1	1.7	SEQ ID NO: 1670	GVNLPGAQVDLPGLSEQDVR
SEQ ID NO: 1671					
1 M S I Q E N I S S L Q L R S W V S K S Q R D L A K S I L I G A P G G P A G Y L R R					
A S V A Q L T Q E L G T A F F Q Q Q L P A A M A D T F L E H L C L L D I D S					
81 E P V A A R S T S I I A T I G P A S R S V E R L K E M I K A G M N I A R L N F S H					
G S H E Y H A E S I A N V R E A V E S F A G S P L S Y R P V A I A L D T K G P					
161 E I R T G I L Q G G P E S E V E L V K G S Q V L V T V D P A F R T R G N A N T V					
W V D Y P N I V R V V P V G G R I Y I D D G L I S L V V Q K I G P E G L V T Q V					
241 E N G G V L G S R K G V N L P G A Q V D L P G L S E Q D V R D L R F G V E H G					
V D I V F A S F V R K A S D V A A V R A A L G P E G H G I K I I S K I E N H E G V					
321 K R F D E I L E V S D G I M V A R G D L G I E I P A E K V F L A Q K M M I G R C					
N L A G K P V V C A T Q M L E S M I T K P R P T R A E T S D V A N A V L D G A D					
401 C I M L S G E T A K G N F P V E A V K M Q H A I A R E A E A A V Y H R Q L F E					
E L R R A A P L S R D P T E V T A I G A V E A A F K C C A A A I I V L T T T G R S					
481 A Q L L S R Y R P R A A V I A V T R S A Q A A R Q V H L C R G V F P L L Y R E					
P P E A I W A D D V D R R V Q F G I E S G K L R G F L R V G D L V I V V T G W R P					
561 G S G Y T N I M R V L S I S					

5.344 glutathione transferase [*Homo sapiens*]
Protein Accession gi|4504183
Mean Expression Ratio 1.01
Median Expression Ratio 1.01
Credible Interval (0.713, 1.41)
Associated Peptides 3
Associated Spectra 5
Coverage 0.205
[0462]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.71	1.0	1.4	SEQ ID NO: 1672	DQQEAAALVDMVNDGVEDLR
1	0.67	1.0	1.5	SEQ ID NO: 1673	FQDGDLTLYQSNTILR
1	0.66	1	1.5	SEQ ID NO: 1674	TVVYFPVR

SEQ ID NO: 1675

1MPPYTVVYFPVVRGRCAALRMLLADQGQSWKEEVVTVETW
QEGSLKASC LYGLPKFQDGDLTLYQSNTILRHLGR T LGLY

81GKDQQEAAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDY
VKALPGQLKPFETLLSQNQGGKTFIVGDQISFADYNLLDLL

161LIHEVLAPGCLDAFPPLLSAYVGRLSARPKLKAFLASPEYV
NLPINGNGKQ

5.345 ATPase, H⁺ transporting, lysosomal 70kD, V1 subunit
A, isoform 1 [*Homo sapiens*]
Protein Accession gi|19913424
Mean Expression Ratio 1.01
Median Expression Ratio 1.01

Credible Interval (0.726, 1.41)
Associated Peptides 5
Associated Spectra 5
Coverage 0.104
[0463]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.68	1.0	1.5	SEQ ID NO: 1676	FTMVQVWPVR
1	0.66	1	1.5	SEQ ID NO: 1677	HFTEFVPLR
1	0.69	1.0	1.5	SEQ ID NO: 1678	SDYAQLLEDMQNAFR
1	0.66	1	1.5	SEQ ID NO: 1679	LPANHPLLTGQR
1	0.7	1.0	1.6	SEQ ID NO: 1680	EILQEEEDLAEIVQLVGK

SEQ ID NO: 1681

1MDFS K L P K I L D E D K E S T F G Y V H G V S G P V V T A C D M A G A A M Y
E L V R V G H S E L V G E I I R L E G D M A T I Q V Y E E T S G V S V G D P V L

81R T G K P L S V E L G P G I M G A I F D G I Q R P L S D I S S Q T Q S I Y I P R G V
N V S A L S R D I K W D F T P C K N L R V G S H I T G G D I Y G I V S E N S

161L I K H K I M L P P R N R G T V T Y I A P P G N Y D T S D V V L E L E F E G V K
E K F T M V Q V W P V R Q V R P V T E K L P A N H P L L T G Q R V L D A L F P C

241V Q G G T T A I P G A F G C G K T V I S Q S L S K Y S N S D V I I Y V G C G E R
G N E M S E V L R D F P E L T M E V D G K V E S I M K R T A L V A N T S N M P V

321A A R E A S I Y T G I T L S E Y F R D M G Y H V S M M A D S T S R W A E A L R
E I S G R L A E M P A D S G Y P A Y L G A R L A S F Y E R A G R V K C L G N P E R

401E G S V S I V G A V S P P G G D F S D P V T S A T L G I V Q V F W G L D K K L A
Q R K H F P S V N W L I S Y S K Y M R A L D E Y Y D K H F T E F V P L R T K A K

-continued

481	E I L Q E E E D L A E I V Q L V G K A S L A E T D K I T L E V A K L I K D D F L
	Q Q N G Y T P Y D R F C P F Y K T V G M L S N M I A F Y D M A R R A V E T T A Q
561	S D N K I T W S I I R E H M G D I L Y K L S S M K F K D P L K D G E A K I K S D
	Y A Q L L E D M Q N A F R S L E D

5.346 DnaJ (Hsp40) homolog, subfamily A, member 1
[*Homo sapiens*]
Protein Accession gil4504511
Mean Expression Ratio 0.986
Median Expression Ratio 0.99
Credible Interval (0.634, 1.49)
Associated Peptides 1
Associated Spectra 2
Coverage 0.0479
[0464]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.63	0.98	1.5	SEQ ID NO: 1682	NVVHQLSVTLLEDLYNGATR
SEQ ID NO: 1683					
1	M V K E T T Y Y D V L G V K P N A T Q E E L K K A Y R K L A L K Y H P D K N P				
	N E G E K F K Q I S Q A Y E V L S D A K K R E L Y D K G G E Q A I K E G G A G G G				
81	F G S P M D I F D M F F G G G R M Q R E R R G K N V V H Q L S V T L E D L Y				
	N G A T R K L A L Q K N V I C D K C E G R G G K K G A V E C C P N C R G T G M Q I				
161	R I H Q I G P G M V Q Q I Q S V C M E C Q G H G E R I S P K D R C K S C N G R				
	K I V R E K K I L E V H I D K G M K D G Q K I T F H G E G D Q E P G L E P G D I I				
241	I V L D Q K D H A V F T R R G E D L F M C M D I Q L V E A L C G F Q K P I S T L				
	D N R T I V I T S H P G Q I V K H G D I K C V L N E G M P I Y R R P Y E K G R L				
321	I I E F K V N F P E N G F L S P D K L S L L E K L L P E R K E V E E T D E M D Q				
	V E L V D F D P N Q E R R R H Y N G E A Y E D D E H H P R G G V Q C Q T S				

5.347 aquaporin 2 [*Homo sapiens*]
Protein Accession gil4502179
Mean Expression Ratio 0.99
Median Expression Ratio 0.991
Credible Interval (0.645, 1.52)

Associated Peptides 2
Associated Spectra 2
Coverage 0.0886
[0465]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.6	0.97	1.5	SEQ ID NO: 1684	QSVELHSPQSLPR
1	0.63	1.0	1.6	SEQ ID NO: 1685	GLEPDTDWEER
SEQ ID NO: 1686					
1	M W E L R S I A F S R A V F A E F L A T L L F V F F G L G S A L N W P Q A L P S V				
	L Q I A M A F G L G I G T L V Q A L G H I S G A H I N P A V T V A C L V G C H				
81	V S V L R A A F Y V A A Q L L G A V A G A A L L H E I T P A D I R G D L A V N A				
	L S N S T T A G Q A V T V E L F L T L Q L V L C I F A S T D E R R G E N P G T P				
161	A L S I G F S V A L G H L L G I H Y T G C S M N P A R S L A P A V V T G K F D D				
	H W V F W I G P L V G A I L G S L L Y N Y V L F P P A K S L S E R L A V L K G L				
241	E P D T D W E E R E V R R R Q S V E L H S P Q S L P R G T K A				

5.348 serine incorporator 1 [*Homo sapiens*]
Protein Accession gi|24308213
Mean Expression Ratio 1.01
Median Expression Ratio 1.01
Credible Interval (0.624, 1.63)
Associated Peptides 1
Associated Spectra 1
Coverage 0.0375
[0466]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	1	1.7	SEQ ID NO: 1687	LTLTSDESTLIEDGGAR

SEQ ID NO: 1688

1M G S V L G L C S M A S W I P C L C G S A P C L L C R C C P S G N N S T V T R L I
Y A L F L L V G V C V A C V M L I P G M E E Q L N K I P G F C E N E K G V V P

81C N I L V G Y K A V Y R L C F G L A M F Y L L L S L L M I K V K S S S D P R A A
V H N G F W F F K F A A A I A I I I G A F F I P E G T F T T V W F Y V G M A G A

161F C F I L I Q L V L L I D F A H S W N E S W V E K M E E G N S R C W Y A A L L S
A T A L N Y L L S L V A I V L F F V Y Y T H P A S C S E N K A F I S V N M L L C

241V G A S V M S I L P K I Q E S Q P R S G L L Q S S V I T V Y T M Y L T W S A M T
N E P E T N C N P S L L S I I G Y N T T S T V P K E G Q S V Q W W H A Q G I I G

321L I L F L L C V F Y S S I R T S N N S Q V N K L T L T S D E S T L I E D G G A R S
D G S L E D G D D V H R A V D N E R D G V T Y S Y S F F H F M L F L A S L Y I

401M M T L T N W Y R Y E P S R E M K S Q W T A V W V K I S S S W I G I V L Y V
W T L V A P L V L T N R D F D

5.349 syntaxin 7 [*Homo sapiens*]
Protein Accession gi|170932494
Mean Expression Ratio 1.01
Median Expression Ratio 1.01
Credible Interval (0.748, 1.35)
Associated Peptides 4
Associated Spectra 8
Coverage NaN
[0467]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.69	1.0	1.5	SEQ ID NO: 1689	EFGSLPTTPSEQR
4	0.72	0.98	1.3	SEQ ID NO: 1690	NLVSWESQTQPQVQVQDEEITEDDLR
1	0.7	1.0	1.5	SEQ ID NO: 1691	QLEADIMDINEIFK

-continued					
A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.72	1.0	1.4	SEQ ID NO: 1692	TLNQLGTPQDSPELR

5.350 carbonic anhydrase XII isoform 2 precursor [*Homo sapiens*]; carbonic anhydrase XII isoform 1 precursor [*Homo sapiens*]
Protein Accession gi|45935383 gi|4502515
Mean Expression Ratio 0.991
Median Expression Ratio 0.993
Credible Interval (0.66, 1.49)
Associated Peptides 1
Associated Spectra 3
Coverage NaN
[0468]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.67	0.99	1.5	SEQ ID NO: 1693	GQEAFVPGFNIEELLPER

5.351 major histocompatibility complex, class II, DR alpha precursor [*Homo sapiens*]
Protein Accession gil52426774
Mean Expression Ratio 1.00
Median Expression Ratio 1.01
Credible Interval (0.754, 1.32)
Associated Peptides 5
Associated Spectra 9
Coverage 0.209
[0469]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.7	0.98	1.4	SEQ ID NO: 1694	FHYLPFLPSTEDVYDCR
3	0.76	1.1	1.5	SEQ ID NO: 1695	NGKPVTTGVSETVFLPR
2	0.73	1.0	1.4	SEQ ID NO: 1696	VEHWGLDEPLLK
1	0.69	1	1.5	SEQ ID NO: 1697	KFHYLPFLPSTEDVYDCR
1	0.66	0.95	1.4	SEQ ID NO: 1698	EDHLFR

SEQ ID NO: 1699

1M A I S G V P V L G F F I I A V L M S A Q E S W A I K E E H V I I Q A E F Y L N P D
Q S G E F M F D F D G D E I F H V D M A K K E T V W R L E E F G R F A S F E

81A Q G A L A N I A V D K A N L E I M T K R S N Y T P I T N V P P E V T V L T N S
P V E L R E P N V L I C F I D K F T P P V V N V T W L R N G K P V T T G V S E T

161V F L P R E D H L F R K F H Y L P F L P S T E D V Y D C R V E H W G L D E P L L
K H W E F D A P S P L P E T T E N V V C A L G L T V G L V G I I I G T I F I I K

241G L R K S N A A E R R G P L

5.352 cytosolic phosphoenolpyruvate carboxykinase 1 [*Homo sapiens*]
Protein Accession gil187281517
Mean Expression Ratio 0.996
Median Expression Ratio 0.994
Credible Interval (0.7, 1.43)
Associated Peptides 3
Associated Spectra 4
Coverage NaN

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.67	1	1.5	SEQ ID NO: 1700	IFHVNWFR
1	0.65	1	1.5	SEQ ID NO: 1701	LLGQMEEEGILR
1	0.65	1	1.5	SEQ ID NO: 1702	FLWPGFGNSR

5.353 glutathione peroxidase 3 precursor [*Homo sapiens*]
Protein Accession gil6006001
Mean Expression Ratio 0.996
Median Expression Ratio 0.994
Credible Interval (0.723, 1.37)
Associated Peptides 4
Associated Spectra 6
Coverage 0.217
[0471]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.7	1	1.4	SEQ ID NO: 1703	FLVGPDGIPIMR
1	0.67	1	1.5	SEQ ID NO: 1704	FYTFLK
1	0.66	0.97	1.4	SEQ ID NO: 1705	QEPGENSEILPTLK
2	0.72	1.0	1.5	SEQ ID NO: 1706	YVRPGGGFVPNFQLFEK

-continued

SEQ ID NO: 1707
1M A R L L Q A S C L L S L L L A G F V S Q S R G Q E K S K M D C H G G I S G T I Y
E Y G A L T I D G E E Y I P F K Q Y A G K Y V L F V N V A S Y U G L T G Q Y I

81E L N A L Q E E L A P F G L V I L G F P C N Q F G K Q E P G E N S E I L P T L K Y
V R P G G G F V P N F Q L F E K G D V N G E K E Q K F Y T F L K N S C P P T S

161E L L G T S D R L F W E P M K V H D I R W N F E K F L V G P D G I P I M R W H
H R T T V S N V K M D I L S Y M R R Q A A L G V K R K

5.354 transmembrane 7 superfamily member 3 [*Homo sapi-*
ens]
Protein Accession gi|7706575

Mean Expression Ratio 1.00

Median Expression Ratio 1.00

Credible Interval (0.7, 1.44)

Associated Peptides 4

Associated Spectra 4

Coverage 0.0842

[0472]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.67	1	1.5	SEQ ID NO: 1708	GRPFFPPHPYK
1	0.68	1.0	1.6	SEQ ID NO: 1709	LQYDVYQYFLPENDLTEEMLLK
1	0.65	0.99	1.5	SEQ ID NO: 1710	QYFLPENDLTEEMLLK
1	0.65	1	1.5	SEQ ID NO: 1711	VTNILDPSYHIPPLR

SEQ ID NO: 1712

1M G F L Q L L V V A V L A S E H R V A G A A E V F G N S S E G L I E F S V G K F
R Y F E L N R P P F P E E A I L H D I S S N V T F L I F Q I H S Q Y Q N T T V S F

81S P T L L S N S S E T G T A S G L V F I L R P E Q S T C T W Y L G T S G I Q P V Q
N M A I L L S Y S E R D P V P G G C N L E F D L D I D P N I Y L E Y N F F E T

161T I K F A P A N L G Y A R G V D P P P C D A G T D Q D S R W R L Q Y D V Y Q Y
F L P E N D L T E E M L L K H L Q R M V S V P Q V K A S A L K V V T L T A N D K T

241S V S F S S L P G Q G V I Y N V I V W D P F L N T S A A Y I P A H T Y A C S F E
A G E G S C A S L G R V S S K V F F T L F A L L G F F I C F F G H R F W K T E L

321F F I G F I I M G F F F Y I L I T R L T P I K Y D V N L I L T A V T G S V G G M F L
V A V W W R F G I L S I C M L C V G L V L G F L I S S V T F F T P L G N L K

401I F H D D G V F W V T F S C I A I L I P V V F M G C L R I L N I L T C G V I G S Y
S V V L A I D S Y W S T S L S Y I T L N V L K R A L N K D F H R A F T N V P F

481Q T N D F I I L A V W G M L A V S G I T L Q I R R E R G R P F F P P H P Y K L W
K Q E R E R R V T N I L D P S Y H I P P L R E R L Y G R L T Q I K G L F Q K E Q

561P A G E R T P L L L

5.355 cathelicidin antimicrobial peptide [*Homo sapiens*]
Protein Accession gil39753970

Mean Expression Ratio 0.997
Median Expression Ratio 0.996
Credible Interval (0.668, 1.49)

Associated Peptides 1
Associated Spectra 3

Coverage 0.0529
[0473]

A	2.5	50	97.5	Sequence ID No.	Sequence
3	0.67	1	1.5	SEQ ID NO: 1713	FALLGDFFR
SEQ ID NO: 1714					
1MKTQRDGHSLGRWSLVLLLLGLVMP LAIIAQVLSYKEAVL					
RAIDGINQRSSDANLYRLLDLDPRPTMDGD PDTPKPV SFT					
81VKE TVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARG					
SFDISCDKDNKRFA LLGDFFRKSK EKIGKEFKRIVQRIKDF					
161LRNLVPRTES					

5.356 transmembrane protein 55B isoform 1 [*Homo sapi-*
ens]; transmembrane protein 55B isoform 2 [*Homo sapiens*]
Protein Accession gil154816186 gil154816184

Mean Expression Ratio 0.995
Median Expression Ratio 0.996
Credible Interval (0.652, 1.53)

Associated Peptides 2
Associated Spectra 2

Coverage NaN
[0474]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	1	1.6	SEQ ID NO: 1715	NTFLWTEFTDR

-continued

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	0.98	1.6	SEQ ID NO: 1716	IINLGPVHPGPLSPPEQPMGVR

5.357 aconitase 1 [*Homo sapiens*]
Protein Accession gil8659555

Mean Expression Ratio 0.996
Median Expression Ratio 0.997
Credible Interval (0.645, 1.56)

Associated Peptides 1
Associated Spectra 2

Coverage 0.0214
[0475]

A	2.5	50	97.5	Sequence ID No.	Sequence
2	0.65	0.99	1.6	SEQ ID NO: 1717	VILQDFTGVPVVDFAAMR
SEQ ID NO: 1718					
1MSNPFAHLAEPLDPVQPGKKFFNLNKL EDSRYGRLPFSIRV					
LLEAAAIRNCDEFLVKKQDIENILHWNVTQHKNIEVPFKP					
81ARVILQDFTGVPAVVDF AAMRD AVKKLGGDPEKINPVCP					
ADLVIDHSIQVDFNRRADSLQKNQDLEFERNRERFEFLKWG					
161SQAFHNMRIIPPGSGIIHQVNLEYLARVVFDQDGYYPDS					
LVGTDSSH TTMIDGLGILGWGVGGIEAEAVMLGQPI SMVLP					
241QVIGYRLMGKPHPLVTSTDIVLTI TKHLRQVG VVGK FVEF					
FGPGVAQLSIAADRATI ANMCP EYGATAA FFPVDEV SITYL					
321VQTGRDEEKLKYIKKY LQAVGMFRDFNDPSQDPDFTQVV					
ELD LKTVVPCCSGPKRPQDKVAVSDMKKDFE SCLGAKQGFK					

-continued

401	G F Q V A P E H H N D H K T F I Y D N T E F T L A H G S V V I A A I T S C T N T
	S N P S V M L G A G L L A K K A V D A G L N V M P Y I K T S L S P G S G V V T Y
481	Y L Q E S G V M P Y L S Q L G F D V V G Y G C M T C I G N S G P L P E P V V E
	A I T Q G D L V A V G V L S G N R N F E G R V H P N T R A N Y L A S P P L V I A Y
561	A I A G T I R I D F E K E P L G V N A K G Q Q V F L K D I W P T R D E I Q A V E
	R Q Y V I P G M F K E V Y Q K I E T V N E S W N A L A T P S D K L F F W N S K S
641	T Y I K S P P F F E N L T L D L Q P P K S I V D A Y V L L N L G D S V T T D H I S
	P A G N I A R N S P A A R Y L T N R G L T P R E F N S Y G S R R G N D A V M A
721	R G T F A N I R L L N R F L N K Q A P Q T I H L P S G E I L D V F D A A E R Y Q
	Q A G L P L I V L A G K E Y G A G S S R D W A A K G P F L L G I K A V L A E S Y
801	E R I H R S N L V G M G V I P L E Y L P G E N A D A L G L T G Q E R Y T I I I P E
	N L K P Q M K V Q V K L D T G K T F Q A V M R F D T D V E L T Y F L N G G I L
881	N Y M I R K M A K

5.358 nicastrin precursor [*Homo sapiens*]
Protein Accession gi|24638433

Associated Peptides 2

Mean Expression Ratio 0.997

Associated Spectra 2

Median Expression Ratio 0.997

Coverage 0.031

Credible Interval (0.656, 1.51)

[0476]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.63	1	1.6	SEQ ID NO: 1719	GKFPVQLENVDSFVELGQVALR
1	0.63	1	1.6	SEQ ID NO: 1720	FPVQLENVDSFVELGQVALR
SEQ ID NO: 1721					
1M A T A G G G S G A D P G S R G L L R L L S F C V L L A G L C R G N S V E R K I					
Y I P L N K T A P C V R L L N A T H Q I G C Q S S I S G D T G V I H V V E K E E					
81D L Q W V L T D G P N P P Y M V L L E S K H F T R D L M E K L K G R T S R I A					
G L A V S L T K P S P A S G F S P S V Q C P N D G F G V Y S N S Y G P E F A H C R					
161E I Q W N S L G N G L A Y E D F S F P I F L L E D E N E T K V I K Q C Y Q D H N					
L S Q N G S A P T F P L C A M Q L F S H M H A V I S T A T C M R R S S I Q S T F					
241S I N P E I V C D P L S D Y N V W S M L K P I N T T G T L K P D D R V V V A A T					
R L D S R S F F W N V A P G A E S A V A S F V T Q L A A A E A L Q K A P D V T T					
321L P R N V M F V F F Q G E T F D Y I G S S R M V Y D M E K G K F P V Q L E N V					
D S F V E L G Q V A L R T S L E L W M H T D P V S Q K N E S V R N Q V E D L L A T					
401L E K S G A G V P A V I L R R P N Q S Q P L P P S S L Q R F L R A R N I S G V V					
L A D H S G A F H N K Y Y Q S I Y D T A E N I N V S Y P E W L S P E E D L N F V					
481T D T A K A L A D V A T V L G R A L Y E L A G G T N F S D T V Q A D P Q T V T					
R L L Y G F L I K A N N S W F Q S I L R Q D L R S Y L G D G P L Q H Y I A V S S P					
561T N T T Y V V Q Y A L A N L T G T V V N L T R E Q C Q D P S K V P S E N K D L					
Y E Y S W V Q G P L H S N E T D R L P R C V R S T A R L A R A L S P A F E L S Q W					
641S S T E Y S T W T E S R W K D I R A R I F L I A S K E L E L I T L T V G F G I L I F					
S L I V T Y C I N A K A D V L F I A P R E P G A V S Y					

5.359 carboxymethylenebutenolidase [*Homo sapiens*]
Protein Accession gi|20270371
Mean Expression Ratio 0.995
Median Expression Ratio 0.997
Credible Interval (0.672, 1.45)
Associated Peptides 3
Associated Spectra 3
Coverage 0.135
[0477]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.64	1	1.6	SEQ ID NO: 1722	AVIVIQDIFGWQLPNTR
1	0.63	1	1.5	SEQ ID NO: 1723	EVQVEHIK
1	0.63	0.98	1.5	SEQ ID NO: 1724	NLIEWLNK

SEQ ID NO: 1725

1M A N E A Y P C P C D I G H R L E Y G G L G R E V Q V E H I K A Y V T K S P V D
A G K A V I V I Q D I F G W Q L P N T R Y I A D M I S G N G Y T T I V P D F F V

81G Q E P W D P S G D W S I F P E W L K T R N A Q K I D R E I S A I L K Y L K Q Q
C H A Q K I G I V G F C W G G T A V H H L M M K Y S E F R A G V S V Y G I V K D

161S E D I Y N L K N P T L F I F A E N D V V I P L K D V S L L T Q K L K E H C K V
E Y Q I K T F S G Q T H G F V H R K R E D C S P A D K P Y I D E A R R N L I E W

241L N K Y M

5.360 major histocompatibility complex, class II, DR beta 3 precursor [*Homo sapiens*]
Protein Accession gi|17986005
Mean Expression Ratio 1
Median Expression Ratio 1

Credible Interval (0.679, 1.47)
Associated Peptides 2
Associated Spectra 3
Coverage 0.094
[0478]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.66	1.0	1.6	SEQ ID NO: 1726	SVSGFYPGSIEVR
2	0.66	1	1.5	SEQ ID NO: 1727	TQPLQHNNLLVCSVSGFYPGSIEVR

SEQ ID NO: 1728

1M V C L K L P G G S S L A A L T V T L M V L S S R L A F A G D T R P R F L E L R
K S E C H F F N G T E R V R Y L D R Y F H N Q E E F L R F D S D V G E Y R A V T

81E L G R P V A E S W N S Q K D L L E Q K R G R V D N Y C R H N Y G V G E S F T
V Q R R V H P Q V T V Y P A K T Q P L Q H H N L L V C S V S G F Y P G S I E V R W

161F R N G Q E E K A G V V S T G L I Q N G D W T F Q T L V M L E T V P R S G E V
Y T C Q V E H P S V T S A L T V E W R A R S E S A Q S K M L S G V G G F V L G L L

241F L G A G L F I Y F R N Q K G H S G L Q P T G F L S

5.361 hypothetical protein LOC51571 [*Homo sapiens*]
Protein Accession gi42734438

Mean Expression Ratio 0.997

Median Expression Ratio 1

Credible Interval (0.648, 1.52)

Associated Peptides 2

Associated Spectra 2

Coverage 0.0988

[0479]

A	2.5	50	97.5	Sequence ID No.	Sequence
1	0.61	1	1.6	SEQ ID NO: 1729	INNVPAGEGENEVNNELANR
1	0.63	1	1.6	SEQ ID NO: 1730	DAEGILEDLQSYR

SEQ ID NO: 1731

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1M G N L L K V L T C T D L E Q G P N F F L D F E N A Q P T E S E K E I Y N Q V N
V V L K D A E G I L E D L Q S Y R G A G H E I R E A I Q H P A D E K L Q E K A W

81G A V V P L V G K L K K F Y E F S Q R L E A A L R G L L G A L T S T P Y S P T Q
H L E R E Q A L A K Q F A E I L H F T L R F D E L K M T N P A I Q N D F S Y Y R

161R T L S R M R I N N V P A E G E N E V N N E L A N R M S L F Y A E A T P M L K
T L S D A T T K F V S E N K N L P I E N T T D C L S T M A S V C R V M L E T P E Y

241R S R F T N E E T V S F C L R V M V G V I I L Y D H V H P V G A F A K T S K I D
M K G C I K V L K D Q P P N S V E G L L N A L R Y T T K H L N D E T T S

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III. Renal Status Assay Measurements

[0480] The ability of a particular renal biomarker assay measurement to distinguish between two populations can be established using ROC analysis. For example, ROC curves established from a “first” subpopulation (i.e., for example, a population predisposed to one or more future changes in renal status) and a “second” subpopulation (i.e., for example, a population not predisposed to one or more future changes in renal status). Calculation of these ROC curves and establishing the area under these ROC curves quantitate the predictive power of the specific assay measurement. In some embodiments, predictive power established by assay measurements described herein comprise an AUC ROC greater than 0.5, preferably at least 0.6, more preferably 0.7, still more preferably at least 0.8, even more preferably at least 0.9, and most preferably at least 0.95.

[0481] A. Immunoassays

[0482] In general, immunoassays involve contacting a sample containing, or suspected of containing, a biomarker of interest with at least one antibody that specifically binds to the biomarker. A detectable signal is then generated indicative of the presence or amount of complexes formed by the binding of polypeptides in the sample to the antibody. The detectable signal is then related to the presence or amount of the biomarker in the sample. Numerous methods and devices have been reported regarding the detection and analysis of biological biomarkers. See, e.g., U.S. Pat. Nos. 6,143,576; 6,113,855; 6,019,944; 5,985,579; 5,947,124; 5,939,272; 5,922,615; 5,885,527; 5,851,776; 5,824,799; 5,679,526; 5,525,524; and 5,480,792, and The Immunoassay

Handbook, David Wild, ed. Stockton Press, New York, 1994, each of which is herein incorporated by reference in its entirety, including all tables, figures and claims.

[0483] Numerous immunoassay devices and methods can utilize labeled molecules in various sandwich, competitive, or non-competitive assay formats, to generate a signal that is related to the presence or amount of the biomarker of interest. Suitable assay formats also include chromatographic, mass spectrographic, and protein “blotting” methods. Additionally, certain methods and devices, such as biosensors and optical immunoassays, may be employed to determine the presence or amount of analytes without the need for a labeled molecule. See, e.g., U.S. Pat. Nos. 5,631,171; and 5,955,377, each of which is herein incorpo-

rated by reference in its entirety, including all tables, figures and claims. Robotic instrumentation for performing these immunoassays are commercially available including, but not limited to, Beckman ACCESS®, Abbott AXSYM®, Roche ELECSYS®, Dade Behring STRATUS® systems. But any suitable immunoassay may be utilized, for example, enzyme-linked immunoassays (ELISA), radioimmunoassays (RIAs), competitive binding assays, and the like.

[0484] Antibodies or other polypeptides may be immobilized onto a variety of solid supports for use in immunoassays. Solid phases that may be used to immobilize specific binding members include, but are not limited to those developed and/or used as solid phases in solid phase binding assays. Examples of suitable solid phases include, but are not limited to, membrane filters, cellulose-based papers, beads (including polymeric, latex and paramagnetic particles), glass, silicon wafers, microparticles, nanoparticles, TentaGels, AgroGels, PEGA gels, SPOCC gels, and multiple-well plates. For example, an assay strip could be prepared by coating the antibody or a plurality of antibodies in an array on solid support. This strip could then be dipped into the test sample and then processed quickly through washes and detection steps to generate a measurable signal, such as a colored spot. Antibodies or other polypeptides may be bound to specific zones of assay devices either by conjugating directly to an assay device surface, or by indirect binding. In an example of the later case, antibodies or other polypeptides may be immobilized on particles or other solid supports, and that solid support immobilized to the device surface.

[0485] In certain embodiments, a urinary renal biomarker assay method comprises an immunoassay. For example, antibodies for use in such assays may specifically bind an epitope of a renal biomarker of interest, and may also bind one or more polypeptides that are “related” thereto, as that term is defined hereinafter. In one embodiment, the renal biomarker of interest is a fully length marker (i.e., for example, a protein). In one embodiment, the renal biomarker of interest is a protein fragment marker (i.e., for example, a peptide). Numerous immunoassay formats are available compatible with body fluid samples including, but not limited to, urine, blood, serum, saliva, tears, and plasma.

[0486] In this regard, detectable signals obtained from an immunoassay may be a direct result of complexes formed between one or more antibodies and the target biomolecule (i.e., for example, an analyte) and polypeptides containing the necessary epitope(s) to which the antibodies bind. While such assays may detect the full length biomarker and the assay result be expressed as a concentration of a biomarker of interest, the signal from the assay may actually be a result of all such “immunoreactive” polypeptides present in the sample. Expression of biomarkers may also be determined by means other than immunoassays, including protein measurements (i.e., for example, dot blots, western blots, chromatographic methods, mass spectrometry, etc.) and nucleic acid measurements (mRNA quantitation). This list is not meant to be limiting.

[0487] The foregoing method steps should not be interpreted to mean that the renal biomarker assay measurements is/are used in isolation in the methods described herein. Rather, additional variables or other clinical indicia may be included in the methods described herein. For example, risk stratification, diagnostic, classification, monitoring, etc. methods as described herein may be combined with one or more clinical indicia relevant to the patient population including, but not limited to, demographic information (e.g., weight, sex, age, race), medical history (e.g., family history, type of surgery, pre-existing disease such as aneurism, congestive heart failure, preeclampsia, eclampsia, diabetes mellitus, hypertension, coronary artery disease, proteinuria, renal insufficiency, or sepsis, type of toxin exposure such as NSAIDs, cyclosporines, tacrolimus, aminoglycosides, foscarnet, ethylene glycol, hemoglobin, myoglobin, ifosfamide, heavy metals, methotrexate, radiopaque contrast agents, or streptozotocin), clinical variables (e.g., blood pressure, temperature, respiration rate), risk scores (APACHE score, PREDICT score, TIMI Risk Score for UA/NSTEMI, Framingham Risk Score), a glomerular filtration rate, an estimated glomerular filtration rate, a urine production rate, a serum or plasma creatinine concentration, a urine creatinine concentration, a fractional excretion of sodium, a urine sodium concentration, a urine creatinine to serum or plasma creatinine ratio, a urine specific gravity, a urine osmolality, a urine urea nitrogen to plasma urea nitrogen ratio, a plasma BUN to creatinine ratio, a renal failure index calculated as urine sodium/(urine creatinine/plasma creatinine), a serum or plasma neutrophil gelatinase (NGAL) concentration, a urine NGAL concentration, a serum or plasma cystatin C concentration, a serum or plasma cardiac troponin concentration, a serum or plasma BNP concentration, a serum or plasma NTproBNP concentration, and a serum or plasma proBNP concentration. Other measures of renal function which may be combined with one or more renal biomarker assay measurements are described hereinafter. In: Harrison’s

Principles of Internal Medicine, 17th Ed., McGraw Hill, New York, pages 1741-1830; and In: Current Medical Diagnosis & Treatment 2008, 47th Ed, McGraw Hill, New York, pages 785-815, each of which are herein incorporated by reference in their entirety.

[0488] When more than one biomarker is measured, the individual biomarkers may be measured in samples obtained at the same time, or may be determined from samples obtained at different (e.g., an earlier or later) times. The individual biomarkers may also be measured on the same or different body fluid samples. For example, one renal biomarker may be measured in a serum or plasma sample and another renal biomarker may be measured in a urine sample. In addition, assignment of a likelihood may combine a renal biomarker assay measurement with temporal changes in one or more additional variables.

[0489] B. Detectable Labels

[0490] Generation of a detectable signal from the detectable label can be performed using various optical, acoustical, and electrochemical methods. Examples of detection modes include, but are not limited to, fluorescence, radiochemical detection, reflectance, absorbance, amperometry, conductance, impedance, interferometry, ellipsometry, etc. In certain of these methods, the solid phase antibody may be coupled to a transducer (e.g., a diffraction grating, electrochemical sensor, etc) for generation of a signal, while in others, a signal is generated by a transducer that is spatially separate from the solid phase antibody (e.g., a fluorometer that employs an excitation light source and an optical detector). This list is not meant to be limiting. Antibody-based biosensors may also be employed to determine the presence or amount of analytes that optionally eliminate the need for a labeled molecule.

[0491] Biological assays require methods for detection, and one of the most common methods for quantitation of assay measurements is to conjugate a detectable label to a protein or nucleic acid that has affinity for one of the components in the biological system being studied. Detectable labels used in the immunoassays described above may include, but are not limited to, molecules that are themselves detectable (e.g., fluorescent moieties, electrochemical labels, ecl (electrochemical luminescence) labels, metal chelates, colloidal metal particles, etc.) as well as molecules that may be indirectly detected by production of a detectable reaction product (e.g., enzymes such as horseradish peroxidase, alkaline phosphatase, etc.) or through the use of a specific binding molecule which itself may be detectable (e.g., a labeled antibody that binds to the second antibody, biotin, digoxigenin, maltose, oligohistidine, 2,4-dinitrobenzene, phenylarsenate, ssDNA, dsDNA, etc.).

[0492] Preparation of solid phases and detectable label conjugates often comprise the use of chemical cross-linkers. Cross-linking reagents may involve at least two reactive groups, and are divided generally into homofunctional cross-linkers (containing identical reactive groups) and heterofunctional cross-linkers (containing non-identical reactive groups). Homobifunctional cross-linkers that couple through amines, sulfhydryls or react non-specifically are available from many commercial sources. Maleimides, alkyl and aryl halides, alpha-haloacyls and pyridyl disulfides are thiol reactive groups and are believed to react with sulfhydryls to form thiol ether bonds, while pyridyl disulfides react with sulfhydryls to produce mixed disulfides. The pyridyl disulfide product is cleavable. Imidoesters are also very

useful for protein-protein cross-links. A variety of heterobifunctional cross-linkers, each combining different attributes for successful conjugation, are commercially available.

[0493] D. Assay Correlations

[0494] In some embodiments, the renal biomarker assay measurement is/are correlated to one or more future changes in renal function. In one embodiment, risk stratification comprises determining a subject's likelihood (i.e., for example, probability) for a future improvement in renal function.

[0495] In one embodiment, the renal biomarker assay measurement is/are correlated to a likelihood of such a future improvement in renal function. In one embodiment, the method correlates a likelihood of such a future injury to renal function. In one embodiment, the risk stratification comprises determining a subject's risk for progression to acute renal failure (ARF).

[0496] In one embodiment, the renal biomarker assay measurement is/are correlated to a likelihood of such progression to acute renal failure (ARF). In one embodiment, the risk stratification method comprises determining a subject's outcome risk.

[0497] In one embodiment, the assay measurement is/are correlated to a likelihood of the occurrence of a clinical outcome related to a renal injury suffered by the subject.

[0498] Consequently, the measured concentration value(s) may each be compared to a threshold value, wherein either a "positive going kidney injury marker", or a "negative going kidney injury marker" is identified. In one embodiment, the risk stratification comprises determining a subject's risk for future reduced renal function. In some embodiments, the method assigns a likelihood, risk, or probability that such that an event of interest is more or less likely to occur within 180 Days of the time at which the body fluid sample is obtained from the subject. In some embodiments, the assigned likelihood, risk, or probability relates to an event of interest occurring within a time period including, but not limited to, 18 months, 120 Days, 90 Days, 60 Days, 45 Days, 30 Days, 21 Days, 14 Days, 7 Days, 5 Days, 96 hours, 72 hours, 48 hours, 36 hours, 24 hours, 12 hours, or less. Alternatively, assigning a risk at 0 hours of the time at which the body fluid sample is obtained from the subject is equivalent to diagnosis of a current condition.

[0499] Selecting a diagnostic threshold involves, among other things, consideration of the probability of disease, distribution of true and false diagnoses at different test thresholds, and estimates of the consequences of treatment (or a failure to treat) based on the diagnosis. For example, when considering administering a specific therapy which is highly efficacious and has a low level of risk, few tests are needed because clinicians can accept substantial diagnostic uncertainty. On the other hand, in situations where treatment options are less effective and more risky, clinicians often need a higher degree of diagnostic certainty. Thus, a cost/benefit analysis is involved in selecting a diagnostic threshold.

[0500] 1. Thresholds

[0501] Suitable thresholds may be determined in a variety of ways. For example, one recommended diagnostic threshold for the diagnosis of acute myocardial infarction uses cardiac troponin, wherein the diagnostic threshold is set at the 97.5th percentile of the cardiac troponin concentration measured in a normal population. Another method to determine a diagnostic threshold comprises measuring serial

samples from the same patient, where a prior "baseline" result is used to monitor for temporal changes in a biomarker level.

[0502] Population studies may also be used to select thresholds. For example, Receiver Operating Characteristic ("ROC") arose from the field of signal detection theory developed during World War II for the analysis of radar images, and ROC analysis is often used to select a threshold to distinguish a "diseased" subpopulation from a "nondiseased" subpopulation. Predictive power balances the occurrences of false positives (i.e., for example, when the person tests positive, but actually does not have the disease) and false negatives (i.e., for example, when the person tests negative, suggesting they are healthy, when they actually do have the disease). To draw a ROC curve, the true positive rate (TPR) and false positive rate (FPR) are determined as the decision threshold is varied continuously. Since TPR is equivalent with sensitivity and FPR is equal to (1-specificity), the ROC graph is sometimes called the sensitivity vs (1-specificity) plot. A perfect test will have an area under the ROC curve of 1.0; a random test will have an area of 0.5. A threshold value is selected to provide an acceptable level of specificity and sensitivity usually determined by summing specificity values with sensitivity values. Consequently, the larger the calculated threshold value the greater the predictive power of the specific assay measurement under analysis.

[0503] In this context, "diseased" is meant to refer to a population having one characteristic (i.e., for example, the presence of a disease or condition or the occurrence of some outcome) and "nondiseased" population lacking the same characteristic. While a single decision threshold is the simplest application of such a method, multiple decision thresholds may be used. For example, below a first threshold, the absence of disease may be assigned with relatively high confidence, and above a second threshold the presence of disease may also be assigned with relatively high confidence. Between the two thresholds may be considered indeterminate. This is meant to be exemplary in nature only.

[0504] In addition to threshold value comparisons, other methods for correlating assay measurements to a patient classification (i.e., for example, occurrence or nonoccurrence of disease, likelihood of an outcome, etc.) include, but are not limited to, decision trees, rule sets, Bayesian methods, and neural network methods. These methods can produce probability values representing the degree to which a subject or patient belongs to one classification out of a plurality of classifications.

[0505] Multiple thresholds may also be used to assess renal status in a subject and/or patient. For example, a multiple thresholding method may combine a "first" subpopulation which is predisposed to one or more future changes in renal status, the occurrence of an injury, a classification, etc., with a "second" subpopulation which is not so predisposed into a single group. This combination group is then subdivided into three or more equal parts (i.e., for example, tertiles, quartiles, quintiles, etc., depending on the number of subdivisions). An odds ratio is assigned to subjects based on which subdivision they fall into. If one considers a tertile embodiment, the lowest or highest tertile can be used as a reference for comparison of the other subdivisions. This reference subdivision is assigned an odds ratio of 1. The second tertile is assigned an odds ratio that is relative to that first tertile. That is, someone in the second

tertile might be 3 times more likely to suffer one or more future changes in renal status in comparison to someone in the first tertile. The third tertile is also assigned an odds ratio that is relative to that first tertile.

[0506] 2. Specificity and Sensitivity

[0507] In some embodiments, a measured concentration of one or more renal biomarkers, or a composite of such biomarkers, may be treated as continuous variables. For example, any particular biomarker concentration can be converted into a corresponding probability of a future reduction in renal function for the subject, the occurrence of an injury, a classification, etc. Alternatively, a threshold value can provide an acceptable level of specificity and sensitivity in separating a population of subjects into “bins” such as a “first” subpopulation (e.g., which is predisposed to one or more future changes in renal status, the occurrence of an injury, a classification, etc.) and a “second” subpopulation which is not so predisposed.

[0508] In one embodiment, a threshold value is selected to separate a first and a second population by one or more of the following measures of test accuracy:

[0509] i) an odds ratio greater than 1, preferably at least about 2 or more or about 0.5 or less, more preferably at least about 3 or more or about 0.33 or less, still more preferably at least about 4 or more or about 0.25 or less, even more preferably at least about 5 or more or about 0.2 or less, and most preferably at least about 10 or more or about 0.1 or less;

[0510] ii) a specificity of greater than 0.5, preferably at least about 0.6, more preferably at least about 0.7, still more preferably at least about 0.8, even more preferably at least about 0.9 and most preferably at least about 0.95, with a corresponding sensitivity greater than 0.2, preferably greater than about 0.3, more preferably greater than about 0.4, still more preferably at least about 0.5, even more preferably about 0.6, yet more preferably greater than about 0.7, still more preferably greater than about 0.8, more preferably greater than about 0.9, and most preferably greater than about 0.95;

[0511] iii) a sensitivity of greater than 0.5, preferably at least about 0.6, more preferably at least about 0.7, still more preferably at least about 0.8, even more preferably at least about 0.9 and most preferably at least about 0.95, with a corresponding specificity greater than 0.2, preferably greater than about 0.3, more preferably greater than about 0.4, still more preferably at least about 0.5, even more preferably about 0.6, yet more preferably greater than about 0.7, still more preferably greater than about 0.8, more preferably greater than about 0.9, and most preferably greater than about 0.95;

[0512] iv) at least about 75% sensitivity, combined with at least about 75% specificity; a positive likelihood ratio (calculated as sensitivity/(1-specificity)) of greater than 1, at least about 2, more preferably at least about 3, still more preferably at least about 5, and most preferably at least about 10; or

[0513] v) a negative likelihood ratio (calculated as (1-sensitivity)/specificity) of less than 1, less than or equal to about 0.5, more preferably less than or equal to about 0.3, and most preferably less than or equal to about 0.1.

[0514] Various measures of test accuracy have been reported and used to determine the effectiveness of a given biomarker. Fischer et al., *Intensive Care Med.* 29:1043-1051 (2003). These accuracy measures include, but are not limited to, sensitivity and specificity, predictive values, likelihood ratios, diagnostic odds ratios, and AUC ROC values. For example, AUC ROC values are equal to the probability that a classifier will rank a randomly chosen positive instance higher than a randomly chosen negative one. Consequently, an AUC ROC value may be thought of as equivalent to the Mann-Whitney U test, which tests for the median difference between scores obtained in the two groups considered if the groups are of continuous data, or to the Wilcoxon test of ranks.

[0515] As discussed above, suitable tests may exhibit one or more of the following results on these various measures: a specificity of greater than 0.5, preferably at least 0.6, more preferably at least 0.7, still more preferably at least 0.8, even more preferably at least 0.9 and most preferably at least 0.95, with a corresponding sensitivity greater than 0.2, preferably greater than 0.3, more preferably greater than 0.4, still more preferably at least 0.5, even more preferably 0.6, yet more preferably greater than 0.7, still more preferably greater than 0.8, more preferably greater than 0.9, and most preferably greater than 0.95; a sensitivity of greater than 0.5, preferably at least 0.6, more preferably at least 0.7, still more preferably at least 0.8, even more preferably at least 0.9 and most preferably at least 0.95, with a corresponding specificity greater than 0.2, preferably greater than 0.3, more preferably greater than 0.4, still more preferably at least 0.5, even more preferably 0.6, yet more preferably greater than 0.7, still more preferably greater than 0.8, more preferably greater than 0.9, and most preferably greater than 0.95; at least 75% sensitivity, combined with at least 75% specificity; a ROC curve area of greater than 0.5, preferably at least 0.6, more preferably 0.7, still more preferably at least 0.8, even more preferably at least 0.9, and most preferably at least 0.95; an odds ratio different from 1, preferably at least about 2 or more or about 0.5 or less, more preferably at least about 3 or more or about 0.33 or less, still more preferably at least about 4 or more or about 0.25 or less, even more preferably at least about 5 or more or about 0.2 or less, and most preferably at least about 10 or more or about 0.1 or less; a positive likelihood ratio (calculated as sensitivity/(1-specificity)) of greater than 1, at least 2, more preferably at least 3, still more preferably at least 5, and most preferably at least 10; and or a negative likelihood ratio (calculated as (1-sensitivity)/specificity) of less than 1, less than or equal to 0.5, more preferably less than or equal to 0.3, and most preferably less than or equal to 0.1.

[0516] G. Conventional Renal Diagnostics

[0517] As noted above, the terms “acute renal (or kidney) injury” and “acute renal (or kidney) failure” as used herein are generally defined, in part, in terms of changes in serum creatinine from a baseline value. Most conventional definitions of ARF have common elements, including but not limited to the use of serum creatinine and, often, urine output. Patients may present with renal dysfunction without an available baseline measure of renal function for use in this comparison. In such an event, one may estimate a baseline serum creatinine value by assuming the patient initially had a normal GFR.

[0518] 1. Glomerular Filtration Rate And Creatinine

[0519] Glomerular filtration rate (GFR) is generally defined as the volume of fluid filtered from the renal (kidney) glomerular capillaries into the Bowman's capsule per unit time. Glomerular filtration rate (GFR) can be calculated by measuring any chemical that has a steady level in the blood, and is freely filtered but neither reabsorbed nor secreted by the kidneys. GFR is typically expressed in units of ml/min:

[0520] By normalizing the GFR to the body surface area, a GFR of approximately 75-100 ml/min per 1.73 m² can be assumed. The rate therefore measured is the quantity of the substance in the urine that originated from a calculable volume of blood.

[0521] There are several different techniques used to calculate or estimate the glomerular filtration rate (GFR or eGFR). In clinical practice, however, creatinine clearance is used to measure GFR. Creatinine is produced naturally by the body (creatinine is a metabolite of creatine, which is found in muscle). It is freely filtered by the glomerulus, but also actively secreted by the renal tubules in very small amounts such that creatinine clearance overestimates actual GFR by 10-20%. This margin of error is acceptable considering the ease with which creatinine clearance is measured.

[0522] Creatinine clearance (CCr) can be calculated if values for creatinine's urine concentration (UCr), urine flow rate (V), and creatinine's plasma concentration (PCr) are known. Since the product of urine concentration and urine flow rate yields creatinine's excretion rate, creatinine clearance is also said to be its excretion rate (UCr×V) divided by its plasma concentration. This is commonly represented mathematically as:

$$C_{Cr} = \frac{U_{Cr} \times V}{P_{Cr}}$$

[0523] Commonly a 24 hour urine collection is undertaken, from empty-bladder one morning to the contents of the bladder the following morning, with a comparative blood test then taken:

$$C_{Cr} = \frac{U_{Cr} \times 24\text{-hour volume}}{P_{Cr} \times 24 \times 60 \text{ mins}}$$

[0524] To allow comparison of results between people of different sizes, the CCr is often corrected for the body surface area (BSA) and expressed compared to the average sized man as ml/min/1.73 m². While most adults have a BSA that approaches 1.7 (1.6-1.9), extremely obese or slim patients should have their CCr corrected for their actual BSA:

$$C_{Cr\text{-corrected}} = \frac{C_{Cr} \times 1.73}{BSA}$$

[0525] The accuracy of a creatinine clearance measurement (even when collection is complete) is limited because as glomerular filtration rate (GFR) falls creatinine secretion is increased, and thus the rise in serum creatinine is less. Thus, creatinine excretion is much greater than the filtered

load, resulting in a potentially large overestimation of the GFR (as much as a twofold difference). However, for clinical purposes it is important to determine whether renal function is stable or getting worse or better. This is often determined by monitoring serum creatinine alone. Like creatinine clearance, the serum creatinine will not be an accurate reflection of GFR in the non-steady-state condition of ARF. Nonetheless, the degree to which serum creatinine changes from baseline will reflect the change in GFR. Serum creatinine is readily and easily measured and it is specific for renal function.

[0526] For purposes of determining urine output on a mL/kg/hr basis, hourly urine collection and measurement is adequate. In the case where, for example, only a cumulative 24-h output was available and no patient weights are provided, minor modifications of the RIFLE urine output criteria have been described. For example, some have assumed an average patient weight of 70 kg, wherein patients are assigned a RIFLE classification based on the following: <35 mL/h (Risk), <21 mL/h (Injury) or <4 mL/h (Failure). Bagshaw et al., *Nephrol. Dial. Transplant.* 23:1203-1210 (2008).

[0527] 2. Treatment Regimen Selection

[0528] Once a renal diagnosis is obtained, the clinician can readily select a treatment regimen that is compatible with the diagnosis, such as initiating renal replacement therapy, withdrawing delivery of compounds that are known to be damaging to the kidney, kidney transplantation, delaying or avoiding procedures that are known to be damaging to the kidney, modifying diuretic administration, initiating goal directed therapy, etc. Various appropriate treatments for numerous diseases have been previously discussed in relation to the methods of diagnosis described herein. See, e.g., Merck Manual of Diagnosis and Therapy, 17th Ed. Merck Research Laboratories, Whitehouse Station, N J, 1999. In addition, since the methods and compositions described herein provide prognostic information, the renal biomarkers of the present invention may be used to monitor a course of treatment. For example, an improved prognostic state or a worsened prognostic state may indicate that a particular treatment is or is not efficacious.

IV. Antibodies

[0529] Antibodies used in the immunoassays described herein preferably specifically bind to a kidney injury marker of the present invention. The term "specifically binds" is not intended to indicate that an antibody binds exclusively to its intended target since, as noted above, an antibody binds to any polypeptide displaying the epitope(s) to which the antibody binds. Rather, an antibody "specifically binds" if its affinity for its intended target is about 5-fold greater when compared to its affinity for a non-target molecule which does not display the appropriate epitope(s). Preferably the affinity of the antibody will be at least about 5 fold, preferably 10 fold, more preferably 25-fold, even more preferably 50-fold, and most preferably 100-fold or more, greater for a target molecule than its affinity for a non-target molecule. In some embodiments, antibodies bind with affinities of at least about 10⁷ M⁻¹, and preferably between about 10⁸ M⁻¹ to about 10⁹ M⁻¹, about 10⁹ M⁻¹ to about 10¹⁰ M⁻¹, or about 10¹⁰ M⁻¹ to about 10¹² M⁻¹.

[0530] Affinity may be calculated as K_d=k_{off}/k_{on} (k_{off} is the dissociation rate constant, K_{on} is the association rate constant and K_d is the equilibrium constant). Affinity can be

determined at equilibrium by measuring the fraction bound (r) of labeled ligand at various concentrations (c). The data are graphed using the Scatchard equation: $r/c = K(n-r)$; where r =moles of bound ligand/mole of receptor at equilibrium; c =free ligand concentration at equilibrium; K =equilibrium association constant; and n =number of ligand binding sites per receptor molecule. By graphical analysis, r/c is plotted on the Y-axis versus r on the X-axis, thus producing a Scatchard plot. Antibody affinity measurement by Scatchard analysis is well known in the art. See, e.g., van Erp et al., *J. Immunoassay* 12:425-443 (1991); and Nelson et al., *Comput. Methods Programs Biomed.* 27: 65-68 (1988).

[0531] Numerous publications discuss the use of phage display technology to produce and screen libraries of polypeptides for binding to a selected analyte. See, e.g., Cwirla et al., *Proc. Natl. Acad. Sci. USA* 87: 6378-6382 (1990); Devlin et al., *Science* 249:404-406 (1990); Scott et al., *Science* 249:386-388 (1990); and Ladner et al., U.S. Pat. No. 5,571, 698 (all references herein incorporated by reference). A basic concept of phage display methods is the establishment of a physical association between DNA encoding a polypeptide to be screened and the polypeptide. This physical association is provided by the phage particle, which displays a polypeptide as part of a capsid enclosing the phage genome which encodes the polypeptide. The establishment of a physical association between polypeptides and their genetic material allows simultaneous mass screening of very large numbers of phage bearing different polypeptides. Phage displaying a polypeptide with affinity to a target bind to the target and these phage are enriched by affinity screening to the target. The identity of polypeptides displayed from these phage can be determined from their respective genomes. Using these methods a polypeptide identified as having a binding affinity for a desired target can then be synthesized in bulk by conventional means. See, e.g., U.S. Pat. No. 6,057,098, which is hereby incorporated in its entirety, including all tables, figures, and claims.

[0532] Antibodies generated by these methods may then be selected by first screening for affinity and specificity with the purified polypeptide of interest and, if required, comparing the results to the affinity and specificity of the antibodies with polypeptides that are desired to be excluded from binding. The screening procedure can involve immobilization of the purified polypeptides in separate wells of microtiter plates. The solution containing a potential antibody or groups of antibodies is then placed into the respective microtiter wells and incubated for about 30 min to 2 h. The microtiter wells are then washed and a labeled secondary antibody (for example, an anti-mouse antibody conjugated to alkaline phosphatase if the raised antibodies are mouse antibodies) is added to the wells and incubated for about 30 min and then washed. Substrate is added to the wells and a color reaction will appear where antibody to the immobilized polypeptide(s) are present.

[0533] Antibodies so identified may then be further analyzed for affinity and specificity in the assay design selected. In the development of immunoassays for a target protein, the purified target protein acts as a standard with which to judge the sensitivity and specificity of the immunoassay using the antibodies that have been selected. Because the binding affinity of various antibodies may differ, certain antibody pairs (e.g., in sandwich assays) may interfere with one

another sterically, etc., assay performance of an antibody may be a more important measure than absolute affinity and specificity of an antibody.

V. Kits

[0534] In some embodiments, the present invention also contemplates devices and kits for performing the methods described herein. Suitable kits comprise reagents sufficient for performing an assay for at least one of the described kidney injury markers, together with instructions for performing the described threshold comparisons.

[0535] In certain embodiments, reagents for performing such assays are provided in an assay device, and such assay devices may be included in such a kit. Preferred reagents can comprise one or more solid phase antibodies, the solid phase antibody comprising antibody that detects the intended biomarker target(s) bound to a solid support. In the case of sandwich immunoassays, such reagents can also include one or more detectably labeled antibodies, the detectably labeled antibody comprising antibody that detects the intended biomarker target(s) bound to a detectable label. Additional optional elements that may be provided as part of an assay device are described hereinafter.

[0536] In some embodiments, the present invention provides kits for the analysis of the described kidney injury markers. The kit comprises reagents for the analysis of at least one test sample which comprise at least one antibody that a kidney injury marker. The kit can also include devices and instructions for performing one or more of the diagnostic and/or prognostic correlations described herein. Preferred kits will comprise an antibody pair for performing a sandwich assay, or a labeled species for performing a competitive assay, for the analyte. Preferably, an antibody pair comprises a first antibody conjugated to a solid phase and a second antibody conjugated to a detectable label, wherein each of the first and second antibodies that bind a kidney injury marker. Most preferably each of the antibodies are monoclonal antibodies. The instructions for use of the kit and performing the correlations can be in the form of labeling, which refers to any written or recorded material that is attached to, or otherwise accompanies a kit at any time during its manufacture, transport, sale or use. For example, the term labeling encompasses advertising leaflets and brochures, packaging materials, instructions, audio or video cassettes, computer discs, as well as writing imprinted directly on kits.

EXPERIMENTAL

Example I

BioMaRK Data Collection Method

Patients and Study Design

[0537] BioMaRK was an observational cohort study conducted as an ancillary study to the Veterans Affairs/National Institutes of Health (VA/NIH) Acute Renal Failure Trial Network study (ATN study). The ATN study was a multicenter, prospective trial of two strategies for renal replacement therapy in critically ill patients with acute kidney injury. Coca et al., "Biomarkers for the diagnosis and risk stratification of acute kidney injury: a systematic review" *Kidney Int.* 73:1008-1016 (2008). Adult patients (18 years or older) with AKI and requiring renal-replacement therapy

(RRT), as well as failure of one or more non-renal organ systems or sepsis were eligible. As a sub-study to the ATN study, 109 patients were enrolled at The University of Pittsburgh Medical Center, The VA Pittsburgh Healthcare System, The Cleveland Clinical Foundation, The University of Texas Health Science Center at Houston, and Washington University Medical Center to undergo serial blood and urine sampling. Incomplete data including unavailability of urine samples precluded inclusion of 33 subjects; consequently the remaining 76 formed the analysis cohort. Approval from the Institutional Review Boards was received from the University of Pittsburgh and all participating sites.

Data Collection/Laboratory Measurements

[0538] Medical records of study participants were prospectively reviewed to retrieve hospitalization data including baseline demographic characteristics, serial renal function, daily urine volume, and severity of illness scores. The presence of sepsis was defined by international consensus criteria. Levy et al., "2001 SCCM/ESICM/ACCP/ATS/SIS International Sepsis Definitions Conference" *Crit Care Med*, 31:1250-1256 (2003). Recovery of renal function was defined by survival and dialysis independence at Day 60 post AKI. For purposes of primary analysis, partial recovery (i.e. failure to return to baseline renal function but free of dialysis) was included in the recovery group. Similarly, all deaths were included in the non-recovery group.

[0539] Fresh urine samples were obtained on Days 1, 7, and 14 post AKI. Immediately upon obtaining a well-mixed 30 ml sample, a protease inhibitor tablet (Roche Diagnostics Corporation, IN, USA) was added. After processing, the sample was frozen (at -80°C .) until analyzed. Samples were assayed in duplicate, and data were analyzed using Bio-Rad Bio-Plex Manager Software (version 4.1). Urine creatinine concentrations were measured using a non-enzymatic assay (DICT-500, BioAssay Systems, CA, USA).

Example II

Proteomics Analysis

[0540] Urine collected in accordance with Example I from fourteen (14) patients with severe AKI was evaluated with an unbiased proteomics discovery platform.

[0541] Data collected from seven (7) patients that did not recover renal function after AKI was compared to data collected from seven (7) patients that did recover renal function after AKI. The two groups were matched for age (e.g., ± 5 yrs) and gender.

[0542] The data presented herein show that approximately thirty (30) proteins were differentially expressed between the Recovery Group and the Non-Recovery Group. A preliminary analysis has categorized these proteins into groups including, but not limited to:

[0543] 1. Ferritin, alpha and beta globin, or catalase that may be involved in providing protection from reactive oxygen species

[0544] 2. Complement factor H or complement component 4 BP that may be involved in regulation of complement activation

[0545] 3. Olfactomedin-4, leucine rich alpha-2 glycoprotein or ring finger protein 167 that may be involved in cell survival and proliferation.

[0546] 4. Inter-alpha globulin inhibitor H4, heparan sulfate proteoglycan 2, (N-acylsphingosine aminohydrolase and saposin) that may be involved in basement membrane, matrix proteins or sphingolipid turnover.

[0547] Although it is not necessary to understand the mechanism of an invention, it is believed that the differential expression of proteins categorized in Group 3 and Group 4 might be directly involved in renal recovery because of their involvement with cell proliferation and/or rebuilding of the basement membrane.

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20170199204A1>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

1. A composition comprising an renal injury biomarker, wherein said biomarker comprises at least a fragment of at least one protein selected from the group consisting of ferritin, beta globin, catalase, alpha globin, epidermal growth factor receptor pathway substrate 8, mucin isoform precursor, ezrin, delta globin, moesin, phosphoprotein isoform, annexin A2, myoglobin, hemopexin, serine proteinase inhibitor, serpine peptidase inhibitor, CD14 antigen precursor, fibronectin isoform preprotein, angiotensinogen preprotein, complement component precursor, carbonic anhydrase, uromodulin precursor, complement factor H, complement component 4 BP, heparan sulfate proteoglycan 2, olfactomedian-4, leucine rich alpha-2 glycoprotein, ring finger protein 167, inter-alpha globulin inhibitor H4, heparan sul-

fate proteoglycan 2, N-acylsphingosine aminohydrolase, serine proteinase inhibitor clade A member 1, mucin 1, clusterin isoform 1, brain abundant membrane attached signal protein 1, dipeptidase 1, fibronectin 1 isoform 5 preprotein, angiotensinogen preprotein, carbonic anhydrase, and uromodulin precursor.

2. The composition of claim 1, wherein said composition further comprises a biological fluid sample.

3. The composition of claim 2, wherein said biological fluid sample is collected from a patient between 1 day and 14 days after a kidney injury.

4. The composition of claim 2, wherein said biological fluid sample is a human urine sample.

5. The composition of claim 1, wherein said renal injury biomarker in said biological fluid sample is at at least one level selected from the group consisting of at least 2.5 fold higher, at least 2.0 fold higher, at least 1.5 fold higher, at least 1.25 fold higher as compared to an expected level in a renal recovery group.

6. The composition of claim 1, wherein said renal injury biomarker in said biological fluid sample is at at least one level selected from the group consisting of at least 2.5 fold lower, at least 2.0 fold lower, at least 1.5 fold lower and at least 1.25 fold lower as compared to an expected level in a renal recovery group.

7-10. (canceled)

11. A kit, comprising:

- a) a first container comprising an antibody is specifically directed to at least one of a plurality of renal injury biomarkers, wherein said biomarkers comprise at least a fragment of a protein selected from the group consisting of ferritin, beta globin, catalase, alpha globin, epidermal growth factor receptor pathway substrate 8, mucin isoform precursor, ezrin, delta globin, moesin, phosphoprotein isoform, annexin A2, myoglobin, hemopexin, serine proteinase inhibitor, serpine peptidase inhibitor, CD14 antigen precursor, fibronectin isoform preprotein, angiotensinogen preprotein, complement component precursor, carbonic anhydrase, uromodulin precursor, complement factor H, complement component 4 BP, heparan sulfate proteoglycan 2, olfactomedian-4, leucine rich alpha-2 glycoprotein, ring finger protein 167, inter-alpha globulin inhibitor H4, heparan sulfate proteoglycan 2, N-acylshingosine aminohydrolase, serine proteinase inhibitor clade A member 1, mucin 1, clusterin isoform 1, brain abundant membrane attached signal protein 1, dipeptidase 1, fibronectin 1 isoform 5 preprotein, angiotensinogen preprotein, carbonic anhydrase, and uromodulin precursor;
- b) instructions for determining whether said biomarker is overexpressed as compared to a renal recovery group comprising individuals without an acute renal injury;
- c) instructions for determining whether said biomarker is underexpressed as compared to said renal recovery group; and

d) instructions for determining a probability value of renal non-recovery for a patient from an acute renal injury by a combination of receiver operated characteristic area under the curve determinations for overexpression or underexpression of said biomarker as compared to a plurality of diagnostic threshold values.

12. The kit of claim 11, wherein said antibody is a monoclonal antibody.

13. The kit of claim 12, wherein said monoclonal antibody is specifically directed to said biomarker protein fragment.

14. The kit of claim 11, further comprising instructions for treating said patient during the development of said renal disease with a treatment regimen selected from the group consisting of: i) said treatment regimen comprising adverse effects when said probability value of non-recovery from said acute injury is greater than 50%, and ii) said treatment regimen without adverse effects when said probability value of non-recovery from said acute renal injury is less than 50%.

15. The kit of claim 14, wherein said instructions identify that said treatment regimen as selected from the group consisting of initiating renal replacement therapy, withdrawing kidney damaging compounds, kidney transplantation, delaying or avoiding kidney damaging procedures and modifying diuretic administration.

16. The kit of claim 11, wherein said interactions identify that said overexpressed biomarker is between approximately 1.5 fold-1.5 fold higher in comparison to said renal recovery group.

17. The kit of claim 11, wherein said instructions identify that said underexpressed biomarker is between approximately 1.5 fold-2.0 fold lower in comparison to said renal recovery group.

18. The kit of claim 11, wherein said instructions identify that said probability value of non-recovery from said acute renal injury is less than 10%.

19. The kit of claim 11, wherein said instructions identify that said probability value of non-recovery from said acute renal injury is greater than 75%.

20. The kit of claim 11, wherein said instructions identify that said probability value of non-recovery from said acute renal injury is greater than 90%.

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