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(57) Abrégé/Abstract:
The present invention encompasses miRNA profiles and type-I IFN/IFNα- induced PD marker profiles in inflammatory or autoimmune disorders, such as myositis. The profiles may also be used in, for example, methods of treating patients, methods of monitoring disease progression of patients, and in diagnosing or providing a prognosis to patients having inflammatory or autoimmune disorders.

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(54) Title: DISEASE MARKERS AND USES THEREOF

(57) Abstract: The present invention encompasses miRNA profiles and type-I IFN/IFNα- induced PD marker profiles in inflammatory or autoimmune disorders, such as myositis. The profiles may also be used in, for example, methods of treating patients, methods of monitoring disease progression of patients, and in diagnosing or providing a prognosis to patients having inflammatory or autoimmune disorders.

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DISEASE MARKERS AND USES THEROF

FIELD OF THE INVENTION

The present invention relates to miRNA markers and interferon (IFN) alpha/type I IFN-inducible pharmacodynamic (PD) markers and methods employing the same.

BACKGROUND OF THE INVENTION

The present invention encompasses miRNA markers and IFNα/type I IFN-inducible PD markers. The present invention further encompasses methods that employ these markers in methods of, *e.g.*, treating patients and prognosing or monitoring disease.

SUMMARY OF THE INVENTION

One embodiment of the invention encompasses a method of treating a patient having a type I IFN or IFNα-mediated disease or disorder. An agent that binds to and modulates type I IFN or IFNα activity is administered to the patient. The patient comprises a differentially regulated miRNA marker profile. The agent neutralizes the differentially regulated miRNA marker profile.

Another embodiment of the invention is a method of neutralizing a differentially regulated miRNA marker profile in a patient in need thereof. An agent that binds to and modulates type I IFN or IFNα activity is administered to the patient. The agent neutralizes the differentially regulated miRNA marker profile of the patient.

A further embodiment of the invention is a method of monitoring or prognosing an autoimmune or inflammatory disease progression of a patient. A first differentially regulated miRNA marker profile is obtained in a first sample from a patient.

In yet another embodiment of the invention is a method of monitoring autoimmune or inflammatory disease progression of a patient receiving treatment with a therapeutic agent. A first miRNA profile is obtained in a first sample from the patient. A therapeutic agent is administered. A second miRNA profile is obtained in a second sample from the patient. The first and the second miRNA profiles are compared. A variance in the first and the second miRNA profiles indicates a level of efficacy of the therapeutic agent.

In another embodiment of the invention is a method of treating a myositis patient. An agent that binds to and modulates type I IFN or IFNα activity is administered to the patient. The agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient.

A further embodiment of the invention encompasses a method of monitoring or prognosing myositis disease progression of a patient. A first IFNα-inducible PD marker expression profile is obtained in a first sample from the patient.

In yet a further embodiment of the invention is a method of monitoring myositis disease progression of a patient receiving treatment with a therapeutic agent. A first IFNα-inducible PD marker expression profile is obtained in a first sample from the patient. A therapeutic agent is administered to the patient. A second IFNα-inducible PD marker expression profile is obtained from a second sample from the patient. The first and the second IFNα-inducible PD marker expression profiles are compared.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1a and 1b: The majority of the most upregulated genes in muscle specimens of DM and PM patients are IFN-α/β-inducible. (a) table showing genes up-regulated in DM patient muscle specimens; (b) IFN-α/β-inducible gene signature score in muscle of DM and PM patients.

Figure 2a and 2b: IFN-α/β-inducible gene signature scores in DM and PM patients decreases as patients disease condition improves. (a) provides IFN-α/β-inducible gene signature scores of DM active patients (DMA), DM improving patients (DMI), PM active patients (PMA), and PM improving patients (PMI). (b) shows that IFN-α/β-inducible gene signature scores decrease in DM patients as they go from active disease to improvement.

Figure 3a – 3c: IFN-α/β-inducible gene signature scores in DM patient whole blood samples correlate with clinical improvement, but not gene signature scores of other cytokines (TNFα, IL1β, IL4, IL10, and IL13) as shown for three, (a) – (c), patients.

Figure 4: IFN-α/β-inducible gene signature scores of a DM patient predicted clinical improvement as well as relapse.

Figure 5a – 5d: Change in IFN-α/β-inducible gene signature score in a PM patient correlates with serum CK level. (a) shows the IFN-α/β-, TNFα-, IL1β-, IL4-, IL10-, IL13-inducible gene signature scores of the PM patient, (b) provides the serum CK activity of the patient, which follows the curve of the IFN-α/β-inducible gene signature; (c) provides the correlation between the various cytokine gene signature scores and serum CK level; (d) is a PCA plot of the PM patient's IFN-α/β-inducible gene signature score relative to that of healthy donors (black circles).

Figure 6: Change in IFN-α/β-inducible gene signature score in a DM patient correlates with serum CK level. (a) shows the patient's serum CK activity over four visits with a physician; (b) shows the IFN-α/β-, TNFα-, IL1β-, IL4-, IL10-, IL13-inducible gene signature scores of the patient over the same four visits; (c) provides the correlation between the various cytokine gene signature scores and serum CK level. The type I IFN gene signature (shown in (b)), as monitored by the neutralization of top 25 inducible genes in the whole blood of the patient, tracked the clinical activity. Visit 1, pre-treatment; Visit 2, followed treatment with Rituximab and steroids (marginal improvement); Visit 3, patient remained stable; Visit 4, patient crashed (sharp increase in serum CK level).

Figure 7a and 7b: The IFN-α/β-inducible gene signature of the DM patient discussed in figure 6 tracks disease progression/regression. (a) heatmap showing neutralization and de-neutralization of genes in the IFN-α/β-inducible signature as patient progresses/regresses; (b) PCA plot tracking the DM patient's IFN-α/β-inducible gene signature score relative to that of healthy donors (black circles).

Figure 8: Scatter plot showing that muscle specimens of IBM patients exhibit IFN-α/β-inducible gene signature overexpression. Scatter plot is of IFN-α/β-gene signature scores for muscle specimens from 14 patients with IBM using two methods: a dynamic list of 25 genes and a static list of 21 genes. Each point represents a patient.

Figure 9a and 9b: IBM patient serum samples show distinct IFN-α/β-gene signature overexpression. (a) IFN-α/β-gene signature scores for whole blood from 9 IBM patients

using two methods: a dynamic list of 25 genes and a static list of 21 genes; (b) scatter plot of IFN-α/β-gene signature scores for whole blood from 9 IBM patients using a dynamic list of 25 genes. Each point represents a patient.

Figure 10a and 10b: Jo1 negative DM patients have higher IFN-α/β-gene signature scores than Jo1 positive DM patients. (a) overexpression of 19 IFN-α/β-inducible genes in DM Jo1 positive and DM Jo1 negative patients; (b) scatter plot of IFN-α/β-gene signature scores for muscle from 3 Jo1 positive and 7 Jo1 negative DM patients using the 19 genes. Each point represents a patient.

Figures 11-104: Probe list with annotation of genes in IL4 signature.

Figures 105-158: Probe list with annotation of genes in IL10 signature.

Figures 159-234: Probe list with annotation of genes in IL13 signature.

Figures 235-381: Probe list with annotation of 807 IFNα-inducible genes.

Figures 382-383: List with unique detector ids, miRNA ids, and sequences.

Figure 384a and 384b: The prevalence of type 1 IFN-inducible genes among those most overexpressed in DM and PM patients can be used to identify type 1 IFN-inducible gene signature score-positive patients. (a) Heatmap representing 24 normal healthy donors, 20 PM patients, and 22 DM patients and 136 probe sets identified as both type 1 IFN-inducible and significantly over-expressed (q-value < 0.05 and fold change > 2), comparing the 42 DM and PM patients to 24 normal healthy donors. The first, black, horizontal bar represents the normal healthy donors; the second horizontal bar, labeled low, represents patients with a weak type 1 IFN-inducible gene signature score (fold change < 4); the third horizontal bar, labeled moderate, represents patients with a moderate type 1 IFN-inducible gene signature score ($4 \leq$ fold change < 10), and the fourth horizontal bar, labeled high, represents patients with a high type 1 IFN-inducible gene signature score (i.e., signature score-positive). (b) Scatter plot of the type 1 IFN-inducible gene signature scores for the same subjects in (a) stratified by normal healthy donors, weak signature score, moderate signature score, and high signature score. IFN=interferon; DM=dermatomyositis; PM=polymyositis.

Figure 385a – 385c: Patient-specific longitudinal type 1 IFN-inducible transcript measurements have utility as biomarkers to measure DM and PM disease activity. (a) Individual gene composite scores and fold-change values using a 13-gene composite score and individual transcript measurements for IFI27, IFI44, IFI44L and RSAD2 for 21 patients at visit 1 and for 36 normal healthy donors. Patients are grouped by relatively low or moderate clinically measured disease activity (MITAX ≤ 6) and high disease activity (MITAX > 6). After multiple testing adjustment, there is no significant difference between normal healthy donors and patients with MITAX ≤ 6 for any of the 4 genes or the 13-gene composite scores. There are significant differences in comparing normal healthy donors vs. patients with MITAX > 6, and comparing patients with MITAX ≤ 6 vs. MITAX > 6, for all genes and gene composite scores (see Table 8). (b) Patient-specific analysis for 18 patients with some variation in MITAX-measured disease activity and (c) 3 patients with no change in MITAX across the study. Gene composite scores, fold-change values, and raw p-values are provided for each of the 18 patients at their visits, with lowest to highest MITAX values over the course of the study. Patients with MITAX variation showed highly significant concordant gene expression changes for all genes/gene composite scores except IFI44 after adjustment; patients without MITAX variation showed essentially no gene expression changes, though the sample size was too small to carry statistical significance. All gene composite scores and fold change values were calculated relative to the median of the 36 normal healthy donors.

Figure 386a and 386b. DM and PM patients demonstrate a correlation between MITAX score and type 1 IFN 13-gene composite score from peripheral blood. (a) Comparisons between MITAX score and the 13-gene composite score for 6 patients (BGE15, BGE99, BGE10, BGE106, BGE119, and BGE147) with at least 4 total visits. The solid black line and rightmost y-axis represent MITAX scores, while the dashed black line and leftmost y-axis represent 13-gene composite scores. The 'H' designation in the plots for BGE15 and BGE147 represent the herald visits. (b) An additional correlation is seen for patient BGE92 between the 13-gene composite score and CK levels. The dashed black line and rightmost y-axis in the leftmost plot represents the CK levels for this patient. DM=dermatomyositis; PM=polymyositis; CK=creatine kinase.

Figure 387a and 387b: Strong elevation of type 1 IFN-inducible gene expression in WB heralding disease relapse in several patients with DM or PM. Three visits occurred in which disease was believed to be clinically stable or improving, yet the patient developed a clinical relapse 6-35 days later. The significant IFN-inducible gene expression increases in each of these 3 visits "heralded" that relapses would soon occur. (a) Tabular listing of expression changes for the 13-gene composite score. Columns show: patient samples; days between herald (V-herald) and relapse (V-relapse) visits; MITAX score changes between V-herald and V-relapse; fold-increases in gene expression from the prior visit to V-herald. (b) Graphical representation of the 13-gene composite scores. Each of the middle visits (#3) is the herald visit; MITAX score was stable or improved compared to the prior visit (#2), but the 13-gene composite scores had significantly increased, possibly heralding the relapses confirmed by increased MITAX scores at the next visit (#4). IFN=interferon; DM=dermatomyositis; PM=polymyositis.

Figure 388a – 388c: Other cytokine-inducible signature scores do not differ between moderate and severe patients with DM or PM and are not correlated with disease activity. (a) Cytokine-inducible gene signatures for TNF-α, IL-1β, IL-10, IL-13, and GM-CSF for 21 patients at visit 1 and for 36 normal healthy donors. Patients are grouped by relatively low or moderate clinically measured disease activity (MITAX $\leq$ 6) and high disease activity (MITAX > 6). After multiple testing adjustment, there is a significant difference between normal healthy donors and patients with a MITAX $\leq$ 6 for all 5 cytokine-inducible gene signatures. There is also a significant difference between normal healthy donors and patients with a MITAX > 6 for all 5 cytokine-inducible gene signatures. However, there is no significant difference between patients with a MITAX $\leq$ 6 vs. MITAX > 6 for any of the 5 cytokine-inducible gene signatures (see Table 8). (b) Patient-specific analysis for 18 patients with some variation in MITAX-measured disease activity and (c) 3 patients with no change in MITAX activity across the study. Cytokine-inducible gene signatures and raw p-values are provided for each of the 18 patients at their visits with lowest to highest MITAX values over the course of the study. Patients with MITAX variation showed no significant concordant gene expression changes for any cytokine-inducible gene signature; patients without MITAX variation showed essentially no gene expression changes either, although the sample size was too small to calculate statistical

significance. All cytokine-inducible gene signatures are calculated relative to the median of the 36 normal healthy donors. DM=dermatomyositis; PM=polymyositis.

Figure 389: Comparison of different cytokine-inducible gene signatures for 24 DM or PM patients at the visits with the highest (upper panel) and lowest (lower panel) MITAX scores. Each row indicates the overexpression of a different cytokine-inducible gene signature. The 3 patients outlined in the box are type 1 IFN-inducible gene signature score-negative. Elevated cytokine-induced gene signature levels for each patient are represented by colors approaching red, while colors approaching blue represent low cytokine-induced gene signature values. IFN=interferon; DM=dermatomyositis; PM=polymyositis.

DETAILED DESCRIPTION

The invention encompasses methods of identifying, diagnosing, treating, and monitoring disease progression in patients. Patients include any animal having a type I IFN or an IFNα-inducible disease, disorder, or condition; or any animal having an inflammatory or autoimmune disease, disorder, or condition. The patient may have the disease, disorder, or condition as a result of experimental research, *e.g.*, it may be an experimental model developed for the disease, disorder, or condition. Alternatively, the patient may have the disease, disorder, or condition in the absence of experimental manipulation. Patients include humans, mice, rats, horses, pigs, cats, dogs, and any animal used for research.

A type I IFN or an IFNα-inducible disease, disorder, or condition is any that exhibits a type I IFN or an IFNα PD marker expression profile or gene signature. A PD marker expression profile and a gene signature will be understood to be equivalent. These diseases, disorders, or conditions include those with an autoimmune component such as systemic lupus erythematosus, insulin dependent diabetes mellitus, inflammatory bowel disease (including Crohn's disease, ulcerative colitis, and Celiac's disease), multiple sclerosis, psoriasis, autoimmune thyroiditis, rheumatoid arthritis, glomerulonephritis, idiopathic inflammatory myositis such as inclusion body myositis or dermatomyositis or polymyositis or nonspecific myositis, or necrotizing myopathy,

Sjogren's syndrome, vasculitis, and sarcoidosis. Other diseases, disorders, or conditions include graft versus host disease and transplant rejection.

If the patient is a myositis patient, the patient may have inclusion body myositis or dermatomyositis or polymyositis. The myositis patient may have a high or a low Myositis Intention to Treat scale (MITAX) score. One of skill in the art would readily be able to determine the MITAX score of a myositis patient. See, for example, Walsh RJ, Pinkus JL, et al. Type I interferon-inducible gene expression in blood is present and reflects disease activity in dermatomyositis and polymyositis. Arthritis Rheum. 2007; 56(11):3784-92, incorporated by reference. A high MITAX score may be about greater than 6. A low MITAX score may be about less than or equal to 6. The myositis patient may alternatively or further have a moderate or strong type I IFN- or IFNα-inducible gene signature score. A type 1 IFN- or IFNα–inducible gene signature score may be weak if assigned a score of about less than 4, moderate if assigned a score around or about greater than 4 but less than 10, and high if assigned a score of about 10 or greater than 10. Those of skill in the art would readily understand and be able to determine type I IFN or IFNα-inducible gene signature score. See, for example, Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008; Volume 2009, Article ID 374312, doi:10.4061/2009/374312, incorporated by reference.

An autoimmune disease, disorder, or condition may be any disease, disorder, or condition in which the immune system triggers an immune response when there are no foreign substances to fight and the body's normally protective immune system causes damage to its own tissues by mistakenly attacking self. These diseases, disorders, or conditions include multiple sclerosis, Crohn's disease, rheumatoid arthritis, alopecia greata, ankylosing spondylitis, antiphospholipid syndrome, autoimmune Addison's disease, autoimmune diseases of the adrenal gland, allergic encephalomyelitis, autoimmune hemolytic anemia, autoimmune hepatitis, autoimmune inflammatory eye disease, autoimmune neonatal thrombocytopenia, autoimmune neutropenia, autoimmune oophoritis and orchitis, autoimmune thrombocytopenia, autoimmune thyroiditis, Behcet's disease, bullous pemphigoid, cardiomyopathy, cardiotomy syndrome, celiac sprue-

dermatitis, chronic active hepatitis, chronic fatigue immune dysfunction syndrome (CFIDS), chronic inflammatory demyelinating polyneuropathy, Churg-Strauss syndrome, cicatrical pemphigoid, CREST syndrome, cold agglutinin disease, Crohn's disease, dense deposit disease, discoid lupus, essential mixed cryoglobulinemia, fibromyalgia-fibromyositis, glomerulonephritis (*e.g.*, IgA nephrophathy), gluten-sensitive enteropathy, Goodpasture 's syndrome, Graves' disease, Guillain-Barre, hyperthyroidism (*i.e.*, Hashimoto's thyroiditis), idiopathic pulmonary fibrosis, idiopathic Addison's disease, idiopathic thrombocytopenia purpura (ITP), IgA neuropathy, juvenile arthritis, lichen planus, lupus erthematosus, Meniere's disease, mixed connective tissue disease, multiple sclerosis, Myasthenia Gravis, myocarditis, type 1 or immune-mediated diabetes mellitus, myasthenia gravis, myocarditis, neuritis, other endocrine gland failure, pemphigus vulgaris, pernicious anemia, polyarteritis nodosa, polychrondritis, Polyendocrinopathies, polyglandular syndromes, polymyalgia rheumatica, polymyositis and dermatomyositis, post-MI, primary agammaglobulinemia, primary biliary cirrhosis, psoriasis, psoriatic arthritis, Raynauld's phenomenon, relapsing polychondritis, Reiter's syndrome, rheumatic heart disease, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, stiff-man syndrome, systemic lupus erythematosus, lupus erythematosus, takayasu arteritis, temporal arteristis/giant cell arteritis, ulcerative colitis, urticaria, uveitis, Uveitis Opthalmia, vasculitides such as dermatitis herpetiformis vasculitis, vitiligo, and Wegener's granulomatosis.

An inflammatory disorder, disease, or condition may include asthma, allergic disorders, inflammatory disorders characterized by type-2 mediated inflammation, pulmonary fibrosis, chronic obstructive pulmonary disease (COPD), encephilitis, inflammatory bowel disease, septic shock, undifferentiated spondyloarthropathy, undifferentiated arthropathy, arthritis, inflammatory osteolysis, and chronic inflammation resulting from chronic viral or bacteria infections.

The patient may comprise a differentially regulated miRNA profile. A differentially regulated miRNA profile may be one in which a tissue sample of the patient exhibits increased expression of one or more miRNAs relative to a control tissue sample of the patient or relative to a healthy control individual. A differentially regulated miRNA profile may be one in which a tissue sample of the patient exhibits decreased

expression of one or more miRNAs relative to a control sample of the patient or relative to a healthy control individual. A differentially regulated miRNA profile may be one in which a tissue sample of the patient exhibits both increased expression of one or more miRNAs relative to a control sample and decreased expression of one or more miRNAs relative to a control sample. The number of miRNAs exhibiting increased expression may be 1, at least 1, 2, at least 2, 3, at least 3, 4, at least 4, 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 50. The number of miRNAs exhibiting decreased expression may be 1, at least 1, 2, at least 2, 3, at least 3, 4, at least 4, 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 50. The differential increase or decrease in expression may be approximately 10% - 500% of the control sample, approximately 10% - 400% of the control sample, approximately 10% - 300% of the control sample, approximately 10% - 250% of the control sample, approximately 10% - 200% of the control sample, approximately 10% - 150% of the control sample, approximately 10% - 100% of the control sample, approximately 10% - 50% of the control sample, approximately 100% - 500% of the control sample, approximately 200% - 500% of the control sample, approximately 300% - 500% of the control sample, approximately 400% - 500% of the control sample, approximately 50% - 100% of the control sample, approximately 100% - 200% of the control sample, approximately 100% - 400% of the control sample, approximately 200% - 400% of the control sample, approximately 10% - 50% of the control sample, approximately 20% - 100% of the control sample, approximately 25% - 75% of the control sample, or approximately 50% - 100% of the control sample. It may be 10, 20, 25, 30, 40, 50, 75, 100, 125, 150, 175, 200, 250, 300, 400, or 500 percent of the control sample.

The any 1, at least 1, 2, at least 2, 3, at least 3, 4, at least 4, 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 50 miRNAs differentially expressed may include any of the miRNAs discussed in Tables 2-5 or figures 382-383. The miRNA may be detected by the detector hsa-miR-34b-4373037 or hsa-miR-1-4373161.

Administration of an agent which binds to and modulates type I IFN or IFNα activity may be administration of a small molecule or a biological agent. If the

therapeutic agent is a small molecule it may be synthesized or identified and isolated from a natural source.

If the therapeutic agent is a biological agent, it may be an antibody specific for any subtype(s) of type I IFN or IFNα. For instance, the antibody may be specific for any one of IFNα1, IFNα2, IFNα4, IFNα5, IFNα6, IFNα7, IFNα8, IFNα10, IFNα14, IFNα17, IFNα21, IFNβ, or IFNω. Alternatively, the antibody may be specific for any two, any three, any four, any five, any six, any seven, any eight, any nine, any ten, any eleven, any twelve type I IFN of IFNα subtypes. If the antibody is specific for more than one type I IFN subtype, the antibody may be specific for IFNα1, IFNα2, IFNα4, IFNα5, IFNα8, IFNα10, and IFNα21; or it may be specific for IFNα1, IFNα2, IFNα4, IFNα5, IFNα8, and IFNα10; or it may be specific for IFNα1, IFNα2, IFNα4, IFNα5, IFNα8, and IFNα21; or it may be specific for IFNα1, IFNα2, IFNα4, IFNα5, IFNα10, and IFNα21. Antibodies specific for type I IFN or IFNα include MEDI-545, any biologic or antibody other than MEDI-545, antibodies described in U.S. patent applications 11/009,410 filed December 10, 2004 and 11/157,494 filed June 20, 2005, 9F3 and other antibodies described in U.S. Patent No. 7,087,726 (Example 1 and Example 2, those disclosed in Table 3 and Table 4, and/or those disclosed in the table entitled "Deposit of Material" on lines 25-54, column 56), NK-2 and YOK5/19 (WO 84/03105), LO-22 (U.S. Patent 4,902,618), 144 BS (U.S. Patent 4,885,166), and EBI-1, EBI-2, and EBI-3 (EP 119476). A therapeutic agent that modulates IFNα activity may neutralize IFNα activity. One of skill in the art is well aware of preparation and formulation of such biological agents and methods of their administration.

The antibody may be a synthetic antibody, a monoclonal antibody, polyclonal antibodies, a recombinantly produced antibody, an intrabody, a multispecific antibody (including bi-specific antibodies), a human antibody, a humanized antibody, a chimeric antibody, a single-chain Fv (scFv) (including bi-specific scFv), a BiTE molecule, a single chain antibody, a Fab fragments, a F(ab') fragment, a disulfide-linked Fv (sdFv), or an epitope-binding fragment of any of the above. The antibody may be any of an immunoglobulin molecule or immunologically active portion of an immunoglobulin molecule. Furthermore, the antibody may be of any isotype. For example, it may be any of isotypes IgG1, IgG2, IgG3 or IgG4. The antibody may be a full-length antibody

comprising variable and constant regions, or an antigen-binding fragment thereof, such as a single chain antibody, or a Fab or Fab'2 fragment. The antibody may also be conjugated or linked to a therapeutic agent, such as a cytotoxin or a radioactive isotope.

A second agent other than the agent that binds to modulates IFNα activity may be administered to the patient. Second agents include, but are not limited to non-steroidal anti-inflammatory drugs such as ibuprofen, naproxen, sulindac, diclofenac, piroxicam, ketoprofen, diflunisal, nabumetone, etodolac, and oxaprozin, indomethacin; anti-malarial drugs such as hydroxychloroquine; corticosteroid hormones, such as prednisone, hydrocortisone, methylprednisolone, and dexamethasone; methotrexate; immunosuppressive agents, such as azathioprine and cyclophosphamide; and biologic agents that, *e.g.*, target T cells such as Alefacept and Efalizumab, or target TNFα, such as, Enbrel, Remicade, and Humira.

Treatment with the agent may result in neutralization of the differentially regulated miRNA profile. Treatment with the agent may result in a decrease in one or more symptoms of the type I IFN or an IFNα-mediated disease or disorder. Treatment with the agent may result in fewer flare-ups related to the type I IFN or an IFNα-mediated disease or disorder. Treatment with the agent may result in improved prognosis for the patient having the type I IFN or an IFNα-mediated disease or disorder. Treatment with the agent may result in a higher quality of life for the patient. Treatment with the agent may alleviate the need to co-administer second agents or may lessen the dosage of administration of the second agent to the patient. Treatment with the agent may reduce the number of hospitalizations of the patient that are related to the type I IFN or an IFNα-mediated disease or disorder.

The agent that binds to and modulates type I IFN or IFNα activity may neutralize a differentially regulated miRNA profile. Neutralization of the differentially regulated miRNA profile may be a reduction in at least one, at least two, at least three, at least five, at least seven, at least eight, at least ten, at least twelve, at least fifteen, at least twenty, at least twenty five, at least thirty, at least thirty five, at least forty, at least forty five, or at least fifty up-regulated miRNAs. The upregulated miRNAs may include any of those detected by or included in Tables 2 or 4 or as shown in figure sheets 382-383. Neutralization of the differentially regulated miRNA profile may be a reduction of at

least 2%, at least 3%, at least 4%, at least 5%, at least 7%, at least 8%, at least 10%, at least 15%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, or at least 90% of any of the at least one, at least two, at least three, at least five, at least seven, at least eight, at least ten, at least twelve, at least fifteen, at least twenty, at least twenty five, at least thirty, at least thirty five, at least forty, at least forty five, or at least fifty genes up-regulated in any differentially regulated miRNA profile. Alternatively, neutralization of the differentially regulated miRNA profile refers to a reduction of expression of up-regulated miRNAs that is within at most 50%, at most 45%, at most 40%, at most 35%, at most 30%, at most 25%, at most 20%, at most 15%, at most 10%, at most 5%, at most 4%, at most 3%, at most 2%, or at most 1% of expression levels of those miRNAs in a control sample. If the agent that binds to and modulates type I IFN or IFNα activity is a biologic agent, such as an antibody, the agent may neutralize the type I IFN or IFNα profile at doses of 0.3 to 30 mg/kg, 0.3 to 10 mg/kg, 0.3 to 3 mg/kg, 0.3 to 1 mg/kg, 1 to 30 mg/kg, 3 to 30 mg/kg, 5 to 30 mg/kg, 10 to 30 mg/kg, 1 to 10 mg/kg, 3 to 10 mg/kg, or 1 to 5 mg/kg.

Neutralization of the differentially regulated miRNA profile may be an increase in down-regulated expression of at least one, at least two, at least three, at least five, at least seven, at least eight, at least ten, at least twelve, at least fifteen, at least twenty, at least twenty five, at least thirty, at least thirty five, at least forty, at least forty five, or at least fifty miRNAs. The downregulated miRNAs may include any of these detected by or included in Tables 3 or 5 or as shown in figure sheets 382-383. Neutralization of down-regulated genes in a differentially regulated miRNA profile is an increase of at least 2%, at least 3%, at least 4%, at least 5%, at least 7%, at least 8%, at least 10%, at least 15%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, or at least 90%, or at least 100%, or at least 125%, or at least 130%, or at least 140%, or at least 150%, or at least 175%, or at least 200%, or at least 250%, or at least 300%, or at least 500% of any of the at least one, at least two, at least three, at least five, at least seven, at least eight, at least ten, at least twelve, at least fifteen, at least twenty, or at least twenty five miRNAs whose expression is downregulated in any miRNA profile. Alternatively, neutralization of the differentially regulated miRNA profile refers to an increase in expression of miRNAs to within at most

50%, at most 45%, at most 40%, at most 35%, at most 30%, at most 25%, at most 20%, at most 15%, at most 10%, at most 5%, at most 4%, at most 3%, at most 2%, or at most 1% of expression levels of those miRNAs in a control sample. If the agent that binds to and modulates type I IFN or IFNα activity is a biologic agent, such as an antibody, the agent may neutralize the differentially regulated miRNA profile at doses of 0.3 to 30 mg/kg, 0.3 to 10 mg/kg, 0.3 to 3 mg/kg, 0.3 to 1 mg/kg, 1 to 30 mg/kg, 3 to 30 mg/kg, 5 to 30 mg/kg, 10 to 30 mg/kg, 1 to 10 mg/kg, 3 to 10 mg/kg, or 1 to 5 mg/kg.

The patient may further comprise a type I IFN or IFNα-inducible PD marker expression profile. The type I IFN or IFNα-inducible PD marker expression profile may be a strong profile, a moderate profile, or a weak profile. The type I IFN or IFNα-inducible PD marker expression profile can readily be designated as strong, moderate, or weak by determining the fold dysregulation of the type I IFN or IFNα-inducible PD marker expression profile of the patient, (*e.g.*, the fold increase in expression of upregulated type I IFN or IFNα-inducible PD markers in the patient), relative to a control sample(s) or control patient(s) and comparing the patient's fold dysregulation to that of other patients having a type I IFN or IFNα-inducible PD marker expression profile. The type I IFN or IFNα-inducible PD marker expression profile may be any disclosed in PCT/US2007/024947 filed December 6, 2007, herein incorporated by reference.

The group of genes that may be included in the type I IFN or IFNα-inducible PD marker expression profile of the patient may be MX1, LY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RASD2, and IFI44. The genes or genes detected by the probes may include IFI44, IFI27, IFI44L, DNAPTP6, LAMP3, LY6E, RSAD2, HERC5, IFI6, ISG15, OAS3, SIGLEC1, OAS2, USP18, RTP4, IFIT1, MX1, OAS1, EPSTI1, PLSCR1, and IFRG28. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The genes may include any at least 2, any at least 3, any at least 4, any at least 5, any at least 6, any at least 7, any at least 8, any at least 9, any at least 10, or any at least 11, or any at least 12, or any at least 13, or any at least 14, or any at least 15, or any at least 16, or any at least 17, or any at least 18, or any at least 19, or at least 20, or any at least 21, or any at least 22, or any at least 23, or any at least 24, or any least 25, or any at least 26, or any at least 27, or any at least 28, or any at least 29, or any at least 30 of

LAMP3, DNAPTP6, FLJ31033, HERC6, SERPING1, EPSTl1, RTP4, OASL, FBXO6, IFIT2, IFI44, OAS3, BATF2, ISG15, IRF7, RSAD2, IFI35, OAS1, LAP3, IFIT1, IFIT5, PLSCR1, IFI44L, MS4A4A, GALM, UBE2L6, TOR1B, SAMD9L, HERC5, TDRD7, TREX1, PARP12, and AXUD1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI27, SIGLEC1, RSAD2, IFI6, IFI44L, IFI44, USP18, IFIT2, SAMD9L, BIRC4BP, DNAPTP6, OAS3, LY6E, IFIT1, LIPA, LOC129607, ISG15, PARP14, MX1, OAS2, OASL, CCL2, HERC5, OAS1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFIT1, IFIT3, IRF7, IFI6, IL6ST, IRF2, LY6E, MARCKS, MX1, MX2, OAS1, EIF2AK2, ISG15, STAT2, OAS3, IFI44, IFI44L, HERC5, RAB8B, LILRA5, RSAD2, and FCHO2. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes SERPING1, IFIT2, IFIT3, IFI6, LY6E, MX1, OAS1, ISG15, IFI27, OAS3, IFI44, LAMP3, DNAPTP6, ETV7, HERC5, OAS2, USP18, XAF1, RTP4, SIGLEC1, and EPSTI1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes SERPING1, IFIT2, IFIT3, IFI6, LY6E, MX1, OAS1, ISG15, IFI27, OAS3, IFI44, LAMP3, DNAPTP6, ETV7, HERC5, OAS2, USP18, XAF1, RTP4, SIGLEC1, EPSTI1, and RSAD2. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes BCL2, BAK1, BAD, BAX, and BCL2L1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes RTP4, RSAD2, HERC5, SIGLEC1, USP18, LY6E, ETV7, SERPING1, IFIT3, OAS1, HSXIAPAF1, G1P3, MX1, OAS3, IFI27, DNAPTP6, LAMP3, EPSTI1, IFI44, OAS2, IFIT2, and ISG15. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes LAMP3, SIGLEC1, DNAPTP6, IFIT2, ETV7, RTP4, SERPING1, HERC5, XAF1, MX1, EPSTI1, OAS2, OAS1, OAS3, IFIT3, IFI6, USP18, RSAD2, IFI44, LY6E, ISG15, and IFI27. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes DNAPTP6, EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, PLSCR1, RSAD2, RTP4, SIGLEC1, and USP18. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes SAMD9L, IFI6, IFI44, IFIT2, ZC3HAV1, ETV6, DAPP1, IL1RN, CEACAM1, OAS1, IFI27, OAS3, IFI44L, HERC5, IFIT1, EPSTI1, ISG15, SERPING1, OASL, GBP1, and MX1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI6, RSAD2, IFI44, IFI44L, IFI27, MX1, IFIT1, ISG15, LAMP3, OAS3, OAS1, EPSTI1, IFIT3, OAS2, SIGLEC1, and USP18. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI6, RSAD2, IFI44, IFI44L, IFI27, MX1, IFIT1, HERC5, ISG15, LAMP3, OAS3, OAS1, EPSTI1, IFIT3, OAS2, LY6E, SIGLEC1, and USP18. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI6, RSAD2, IFI44, IFI44L, IFI27, MX1, and IFIT1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes SAMD9L, IFI6, IFI44, IFIT2, OAS1, IFI27, OAS3, IFI44L, HERC5, IFIT1, EPSTI1, ISG15, SERPING1, OASL, GBP1, and MX1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI27, RSAD2, IFI44L, IFI44, OAS1, IFIT1, ISG15, OAS3, HERC5, MX1, ESPTI1, IFIT3, and IFI6. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI44L, RSAD2, IFI27, and IFI44. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI44L and RSAD2. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least gene IFI444L. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least gene RSAD2. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The patient comprising the differentially regulated miRNA profile may further comprise downregulated type I IFN or IFNα PD marker(s). The downregulated PD markers may include any one, any two, any three, any four, any five, any six, or any seven, of genes CYP1B1, TGST1, RRAGD, IRS2, MGST1, TGFBR3, and RGS2.

The patient comprising the differentially regulated miRNA profile may further comprise upregulation of expression of any number of IFNα or type-I IFN subtypes. The IFNα or type-I IFN subtypes may include any more than one, more than two, more than three, more than four, more than five, more than six, more than seven, more than eight, more than nine, or more than ten IFNα or type-I IFN subtypes. These subtypes may include IFNα1, IFNα2, IFNα4, IFNα5, IFNα6, IFNα7, IFNα8, IFNα10, IFNα14, IFNα17, IFNα21, IFNβ, or IFNω. The patient may comprise upregulation of expression of IFN subtypes IFNα1, IFNα2, IFNα8, and IFNα14.

The patient comprising the differentially regulated miRNA profile may further comprise upregulation of expression of IFNα receptors, either IFNAR1 or IFNAR2, or both, or TNFα, or IFNγ, or IFNγ receptors (either IFNGR1, IFNGR2, or both IFNGR1 and IFNGR2). The patient may simply be identified as one who comprises upregulation of expression of IFNα receptors, either IFNAR1 or IFNAR2, or both, or TNFα, or IFNγ, or IFNγ receptors (either IFNGR1, IFNGR2, or both IFNGR1 and IFNGR2).

The upregulation or downregulation of the type I IFN or IFNα-inducible PD markers in the patient's expression profile may be by any degree relative to that of a sample from a control (which may be from a sample that is not disease tissue of the patient (e.g., non-lesional skin of a psoriasis patient) or from a healthy person not afflicted with the disease or disorder). The degree upregulation or downregulation may be at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 100%, at least 125%, at least 150%, or at least 200%, or at least 300%, or at least 400%, or at least 500% that of the control or control sample.

Furthermore, the patient may overexpress or have a tissue that overexpresses a type I IFN subtype at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 100%, at least 125%, at least 150%, or at least 200%, or at least 300%, or at least 400%, or at least 500% that of the control. The type I IFN subtype may be any one of IFNα1, IFNα2, IFNα4, IFNα5, IFNα6, IFNα7, IFNα8, IFNα10, IFNα14, IFNα17, IFNα21, IFNβ, or IFNω. The type I IFN subtypes may include all of IFNα1, IFNα2, IFNα8, and IFNα14.

The patient may further comprise or alternatively comprise alterations in levels of proteins in serum. The patient may have increased serum levels of proteins such as adiponectin, alpha-fetoprotein, apolipoprotein CIII, beta-2 microglobulin, cancer antigen 125, cancer antigen 19-9, eotaxin, FABP, factor VII, ferritin, IL-10, IL-12p70, IL-16, IL-18, IL-1ra, IL-3, MCP-1, MMP-3, myoglobin, SGOT, tissue factor, TIMP-1, TNF RII, TNF-alpha, VCAM-1, or vWF. The patient may have increased serum levels of any 1, 2,3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 14, 15, 16, 17, 18, 19, 20, 21, o22, 23, 24, 25, or 26 of these proteins in serum. The increased level may be at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 100%, at least 125%, at least 150%, or at least 200%, or at least 300%, or at least 400%, or at least 500% that of a control, e.g., a healthy subject. The alteration may be a decrease in serum levels of proteins such as BDNK, complement 3, CD40 ligand, EGF, ENA-78, EN-RAGE, IGF-1, MDC, myeloperoxidase, RANTES, or thrombopoietin, The patient may have decreased serum levels of any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 or these proteins. The decreased level may be at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, or at least 100% that of a control, e.g., a healthy subject. The PD marker profile may comprise one or more of these increased or decreased serum levels of proteins.

The patient may further comprise auto-antibodies that bind to any one of the following auto-antigens: (a) Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78; (b) surfeit 5, transcript variant c; (c) proteasome (posome, macropain) activator subunit 3 (PA28 gamma; Ki) transc; (d) retinoic acid receptor, alpha; (e) Heat shock 10 kDa protein 1 (chaperonin 10); (f) tropomyosin 3; (g) pleckstrin homology-like domain, family A, member 1; (h) cytoskeleton-associated protein 1; (i) Sjogren syndrome antigen A2 (60 kDa, ribonucleoprotein auto-antigen SS-A/Ro); (j) NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex 1, 8 kDa; (k) NudE nuclear distribution gene E homolog 1 (A. nidulans); (l) MutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli); (m) leucine rich repeat (in FLII) interacting protein 2; (n) tropomyosin 1 (alpha); (o) spastic paraplegia 20, spartin (Troyer syndrome); (p) preimplantation protein, transcript variant 1; (r) mitochondrial ribosomal protein L45; (s)

Lin-28 homolog (C. elegans); (t) heat shock 90 kDa protein 1, alpha; (u) dom-3 homolog Z (C. elegans); (v) dynein, cytoplasmic, light intermediate polypeptide 2; (w) Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein); (x) synovial sarcoma, X breakpoint 2, transcript variant 2; (y) moesin; (z) homer homolog (Drosophila), transcript variant 1; (aa) GCN5 general control of amino-acid synthesis 5-like 2 (yeast); (bb) eukaryotic translation elongation factor 1 gamma; (cc) eukaryotic translation elongation factor 1, delta; (dd) DNA-damage-inducible transcript 3; (ee) CCAAT/enhancer binding protein (C/EBP) gamma; and any other auto-antigen described in provisional application entitled "Auto-antibody markers of autoimmune disease" filed May 3, 2007 or in provisional application entitled entitled "Auto-antibody markers of autoimmune disease" to be filed November 6, 2007 (for example, but not limited to, those described on Tables 2, 4, 5, and 9). The patient may comprise auto-antibodies that bind to any number of these auto-antigens, *e.g.*, any at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25.

Administration of the agent that binds to and modulates type I IFN or an IFNα activity may further neutralize a type I IFN or IFNα-inducible profile to within at least 2%, at least 3%, at least 4%, at least 5%, at least 7%, at least 8%, at least 10%, at least 15%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, or at least 90% that of a control sample.

In methods of monitoring or prognosing disease progression of a patient, samples from the patient may be obtained before and after administration of an agent.

Samples include any biological fluid or tissue, such as whole blood, serum, muscle, saliva, urine, synovial fluid, bone marrow, cerebrospinal fluid, nasal secretions, sputum, amniotic fluid, bronchoalveolar lavage fluid, peripheral blood mononuclear cells, total white blood cells, lymph node cells, spleen cells, tonsil cells, or skin. The samples may be obtained by any means known in the art.

miRNA profiles are obtained in the (before and after agent administration) samples. The miRNA profiles in the samples are compared. Comparison may be of the number of miRNAs present in the samples or may be of the quantity of miRNAs present

in the samples, or any combination thereof. Variance indicating efficacy of the therapeutic agent may be indicated if the number or level (or any combination thereof) of up-regulated miRNAs decreases in the sample obtained after administration of the therapeutic agent relative to the sample obtained before administration of the therapeutic agent. The number of up-regulated miRNAs may decrease by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10. The level of any given up-regulated miRNAs may decrease by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. The number of up-regulated miRNAs with decreased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. Any combination of decreased number and decreased level of up-regulated miRNAs may indicate efficacy. Variance indicating efficacy of the therapeutic agent may be indicated if the number or level (or any combination thereof) of down-regulated miRNAs decreases in the sample obtained after administration of the therapeutic agent relative to the sample obtained before administration of the therapeutic agent. The number of down-regulated miRNAs may decrease by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10. The level of any given down-regulated miRNA may increase by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. The number of down-regulated miRNAs with increased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. Any combination of decreased number and increased level of down-regulated miRNAs may indicate efficacy.

The sample obtained from the patient may be obtained prior to a first administration of the agent, *i.e.*, the patient is naïve to the agent. Alternatively, the sample obtained from the patient may occur after administration of the agent in the course of treatment. For example, the agent may have been administered prior to the initiation of the monitoring protocol. Following administration of the agent an additional samples may be obtained from the patient and type I IFN or IFNα inducible PD markers

in the samples are compared. The samples may be of the same or different type, e.g., each sample obtained may be a blood sample, or each sample obtained may be a serum sample. The type I IFN or IFNα inducible PD markers detected in each sample may be the same, may overlap substantially, or may be similar.

The samples may be obtained at any time before and after the administration of the therapeutic agent. The sample obtained after administration of the therapeutic agent may be obtained at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 12, or at least 14 days after administration of the therapeutic agent. The sample obtained after administration of the therapeutic agent may be obtained at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 weeks after administration of the therapeutic agent. The sample obtained after administration of the therapeutic agent may be obtained at least 2, at least 3, at least 4, at least 5, or at least 6 months following administration of the therapeutic agent.

Additional samples may be obtained from the patient following administration of the therapeutic agent. At least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 12, at least 15, at least 20, at least 25 samples may be obtained from the patient to monitor progression or regression of the disease or disorder over time. Disease progression may be monitored over a time period of at least 1 week, at least 2 weeks, at least 3 weeks, at least 4 weeks, at least 5 weeks, at least 6 weeks, at least 7 weeks, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, at least 1 year, at least 2 years, at least 3 years, at least 4 years, at least 5 years, at least 10 years, or over the lifetime of the patient. Additional samples may be obtained from the patient at regular intervals such as at monthly, bi-monthly, once a quarter year, twice a year, or yearly intervals. The samples may be obtained from the patient following administration of the agent at regular intervals. For instance, the samples may be obtained from the patient at one week following each administration of the agent, or at two weeks following each administration of the agent, or at three weeks following each administration of the agent, or at one month following each administration of the agent, or at two months following each administration of the agent. Alternatively, multiple samples may be obtained from the patient following each administration of the agent.

Disease progression in a patient may similarly be monitored in the absence of administration of an agent. Samples may periodically be obtained from the patient having the disease or disorder. Disease progression may be identified if the number of miRNAs increases in a later-obtained sample relative to an earlier obtained sample. The number of miRNAs may increase by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10. Disease progression may be identified if level of any given up-regulated miRNAs increases by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. Disease progression may be identified if level of any given down-regulated miRNAs decreases by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. The number of up-regulated miRNAs with increased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. The number of down-regulated miRNAs with decreased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. Any combination of increased number and increased level of up-regulated miRNA may indicate disease progression. Alternatively, or in combination, any combination of decreased number and decreased level of down-regulated type miRNA may indicate disease progression. Disease regression may also be identified in a patient having a disease or disorder, not treated by an agent. In this instance, regression may be identified if the number of miRNAs decreases in a later-obtained sample relative to an earlier obtained sample. The number of miRNAs may decrease by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10. Disease regression may be identified if level of any given up-regulated miRNA decreases by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. Disease regression may be identified if level of any given down-regulated miRNA increases by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. The number

of up-regulated miRNAs with decreased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. The number of down-regulated miRNAs with increased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. Disease progression or disease regression may be monitored by obtaining samples over any period of time and at any interval. Disease progression or disease regression may be monitored by obtaining samples over the course of at least 1 week, at least 2 weeks, at least 3 weeks, at least 4 weeks, at least 5 weeks, at least 6 weeks, at least 7 weeks, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, at least 1 year, at least 2 years, at least 3 years, at least 4 years, at least 5 years, at least 10 years, or over the lifetime of the patient. Disease progression or disease regression may be monitored by obtaining samples at least monthly, bi-monthly, once a quarter year, twice a year, or yearly. The samples need not be obtained at strict intervals.

Variance in the samples may guide treatment strategy of a disease or disorder. Treatment strategy may be dosage of a particular therapeutic, or may be removal or addition of particular therapeutics administered to a patient.

The invention also encompasses methods employing IFNα-inducible PD markers to treat, diagnose, prognose, and monitor myositis. These IFNα-inducible PD markers can also be used to guide dosage and treatment of myositis patients or models of myositis disease.

The type I IFN or IFNα-inducible PD marker expression profile may comprise upregulation or downregulation of any type I IFN or IFNα-inducible PD marker expression profile genes or group of genes relative to a control, e.g. healthy, patient or sample of non-disease tissue of a patient. The gene or group of genes may include any at least 2, any at least 3, any at least 4, any at least 5, any at least 6, any at least 7, any at least 8, any at least 9, any at least 10, any at least 11, any at least 12, any at least 13, any at least 14, any at least 15, any at least 16, any at least 17, any at least 18, any at least 19, any at least 20, any at least 21, any at least 22, any at least 23, any at least 24, any at least 25, any at least 26, any at least 27, any at least 28, any at least 29, any at least 30, any at

least 40, any at least 50 genes, any at least 75 gene, any at least 100 genes, or any at least 150 genes.

The IFNα-inducible PD markers in an expression profile may include at least genes EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, RSAD2, RTP4, SIGLEC1, USP18. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI27, SIGLEC1, RSAD2, IFI6, IFI44L, IFI44, USP18, IFIT2, SAMD9L, BIRC4BP, DNAPTP6, OAS3, LY6E, IFIT1, LIPA, LOC129607, ISG15, PARP14, MX1, OAS2, OASL, CCL2, HERC5, OAS1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFIT1, IFIT3, IRF7, IFI6, IL6ST, IRF2, LY6E, MARCKS, MX1, MX2, OAS1, EIF2AK2, ISG15, STAT2, OAS3, IFI44, IFI44L, HERC5, RAB8B, LILRA5, RSAD2, and FCHO2. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes SERPING1, IFIT2, IFIT3, IFI6, LY6E, MX1, OAS1, ISG15, IFI27, OAS3, IFI44, LAMP3, DNAPTP6, ETV7, HERC5, OAS2, USP18, XAF1, RTP4, SIGLEC1, and EPSTI1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes SERPING1, IFIT2, IFIT3, IFI6, LY6E, MX1, OAS1, ISG15, IFI27, OAS3, IFI44, LAMP3, DNAPTP6, ETV7, HERC5, OAS2, USP18, XAF1, RTP4, SIGLEC1, EPSTI1, and RSAD2. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes RTP4, RSAD2, HERC5, SIGLEC1, USP18, LY6E, ETV7, SERPING1, IFIT3, OAS1, HSXIAPAF1, G1P3, MX1, OAS3, IFI27, DNAPTP6, LAMP3, EPSTI1, IFI44,

OAS2, IFIT2, and ISG15. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes LAMP3, SIGLEC1, DNAPTP6, IFIT2, ETV7, RTP4, SERPING1, HERC5, XAF1, MX1, EPSTI1, OAS2, OAS1, OAS3, IFIT3, IFI6, USP18, RSAD2, IFI44, LY6E, ISG15, and IFI27. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes DNAPTP6, EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, PLSCR1, RSAD2, RTP4, SIGLEC1, and USP18. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes SAMD9L, IFI6, IFI44, IFIT2, ZC3HAV1, ETV6, DAPP1, IL1RN, CEACAM1, OAS1, IFI27, OAS3, IFI44L, HERC5, IFIT1, EPSTI1, ISG15, SERPING1, OASL, GBP1, and MX1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI6, RSAD2, IFI44, IFI44L, IFI27, MX1, IFIT1, ISG15, LAMP3, OAS3, OAS1, EPSTI1, IFIT3, OAS2, SIGLEC1, and USP18. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI6, RSAD2, IFI44, IFI44L, IFI27, MX1, IFIT1, HERC5, ISG15, LAMP3, OAS3, OAS1, EPSTI1, IFIT3, OAS2, LY6E, SIGLEC1, and USP18. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI6, RSAD2, IFI44, IFI44L, IFI27, MX1, and IFIT1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI6, RSAD2, IFI44, IFI44L, and IFI27. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes SAMD9L, IFI6, IFI44, IFIT2, OAS1, IFI27, OAS3, IFI44L, HERC5, IFIT1, EPSTI1, ISG15, SERPING1, OASL, GBP1, and MX1. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI27, RSAD2, IFI44L, IFI44, OAS1, IFIT1, ISG15, OAS3, HERC5, MX1, ESPTI1, IFIT3, and IFI6. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI44L, RSAD2, IFI27, and IFI44. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI44L and RSAD2. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least gene IFI444L. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least gene RSAD2. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include at least genes IFI27, IL-121R beta2, IL-15R alpha, IL-15, suppressor of cytokine signaling 1 (SOCS1), janus kinase 2, CXCL11 (T-TAC), TNFSF13B (BAFF), TRAF-type domain 1 (TRAFD1), SERPING1, CD274 (PD1-L), indoleamine 2,3 dioxygenase (INDO), lymphocyte-activation gene 3 (LAG3), and caspase 5. The IFNα-inducible PD markers in

such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

IFNα-inducible PD markers or a PD marker profile may include any at least 5 genes such as, for example: MX1, LLY6E, IFI27, OAS1, IFIT1; or MX1, LLY6E, IFI27, OAS1, IFI6; or MX1, LLY6E, IFI27, OAS1, IFI44L; or MX1, LLY6E, IFI27, OAS1, ISG15; or MX1, LLY6E, IFI27, OAS1, LAMP3; or MX1, LLY6E, IFI27, OAS1, OASL; or MX1, LLY6E, IFI27, OAS1, RSAD2; or MX1, LLY6E, IFI27, OAS1, IFI44; or MX1, LLY6E, IFI27, OAS1, IFIT2; or MX1, LLY6E, IFI27, OAS1, OAS3; or MX1, LLY6E, IFI27, OAS1, USP18; or MX1, LLY6E, IFI27, OAS1, SIGLEC1; or MX1, LLY6E, IFI27, OAS1, HERC5; or MX1, LLY6E, IFI27, OAS1, DNAPTP6; or MX1, LLY6E, IFI27, OAS1, LOC129607; or MX1, LLY6E, IFI27, OAS1, EPSTI1; or MX1, LLY6E, IFI27, OAS1, BIRC4BP; or MX1, LLY6E, IFI27, OAS1, SIGLEC1; or MX1, LLY6E, IFI27, OAS1, gene detected by probe 229450_at; or MX1, LLY6E, IFI27, OAS1, gene detected by probe 235276_at; or LLY6E, IFI27, OAS1, IFIT1, IFI6; or LLY6E, IFI27, OAS1, IFIT1, IFI44L; or LLY6E, IFI27, OAS1, IFIT1, ISG15; or LLY6E, IFI27, OAS1, IFIT1, LAMP3; or LLY6E, IFI27, OAS1, IFIT1, OASL; or LLY6E, IFI27, OAS1, IFIT1, RSAD2; or LLY6E, IFI27, OAS1, IFIT1, IFI44; or LLY6E, IFI27, OAS1, IFIT1, IFIT2; or LLY6E, IFI27, OAS1, IFIT1, OAS3; or LLY6E, IFI27, OAS1, IFIT1, USP18; or LLY6E, IFI27, OAS1, IFIT1, SIGLEC1; or LLY6E, IFI27, OAS1, IFIT1, HERC5; or LLY6E, IFI27, OAS1, IFIT1, DNAPTP6; or LLY6E, IFI27, OAS1, IFIT1, LOC129607; or LLY6E, IFI27, OAS1, IFIT1, EPSTI1; or LLY6E, IFI27, OAS1, IFIT1, BIRC4BP; or LLY6E, IFI27, OAS1, IFIT1, SIGLEC1; or LLY6E, IFI27, OAS1, IFIT1, gene detected by probe 229450_at; or LLY6E, IFI27, OAS1, IFIT1, gene detected by probe 235276_at; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15; or IFI27, OAS1, IFIT1, IFI6, LAMP3; or IFI27, OAS1, IFIT1, IFI6, OASL; or IFI27, OAS1, IFIT1, IFI6, RSAD2; or IFI27, OAS1, IFIT1, IFI6, IFI44; or IFI27, OAS1, IFIT1, IFI6, IFIT2; or IFI27, OAS1, IFIT1, IFI6, OAS3; or IFI27, OAS1, IFIT1, IFI6, USP18; or IFI27, OAS1, IFIT1, IFI6, SIGLEC1; or IFI27, OAS1, IFIT1, IFI6, HERC5; or IFI27, OAS1, IFIT1, IFI6, DNAPTP6; or IFI27, OAS1, IFIT1, IFI6, LOC129607; or IFI27, OAS1, IFIT1, IFI6, EPSTI1; or IFI27, OAS1, IFIT1, IFI6, BIRC4BP; or IFI27, OAS1, IFIT1, IFI6, SIGLEC1; or IFI27, OAS1, IFIT1, IFI6, gene detected by probe 229450_at; or IFI27,

OAS1, IFIT1, IFI6, gene detected by probe 235276_at; or OAS1, IFIT1, IFI6, IFI44L, ISG15; or OAS1, IFIT1, IFI6, IFI44L, LAMP3; or OAS1, IFIT1, IFI6, IFI44L, OASL; or OAS1, IFIT1, IFI6, IFI44L, RSAD2; or OAS1, IFIT1, IFI6, IFI44L, IFI44; or OAS1, IFIT1, IFI6, IFI44L, IFIT2; or OAS1, IFIT1, IFI6, IFI44L, OAS3; or OAS1, IFIT1, IFI6, IFI44L, USP18; or OAS1, IFIT1, IFI6, IFI44L, SIGLEC1; or OAS1, IFIT1, IFI6, IFI44L, HERC5; or OAS1, IFIT1, IFI6, IFI44L, DNAPTP6; or OAS1, IFIT1, IFI6, IFI44L, LOC129607; or OAS1, IFIT1, IFI6, IFI44L, EPSTI1; or OAS1, IFIT1, IFI6, IFI44L, BIRC4BP; or OAS1, IFIT1, IFI6, IFI44L, SIGLEC1; or OAS1, IFIT1, IFI6, IFI44L, gene detected by probe 229450_at; or OAS1, IFIT1, IFI6, IFI44L, gene detected by probe 235276_at; or IFIT1, IFI6, IFI44L, ISG15, LAMP3; or IFIT1, IFI6, IFI44L, ISG15, OASL; or IFIT1, IFI6, IFI44L, ISG15, RSAD2; or IFIT1, IFI6, IFI44L, ISG15, IFI44; or IFIT1, IFI6, IFI44L, ISG15, IFIT2 or IFIT1, IFI6, IFI44L, ISG15, OAS3; or IFIT1, IFI6, IFI44L, ISG15, USP18; or IFIT1, IFI6, IFI44L, ISG15, SIGLEC1; or IFIT1, IFI6, IFI44L, ISG15, HERC5; or IFIT1, IFI6, IFI44L, ISG15, DNAPTP6; or IFIT1, IFI6, IFI44L, ISG15, LOC129607; or IFIT1, IFI6, IFI44L, ISG15, EPSTI1; or IFIT1, IFI6, IFI44L, ISG15, BIRC4BP; or IFIT1, IFI6, IFI44L, ISG15, gene detected by probe 229450_at; or IFIT1, IFI6, IFI44L, ISG15, gene detected by probe 235276_at; or IFI6, IFI44L, ISG15, LAMP3, HERC5; or IFI6, IFI44L, ISG15, LAMP3, DNAPTP6; or IFI6, IFI44L, ISG15, LAMP3, LOC129607; or IFI6, IFI44L, ISG15, LAMP3, EPSTI1; or IFI6, IFI44L, ISG15, LAMP3, BIRC4BP; or IFI6, IFI44L, ISG15, LAMP3, gene detected by probe 229450_at; or IFI6, IFI44L, ISG15, LAMP3, gene detected by probe 235276_at; or IFI6, IFI44L, ISG15, LAMP3, SIGLEC1; or IFI6, IFI44L, ISG15, LAMP3, USP18; or IFI6, IFI44L, ISG15, LAMP3, OAS3; or IFI6, IFI44L, ISG15, LAMP3, IFIT2; or IFI6, IFI44L, ISG15, LAMP3, IFI44; or IFI6, IFI44L, ISG15, LAMP3, RSAD2; or IFI6, IFI44L, ISG15, LAMP3, OASL; or IFI44L, ISG15, LAMP3, OASL, RSAD2; or IFI44L, ISG15, LAMP3, OASL, IFI44; or IFI44L, ISG15, LAMP3, OASL, IFIT2; or IFI44L, ISG15, LAMP3, OASL, OAS3; or IFI44L, ISG15, LAMP3, OASL, USP18; or IFI44L, ISG15, LAMP3, OASL, SIGLEC1; or IFI44L, ISG15, LAMP3, OASL, HERC5; or IFI44L, ISG15, LAMP3, OASL, DNAPTP6; or IFI44L, ISG15, LAMP3, OASL, LOC129607; or IFI44L, ISG15, LAMP3, OASL, EPSTI1;or IFI44L, ISG15, LAMP3, OASL, BIRC4BP; or IFI44L, ISG15, LAMP3, OASL, gene

detected by probe 229450_at; or IFI44L, ISG15, LAMP3, OASL, gene detected by probe 235276_at; or ISG15, LAMP3, OASL, RSAD2, IFI44; or ISG15, LAMP3, OASL, RSAD2, IFIT2; or ISG15, LAMP3, OASL, RSAD2, OAS3; or ISG15, LAMP3, OASL, RSAD2, USP18; or ISG15, LAMP3, OASL, RSAD2, SIGLEC1; or ISG15, LAMP3, OASL, RSAD2, HERC5; or ISG15, LAMP3, OASL, RSAD2, DNAPTP6; or ISG15, LAMP3, OASL, RSAD2, LOC129607; or ISG15, LAMP3, OASL, RSAD2, EPSTI1; or ISG15, LAMP3, OASL, RSAD2, BIRC4BP; or ISG15, LAMP3, OASL, RSAD2, gene detected by probe 229450_at; or ISG15, LAMP3, OASL, RSAD2, gene detected by probe 235276_at; or LAMP3, OASL, RSAD2, IFI44, IFIT2; or LAMP3, OASL, RSAD2, IFI44, OAS3; or LAMP3, OASL, RSAD2, IFI44, USP18; or LAMP3, OASL, RSAD2, IFI44, SIGLEC1; or LAMP3, OASL, RSAD2, IFI44, HERC5; or LAMP3, OASL, RSAD2, IFI44, DNAPTP6; or LAMP3, OASL, RSAD2, IFI44, LOC129607; or LAMP3, OASL, RSAD2, IFI44, EPSTI1; or LAMP3, OASL, RSAD2, IFI44, BIRC4BP; or LAMP3, OASL, RSAD2, IFI44, gene detected by probe 229450_at; or LAMP3, OASL, RSAD2, IFI44, gene detected by probe 235276_at; or OASL, RSAD2, IFI44, IFIT2, OAS3; or OASL, RSAD2, IFI44, IFIT2, USP18; or OASL, RSAD2, IFI44, IFIT2, SIGLEC1; or OASL, RSAD2, IFI44, IFIT2, HERC5; or OASL, RSAD2, IFI44, IFIT2, DNAPTP6; or OASL, RSAD2, IFI44, IFIT2, LOC129607; or OASL, RSAD2, IFI44, IFIT2, EPSTI1; or OASL, RSAD2, IFI44, IFIT2, BIRC4BP; or OASL, RSAD2, IFI44, IFIT2, gene detected by probe 229450_at; or OASL, RSAD2, IFI44, IFIT2, gene detected by probe 235276_at; or RSAD2, IFI44, IFIT2, OAS3, USP18; or RSAD2, IFI44, IFIT2, OAS3, SIGLEC1; or RSAD2, IFI44, IFIT2, OAS3, HERC5; or RSAD2, IFI44, IFIT2, OAS3, DNAPTP6; or RSAD2, IFI44, IFIT2, OAS3, LOC129607; or RSAD2, IFI44, IFIT2, OAS3, EPSTI1; or RSAD2, IFI44, IFIT2, OAS3, BIRC4BP; or RSAD2, IFI44, IFIT2, OAS3, gene detected by probe 229450_at; or RSAD2, IFI44, IFIT2, OAS3, gene detected by probe 235276_at; or IFI44, IFIT2, OAS3, USP18, SIGLEC1; or IFI44, IFIT2, OAS3, USP18, HERC5; or IFI44, IFIT2, OAS3, USP18, DNAPTP6; or IFI44, IFIT2, OAS3, USP18, LOC129607; or IFI44, IFIT2, OAS3, USP18, EPSTI1; or IFI44, IFIT2, OAS3, USP18, BIRC4BP; or IFI44, IFIT2, OAS3, USP18, gene detected by probe 229450_at; or IFI44, IFIT2, OAS3, USP18, gene detected by probe 235276_at; or IFIT2, OAS3, USP18, SIGLEC1, HERC5; or IFIT2, OAS3, USP18, SIGLEC1, DNAPTP6; or

IFIT2, OAS3, USP18, SIGLEC1, LOC129607; or IFIT2, OAS3, USP18, SIGLEC1, EPSTI1; or IFIT2, OAS3, USP18, SIGLEC1, BIRC4BP; or IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 229450_at; or IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 235276_at; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6; or OAS3, USP18, SIGLEC1, HERC5, LOC129607; or OAS3, USP18, SIGLEC1, HERC5, EPSTI1; or OAS3, USP18, SIGLEC1, HERC5, BIRC4BP; or OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 229450_at; or OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 235276_at; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607; or USP18, SIGLEC1, HERC5, DNAPTP6, EPSTI1; or USP18, SIGLEC1, HERC5, DNAPTP6, BIRC4BP; or USP18, SIGLEC1, HERC5, DNAPTP6, gene detected by probe 229450_at; or USP18, SIGLEC1, HERC5, DNAPTP6, gene detected by probe 235276_at; or SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1; or SIGLEC1, HERC5, DNAPTP6, LOC129607, BIRC4BP; or SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 229450_at; or SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 235276_at; or HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP; or HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 229450_at; or HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 235276_at; or DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at; or DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 235276_at; or LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at, gene detected by probe 235276_at. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include any at least 6 genes such as, for example: MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI44L; or MX1, LLY6E, IFI27, OAS1, IFIT1, ISG15; or MX1, LLY6E, IFI27, OAS1, IFIT1, LAMP3; or MX1, LLY6E, IFI27, OAS1, IFIT1, OASL; or MX1, LLY6E, IFI27, OAS1, IFIT1, RSAD2; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI44; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFIT2; or MX1, LLY6E, IFI27, OAS1, IFIT1, OAS3; or MX1, LLY6E, IFI27, OAS1, IFIT1, USP18; or MX1, LLY6E, IFI27, OAS1, IFIT1, SIGLEC1; or MX1, LLY6E, IFI27, OAS1, IFIT1, HERC5; or MX1, LLY6E, IFI27, OAS1, IFIT1, DNAPTP6; or MX1, LLY6E, IFI27, OAS1, IFIT1,

LOC129607; or MX1, LLY6E, IFI27, OAS1, IFIT1, EPSTI1; or MX1, LLY6E, IFI27, OAS1, IFIT1, BIRC4BP;or MX1, LLY6E, IFI27, OAS1, IFIT1, gene detected by probe 229450_at; or MX1, LLY6E, IFI27, OAS1, IFIT1, gene detected by probe 235276_at; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L; or LLY6E, IFI27, OAS1, IFIT1, IFI6, ISG15; or LLY6E, IFI27, OAS1, IFIT1, IFI6, LAMP3; or LLY6E, IFI27, OAS1, IFIT1, IFI6, OASL ; or LLY6E, IFI27, OAS1, IFIT1, IFI6, RSAD2; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFIT2; or LLY6E, IFI27, OAS1, IFIT1, IFI6, OAS3; or LLY6E, IFI27, OAS1, IFIT1, IFI6, USP18; or LLY6E, IFI27, OAS1, IFIT1, IFI6, SIGLEC1; or LLY6E, IFI27, OAS1, IFIT1, IFI6, HERC5; or LLY6E, IFI27, OAS1, IFIT1, IFI6, DNAPTP6; or LLY6E, IFI27, OAS1, IFIT1, IFI6, LOC129607; or LLY6E, IFI27, OAS1, IFIT1, IFI6, EPSTI1; or LLY6E, IFI27, OAS1, IFIT1, IFI6, BIRC4BP; or LLY6E, IFI27, OAS1, IFIT1, IFI6, gene detected by probe 229450_at; or LLY6E, IFI27, OAS1, IFIT1, IFI6, gene detected by probe 235276_at; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15; or IFI27, OAS1, IFIT1, IFI6, IFI44L, LAMP3; or IFI27, OAS1, IFIT1, IFI6, IFI44L, OASL; or IFI27, OAS1, IFIT1, IFI6, IFI44L, RSAD2; or IFI27, OAS1, IFIT1, IFI6, IFI44L, IFI44; or IFI27, OAS1, IFIT1, IFI6, IFI44L, IFIT2; or IFI27, OAS1, IFIT1, IFI6, IFI44L, OAS3; or IFI27, OAS1, IFIT1, IFI6, IFI44L, USP18; or IFI27, OAS1, IFIT1, IFI6, IFI44L, SIGLEC1; or IFI27, OAS1, IFIT1, IFI6, IFI44L, HERC5; or IFI27, OAS1, IFIT1, IFI6, IFI44L, DNAPTP6; or IFI27, OAS1, IFIT1, IFI6, IFI44L, LOC129607; or IFI27, OAS1, IFIT1, IFI6, IFI44L, EPSTI1; or IFI27, OAS1, IFIT1, IFI6, IFI44L, BIRC4BP; or IFI27, OAS1, IFIT1, IFI6, IFI44L, gene detected by probe 229450_at; or IFI27, OAS1, IFIT1, IFI6, IFI44L, gene detected by probe 235276_at; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3; or OAS1, IFIT1, IFI6, IFI44L, ISG15, OASL; or OAS1, IFIT1, IFI6, IFI44L, ISG15, RSAD2; or OAS1, IFIT1, IFI6, IFI44L, ISG15, IFI44; or OAS1, IFIT1, IFI6, IFI44L, ISG15, IFIT2; or OAS1, IFIT1, IFI6, IFI44L, ISG15, OAS3; or OAS1, IFIT1, IFI6, IFI44L, ISG15, USP18; or OAS1, IFIT1, IFI6, IFI44L, ISG15, SIGLEC1; or OAS1, IFIT1, IFI6, IFI44L, ISG15, HERC5; or OAS1, IFIT1, IFI6, IFI44L, ISG15, DNAPTP6; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LOC129607; or OAS1, IFIT1, IFI6, IFI44L, ISG15, EPSTI1; or OAS1, IFIT1, IFI6, IFI44L, ISG15, BIRC4BP; or OAS1, IFIT1, IFI6, IFI44L, ISG15, gene detected by probe 229450_at; or OAS1, IFIT1, IFI6, IFI44L, ISG15, gene detected

by probe 235276_at; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, RSAD2; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, IFI44; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, IFIT2; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OAS3; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, USP18; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, SIGLEC1; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, HERC5; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, DNAPTP6; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, LOC129607; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, EPSTI1; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, BIRC4BP; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, gene detected by probe 229450_at; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, gene detected by probe 235276_at; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2; or IFI6, IFI44L, ISG15, LAMP3, OASL, IFI44; or IFI6, IFI44L, ISG15, LAMP3, OASL, IFIT2; or IFI6, IFI44L, ISG15, LAMP3, OASL, OAS3; or IFI6, IFI44L, ISG15, LAMP3, OASL, USP18; or IFI6, IFI44L, ISG15, LAMP3, OASL, SIGLEC1; or IFI6, IFI44L, ISG15, LAMP3, OASL, HERC5; or IFI6, IFI44L, ISG15, LAMP3, OASL, DNAPTP6; or IFI6, IFI44L, ISG15, LAMP3, OASL, LOC129607; or IFI6, IFI44L, ISG15, LAMP3, OASL, EPSTI1; or IFI6, IFI44L, ISG15, LAMP3, OASL, BIRC4BP; or IFI6, IFI44L, ISG15, LAMP3, OASL, gene detected by probe 229450_at; or IFI6, IFI44L, ISG15, LAMP3, OASL, gene detected by probe 235276_at; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFIT2; or IFI44L, ISG15, LAMP3, OASL, RSAD2, OAS3; or IFI44L, ISG15, LAMP3, OASL, RSAD2, USP18; or IFI44L, ISG15, LAMP3, OASL, RSAD2, SIGLEC1; or IFI44L, ISG15, LAMP3, OASL, RSAD2, HERC5; or IFI44L, ISG15, LAMP3, OASL, RSAD2, DNAPTP6; or IFI44L, ISG15, LAMP3, OASL, RSAD2, LOC129607; or IFI44L, ISG15, LAMP3, OASL, RSAD2, EPSTI1; or IFI44L, ISG15, LAMP3, OASL, RSAD2, BIRC4BP; or IFI44L, ISG15, LAMP3, OASL, RSAD2, gene detected by probe 229450_at; or IFI44L, ISG15, LAMP3, OASL, RSAD2, gene detected by probe 235276_at; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2; or ISG15, LAMP3, OASL, RSAD2, IFI44, OAS3; or ISG15, LAMP3, OASL, RSAD2, IFI44, USP18; or ISG15, LAMP3, OASL, RSAD2, IFI44, SIGLEC1; or ISG15, LAMP3, OASL, RSAD2, IFI44, HERC5; or ISG15, LAMP3, OASL, RSAD2, IFI44, DNAPTP6; or ISG15, LAMP3, OASL, RSAD2, IFI44, LOC129607; or ISG15, LAMP3, OASL, RSAD2, IFI44, EPSTI1; or ISG15, LAMP3, OASL, RSAD2, IFI44,

BIRC4BP; or ISG15, LAMP3, OASL, RSAD2, IFI44, gene detected by probe 229450_at; or ISG15, LAMP3, OASL, RSAD2, IFI44, gene detected by probe 235276_at; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3; or LAMP3, OASL, RSAD2, IFI44, IFIT2, USP18; or LAMP3, OASL, RSAD2, IFI44, IFIT2, SIGLEC1; or LAMP3, OASL, RSAD2, IFI44, IFIT2, HERC5; or LAMP3, OASL, RSAD2, IFI44, IFIT2, DNAPTP6; or LAMP3, OASL, RSAD2, IFI44, IFIT2, LOC129607; or LAMP3, OASL, RSAD2, IFI44, IFIT2, EPSTI1; or LAMP3, OASL, RSAD2, IFI44, IFIT2, BIRC4BP; or LAMP3, OASL, RSAD2, IFI44, IFIT2, gene detected by probe 229450_at; or LAMP3, OASL, RSAD2, IFI44, IFIT2, gene detected by probe 235276_at; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18; or OASL, RSAD2, IFI44, IFIT2, OAS3, SIGLEC1; or OASL, RSAD2, IFI44, IFIT2, OAS3, HERC5; or OASL, RSAD2, IFI44, IFIT2, OAS3, DNAPTP6; or OASL, RSAD2, IFI44, IFIT2, OAS3, LOC129607; or OASL, RSAD2, IFI44, IFIT2, OAS3, EPSTI1; or OASL, RSAD2, IFI44, IFIT2, OAS3, BIRC4BP; or OASL, RSAD2, IFI44, IFIT2, OAS3, gene detected by probe 229450_at; or OASL, RSAD2, IFI44, IFIT2, OAS3, gene detected by probe 235276_at; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1; or RSAD2, IFI44, IFIT2, OAS3, USP18, HERC5; or RSAD2, IFI44, IFIT2, OAS3, USP18, DNAPTP6; or RSAD2, IFI44, IFIT2, OAS3, USP18, LOC129607; or RSAD2, IFI44, IFIT2, OAS3, USP18, EPSTI1; or RSAD2, IFI44, IFIT2, OAS3, USP18, BIRC4BP; or RSAD2, IFI44, IFIT2, OAS3, USP18, gene detected by probe 229450_at; or RSAD2, IFI44, IFIT2, OAS3, USP18, gene detected by probe 235276_at; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, DNAPTP6; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, LOC129607; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, EPSTI1; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, BIRC4BP; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 229450_at; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 235276_at; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, LOC129607; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, EPSTI1; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, BIRC4BP; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 229450_at; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 235276_at; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607; or OAS3, USP18, SIGLEC1, HERC5,

DNAPTP6, EPSTI1; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, BIRC4BP; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, gene detected by probe 229450_at; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, gene detected by probe 235276_at; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, BIRC4BP; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 229450_at; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 235276_at; or SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP; or SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 229450_at; or SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 235276_at ; or HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at; or HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 235276_at; or DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at, gene detected by probe 235276_at. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include any at least 7 genes such as, for example: MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, ISG15; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, LAMP3; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, OASL; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, RSAD2; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFIT2; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, OAS3; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, USP18; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, SIGLEC1; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, HERC5; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, DNAPTP6; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, LOC129607; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, EPSTI1; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, BIRC4BP; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, gene detected by probe 229450_at; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, gene detected by probe 235276_at; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, LAMP3; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, OASL; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L,

RSAD2; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, IFI44; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, IFIT2; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, OAS3; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, USP18; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, SIGLEC1; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, HERC5; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, DNAPTP6; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, LOC129607; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, EPSTI1; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, BIRC4BP; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, gene detected by probe 229450_at; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, gene detected by probe 235276_at; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, OASL; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, RSAD2; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, IFI44; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, IFIT2; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, OAS3; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, USP18; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, SIGLEC1; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, HERC5; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, DNAPTP6; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LOC129607; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, EPSTI1; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, BIRC4BP; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, gene detected by probe 229450_at; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, gene detected by probe 235276_at; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, RSAD2; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, IFI44; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, IFIT2; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OAS3; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, USP18; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, SIGLEC1; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, HERC5; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, DNAPTP6; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, LOC129607; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, EPSTI1; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, BIRC4BP; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, gene detected by probe 229450_at; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, gene detected by probe 235276_at; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, IFI44; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, IFIT2; or IFIT1, IFI6, IFI44L, ISG15,

LAMP3, OASL, OAS3; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, USP18; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, SIGLEC1; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, HERC5; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, DNAPTP6; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, LOC129607; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, EPSTI1; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, BIRC4BP; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, gene detected by probe 229450_at; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, gene detected by probe 235276_at; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFIT2; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, OAS3; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, USP18; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, SIGLEC1; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, HERC5; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, DNAPTP6; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, LOC129607; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, EPSTI1; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, BIRC4BP; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, gene detected by probe 229450_at; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, gene detected by probe 235276_at; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, OAS3; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, USP18; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, SIGLEC1; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, HERC5; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, DNAPTP6; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, LOC129607; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, EPSTI1; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, BIRC4BP; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, gene detected by probe 229450_at; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, gene detected by probe 235276_at; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, USP18; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, SIGLEC1; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, HERC5; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, DNAPTP6; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, LOC129607; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, EPSTI1; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, BIRC4BP; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, gene detected

by probe 229450_at; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, gene detected by probe 235276_at; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, SIGLEC1; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, HERC5; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, DNAPTP6; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, LOC129607; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, EPSTI1; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, BIRC4BP; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, gene detected by probe 229450_at; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, gene detected by probe 235276_at; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, HERC5; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, DNAPTP6; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, LOC129607; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, EPSTI1; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, BIRC4BP; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, gene detected by probe 229450_at; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, gene detected by probe 235276_at; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, DNAPTP6; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, LOC129607; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, EPSTI1; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, BIRC4BP; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 229450_at; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 235276_at; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, LOC129607; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, EPSTI1; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, BIRC4BP; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 229450_at; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 235276_at; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, EPSTI1; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, BIRC4BP; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, gene detected by probe 229450_at ; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, gene detected by probe 235276_at; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1; or OAS3, USP18, SIGLEC1, HERC5,

DNAPTP6, LOC129607, BIRC4BP; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 229450_at; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 235276_at; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 229450_at; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 235276_at; or SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at; or SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 235276_at; or HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at, gene detected by probe 235276_at. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include any at least 8 genes such as, for example: MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, LAMP3; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, OASL; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, RSAD2; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, IFI44; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, IFIT2; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, OAS3; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, USP18; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, SIGLEC1; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, HERC5; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, DNAPTP6; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, LOC129607; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, EPSTI1; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, BIRC4BP; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, gene detected by probe 229450_at; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, gene detected by probe 235276_at; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, OASL; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, RSAD2; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, IFI44; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, IFIT2; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, OAS3; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, USP18; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L,

ISG15, SIGLEC1; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, HERC5; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, DNAPTP6; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LOC129607; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, EPSTI1; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, BIRC4BP; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, gene detected by probe 229450_at; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, gene detected by probe 235276_at; orIFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, RSAD2; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, IFI44; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, IFIT2; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OAS3; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, USP18; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, SIGLEC1; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, HERC5; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, DNAPTP6; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, LOC129607; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, EPSTI1; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, gene detected by probe 229450_at; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, BIRC4BP; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, gene detected by probe 235276_at; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, IFI44; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, IFIT2; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, OAS3; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, USP18; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, SIGLEC1; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, HERC5; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, DNAPTP6; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, LOC129607; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, EPSTI1; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, BIRC4BP; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, gene detected by probe 229450_at; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, gene detected by probe 235276_at; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFIT2; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, OAS3; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, USP18; or IFIT1, IFI6, IFI44L,

ISG15, LAMP3, OASL, RSAD2, SIGLEC1; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, HERC5; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, DNAPTP6; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, LOC129607; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, EPSTI1; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, BIRC4BP; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, gene detected by probe 229450_at; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, gene detected by probe 235276_at; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, OAS3; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, USP18; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, SIGLEC1; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, HERC5; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, DNAPTP6; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, LOC129607; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, EPSTI1; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, BIRC4BP; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, gene detected by probe 229450_at; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, gene detected by probe 235276_at; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, USP18; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, SIGLEC1; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, HERC5; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, DNAPTP6; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, LOC129607; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, EPSTI1; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, BIRC4BP; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, gene detected by probe 229450_at; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, gene detected by probe 235276_at; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, SIGLEC1; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, HERC5; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, DNAPTP6; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, LOC129607; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, EPSTI1; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, BIRC4BP; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, gene detected by

probe 229450_at; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, gene detected by probe 235276_at; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, HERC5; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, DNAPTP6; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, LOC129607; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, EPSTI1; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, BIRC4BP; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, gene detected by probe 229450_at; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, gene detected by probe 235276_at; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, DNAPTP6; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, LOC129607; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, EPSTI1; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, BIRC4BP; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 229450_at; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 235276_at; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, LOC129607; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, EPSTI1; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 229450_at; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, BIRC4BP; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 235276_at; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, EPSTI1; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, BIRC4BP; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, gene detected by probe 229450_at; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, gene detected by probe 235276_at; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, BIRC4BP; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 229450_at; or IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 235276_at; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP; or

OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 229450_at; or OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 235276_at; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at; or USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 235276_at; or SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at, gene detected by probe 235276_at. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include any at least 12 genes such as, for example: MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFIT2; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, OAS3; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, USP18; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, SIGLEC1; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, HERC5; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, DNAPTP6; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, LOC129607; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, EPSTI1; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, BIRC4BP; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, gene detected by probe 229450_at; or MX1, LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, gene detected by probe 235276_at; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, OAS3; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, USP18; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, SIGLEC1; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, HERC5; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2,

IFI44, DNAPTP6; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, LOC129607; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, EPSTI1; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, BIRC4BP; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, gene detected by probe 229450_at; or LLY6E, IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, gene detected by probe 235276_at; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, USP18; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, SIGLEC1; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, HERC5; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, DNAPTP6; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, LOC129607; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, EPSTI1; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, BIRC4BP; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, gene detected by probe 229450_at; or IFI27, OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, gene detected by probe 235276_at; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, SIGLEC1; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, HERC5; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, DNAPTP6; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, LOC129607; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, EPSTI1; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, BIRC4BP; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, gene detected by probe 229450_at; or OAS1, IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, gene detected by probe 235276_at; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, HERC5; or

IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, DNAPTP6; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, LOC129607; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, EPSTI1; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, BIRC4BP; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, gene detected by probe 229450_at; or IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, gene detected by probe 235276_at; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, DNAPTP6; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, LOC129607; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, EPSTI1; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, BIRC4BP; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 229450_at; or IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, gene detected by probe 235276_at; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, LOC129607; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, EPSTI1; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, BIRC4BP; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 229450_at; or IFI44L, ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, gene detected by probe 235276_at; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, EPSTI1; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, BIRC4BP; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, gene detected by probe 229450_at; or ISG15, LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, gene

detected by probe 235276_at; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, BIRC4BP; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 229450_at; or LAMP3, OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, gene detected by probe 235276_at; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 229450_at; or OASL, RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, gene detected by probe 235276_at; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at; or RSAD2, IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at; or IFI44, IFIT2, OAS3, USP18, SIGLEC1, HERC5, DNAPTP6, LOC129607, EPSTI1, BIRC4BP, gene detected by probe 229450_at gene detected by probe 235276_at. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include alterations in any one or more of serum protein levels of adiponectin, alpha-fetoprotein, apolipoprotein CIII, beta-2 microglobulin, cancer antigen 125, cancer antigen 19-9, eotaxin, FABP, factor VII, ferritin, IL-10, IL-12p70, IL-16, IL-18, IL-1ra, IL-3, MCP-1, MMP-3, myoglobin, SGOT, tissue factor, TIMP-1, TNF RII, TNF-alpha, VCAM-1, vWF, BDNK, complement 3, CD40 ligand, EGF, ENA-78, EN-RAGE, IGF-1, MDC, myeloperoxidase, RANTES, or thrombopoietin. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include alterations in any one or more of serum protein levels of adiponectin, alpha-fetoprotein, apolipoprotein CIII, beta-2 microglobulin, cancer antigen 125, cancer antigen 19-9, eotaxin, FABP, factor VII, ferritin, IL-10, IL-12p70, IL-16, IL-18, IL-1ra, IL-3, MCP-1,

MMP-3, myoglobin, SGOT, tissue factor, TIMP-1, TNF RII, TNF-alpha, VCAM-1, or vWF. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

The IFNα-inducible PD markers in an expression profile may include alterations in any one or more of serum protein levels of BDNK, complement 3, CD40 ligand, EGF, ENA-78, EN-RAGE, IGF-1, MDC, myeloperoxidase, RANTES, or thrombopoietin. The IFNα-inducible PD markers in such an expression profile may further include at least one or more gene listed in drawing sheets 235-381.

An IFNα-inducible PD marker expression profile may further include genes whose expression or activity is down-regulated in cells exposed to non-baseline IFNα levels. The genes may include any one or more of SLC4A1, PRSS33, FCER1A, BACH2, KLRB1, D4S234E, T cell receptor alpha locus/T cell receptor delta locus, FEZ1, AFF3, CD160, ABCB1, PTCH1, OR2W3, IGHD, NOG, NR3C2, TNS1, PDZK1IP1, SH2D1B, STRBP, ZMYND11, TMOD1, FCRLA, DKFZp761P0423, EPB42, NR6A1, LOC341333, MS4A1, IGHM, SIGLECP3, KIR2DS2, PKIA, BLR1, C5orf4, MYLK, LOC283663, MAD1L1, CXCL5, D4S234E, FCRLA, KRT1, c16orf74, ABCB4, or GPRASP1.

PD markers may be upregulated or may be downregulated relative to those of healthy subjects or non-afflicted patient tissues. The upregulation or downregulation of the type I IFN or IFNα-inducible PD markers in the patient's expression profile may be by any degree relative to that of a sample from a control (which may be from a sample that is not disease tissue of the patient (e.g., non-lesional skin of a psoriasis patient) or from a healthy person not afflicted with the disease or disorder). The degree upregulation or downregulation may be at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 100%, at least 125%, at least 150%, or at least 200%, or at least 300%, or at least 400%, or at least 500% that of the control or control sample.

A patient comprising the type I IFN or IFNα-inducible PD marker expression profile may further comprise upregulation of expression of any number of IFNα or type-I IFN subtypes. The IFNα or type-I IFN subtypes may include any more than one, more than two, more than three, more than four, more than five, more than six, more than

seven, more than eight, more than nine, or more than ten IFNα or type-I IFN subtypes. These subtypes may include IFNα1, IFNα2, IFNα4, IFNα5, IFNα6, IFNα7, IFNα8, IFNα10, IFNα14, IFNα17, IFNα21, IFNβ, or IFNω. The patient may comprise upregulation of expression of IFN subtypes IFNα1, IFNα2, IFNα8, and IFNα14. The upregulation of expression may be at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 100%, at least 125%, at least 150%, or at least 200%, or at least 300%, or at least 400%, or at least 500% that of the control.

A patient comprising a type I IFN or IFNα-inducible PD marker expression profile may further comprise upregulation of expression of IFNα receptors, either IFNAR1 or IFNAR2, or both, or TNFα, or IFNγ, or IFNγ receptors (either IFNGR1, IFNGR2, or both IFNGR1 and IFNGR2). The patient may simply be identified as one who comprises upregulation of expression of IFNα receptors, either IFNAR1 or IFNAR2, or both, or TNFα, or IFNγ, or IFNγ receptors (either IFNGR1, IFNGR2, or both IFNGR1 and IFNGR2).

The patient may further comprise or alternatively comprise alterations in levels of proteins in serum. The patient may have increased serum levels of proteins such as adiponectin, alpha-fetoprotein, apolipoprotein CIII, beta-2 microglobulin, cancer antigen 125, cancer antigen 19-9, eotaxin, FABP, factor VII, ferritin, IL-10, IL-12p70, IL-16, IL-18, IL-1ra, IL-3, MCP-1, MMP-3, myoglobin, SGOT, tissue factor, TIMP-1, TNF RII, TNF-alpha, VCAM-1, or vWF. The patient may have increased serum levels of any 1, 2,3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 14, 15, 16, 17, 18, 19, 20, 21, o22, 23, 24, 25, or 26 of these proteins in serum. The increased level may be at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, at least 100%, at least 125%, at least 150%, or at least 200%, or at least 300%, or at least 400%, or at least 500% that of a control, e.g., a healthy subject. The alteration may be a decrease in serum levels of proteins such as BDNK, complement 3, CD40 ligand, EGF, ENA-78, EN-RAGE, IGF-1, MDC, myeloperoxidase, RANTES, or thrombopoietin, The patient may have decreased serum levels of any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 or these proteins. The decreased level may be at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at

least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 90%, or at least 100% that of a control, e.g., a healthy subject. The PD marker profile may comprise one or more of these increased or decreased serum levels of proteins.

The patient may further comprise auto-antibodies that bind to any one of the following auto-antigens: (a) Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78; (b) surfeit 5, transcript variant c; (c) proteasome (posome, macropain) activator subunit 3 (PA28 gamma; Ki) transc; (d) retinoic acid receptor, alpha; (e) Heat shock 10 kDa protein 1 (chaperonin 10); (f) tropomyosin 3; (g) pleckstrin homology-like domain, family A, member 1; (h) cytoskeleton-associated protein 1; (i) Sjogren syndrome antigen A2 (60 kDa, ribonucleoprotein auto-antigen SS-A/Ro); (j) NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex 1, 8 kDa; (k) NudE nuclear distribution gene E homolog 1 (A. nidulans); (l) MutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli); (m) leucine rich repeat (in FLII) interacting protein 2; (n) tropomyosin 1 (alpha); (o) spastic paraplegia 20, spartin (Troyer syndrome); (p) preimplantation protein, transcript variant 1; (r) mitochondrial ribosomal protein L45; (s) Lin-28 homolog (C. elegans); (t) heat shock 90 kDa protein 1, alpha; (u) dom-3 homolog Z (C. elegans); (v) dynein, cytoplasmic, light intermediate polypeptide 2; (w) Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein); (x) synovial sarcoma, X breakpoint 2, transcript variant 2; (y) moesin; (z) homer homolog (Drosophila), transcript variant 1; (aa) GCN5 general control of amino-acid synthesis 5-like 2 (yeast); (bb) eukaryotic translation elongation factor 1 gamma; (cc) eukaryotic translation elongation factor 1, delta; (dd) DNA-damage-inducible transcript 3; (ee) CCAAT/enhancer binding protein (C/EBP) gamma; and any other auto-antigen described in provisional application entitled “Auto-antibody markers of autoimmune disease” filed May 3, 2007 or in provisional application entitled entitled “Auto-antibody markers of autoimmune disease” filed November 6, 2007 (for example, but not limited to, those described on Tables 2, 4, 5, and 9). The patient may comprise auto-antibodies that bind to any number of these auto-antigens, *e.g.*, any at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25.

A therapeutic agent may be administered to a myositis patient. A therapeutic agent may be any molecule that binds to and modulates type I IFN or IFNα activity. The therapeutic agent may be a small molecule or a biological agent. If the therapeutic agent is a small molecule it may be synthesized or identified and isolated from a natural source.

If the therapeutic agent is a biological agent, it may be an antibody specific for any subtype(s) of type I IFN or IFNα. For instance, the antibody may be specific for any one of IFNα1, IFNα2, IFNα4, IFNα5, IFNα6, IFNα7, IFNα8, IFNα10, IFNα14, IFNα17, IFNα21, IFNβ, or IFNω. Alternatively, the antibody may be specific for any two, any three, any four, any five, any six, any seven, any eight, any nine, any ten, any eleven, any twelve type I IFN of IFNα subtypes. If the antibody is specific for more than one type I IFN subtype, the antibody may be specific for IFNα1, IFNα2, IFNα4, IFNα5, IFNα8, IFNα10, and IFNα21; or it may be specific for IFNα1, IFNα2, IFNα4, IFNα5, IFNα8, and IFNα10; or it may be specific for IFNα1, IFNα2, IFNα4, IFNα5, IFNα8, and IFNα21; or it may be specific for IFNα1, IFNα2, IFNα4, IFNα5, IFNα10, and IFNα21. Antibodies specific for type I IFN or IFNα include MEDI-545, any biologic or antibody other than MEDI-545, antibodies described in U.S. patent applications 11/009,410 filed December 10, 2004 and 11/157,494 filed June 20, 2005, 9F3 and other antibodies described in U.S. Patent No. 7,087,726 (Example 1 and Example 2, those disclosed in Table 3 and Table 4, and/or those disclosed in the table entitled "Deposit of Material" on lines 25-54, column 56), NK-2 and YOK5/19 (WO 84/03105), LO-22 (U.S. Patent 4,902,618), 144 BS (U.S. Patent 4,885,166), and EBI-1, EBI-2, and EBI-3 (EP 119476). A therapeutic agent that modulates IFNα activity may neutralize IFNα activity. One of skill in the art is well aware of preparation and formulation of such biological agents and methods of their administration.

The antibody may be a synthetic antibody, a monoclonal antibody, polyclonal antibodies, a recombinantly produced antibody, an intrabody, a multispecific antibody (including bi-specific antibodies), a human antibody, a humanized antibody, a chimeric antibody, a single-chain Fv (scFv) (including bi-specific scFv), a BiTE molecule, a single chain antibody, a Fab fragments, a F(ab') fragment, a disulfide-linked Fv (sdFv), or an epitope-binding fragment of any of the above. The antibody may be any of an immunoglobulin molecule or immunologically active portion of an immunoglobulin

molecule. Furthermore, the antibody may be of any isotype. For example, it may be any of isotypes IgG1, IgG2, IgG3 or IgG4. The antibody may be a full-length antibody comprising variable and constant regions, or an antigen-binding fragment thereof, such as a single chain antibody, or a Fab or Fab'2 fragment. The antibody may also be conjugated or linked to a therapeutic agent, such as a cytotoxin or a radioactive isotope.

A second agent other than the agent that binds to modulates IFNα activity may be administered to a myositis patient. Second agents include, but are not limited to non-steroidal anti-inflammatory drugs such as ibuprofen, naproxen, sulindac, diclofenac, piroxicam, ketoprofen, diflunisal, nabumetone, etodolac, and oxaprozin, indomethacin; anti-malarial drugs such as hydroxychloroquine; corticosteroid hormones, such as prednisone, hydrocortisone, methylprednisolone, and dexamethasone; methotrexate; immunosuppressive agents, such as azathioprine and cyclophosphamide; and biologic agents that, *e.g.*, target T cells such as Alefacept and Efalizumab, or target TNFα, such as, Enbrel, Remicade, and Humira.

Treatment with the agent may result in neutralization of the type I IFN or IFNα-inducible profile. Treatment with the agent may result in a decrease in one or more symptoms of myositis or disease flare-ups. The symptoms may include muscle weakness, difficulty swallowing, difficulty breathing, fever, weight loss, pain, muscle tenderness, arthritis, and rash. Treatment with the agent may result in improved prognosis. Treatment with the agent may result in a higher quality of life for the patient. Treatment with the agent may alleviate the need to co-administer second agents or may lessen the dosage of administration of the second agent to the patient. Treatment with the agent may reduce the number of hospitalizations of the patient.

The agent that binds to and modulates type I IFN or IFNα activity may neutralize a type I IFN or IFNα-inducible profile. Neutralization of the type I IFN or IFNα-inducible profile may be a reduction in at least one, at least two, at least three, at least five, at least seven, at least eight, at least ten, at least twelve, at least fifteen, at least twenty, at least twenty five, at least thirty, at least thirty five, at least forty, at least forty five, or at least fifty genes up-regulated by type I IFN or IFNα. The genes upregulated by type I IFN or IFNα may be any group of genes in Figures 235-381 or as discussed above. Neutralization of the type I IFN or IFNα-inducible profile is a reduction of at least 2%, at

least 3%, at least 4%, at least 5%, at least 7%, at least 8%, at least 10%, at least 15%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, or at least 90% of any of the at least one, at least two, at least three, at least five, at least seven, at least eight, at least ten, at least twelve, at least fifteen, at least twenty, at least twenty five, at least thirty, at least thirty five, at least forty, at least forty five, or at least fifty genes up-regulated in any type I IFN or IFNα-inducible profile. Alternatively, neutralization of the type I IFN or IFNα-inducible profile may refer to a reduction of expression of up-regulated type I IFN or IFNα-inducible genes that is within at most 50%, at most 45%, at most 40%, at most 35%, at most 30%, at most 25%, at most 20%, at most 15%, at most 10%, at most 5%, at most 4%, at most 3%, at most 2%, or at most 1% of expression levels of those type I IFN or IFNα-inducible genes in a control sample. If the agent that binds to and modulates type I IFN or IFNα activity is a biologic agent, such as an antibody, the agent may neutralize the type I IFN or IFNα profile at doses of 0.3 to 30 mg/kg, 0.3 to 10 mg/kg, 0.3 to 3 mg/kg, 0.3 to 1 mg/kg, 1 to 30 mg/kg, 3 to 30 mg/kg, 5 to 30 mg/kg, 10 to 30 mg/kg, 1 to 10 mg/kg, 3 to 10 mg/kg, or 1 to 5 mg/kg.

Neutralization of the type I IFN or IFNα-inducible profile may be increased expression of at least one, at least two, at least three, at least five, at least seven, at least eight, at least ten, at least twelve, at least fifteen, at least twenty, at least twenty five, at least thirty, at least thirty five, at least forty, at least forty five, or at least fifty genes whose expression is reduced by type I IFN or IFNα. The genes whose expression is reduced by type I IFN or IFNα may be any group of genes in Figures 235-381 or as discussed above. Neutralization of down-regulated genes in a type I IFN or IFNα-inducible profile may be an increase of at least 2%, at least 3%, at least 4%, at least 5%, at least 7%, at least 8%, at least 10%, at least 15%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, or at least 90%, or at least 100%, or at least 125%, or at least 130%, or at least 140%, or at least 150%, or at least 175%, or at least 200%, or at least 250%, or at least 300%, or at least 500% of any of the at least one, at least two, at least three, at least five, at least seven, at least eight, at least ten, at least twelve, at least fifteen, at least twenty, or at least twenty five genes whose expression is downregulated in any type I IFN or IFNα-

inducible profile. Alternatively, neutralization of the type I IFN or IFNα-inducible profile refers to an increase in expression of type I IFN or IFNα-inducible genes to within at most 50%, at most 45%, at most 40%, at most 35%, at most 30%, at most 25%, at most 20%, at most 15%, at most 10%, at most 5%, at most 4%, at most 3%, at most 2%, or at most 1% of expression levels of those type I IFN or IFNα-inducible (downregulated) genes in a control sample. If the agent that binds to and modulates type I IFN or IFNα activity is a biologic agent, such as an antibody, the agent may neutralize the type I IFN or IFNα profile at doses of 0.3 to 30 mg/kg, 0.3 to 10 mg/kg, 0.3 to 3 mg/kg, 0.3 to 1 mg/kg, 1 to 30 mg/kg, 3 to 30 mg/kg, 5 to 30 mg/kg, 10 to 30 mg/kg, 1 to 10 mg/kg, 3 to 10 mg/kg, or 1 to 5 mg/kg.

The agent that binds to and modulates type I IFN or IFNα activity may further or alternatively neutralize expression of one or more type I IFN or IFNα subtypes. The IFNα or type-I IFN subtypes may include any more than one, more than two, more than three, more than four, more than five, more than six, more than seven, more than eight, more than nine, or more than ten IFNα or type-I IFN subtypes. These subtypes may include IFNα1, IFNα2, IFNα4, IFNα5, IFNα6, IFNα7, IFNα8, IFNα10, IFNα14, IFNα17, IFNα21, IFNβ, or IFNω. These subtypes may include all of IFNα1, IFNα2, IFNα8, and IFNα14. Alternatively, these subtypes may include IFNα1, IFNα2, IFNα4, IFNα5, IFNα8, IFNα10, IFNα21. Neutralization of the IFNα or type-I IFN subtypes may be a reduction of at least 2%, at least 3%, at least 4%, at least 5%, at least 7%, at least 8%, at least 10%, at least 15%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, or at least 90% of any of the at least one, at least two, at least three, at least five, at least seven, at least eight, or at least ten of the subtypes. Neutralization of the IFNα or type-I IFN subtypes may be a reduction in expression of IFNα or type-I IFN subtype genes that is within at most 50%, at most 45%, at most 40%, at most 35%, at most 30%, at most 25%, at most 20%, at most 15%, at most 10%, at most 5%, at most 4%, at most 3%, at most 2%, or at most 1% of expression levels of those IFNα or type I IFN subtypes in a control sample. If the agent that binds to and modulates IFNα activity or type I IFN activity is a biologic agent, such as an antibody, the agent may neutralize the IFNα or type I IFN subtypes at doses of 0.3 to 30 mg/kg, 0.3 to 10 mg/kg, 0.3 to 3 mg/kg, 0.3 to 1

mg/kg, 1 to 30 mg/kg, 3 to 30 mg/kg, 5 to 30 mg/kg, 10 to 30 mg/kg, 1 to 10 mg/kg, 3 to 10 mg/kg, or 1 to 5 mg/kg.

The agent that binds to and modulates type I IFN or IFNα activity may further or alternatively neutralize expression of IFNα receptors, either IFNAR1 or IFNAR2, or both, or TNFα, or IFNγ, or IFNγ receptors (either IFNGR1, IFNGR2, or both IFNGR1 and IFNGR2). Neutralization of expression of IFNα receptors, either IFNAR1 or IFNAR2, or both, or TNFα, or IFNγ, or IFNγ receptors (either IFNGR1, IFNGR2, or both IFNGR1 and IFNGR2) may be a reduction of at least 2%, at least 3%, at least 4%, at least 5%, at least 7%, at least 8%, at least 10%, at least 15%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, or at least 90% of any of the at least one, at least two, at least three, at least five, or at least six of these genes. Neutralization of expression of IFNα receptors, either IFNAR1 or IFNAR2, or TNFα, or IFNγ, or IFNγ receptors (either IFNGR1, IFNGR2, or both IFNGR1 and IFNGR2) is a reduction of expression of at most 50%, at most 45%, at most 40%, at most 35%, at most 30%, at most 25%, at most 20%, at most 15%, at most 10%, at most 5%, at most 4%, at most 3%, at most 2%, or at most 1% of expression levels of these genes in a control sample. If the agent that binds to and modulates type I IFN or IFNα activity is a biologic agent, such as an antibody, the agent may neutralize expression of IFNα receptors IFNAR1 or IFNAR2, or TNFα, or IFNγ, or IFNγ receptors IFNGR1 or IFNGR2 at doses of 0.3 to 30 mg/kg, 0.3 to 10 mg/kg, 0.3 to 3 mg/kg, 0.3 to 1 mg/kg, 1 to 30 mg/kg, 3 to 30 mg/kg, 5 to 30 mg/kg, 10 to 30 mg/kg, 1 to 10 mg/kg, 3 to 10 mg/kg, or 1 to 5 mg/kg.

The agent that binds to and modulates type I IFN or IFNα activity may further or alternatively neutralize alterations of levels of proteins in serum, *e.g.*, increase levels of those proteins whose serum levels are downregulated or decrease levels of those proteins whose serum levels are upregulated to levels closer to those of control subjects. Neutralization of expression of proteins in serum, such as adiponectin, alpha-fetoprotein, apolipoprotein CIII, beta-2 microglobulin, cancer antigen 125, cancer antigen 19-9, eotaxin, FABP, factor VII, ferritin, IL-10, IL-12p70, IL-16, IL-18, IL-1ra, IL-3, MCP-1, MMP-3, myoglobin, SGOT, tissue factor, TIMP-1, TNF RII, TNF-alpha, VCAM-1, vWF, BDNK, complement 3, CD40 ligand, EGF, ENA-78, EN-RAGE, IGF-1, MDC,

myeloperoxidase, RANTES, or thrombopoietin may be by bringing the level of at least one, at least two, at least three, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least twelve, at least fifteen, at least twenty, or at least 25 of these proteins to within at least 2%, at least 3%, at least 4%, at least 5%, at least 7%, at least 8%, at least 10%, at least 15%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, or at least 90% levels of the protein in serum of a healthy subject. If the agent that binds to and modulates type I IFN or IFNα activity is a biologic agent, such as an antibody, the agent may neutralize levels of the serum proteins, *e.g.*, adiponectin, alpha-fetoprotein, apolipoprotein CIII, beta-2 microglobulin, cancer antigen 125, cancer antigen 19-9, eotaxin, FABP, factor VII, ferritin, IL-10, IL-12p70, IL-16, IL-18, IL-1ra, IL-3, MCP-1, MMP-3, myoglobin, SGOT, tissue factor, TIMP-1, TNF RII, TNF-alpha, VCAM-1, vWF, BDNK, complement 3, CD40 ligand, EGF, ENA-78, EN-RAGE, IGF-1, MDC, myeloperoxidase, RANTES, or thrombopoietin, at doses of 0.3 to 30 mg/kg, 0.3 to 10 mg/kg, 0.3 to 3 mg/kg, 0.3 to 1 mg/kg, 1 to 30 mg/kg, 3 to 30 mg/kg, 5 to 30 mg/kg, 10 to 30 mg/kg, 1 to 10 mg/kg, 3 to 10 mg/kg, or 1 to 5 mg/kg.

The agent that binds to and modulates type I IFN or IFNα activity may further or alternatively reduce number or level of auto-antibodies that bind to any one, any at least 2, any at least 3, any at least 4, any at least 5, any at least 6, any at least 7, any at least 8, any at least 9, any at least 10, any at least 15, or any at least 20 of the following auto-antigens: (a) Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78; (b) surfeit 5, transcript variant c; (c) proteasome (posome, macropain) activator subunit 3 (PA28 gamma; Ki) transc; (d) retinoic acid receptor, alpha; (e) Heat shock 10 kDa protein 1 (chaperonin 10); (f) tropomyosin 3; (g) pleckstrin homology-like domain, family A, member 1; (h) cytoskeleton-associated protein 1; (i) Sjogren syndrome antigen A2 (60 kDa, ribonucleoprotein auto-antigen SS-A/Ro); (j) NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex 1, 8 kDa; (k) NudE nuclear distribution gene E homolog 1 (A. nidulans); (l) MutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli); (m) leucine rich repeat (in FLII) interacting protein 2; (n) tropomyosin 1 (alpha); (o) spastic paraplegia 20, spartin (Troyer syndrome); (p) preimplantation protein, transcript variant 1; (r) mitochondrial ribosomal protein L45; (s) Lin-28 homolog (C.

elegans); (t) heat shock 90 kDa protein 1, alpha; (u) dom-3 homolog Z (C. elegans); (v) dynein, cytoplasmic, light intermediate polypeptide 2; (w) Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein); (x) synovial sarcoma, X breakpoint 2, transcript variant 2; (y) moesin; (z) homer homolog (Drosophila), transcript variant 1; (aa) GCN5 general control of amino-acid synthesis 5-like 2 (yeast); (bb) eukaryotic translation elongation factor 1 gamma; (cc) eukaryotic translation elongation factor 1, delta; (dd) DNA-damage-inducible transcript 3; (ee) CCAAT/enhancer binding protein (C/EBP) gamma; and any other auto-antigen described in provisional application entitled "Auto-antibody markers of autoimmune disease" filed May 3, 2007; and any other auto-antigen described in provisional application entitled "Auto-antibody markers of autoimmune disease" filed November 6, 2007 (for example, but not limited to, those described on Tables 2, 4, 5, and 9). Reduction in level of auto-antibody may be a reduction of at least 2%, at least 3%, at least 4%, at least 5%, at least 7%, at least 8%, at least 10%, at least 15%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, or at least 90% in presence of any of the auto-antibodies. If the agent that binds to and modulates type I IFN or IFNα activity is a biologic agent, such as an antibody, the agent may reduce number or level or auto-antibodies at doses of 0.3 to 30 mg/kg, 0.3 to 10 mg/kg, 0.3 to 3 mg/kg, 0.3 to 1 mg/kg, 1 to 30 mg/kg, 3 to 30 mg/kg, 5 to 30 mg/kg, 10 to 30 mg/kg, 1 to 10 mg/kg, 3 to 10 mg/kg, or 1 to 5 mg/kg.

The agent that binds to and modulates type I IFN or IFNα activity may not neutralize expression of genes that are not included in an interferon-inducible signature or PD marker profile.

Monitoring disease progression may be performed by obtaining patient samples before and after administration of an agent, *e.g.*, an agent that binds to and modulates type I IFN or IFNα activity, or an agent that binds to and does not modulate type I IFN or IFNα activity, or a combination of agents that may or may not include an agent that binds to and modulates type I IFN or IFNα activity. Samples include any biological fluid or tissue, such as whole blood, saliva, urine, synovial fluid, bone marrow, cerebrospinal fluid, nasal secretions, sputum, amniotic fluid, bronchoalveolar lavage fluid, peripheral

blood mononuclear cells, total white blood cells, lymph node cells, spleen cells, tonsil cells, or skin. The samples may be obtained by any means known in the art.

Type I IFN or IFNα inducible PD marker expression profiles are obtained in the (before and after agent administration) samples. The type I IFN or IFNα inducible PD marker expression profiles in the samples are compared. Comparison may be of the number of type I IFN or IFNα inducible PD markers present in the samples or may be of the quantity of type I IFN or IFNα inducible PD markers present in the samples, or any combination thereof. Variance indicating efficacy of the therapeutic agent may be indicated if the number or level (or any combination thereof) of up-regulated type I IFN or IFNα inducible PD markers decreases in the sample obtained after administration of the therapeutic agent relative to the sample obtained before administration of the therapeutic agent. The number of up-regulated type I IFN or IFNα inducible PD markers may decrease by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10. The level of any given up-regulated type I IFN or IFNα inducible PD marker may decrease by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. The number of up-regulated type I IFN or IFNα inducible PD markers with decreased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. Any combination of decreased number and decreased level of up-regulated type I IFN or IFNα inducible PD markers may indicate efficacy. Variance indicating efficacy of the therapeutic agent may be indicated if the number or level (or any combination thereof) of down-regulated type I IFN or IFNα inducible PD markers decreases in the sample obtained after administration of the therapeutic agent relative to the sample obtained before administration of the therapeutic agent. The number of down-regulated type I IFN or IFNα inducible PD markers may decrease by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10. The level of any given down-regulated type I IFN or IFNα inducible PD marker may increase by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. The number of down-regulated type I IFN or IFNα inducible PD markers

with increased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. Any combination of decreased number and increased level of down-regulated type I IFN or IFNα inducible PD markers may indicate efficacy.

The sample obtained from the patient may be obtained prior to a first administration of the agent, *i.e.*, the patient is naïve to the agent. Alternatively, the sample obtained from the patient may occur after administration of the agent in the course of treatment. For example, the agent may have been administered prior to the initiation of the monitoring protocol. Following administration of the agent an additional samples may be obtained from the patient and type I IFN or IFNα inducible PD markers in the samples are compared. The samples may be of the same or different type, e.g., each sample obtained may be a blood sample, or each sample obtained may be a serum sample. The type I IFN or IFNα inducible PD markers detected in each sample may be the same, may overlap substantially, or may be similar.

The samples may be obtained at any time before and after the administration of the therapeutic agent. The sample obtained after administration of the therapeutic agent may be obtained at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 12, or at least 14 days after administration of the therapeutic agent. The sample obtained after administration of the therapeutic agent may be obtained at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 weeks after administration of the therapeutic agent. The sample obtained after administration of the therapeutic agent may be obtained at least 2, at least 3, at least 4, at least 5, or at least 6 months following administration of the therapeutic agent.

Additional samples may be obtained from the patient following administration of the therapeutic agent. At least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 12, at least 15, at least 20, at least 25 samples may be obtained from the patient to monitor progression or regression of the disease or disorder over time. Disease progression may be monitored over a time period of at least 1 week, at least 2 weeks, at least 3 weeks, at least 4 weeks, at least 5 weeks, at least 6 weeks, at least 7 weeks, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, at least 1 year, at least 2 years, at least 3 years, at least 4 years,

at least 5 years, at least 10 years, or over the lifetime of the patient. Additional samples may be obtained from the patient at regular intervals such as at monthly, bi-monthly, once a quarter year, twice a year, or yearly intervals. The samples may be obtained from the patient following administration of the agent at regular intervals. For instance, the samples may be obtained from the patient at one week following each administration of the agent, or at two weeks following each administration of the agent, or at three weeks following each administration of the agent, or at one month following each administration of the agent, or at two months following each administration of the agent. Alternatively, multiple samples may be obtained from the patient following an or each administration of the agent.

Disease progression in a patient may similarly be monitored in the absence of administration of an agent. Samples may periodically be obtained from the patient having the disease or disorder. Disease progression may be identified if the number of type I IFN or IFNα inducible PD markers increases in a later-obtained sample relative to an earlier obtained sample. The number of type I IFN or IFNα inducible PD markers may increase by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10. Disease progression may be identified if level of any given up-regulated type I IFN or IFNα inducible PD marker increases by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. Disease progression may be identified if level of any given down-regulated type I IFN or IFNα inducible PD marker decreases by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. The number of up-regulated type I IFN or IFNα inducible PD markers with increased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. The number of down-regulated type I IFN or IFNα inducible PD markers with decreased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. Any combination of increased number and increased level of up-regulated type I IFN or IFNα inducible PD marker may indicate disease progression. Alternatively, or in

combination, any combination of decreased number and decreased level of down-regulated type I IFN or IFNα inducible PD marker may indicate disease progression. Disease regression may also be identified in a patient having a disease or disorder, not treated by an agent. In this instance, regression may be identified if the number of type I IFN or IFNα inducible PD markers decreases in a later-obtained sample relative to an earlier obtained sample. The number of type I IFN or IFNα inducible PD markers may decrease by at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10. Disease regression may be identified if level of any given up-regulated type I IFN or IFNα inducible PD marker decreases by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. Disease regression may be identified if level of any given down-regulated type I IFN or IFNα inducible PD marker increases by at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. The number of up-regulated type I IFN or IFNα inducible PD markers with decreased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. The number of down-regulated type I IFN or IFNα inducible PD markers with increased levels may be at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, or at least 35. Disease progression or disease regression may be monitored by obtaining samples over any period of time and at any interval. Disease progression or disease regression may be monitored by obtaining samples over the course of at least 1 week, at least 2 weeks, at least 3 weeks, at least 4 weeks, at least 5 weeks, at least 6 weeks, at least 7 weeks, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, at least 1 year, at least 2 years, at least 3 years, at least 4 years, at least 5 years, at least 10 years, or over the lifetime of the patient. Disease progression or disease regression may be monitored by obtaining samples at least monthly, bi-monthly, once a quarter year, twice a year, or yearly. The samples need not be obtained at strict intervals.

The invention also encompasses kits and probes. The probes may be any molecule that detects any expression or activity of any gene that may be included in an IFNα-inducible PD marker expression profile.

Applicants provide a set of non-limiting embodiments to describe some of the aspects of the invention.

Embodiments

1. A method of treating a patient having a type I IFN or an IFNα-mediated disease or disorder comprising:

administering an agent that binds to and modulates type I IFN or IFNα activity;

wherein the patient comprises a differentially regulated miRNA marker profile; and

wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient.

2. The method of embodiment 1 further comprising detecting neutralization of the differentially regulated miRNA marker profile of the patient.

3. The method of embodiment 1 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 2 or 4.

4. The method of embodiment 3 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 2 or 4.

5. The method of embodiment 4 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 2 or 4.

6. The method of embodiment 5 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 2 or 4.

7. The method of embodiment 6 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 2 or 4.

8. The method of embodiment 3 wherein the at least one of the miRNAs is detected by the detector hsa-miR-34b-4373037.

9. The method of embodiment 1 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

10. The method of embodiment 9 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

11. The method of embodiment 10 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

12. The method of embodiment 11 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

13. The method of embodiment 12 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

14. The method of embodiment 9 wherein the at least one of the miRNAs is detected by the detector hsa-miR-1-4373161.

15. The method of embodiment 3 wherein the differentially regulated miRNA marker profile further comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

16. The method of embodiment 15 wherein the down-regulated expression or activity is of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

17. The method of embodiment 16 wherein the down-regulated expression or activity is of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

18. The method of embodiment 17 wherein the down-regulated expression or activity is of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

19. The method of embodiment 18 wherein the down-regulated expression or activity is of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

20. The method of embodiment 15 wherein the at least one of the miRNAs detected by the detectors identified in Tables 3 or 5 is hsa-miR-1-4373161.

21. The method of embodiment 1 wherein the agent is a biologic agent.

22. The method of embodiment 21 wherein the agent is an antibody.

23. The method of embodiment 22 wherein the antibody is MEDI-545.

24. The method of embodiment 22 wherein the antibody is specific for one or more type I IFN or IFNα subtype but is not MEDI-545.

25. The method of embodiment 1 wherein the administering the agent alleviates one or more symptoms of the disease or disorder.

26. The method of embodiment 22 wherein the antibody is administered at a dose between approximately .03 and 30 mg/kg.

27. The method of embodiment 26 wherein the antibody is administered at a dose between 0.3 and 3 mg/kg.

28. The method of embodiment 27 wherein the antibody is administered at a dose between .03 and 1 mg/kg.

29. The method of any one of embodiments 21 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 10%.

30. The method of embodiment 29 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 20%.

31. The method of embodiment 30 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 30%.

32. The method of embodiment 31 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 40%.

33. The method of embodiment 32 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 50%.

34. The method of embodiment 1 wherein the disease or disorder is one of lupus, psoriasis, vasculitis, sarcoidosis, Sjogren's syndrome, or myositis.

35. The method of embodiment 34 wherein the disease or disorder is myositis.

36. The method of embodiment 1 wherein the patient further comprises up-regulated expression or activity of at least IFNα subtypes 1, 2, 8, and 14.

37. The method of embodiment 2 wherein the differentially regulated miRNA marker profile is detected in whole blood of the patient.

38. The method of embodiment 2 wherein the differentially regulated miRNA marker profile is detected in muscle tissue of the patient.

39. The method of embodiment 1 wherein the differentially regulated miRNA marker profile is strong or moderate.

40. A method of neutralizing a differentially regulated miRNA marker profile in a patient in need thereof, comprising:

administering an agent that binds to and modulates type I IFN or IFNα activity to the patient;

wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient.

41. The method of embodiment 40 further comprising detecting neutralization of the differentially regulated miRNA marker profile of the patient.

42. The method of embodiment 40 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 2 or 4.

43. The method of embodiment 42 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 2 or 4.

44. The method of embodiment 43 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 2 or 4.

45. The method of embodiment 44 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 2 or 4.

46. The method of embodiment 45 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 2 or 4.

47. The method of embodiment 42 wherein the at least one of the miRNAs is detected by the detector hsa-miR-34b-4373037.

48. The method of embodiment 40 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

49. The method of embodiment 48 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

50. The method of embodiment 49 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

51. The method of embodiment 50 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

52. The method of embodiment 51 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

53. The method of embodiment 48 wherein the at least one of the miRNAs is detected by the detector hsa-miR-1-4373161.

54. The method of embodiment 42 wherein the differentially regulated miRNA marker profile further comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

55. The method of embodiment 54 wherein the down-regulated expression or activity is of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

56. The method of embodiment 55 wherein the down-regulated expression or activity is of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

57. The method of embodiment 56 wherein the down-regulated expression or activity is of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

58. The method of embodiment 57 wherein the down-regulated expression or activity is of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

59. The method of embodiment 54 wherein the at least one of the miRNAs detected by the detectors identified in Tables 3 or 5 is hsa-miR-1-4373161.

60. The method of embodiment 40 wherein the agent is a biologic agent.

61. The method of embodiment 60 wherein the agent is an antibody.

62. The method of embodiment 61 wherein the antibody is MEDI-545.

63. The method of embodiment 61 wherein the antibody is specific for one or more type I IFN or IFNα subtype but is not MEDI-545.

64. The method of embodiment 40 wherein the administering the agent alleviates one or more symptoms of the disease or disorder.

65. The method of embodiment 61 wherein the antibody is administered at a dose between approximately .03 and 30 mg/kg.

66. The method of embodiment 65 wherein the antibody is administered at a dose between 0.3 and 3 mg/kg.

67. The method of embodiment 66 wherein the antibody is administered at a dose between .03 and 1 mg/kg.

68. The method of embodiment 40 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 10%.

69. The method of embodiment 68 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 20%.

70. The method of embodiment 69 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 30%.

71. The method of embodiment 70 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 40%.

72. The method of embodiment 71 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 50%.

73. The method of embodiment 40 wherein the patient has been diagnosed with one of lupus, psoriasis, vasculitis, sarcoidosis, Sjogren's syndrome, or myositis.

74. The method of embodiment 73 wherein the patient has been diagnosed with myositis.

75. The method of embodiment 40 wherein the patient further comprises up-regulated expression or activity of at least IFNα subtypes 1, 2, 8, and 14.

76. The method of embodiment 41 wherein the differentially regulated miRNA marker profile is detected in whole blood of the patient.

77. The method of embodiment 41 wherein the differentially regulated miRNA marker profile is detected in muscle tissue of the patient.

78. The method of embodiment 40 wherein the differentially regulated miRNA marker profile is strong or moderate.

79. A method of monitoring or prognosing an inflammatory disease progression of a patient comprising:

obtaining a first differentially regulated miRNA marker profile in a first sample from a patient.

80. The method of embodiment 79 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 2 or 4.

81. The method of embodiment 80 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 2 or 4.

82. The method of embodiment 81 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 2 or 4.

83. The method of embodiment 82 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 2 or 4.

84. The method of embodiment 83 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 2 or 4.

85. The method of embodiment 80 wherein the at least one of the miRNAs is detected by the detector hsa-miR-34b-4373037.

86. The method of embodiment 79 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

87. The method of embodiment 86 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

88. The method of embodiment 87 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

89. The method of embodiment 88 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

90. The method of embodiment 89 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

91. The method of embodiment 86 wherein the at least one of the miRNAs is detected by the detector hsa-miR-1-4373161.

92. The method of embodiment 80 wherein the first differentially regulated miRNA marker profile further comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

93. The method of embodiment 92 wherein the down-regulated expression or activity is of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

94. The method of embodiment 93 wherein the down-regulated expression or activity is of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

95. The method of embodiment 94 wherein the down-regulated expression or activity is of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

96. The method of embodiment 95 wherein the down-regulated expression or activity is of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

97. The method of embodiment 92 wherein the at least one of the miRNAs detected by the detectors identified in Tables 3 or 5 is hsa-miR-1-4373161.

98. The method of embodiment 79 wherein the first first differentially regulated miRNA marker profile is a strong profile and the patient prognosis is disease progression.

99. The method of embodiment 98 wherein the strong profile comprises a differential expression of the miRNAs of at least 10-fold that of a healthy individual.

100. The method of embodiment 98 wherein the autoimmune disease is myositis.

101. The method of embodiment 79 wherein the first IFNα-inducible PD marker expression profile is a weak profile and the patient prognosis is disease regression.

102. The method of embodiment 101 wherein the weak profile comprises a differential expression of the miRNAs no more than 2-fold that of a healthy individual.

103. The method of embodiment 98 wherein the strong profile indicates to a physician to change disease treatment.

104. The method of embodiment 79 further comprising:

obtaining a second differentially regulated miRNA marker profile in a second sample from a patient;

wherein an increase in number or level of miRNA markers in the second relative to the first profile prognoses disease progression; or

wherein a decrease in number or level of miRNA markers in the second relative to the first profile prognoses disease regression.

105. A method of monitoring autoimmune or inflammatory disease progression of a patient receiving treatment with a therapeutic agent comprising:

obtaining a first miRNA profile in a first sample from the patient;

administering a therapeutic agent ;

obtaining a second miRNA profile in a second sample from the patient; and

comparing the first and the second miRNA profiles,

wherein a variance in the first and the second miRNA profiles indicates a level of efficacy of the therapeutic agent.

106. The method of embodiment 105 wherein the first miRNA profile comprises up-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 2 or 4.

107. The method of embodiment 106 wherein the first miRNA profile comprises up-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 2 or 4.

108. The method of embodiment 107 wherein the first miRNA profile comprises up-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 2 or 4.

109. The method of embodiment 108 wherein the first miRNA marker profile comprises up-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 2 or 4.

110. The method of embodiment 109 wherein the first miRNA profile comprises up-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 2 or 4.

111. The method of embodiment 106 wherein the at least one of the miRNAs is detected by the detector hsa-miR-34b-4373037.

112. The method of embodiment 105 wherein the first miRNA profile comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

113. The method of embodiment 112 wherein the first miRNA profile comprises down-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

114. The method of embodiment 113 wherein the first miRNA profile comprises down-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

115. The method of embodiment 114 wherein the first miRNA profile comprises down-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

116. The method of embodiment 115 wherein the first miRNA profile comprises down-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

117. The method of embodiment 112 wherein the at least one of the miRNAs is detected by the detector hsa-miR-1-4373161.

118. The method of embodiment 106 wherein the first miRNA profile further comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

119. The method of embodiment 118 wherein the down-regulated expression or activity is of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

120. The method of embodiment 119 wherein the down-regulated expression or activity is of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

121. The method of embodiment 120 wherein the down-regulated expression or activity is of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

122. The method of embodiment 121 wherein the down-regulated expression or activity is of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

123. The method of embodiment 118 wherein the at least one of the miRNAs detected by the detectors identified in Tables 3 or 5 is hsa-miR-1-4373161.

124. The method of embodiment 105 wherein the autoimmune or inflammatory disease is lupus, idiopathic inflammatory myositis, Sjogren's syndrome, vasculitis, sarcoidosis, or psoriasis.

125. The method of embodiment 124 wherein the autoimmune disease is idiopathic inflammatory myositis.

126. The method of embodiment 105 wherein the therapeutic agent is a small molecule or a biologic agent.

127. The method of embodiment 126 wherein the biologic agent is an antibody.

128. The method of embodiment 127 wherein the antibody is MEDI-545.

129. The method of embodiment 105 wherein the first miRNA profile is obtained prior to administration of the therapeutic agent.

130. The method of embodiment 105 wherein the first miRNA profile is obtained at the time of administration of the therapeutic agent.

131. The method of embodiment 105 wherein the first and the second sample are whole blood, muscle, or serum.

132. The method of embodiment 105 further comprising obtaining a third miRNA profile in a third sample from the patient.

133. The method of embodiment 132 further comprising obtaining a fourth miRNA profile in a fourth sample from the patient.

134. The method of embodiment 133 further comprising obtaining a fifth miRNA profile in a fifth sample from the patient.

135. The method of embodiment 134 further comprising obtaining a sixth miRNA profile in a sixth sample from the patient.

136. The method of embodiment 105 wherein the second sample is obtained at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following administration of the therapeutic agent.

137. The method of embodiment 132 wherein the third sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the second sample.

138. The method of embodiment 133 wherein the fourth sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the third sample.

139. The method of embodiment 134 wherein the fifth sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the fourth sample.

140. The method of embodiment 105 wherein variance is a decrease in differential miRNA levels of the patient relative to healthy levels.

141. The method of embodiment 105 wherein variance is an increase in differential miRNA levels of the patient relative to healthy levels.

142. The method of embodiment 141 wherein the increase in differential miRNA levels indicates poor disease prognosis or disease will flare.

143. The method of embodiment 141 wherein the increase in differential miRNA levels of the patients indicates a change in treatment of the patient.

144. A method of treating a myositis patient comprising:

administering an agent that binds to and modulates type I IFN or IFNα activity;

wherein the patient comprises a type I IFN or IFNα-inducible PD marker expression profile;

and wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient.

145. The method of embodiment 144 further comprising detecting neutralization of the type I IFN or IFNα-inducible PD marker expression profile of the patient.

146. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes MX1, LY6E, IFI27, OAS1 IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, and IFI44.

147. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes LAMP3, SIGLEC1, DNAPTP6, IFIT2, ETV7, RTP4, SERPING1, HERC5, XAF1, MX1, EPSTI1, OAS2, OAS1, OAS3, IFIT3, IFI6, USP18, RSAD2, IFI44, LY6E, ISG15, and IFI27.

148. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, RSAD2, RTP4, SIGLEC1, and USP18

149. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes DNAPTP6, EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, PLSCR1, RSAD2, RTP4, SIGLEC1, and USP18.

150. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes SAMD9L, IFI6, IFI44, IFIT2, OAS1, IFI27, OAS3, IFI44L, HERC5, IFIT1, EPSTI1, ISG15, SERPING1, OASL, GBP1, and MX1.

151. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI6, RSAD2, IFI44, IFI44L, IFI27, MX1, IFIT1, ISG15, LAMP3, OAS3, OAS1, EPSTI1, IFIT3, OAS2, SIGLEC1, and USP18.

152. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI6, RSAD2, IFI44, IFI44L, and IFI27.

153. The method of embodiment 144 wherein the agent is a biologic agent.

154. The method of embodiment 153 wherein the agent is an antibody.

155. The method of embodiment 154 wherein the antibody is MEDI-545.

156. The method of embodiment 154 wherein the antibody is specific for one or more type I IFN or IFNα subtype but is not MEDI-545.

157. The method of embodiment 144 wherein the administering the agent alleviates one or more myositis symptoms.

158. The method of embodiment 154 wherein the antibody is administered at a dose between approximately .03 and 30 mg/kg.

159. The method of embodiment 158 wherein the antibody is administered at a dose between 0.3 and 3 mg/kg.

160. The method of embodiment 159 wherein the antibody is administered at a dose between .03 and 1 mg/kg.

161. The method of any one of embodiments 153-155 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 10%.

162. The method of embodiment 144 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 20%.

163. The method of embodiment 162 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 30%.

164. The method of embodiment 163 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 40%.

165. The method of embodiment 164 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 50%.

166. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of at least IFNα subtypes 1, 2, 8, and 14.

167. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises transcripts of PD marker genes.

168. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises polypeptides expressed from PD marker genes.

169. A method of monitoring or prognosing myositis disease progression of a patient comprising:

obtaining a first IFNα-inducible PD marker expression profile in a first sample from a patient.

170. The method of embodiment 169 wherein the first IFNα-inducible PD marker expression profile is a strong profile and the patient prognosis is myositis disease progression.

171. The method of embodiment 170 wherein the first IFNα-inducible PD marker expression profile comprises overexpression or activity of genes EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, RSAD2, RTP4, SIGLEC1, and USP18.

172. The method of embodiment 169 wherein the first IFNα-inducible PD marker expression profile is a weak profile and the patient prognosis is myositis disease regression.

173. The method of embodiment 169 further comprising:

obtaining a second IFNα-inducible PD marker expression profile in a second sample from the patient;

wherein an increase in number or level of type I IFN or IFNα inducible PD markers in the second relative to the first expression profile prognoses myositis disease progression; or

wherein a decrease in number or level of type I IFN or IFNα inducible PD markers in the second relative to the first expression profile prognoses myositis disease regression.

174. A method of monitoring myositis disease progression of a patient receiving treatment with a therapeutic agent comprising:

obtaining a first IFNα-inducible PD marker expression profile in a first sample from the patient;

administering a therapeutic agent;

obtaining a second IFNα-inducible PD marker expression profile in a second sample from the patient; and

comparing the first and the second IFNα-inducible PD marker expression profiles,

wherein a variance in the first and the second IFNα-inducible PD marker expression profiles indicates a level of efficacy of the therapeutic agent.

175. The method of embodiment 174 wherein the first type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes profile comprises overexpression or activity of genes EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, RSAD2, RTP4, SIGLEC1, and USP18.

176. The method of embodiment 174 wherein the variance is a decrease in up-regulated expression of activity levels of the genes.

177. The method of embodiment 174 wherein the therapeutic agent is a small molecule or a biologic agent.

178. The method of embodiment 177 wherein the therapeutic agent is biologic agent that binds to and modulates IFNα activity

179. The method of embodiment 178 wherein the biologic agent is an antibody.

180. The method of embodiment 179 wherein the antibody is MEDI-545.

181. The method of embodiment 179 wherein the antibody binds to at least one IFNα subtype but is not MEDI-545.

182. The method of embodiment 174 wherein the first IFNα-inducible PD marker expression profile is obtained prior to administration of the therapeutic agent.

183. The method of embodiment 174 wherein the first IFNα-inducible PD marker expression profile is obtained at the time of administration of the therapeutic agent.

184. The method of embodiment 174 wherein the first and the second sample are whole blood, muscle, or serum.

185. The method of embodiment 174 further comprising obtaining a third IFNα-inducible PD marker expression profile in a third sample from the patient.

186. The method of embodiment 185 further comprising obtaining a fourth IFNα-inducible PD marker expression profile in a fourth sample from the patient.

187. The method of embodiment 186 further comprising obtaining a fifth IFNα-inducible PD marker expression profile in a fifth sample from the patient.

188. The method of embodiment 187 further comprising obtaining a sixth IFNα-inducible PD marker expression profile in a sixth sample from the patient.

189. The method of embodiment 174 wherein the second sample is obtained at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following administration of the therapeutic agent.

190. The method of embodiment 185 wherein the third sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the second sample.

191. The method of 186 wherein the fourth sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the third sample.

192. The method of embodiment 187 wherein the fifth sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the fourth sample.

193. The method of embodiment 174 wherein variance is a decrease in up-regulated expression or activity of the gene.

194. The method of embodiment 193 wherein the decrease is at least 10%, at least 20%, at least 25%, at least 30%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%.

195. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI27, RSAD2, IFI44L, IFI44, OAS1, IFIT1, ISG15, OAS3, HERC5, MX1, ESPTI1, IFIT3, and IFI6.

196. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L, RSAD2, IFI27, and IFI44.

197. The method of embodiment 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L and RSAD2.

198. The method of embodiment 169 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI27, RSAD2, IFI44L, IFI44, OAS1, IFIT1, ISG15, OAS3, HERC5, MX1, ESPTI1, IFIT3, and IFI6.

199. The method of embodiment 169 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L, RSAD2, IFI27, and IFI44.

200. The method of embodiment 169 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L and RSAD2.

201. The method of embodiment 174 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI27, RSAD2, IFI44L, IFI44, OAS1, IFIT1, ISG15, OAS3, HERC5, MX1, ESPTI1, IFIT3, and IFI6.

202. The method of embodiment 174 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L, RSAD2, IFI27, and IFI44.

203. The method of embodiment 174 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L and RSAD2.

204. The method of embodiment 1 wherein the patient has a strong type I IFN or IFNα-inducible gene signature score.

205. The method of embodiment 1 wherein the patient has a moderate type I IFN or IFNα-inducible gene signature score.

206. The method of embodiment 204 wherein the strong score is greater than or equal to 10.

207. The method of embodiment 205 wherein the moderate score is greater than or equal to 4 but less than 10.

208. The method of embodiment 35 or 74 wherein the myositis is DM or PM.

209. The method of embodiment 144 wherein the myositis patient is a DM or PM patient.

210. The method of embodiment 144 wherein the myositis patient comprises a MITAX score greater than 6.

211. The method of embodiment 144 wherein the type I IFN or IFNα-inducible gene signature score is strong.

212. The method of embodiment 144 wherein the type I IFN or IFNα-inducible gene signature score is moderate.

213. The method of embodiment 211 wherein the score is greater than or equal to 10.

214. The method of embodiment 212 wherein the score is greater than or equal to 4 but less than 10.

215. The method of embodiment 174 wherein the first IFNα-inducible PD marker expression profile comprises a strong type I IFN or IFNα-inducible gene signature score.

216. The method of embodiment 215 wherein the strong score is a score greater than or equal to 10.

217. The method of embodiment 174 wherein the first IFNα-inducible PD marker expression profile comprises a moderate type I IFN or IFNα-inducible gene signature score.

218. The method of embodiment 217 wherein the moderate score is a score greater than or equal to 4 but less than 10.

All publications, patents and patent applications mentioned in this specification are herein incorporated by reference into the specification to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference.

This application incorporates by reference, for all purposes, U.S. Provisional Application Serial No. 60/873,008 filed December 6, 2006, U.S. Provisional Application Serial No. 60/907,762 filed April 16, 2007, U.S. Provisional Application Serial No. 60/924,219 filed May 3, 2007, U.S. Provisional Application Serial No. 60/924,584 filed May 21, 2007, U.S. Provisional Application Serial No. 60/960,187 filed September 19, 2007, U.S. Provisional Application Serial No. 60/996,176 filed November 5, 2007 and PCT application No. PCT/US2007/024947 filed December 6, 2007. This application also incorporates by reference, for all purposes, U.S. Provisional Application Serial No. 61/129,366 filed June 20, 2008 and PCT application No. PCT/US2008/062646 filed May 5, 2008. This application also incorporates by reference, for all purposes, U.S. Provisional Application Serial No. 60/924,220 filed May 3, 2007, U.S. Provisional Application entitled "Auto-Antibody Markers of Autoimmune Disease" filed November 6, 2007 (serial number 60/996,219), U.S. Provisional Application entitled "Auto-Antibody Markers of Autoimmune Disease" filed December 6, 2007 (serial number 60/996,820), and PCT application No. PCT/US2008/062639 filed May 5, 2008.

Furthermore, this application claims priority to U.S. Provisional Application Serial No. 61/006,963 filed February 8, 2008, herein incorporated by reference for all purposes.

The set of examples that follow are provided for the purpose of illustration only and the invention should in no way be construed as being limited to these examples.

EXAMPLES

Example 1a: The majority of the most up-regulated genes in DM patient muscle samples are IFNα/β-inducible

DM muscle samples were examined to determine which genes were most up-regulated in DM patients.

Total RNA extraction and microarray processing: Total RNA was extracted from PAXgene muscle biopsies using the Qiagen RNeasy Fibrous Tissue Mini (Hilden, Germany). RNA purity and concentration were determined spectrophotometrically (260/280 > 1.9). RNA quality was assessed on an Agilent 2100 Bioanalyzer using the RNA 6000 Nano LabChip®.

Generation of biotin-labeled amplified cRNA, from 2ug of total RNA, was accomplished with the Affymetrix GeneChip® One-Cycle cDNA Synthesis kit and the Affymetrix GeneChip® IVT Labeling kit. Concentration and purity of the cRNA product were determined spectrophotometrically. Twenty micrograms of each biotin-labeled cRNA was fragmented for hybridization on Affymetrix Human Genome U133 Plus 2.0 GeneChip® arrays. Fragmented cRNA was prepared for hybridization as outlined in the Affymetrix GeneChip® manual. Hybridization was conducted overnight in a model 320 rotating hybridization oven set at 45°C. All GeneChip® wash and staining procedures were performed on an Affymetrix Model 450 Fluidics station. Arrays were scanned on an Affymetrix GeneChip® Scanner 3000. Data capture and initial array quality assessment were performed with the GeneChip Operating Software (GCOS) tool.

Results: The majority of the most up-regulated genes in muscle specimens of DM patients are IFNα/β-inducible. See Figure 1a, which provides a list of the most up-regulated genes in the DM patient muscle samples, and fold-up-regulation of those genes in the DM patient muscle samples relative to healthy control muscle samples. See also Figure 1b which provides a scatter plot of the IFNα/β-inducible gene signature score in muscle of DM and PM patients.

Example 1b: Overexpression of type I IFN-inducible genes in the majority of DM or PM patient blood samples

Prevalence and magnitude of overexpression of type I IFN-inducible genes in the blood of DM and PM patients were evaluated.

Patients and patient samples: Two groups of patients were used in this study. The first group included 24 myositis patients (15 with DM and 9 with PM) from a single hospital center prospectively enrolled into a longitudinal exploratory study of the association between whole genome gene expression in peripheral WB samples and clinical features including disease activity. Clinical data from a total of 150 patient-visits and gene expression data from 80 patient-visits were collected over a period of up to 6 years (mean period of participation in this study was 1.9 years). Clinical features of those patients are summarized in Table 6, below.

Table 6. Clinical features for 24 DM or PM patients.

Disease, patient/ age/gender	# of Serial Visit Blood Profiling / Duration of Study (months)	Disease Duration Initial Visit (months)	Treatment Initial Visit	Treatment Duration at Initial Visit (months)	CK level, range, (units/liter)	MITAX SCORE Initial (Min,Max)	Other diagnoses
Dermatomyositis (N=15)							
BGE79/46/F	3 (32)	72	None	0	260 - 816	12 (6,12)	Calcinosis
BGE99/21/M	7 (21)	3	None	0	90 - 352	12 (1,12)	-
BGE143/43/F	3 (6)	290	None	0	46 - 290	12 (1,12)	-
BGE147/57/F	7 (13)	18	None	0	36 - 252	9 (4,9)	-
BGE10/38/F	6 (42)	108	Pred/IVIG	4	127 – 4590	12 (6,12)	-
BGE15/62/F	4 (78)	36	Pred/ Myco	12	25 - 80	2 (0,6)	-
BGE17/70/F	2 (63)	24	Pred/ IVIG/Myco	6	19 - 52	2 (2,2)	-
BGE19/61/F	2 (27)	12	Pred/Myco	24	34 - 6554	2 (2,6)	Breast cancer
BGE46/25/F	2 (4)	8	Pred	0.1	126 - 393	12 (6,12)	-
BGE80/44/F	2 (23)	1	Pred	1	71 - 87	2 (2,6)	-
BGE92/27/F	4 (6)	17	Pred	11	1140 - 32877	13 (13,13)	ILD, Jo-1
BGE95/53/M	2 (13)	25	MTX	23	260 - 6416	2 (2,13)	Diabetes
BGE126/58/F	2 (2)	2	Prednisone	0.2	46 - 350	12 (1,12)	-
BGE140/46/F	**3 (11)**	**42**	**Pred/MTX**	**36**	**1831 - 1925**	**12 (6,12)**	**-**
BGE155/46/F	2 (5)	15	Pred	14	860 - 4107	3 (3,12)	ILD, Jo-1
Polymyositis (N=9)							
BGE106/59/F	4 (13)	2	None	0	53 - 4720	9 (1,9)	-
BGE119/47/F	6 (12)	5	None	0	62 - 1256	9 (1,9)	ILD/MCTD
BGE3/55/F	**4 (47)**	**26**	**Pred/Myco**	**20**	**498 - 2094**	**6 (6,6)**	**-**
BGE11/65/F	2 (49)	81	Aza/IVIG	48	66 - 1156	3 (1,3)	ILD; Jo-1
BGE47/72/F	3 (45)	11	Pred/Myco	9	209 - 3027	9 (3,9)	-
BGE50/40/F	2 (26)	2	Pred/IVIG	2	74 - 663	3 (1,3)	-
BGE91/55/F	2 (4)	6	MTX	5	123	3 (3,3)	-
BGE100/57/M	3 (15)	12	Pred/MTX	4	329 - 820	3 (3,3)	-
BGE128/84/F	**3 (7)**	**80**	**Pred**	**76**	**150 - 1437**	**1 (1,9)**	**-**

Early cross-sectional studies of some of these patients after one or two visits were previously reported (Walsh RJ, Pinkus JL, et al. Type I interferon-inducible gene expression in blood is present and reflects disease activity in dermatomyositis and polymyositis. Arthritis Rheum. 2007; 56(11):3784-92); the current study increased the number of enrolled patients and performed a longitudinal analysis of up to 7 visits per patient. Diagnostic criteria for DM and PM are as previously reported (Walsh RJ, Pinkus JL, et al. Type I interferon-inducible gene expression in blood is present and reflects

disease activity in dermatomyositis and polymyositis. Arthritis Rheum. 2007; 56(11):3784-92). WB samples were collected at routine clinical follow-up visits. Disease activity was assessed at each visit using the Myositis Intention to Treat scale (MITAX) as previously described (Walsh RJ, Pinkus JL, et al. Type I interferon-inducible gene expression in blood is present and reflects disease activity in dermatomyositis and polymyositis. Arthritis Rheum. 2007; 56(11):3784-92). Clinical parameters, including the MITAX score (Rider LG, Miller FW. Idiopathic inflammatory muscle disease: clinical aspects. Baillieres Best Pract Res Clin Rheumatol. 2000; 14(1):37-54), were assessed blinded to gene expression data. WB samples were not collected according to any predefined schedule. Patients gave informed consent in order to participate. These studies were approved by institutional review board (IRB) at Brigham and Women's Hospital.

The second group of myositis patients (18) was studied for single blood samples obtained at screening visits for a clinical trial in patients with DM or PM. These blood samples were used for initial evaluation of the prevalence of cytokine-inducible gene signatures across patients seen by multiple investigators at multiple centers, and were collected with informed consent under IRB approved protocols. These subjects were at least 18 years of age and had probable or definite DM or PM according to the Bohan and Peter criteria (Bohan A, Peter JB. Polymyositis and dermatomyositis. N Engl J Med. 1975 Feb 13;292(7):344-7; Bohan A, Peter JB. Polymyositis and dermatomyositis. N Engl J Med. 1975 Feb 20;292(8):403-7) and active disease. WB samples were collected in PAXgene RNA tubes at clinical visits prior to treatment. All subjects had to have at least 2 of the following: strength in manual muscle testing (MMT) $\geq$ 80/150 but $\leq$ 125/150 using the MMT-8 muscle group testing; patient global activity assessment by visual analogue scale $\geq$ 2.0 cm on a 10-cm scale; physician global activity assessment by visual analogue scale $\geq$ 2.0 cm on a 10-cm scale, CLINHQA disability index $\geq$ 0.25; and global extramuscular activity assessment $\geq$ 1.0 on a 10 cm visual analogue scale. Subjects with PM were required to have documentation of a muscle biopsy result consistent with the diagnosis of PM. At screening, subjects could not be receiving > 35 mg prednisone or equivalent per day, hydroxychloroquine > 600 mg/day, mycophenolate mofetil > 3 g/day, methotrexate > 25 mg/week, azathioprine > 3 mg/kg/day, leflunomide > 20 mg/day, or any dose of cyclophosphamide, cyclosporine, or thalidomide.

Normal blood samples were from 36 healthy donors as described (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008; Volume 2009, Article ID 374312, doi:10.4061/2009/374312; Walsh RJ, Pinkus JL, et al. Type I interferon-inducible gene expression in blood is present and reflects disease activity in dermatomyositis and polymyositis. Arthritis Rheum. 2007; 56(11):3784-92), and were collected with informed consent under IRB approved protocols.

Total RNA extraction, microarray assays, and TaqMan QRT-PCR assays: RNA isolation from WB used PAXgene tubes or buffy coat samples, and Affymetrix U133 Plus 2.0 microarray assays were carried out as previously described (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008; Volume 2009, Article ID 374312, doi:10.4061/2009/374312; Walsh RJ, Pinkus JL, et al. Type I interferon-inducible gene expression in blood is present and reflects disease activity in dermatomyositis and polymyositis. Arthritis Rheum. 2007; 56(11):3784-92). RNA was isolated using the PAXgene tube collection method for 24 normal healthy donor samples, while 12 normal healthy donor samples were processed with the buffy coat method. These normal healthy donor samples were used as baselines for the patient samples processed by one of the two approaches in order to eliminate any variability due to sample processing differences.

Fluidigm's Biomark system dynamic array platform (Fluidigm Corp, South San Francisco, CA, USA) was used to measure expression levels of the type 1 IFN-inducible genes, a panel of cytokine-inducible genes, and selected immune response genes in the WB of 15 patients with DM or PM. The general procedures for sample processing and data analysis were as described previously (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008; Volume 2009, Article ID 374312, doi:10.4061/2009/374312).

Microarray data analysis: Microarray data analysis was performed as previously described (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008; Volume 2009, Article ID 374312, doi:10.4061/2009/374312; Yao Y, Jallal J, et al. Type I IFN as a potential therapeutic target for psoriasis. PLoS ONE 2008; 3(7): e2737. doi:10.1371/journal.pone.0002737), using GC-Content Robust Multichip Analysis (GCRMA), which was implemented in the Bioconductor (http://www.bioconductor.org/) GCRMA package. All two-group comparisons involving the gene signature scores were calculated using a two-sample Wilcoxon-Mann-Whitney test, while paired comparisons were calculated using a Wilcoxon signed-rank test. All p-values reported are unadjusted for multiple testing, although significance is stated for adjusted p-values, using a Bonferroni correction. For identification of patients with a positive type 1 IFN-inducible gene signature score, we calculated significance analysis of microarrays (SAM) with false discovery rate (FDR) adjustment in R (R Development Core Team, University of Auckland, New Zealand).

Results: Affymetrix human genome U133 plus 2.0 GeneChip® was employed to profile the peripheral WB of 42 patients with DM or PM (22 DM and 20 PM patients; from first and second patient groups). 1,072 and 703 transcripts were observed to be upregulated and downregulated (fold change >2, $q<0.05$), respectively, in the blood of patients with DM or PM compared with healthy controls. Of the 1,072 upregulated transcripts, 136 were type 1 IFN-inducible as defined by ex vivo stimulation of WB with type I IFN family members as described (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008;Volume 2009, Article ID 374312, doi:10.4061/2009/374312). A heatmap visualizing the expression of the 136 transcripts in WB of 42 patients with DM or PM, as compared to 24 healthy controls, is shown in Figure 384a. The type 1 IFN-inducible gene signature scores calculated using the dynamic 25 most overexpressed type 1 IFN-inducible genes (dynamic list potentially different between patients) in the blood of individual normal controls and patients with DM or PM are shown in Figure 384b. The patients evaluated

in the study exhibited different degrees of overexpression of type 1 IFN-inducible genes in the blood, and this included a distinct population of patients with DM or PM that had weak type 1 IFN-inducible gene signatures (score < 4). Normal donors and these weak signature score patients are represented by the first and second horizontal bars, respectively, in Figure 384b. Based on classification criteria (in which a type 1 IFN-inducible gene signature was weak if it was assigned a score of less than 4, moderate if it was assigned a score that was greater than or equal to 4 but less than 10, and high if it was assigned a score greater than or equal to 10) 17% of patients with DM or PM had weak or no overexpression of type 1 IFN-inducible gene signature in the blood. A total of 45% and 38% of the patients had moderate or high type 1 IFN-inducible gene signatures, respectively. Thus, the overwhelming majority of patients with DM or PM showed moderate to high overexpression of type 1 IFN-inducible gene signature in the blood.

Example 1c: Selection of a 13-gene panel to evaluate type 1 IFN signaling pathway activity in patients with DM or PM

Based on the results of Example 1b, a small panel of type 1 IFN–inducible genes was selected that could be used to evaluate the activation of the type 1 IFN signaling pathway in the blood of DM and PM patients.

Ranking genes most overexpressed in the peripheral WB of patients with DM and PM: To identify the most overexpressed probe sets across the 42 DM and PM patients used in the study described in Example 1b, fold-change values were calculated between each patient individually and the median of 24 healthy donors for each probe set on the Affymetrix U133 Plus 2.0 array. For each patient, the fold-change values were then ranked in descending order. The median ranking was calculated for each probe set and the top 200 overall probe sets were selected. The 807 probe sets that have been previously identified as type 1 IFN-inducible (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008;Volume 2009, Article ID 374312, doi:10.4061/2009/374312) were intersected with these 200 probe sets, and those probe sets in common were summated to identify type 1 IFN-inducible genes that were overexpressed in peripheral WB of patients with DM or PM.

Results: Composite scores of relative expression of multiple genes can provide a robust measurement of pathway activity, as described previously (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008; Volume 2009, Article ID 374312, doi:10.4061/2009/374312, Yao, Y, Jallal J, et al. Neutralization of IFN-α/β–Inducible Genes and Downstream Effect in a Phase I Trial of an Anti–IFN-α Monoclonal Antibody in SLE. Accepted by Arthritis Rheum.). The average fold ranks for the 100 most overexpressed genes in peripheral WB of the 42 patients with DM or PM are listed in Table 7, shown below.

Table 7. Average fold ranking of the 100 most overexpressed probes in WB of 42 patients with DM or PM.

median ranking	Unigene	Gene Title	Gene Symbol	Entrez Gene	IFIG
27	Hs.17518	radical S-adenosyl methionine domain containing 2	RSAD2	91543	TRUE
27	Hs.532634	interferon, alpha-inducible protein 27	IFI27	3429	TRUE
36	Hs.17518	radical S-adenosyl methionine domain containing 2	RSAD2	91543	TRUE
42	Hs.389724	interferon-induced protein 44-like	IFI44L	10964	TRUE
62	Hs.118633	2'-5'-oligoadenylate synthetase-like	OASL	8638	TRUE
87	Hs.529517	lactotransferrin /// similar to lactotransferrin	LTF /// LOC728320	4057 /// 643349	FALSE
88	Hs.82316	interferon-induced protein 44	IFI44	10561	TRUE
89	Hs.7155	hypothetical protein LOC129607	LOC129607	129607	TRUE
98	Hs.20315	interferon-induced protein with tetratricopeptide repeats 1	IFIT1	3434	TRUE
120		2',5'-oligoadenylate synthetase 1, 40/46kDa	OAS1	4938	TRUE
169	Hs.440934	arginase, liver	ARG1	383	FALSE
171	Hs.546523	Full-length cDNA clone CS0DK002YF13 of HeLa cells Cot 25-normalized of Homo sapiens (human)	---	---	TRUE
198	Hs.509163	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	ERGIC1	57222	FALSE
283	Hs.567533	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	YOD1	55432	FALSE
354	Hs.480042	annexin A3	ANXA3	306	TRUE
380	---	tubulin, beta 2A	TUBB2A	7280	FALSE
387	Hs.130759	phospholipid scramblase 1	PLSCR1	5359	TRUE
394	Hs.528634	2'-5'-oligoadenylate synthetase 3, 100kDa	OAS3	4940	TRUE
395	Hs.591391	defensin, alpha 4, corticostatin	DEFA4	1669	FALSE
413	Hs.351811	C-type lectin domain family 4, member D	CLEC4D	338339	FALSE
421	Hs.29683	hect domain and RLD 5	HERC5	51191	TRUE
422	Hs.437322	tumor necrosis factor, alpha-induced protein 6	TNFAIP6	7130	TRUE
441	Hs.632594	glycophorin B (MNS blood group)	GYPB	2994	FALSE
443	Hs.12114	vanin 1 /// vanin 1	VNN1	8876	FALSE
470	Hs.469521	interleukin 18 receptor 1	IL18R1	8809	FALSE
487	Hs.252839	interferon-induced protein with tetratricopeptide repeats 5	IFIT5	24138	FALSE
493	Hs.89497	lamin B1	LMNB1	4001	TRUE
494	Hs.130759	phospholipid scramblase 1	PLSCR1	5359	TRUE
508	Hs.517307	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	MX1	4599	TRUE
517	Hs.546467	epithelial stromal interaction 1 (breast)	EPSTI1	94240	TRUE
527	Hs.89714	chemokine (C-X-C motif) ligand 5	CXCL5	6374	FALSE
529	Hs.35861	transmembrane protein 158	TMEM158	25907	FALSE
548	Hs.524760	2',5'-oligoadenylate synthetase 1, 40/46kDa	OAS1	4938	TRUE
556	---	PRO1073 protein	PRO1073	29005	FALSE
556	Hs.47338	interferon-induced protein with tetratricopeptide repeats 3	IFIT3	3437	TRUE
566	Hs.29692	hypothetical protein FLJ36031	FLJ36031	168455	FALSE
608	Hs.523847	interferon, alpha-inducible protein 6	IFI6	2537	TRUE
630	Hs.414332	2'-5'-oligoadenylate synthetase 2, 69/71kDa	OAS2	4939	TRUE
634	Hs.546467	Epithelial stromal interaction 1 (breast)	EPSTI1	94240	TRUE
701	Hs.179608	dehydrogenase/reductase (SDR family) member 9	DHRS9	10170	FALSE
706	Hs.441975	XIAP associated factor-1	BIRC4BP	54739	TRUE
725	---	PRO1073 protein	PRO1073	29005	FALSE
742	Hs.642877	Metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	MALAT1	378938	FALSE
747	---	---	---	---	TRUE
752	Hs.310591	solute carrier family 22 (organic cation transporter), member 4	SLC22A4	6583	FALSE
753	Hs.351811	C-type lectin domain family 4, member D	CLEC4D	338339	FALSE
767	Hs.380781	defensin, alpha 1 /// defensin, alpha 3, neutrophil-specific	DEFA1 /// DEFA3	1667 /// 1668	FALSE
810	Hs.437609	interferon-induced protein with tetratricopeptide repeats 2	IFIT2	3433	TRUE
815	Hs.218040	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	ITGB3	3690	FALSE
831	Hs.446125	male germ cell-associated kinase	MAK	4117	FALSE
831	Hs.458485	ISG15 ubiquitin-like modifier	ISG15	9636	TRUE
859	Hs.25333	interleukin 1 receptor, type II	IL1R2	7850	FALSE
859	Hs.99960	membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	MS4A3	932	FALSE
929	Hs.280604	protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform (calcineurin B, type I)	PPP3R1	5534	FALSE
930	Hs.570423	SAM domain, SH3 domain and nuclear localization signals 1	SAMSN1	64092	FALSE
949	Hs.504687	myosin, light chain 9, regulatory	MYL9	10398	FALSE
978	Hs.82316	Interferon-induced protein 44	IFI44	10561	TRUE
987	Hs.512682	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	CEACAM1	634	TRUE
998	Hs.534956	Fc fragment of IgG, high affinity Ib, receptor (CD64)	FCGR1B	2209	FALSE
1007	Hs.489118	sterile alpha motif domain containing 9-like	SAMD9L	219285	TRUE
1024	Hs.166120	interferon regulatory factor 7	IRF7	3665	TRUE
1049	Hs.495731	BMX non-receptor tyrosine kinase	BMX	660	FALSE
1067	Hs.69328	lymphocyte antigen 96	LY96	23643	FALSE
1091	Hs.631534	Fc fragment of IgA, receptor for	FCAR	2204	FALSE
1099	Hs.437322	tumor necrosis factor, alpha-induced protein 6	TNFAIP6	7130	TRUE
1115	Hs.154654	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	1545	FALSE
1127	Hs.631544	chromosome 19 open reading frame 33	C19orf33	64073	FALSE
1140	Hs.591715	Sin3A-associated protein, 30kDa	SAP30	8819	FALSE
1163	Hs.529317	hect domain and RLD 6	HERC6	55008	TRUE
1173	---	microRNA 21	MIRN21	406991	FALSE
1185	Hs.198365	2,3-bisphosphoglycerate mutase /// 2,3-bisphosphoglycerate mutase	BPGM	669	FALSE
1191	Hs.170009	transforming growth factor, alpha	TGFA	7039	FALSE
1192	Hs.301921	chemokine (C-C motif) receptor 1	CCR1	1230	TRUE
1196	Hs.227777	protein tyrosine phosphatase type IVA, member 1	PTP4A1	7803	TRUE
1199	Hs.591421	lysophosphatidylglycerol acyltransferase 1	LPGAT1	9926	FALSE
1202	Hs.631534	Fc fragment of IgA, receptor for	FCAR	2204	FALSE
1225	Hs.514554	KIAA1618	KIAA1618	57714	TRUE
1225	Hs.306834	FK506 binding protein 1B, 12.6 kDa	FKBP1B	2281	FALSE
1232	Hs.728	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	RNASE2	6036	FALSE
1234	Hs.529019	bactericidal/permeability-increasing protein	BPI	671	FALSE
1251	Hs.334019	complement component (3b/4b) receptor 1 (Knops blood group)	CR1	1378	FALSE
1255	Hs.74368	cytoskeleton-associated protein 4	CKAP4	10970	FALSE
1261	Hs.142074	ring finger protein 149 /// similar to ring finger protein 149	RNF149 /// LOC731208	284996	FALSE
1275	Hs.127126	cytoplasmic polyadenylation element binding protein 4	CPEB4	80315	FALSE
1278	Hs.136398	Zinc finger, CCHC domain containing 6	ZCCHC6	79670	FALSE
1279	Hs.114191	zinc finger, CCHC domain containing 2	ZCCHC2	54877	FALSE
1314	Hs.494977	multiple EGF-like-domains 9	MEGF9	1955	FALSE
1331	Hs.523529	Similar to SLIT-ROBO Rho GTPase-activating protein 2 (srGAP2) (Formin-binding protein 2)	LOC653464	653464	TRUE
1331	Hs.24701	CDNA FLJ37917 fis, clone CTONG1000137	---	---	FALSE
1336	Hs.78919	X-linked Kx blood group (McLeod syndrome)	XK	7504	FALSE
1353	Hs.165762	FCH domain only 2	FCHO2	115548	FALSE
1383	Hs.441975	XIAP associated factor-1	BIRC4BP	54739	TRUE
1396	Hs.497951	hypothetical protein LOC284701	LOC284701	284701	FALSE
1397	Hs.644621	chromosome 14 open reading frame 45	C14orf45	80127	FALSE
1399	Hs.631534	Fc fragment of IgA, receptor for	FCAR	2204	FALSE
1400	Hs.128474	contactin associated protein-like 3	CNTNAP3	389734	FALSE
1409	Hs.635313	chromatin modifying protein 5	CHMP5	51510	FALSE
1413	Hs.234681	leucine rich repeat containing 57	LRRC57	255252	FALSE
1422	Hs.204238	lipocalin 2 (oncogene 24p3)	LCN2	3934	FALSE
1433	Hs.407926	rapamycin-insensitive companion of mTOR	RICTOR	253260	FALSE

The 13 type 1 IFN-inducible genes used to calculate the composite gene signature score were marked in red (RSAD2, IFI27, IFI44L, IFI44, IFIT1, OAS1, OAS3, HERC5, MX1, EPSTI1, IFIT3, IFI6, and ISG15).

The thirteen overexpressed type 1 IFN-inducible genes were selected from this group in order to construct a type 1 IFN-inducible gene signature score reflecting type 1 IFN signaling pathway activation in the blood of DM and PM patients. The 13 selected genes were: the 6 most overexpressed type 1 IFN-inducible genes in the blood of DM and PM patients (IFI27, RSAD2, IFI44L, IFI44, OAS1, IFIT1), plus ISG15, one of the most overexpressed type 1 IFN-inducible genes in DM muscle specimens (Greenberg SA, Tawil R, et al. Interferon-alpha/beta-mediated innate immune mechanisms in dermatomyositis. Ann Neurol 2005; 57(5):664-78), and 6 well characterized type 1 IFN-inducible genes (OAS3, HERC5, MX1, ESPTI1, IFIT3, and IFI6). Gene signature scores with this 13-gene panel (a subset of the 21-gene panel for SLE) correlated very well (r=0.98) with scores for the 21-gene panel of type 1 IFN-inducible genes used to characterize type 1 IFN signaling pathway activation in SLE (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008; Volume 2009, Article ID 374312, doi:10.4061/2009/374312), and also with the alternative gene signature score approach using the dynamic top 25 most overexpressed type 1 IFN-inducible genes (r=0.82) in individual patients (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008; Volume 2009, Article ID 374312, doi:10.4061/2009/374312, Yao, Y, Jallal J, et al. Neutralization of IFN-α/β–Inducible Genes and Downstream Effect in a Phase I Trial of an Anti–IFN-α Monoclonal Antibody in SLE. Accepted by Arthritis Rheum.).

Besides among the most overexpressed type 1 IFN-inducible genes in the blood of patients with DM or PM, stronger overexpression of mRNAs of IFI27, RSAD2, IFI44LL and IFI44 was generally observed in DM and PM patients with high disease activity. For the 12 patients with high disease activity (MITAX > 6; see Table 6, above), at their peak MITAX score during the study, average fold changes of mRNAs of IFI27, RSAD2, IFI44LL and IFI44, compared to the average of 36 normal controls, were 89-, 53-, 90- and 19-fold, respectively. QRT-PCR was also used to validate the microarray results for

these 4 genes. WB samples from 15 patients (9 DM, 6 PM) were selected for the purpose. QRT-PCR measurements for these 4 individual genes correlated highly with microarray measurements (IFI27 r=0.96; IFI44 r=0.95; IFI44L r=0.98; and RSAD2 r=0.98).

Example 1d: Correlation of the 13 gene IFNα/β-inducible gene signature score with myositis disease activity

Longitudinal studies conducted for 24 DM and PM patients identified an association of the 13 gene type I IFN-inducible signature and disease activity (MITAX).

Linear mixed model for longitudinal analysis: A repeated measures analysis was conducted for only those patients with at least 3 follow-up visits (total N=53 follow-up visits for 12 patients). Ten different regression models were fit where MITAX score (low and high disease activity as defined previously) was regressed on the following, all modeled as random effects: 13-gene composite score, RSAD2, IFI27, IFI44, and IFI44L. Treatment status at the initial visit was used as a binary covariate (*i.e.*, any treatment/no treatment) and modeled as a fixed effect in each model in order to control for the influence of medication on gene expression changes.

Results: Of the 24 DM and PM patients evaluated, 3 of the patients (specifically BGE128, BGE140 and BGE3) had low IFN-inducible gene signature scores always < 1 and never differed from scores of normal controls throughout their course. This was the case even when their disease activities as measured by MITAX scores changed significantly.

The remaining 21 patients in the longitudinal study were stratified into a two-group comparison with low (MITAX score ≤ 6; 9 patients) and high (MITAX score > 6; 12 patients) disease activity. Both of these categories demonstrated an association with type 1 IFN-inducible gene expression (13-gene score p=0.002, IFI27 p=0.002, and RSAD2 p=0.003 – all significant after adjustment; see Table 8 and Figure 385a). In a comparison between a panel of 36 normal healthy donors and patients with high disease activity, the difference using both the 13-gene composite score and 4 individual genes was found to be highly significant (Table 8; Figure 385a). These results suggested that both the type 1 IFN-inducible 13-gene signature score and the expression of the 4

individual type 1 IFN-inducible genes correlated strongly with disease activity of DM and PM patients.

Table 8: P-values for DM and PM patients at visit one for 4 type 1 IFN-inducible genes, the 13-gene composite score, and 5 cytokine-inducible gene signature scores.

	Normal vs MITAX≤6	Normal vs MITAX>6	MITAX≤6 vs MITAX>6
13-gene	0.032	<0.0001	0.002
RSAD2	0.10	<0.0001	0.003
IFI44L	0.024	<0.0001	0.006
IFI44	0.021	<0.0001	0.01
IFI27	0.005	<0.0001	0.002
GM-CSF	<0.0001	<0.0001	0.46
TNF-a	<0.0001	<0.0001	0.86
IL-1B	0.001	0.0001	0.97
IL-10	0.0002	<0.0001	0.70
IL-13	<0.0001	<0.0001	0.97

Two-group comparisons are between normal donors, patients with high disease activity (MITAX score > 6 at visit 1), and patients with low disease activity (MITAX score ≤ 6 at visit 1). All p-values are unadjusted.

These biomarkers also showed high correlation with clinical disease activity within individual patients during longitudinal follow up. Patients (N=18) with any variation in disease activity among their visits showed strong correlation between MITAX score changes and changes in both the 13-gene composite score (p=0.0002) and individual gene expression levels (IFI27 p=0.0002, RSAD2 p=0.0002, and IFI44L p=0.0002 – all significant after adjustment; Figure 385b). IFI44 was not significant after adjustment. Furthermore, both the 13-gene score and expression of mRNAs of RSAD2 and IFI44L increased in all 18 patients from low to high MITAX scores. The expression of IFI44 mRNA decreased in 2 patients from low to high MITAX scores. These results suggest that the composite score is likely more robustly correlated with disease activity than individual genes. Patients (N=3) with no variation in disease activity showed no real changes in expression levels of these genes (Figure 385c).

Furthermore, major clinical disease activity changes were associated with major changes in the 13-gene composite signature score. Among the 80 patient-visits were 50 pairs of consecutive visits. Among these 50 were 14 major changes in disease activity (change in MITAX score of > 3; 10 improvements, 4 worsening events). All 14 changes

were associated with major changes in both the 13-gene composite score and the expression of 4 individual type 1 IFN-inducible genes in the concordant direction (13-gene composite score, IFI44L and IFI27 provide the best correlation; Table 9).

Table 9. Major changes in disease activity are associated with major changes in the expression of type 1 IFN-inducible genes in the blood of patients with DM or PM.

Sample	Category	MITAX Change	Interval (Days)	RSAD2	IFI44L	IFI44	IFI27	13-gene score
10v2	Improvement	12→6	103	-94%	-99%	-83%	-96%	-89%
46v2	Improvement	12→6	124	-83%	-50%	-72%	-21%	-63%
47v4	Improvement	9→3	432	-66%	-95%	6128%	-61%	-69%
79v2	Improvement	12→6	35	-98%	-99%	-65%	-95%	-91%
99v2	Improvement	12→3	66	-98%	-99%	-86%	-99%	-92%
106v2	Improvement	9→1	214	-86%	-98%	-84%	-80%	-72%
119v2	Improvement	9→3	45	-97%	-98%	-96%	-83%	-92%
126v2	Improvement	12→1	64	-77%	-84%	-85%	-44%	-76%
140v2	Improvement	12→6	80	-74%	-69%	-66%	-95%	-46%
143v2	Improvement	12→1	61	-98%	-97%	-94%	-99%	-94%
155v2	Improvement	12→3	140	-30%	-45%	63%	-57%	-12%
15v3/4*	Relapse	0→6*	854	1740%	1612%	2213%	1420%	715%
19v3	Relapse	2→6	182	387%	847%	8259%	1675%	636%
95v2	Relapse	2→13	380	11338%	9256%	1748%	4962%	3022%
128v2	Relapse	1→9	133	-24%	145%	-27%	1394%	119%
147v4	Relapse	4→9	6	17%	32%	149%	64%	112%

Gene expression changes are shown as the % change in fold ratio from prior to current visit for each of 4 transcripts (RSAD2, IFI44L, IFI44, and IFI27) and the 13-gene composite score. Improvement (reduction in MITAX score) was associated with marked reduction in these type 1 IFN-inducible transcript levels and relapse was associated with marked increases (1 outlier among 56 measurements is present). One visit (marked *; 15v4) was proceeded by a "herald" visit indicating impending relapse; the MITAX change from 15v3 to 15v4 represents a 35 day interval , but type 1 IFN-inducible gene expression had already risen at 15v3 (change shown from 15v2 to 15v3).

Seven patients had WB samples collected in at least 4 visits. All patients showed strong correlation between changes in disease activity and 13-gene composite scores (Figure 386a). For 6 of these patients, this was evident using the MITAX score as the disease activity measure; with one refractory patient (BGE92), a limitation of the MITAX score (it reaches a maximum at 13 and cannot increase with further increases in disease activity) limited its use, but the serum CK (increasing from 3,369 to 32,877 IU/L) reflected the changes in disease activity and correlated strongly with the changes in the 13-gene composite score (Figure 386b).

A general summary of association between clinical disease activity and type 1 IFN-inducible gene expression changes across all patients was performed using a linear mixed model. An advantage of linear mixed model analysis is the ability to improve estimates by pooling information across patients. The 13-gene composite score was found

to be the most significantly correlated with disease clinical activity (p=0.0007), with IFI44L (p=0.001) and RSAD2 (p=0.002) the next well-correlated (still significant after adjustment) for the 12 patients with at least 3 follow-up measurements, after controlling for treatment status.

Furthermore, three patients appeared to have "herald" visits, or visits in which MITAX score disease activity was low but the 13-gene composite score was significantly increased relative to the prior visit (Figure 387). Shortly after these "herald" visits (7-35 days), each of the three patients relapsed into disease.

Example 2a: IFNα/β-inducible gene signature scores predict myositis disease activity

DM and PM patients, from a study separate from Example 1b-d patients, were likewise monitored to determine whether disease progression and/or regression could be predicted by changes in IFNα/β-inducible gene signature.

Total RNA extraction and microarray processing: Total RNA was extracted from PAXgene blood using the PAXgene Blood RNA kit. RNA purity and concentration were determined spectrophotometrically (260/280 > 1.9). RNA quality was assessed on an Agilent 2100 Bioanalyzer using the RNA 6000 Nano LabChip®.

Generation of biotin-labeled amplified cRNA, from 2ug of total RNA, was accomplished with the Affymetrix GeneChip® One-Cycle cDNA Synthesis kit and the Affymetrix GeneChip® IVT Labeling kit. Concentration and purity of the cRNA product were determined spectrophotometrically. Twenty micrograms of each biotin-labeled cRNA was fragmented for hybridization on Affymetrix Human Genome U133 Plus 2.0 GeneChip® arrays. Fragmented cRNA was prepared for hybridization as outlined in the Affymetrix GeneChip® manual. Hybridization was conducted overnight in a model 320 rotating hybridization oven set at 45°C. All GeneChip® wash and staining procedures were performed on an Affymetrix Model 450 Fluidics station. Arrays were scanned on an Affymetrix GeneChip® Scanner 3000. Data capture and initial array quality assessment were performed with the GeneChip Operating Software (GCOS) tool.

Serum CK levels: Serum CK levels were obtained from Steven Greenberg (Brigham and Women's Hospital, Inc.).

Calculation of IFN gene signature using static list of 21 genes: 21 genes were identified by their prevalence and magnitude of overexpression in Myositis patients as

compared to those of normal controls. It includes a standard list of the same 21 genes (i.e. 21 probes that map to 21 unique genes) for each Myositis patient. These genes include DNA polymerase-transactivated protein 6 - DNAPTP6; epithelial stromal interaction 1 (breast) - EPSTI1; hect domain and RLD 5 - HERC5; interferon, alpha-inducible protein 27 - IFI27; Interferon-induced protein 44 - IFI44; interferon-induced protein 44-like - IFI44L; interferon, alpha-inducible protein 6 - IFI6; interferon-induced protein with tetratricopeptide repeats 1 - IFIT1; interferon-induced protein with tetratricopeptide repeats 3 - IFIT3; ISG15 ubiquitin-like modifier; lysosomal-associated membrane protein 3 - LAMP3; lymphocyte antigen 6 complex, locus E - LY6E; myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 - MX1; 2',5'-oligoadenylate synthetase 1, 40/46kDa - OAS1; 2'-5'-oligoadenylate synthetase 2, 69/71kDa - OAS2; 2'-5'-oligoadenylate synthetase 3, 100kDa - OAS3; Phospholipid scramblase 1 - PLSCR1; radical S-adenosyl methionine domain containing 2 - RSAD2; receptor (chemosensory) transporter protein 4 - RTP4; sialic acid binding Ig-like lectin 1, sialoadhesin - SIGLEC1; ubiquitin specific peptidase 18 - USP18. The fold change is calculated between Myositis patients at day 0 (predose) and the average of 24 normal healthy controls. The median of these 21 fold change values is then computed for each Myositis patient and this value is used as the IFN-α/β-inducible gene signature score.

TNFα, IL1β, IL4, IL10, and IL13 gene signatures: Calculation of TNFα, IL1β, IL4, IL10, and IL13 gene signatures were calculated similarly to way that the IFN-α/β-inducible gene signature. However, because the initial number of cytokine-inducible genes that were identified differs for each cytokine, the percentage rather than absolute number of genes was used. For example, using the IFN-α/β–inducible gene signature as the standard, the top 25 of the 807 genes were selected for each patient (dynamic gene list). This represents approximately 3.5% of the IFN-α/β–inducible genes determined. This percentage of genes was maintained for each of the other cytokines to calculate the gene signature for each patient. The IL1β genes from which the IL1β signature was derived included: zinc finger CCCH-type containing 12A - ZC3H12A; ureidopropionase, beta - UPB1; SAM domain, SH3 domain and nuclear localisation signals, 1 - SAMSN1; nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta – NFKBIZ; pentraxin-related gene, rapidly induced by IL-1 beta - PTX3;

peptidase inhibitor 3, skin-derived (SKALP) - PI3; IBR domain containing 2 - IBRDC2; ATG7 autophagy related 7 homolog (S. cerevisiae) - ATG7; adenosine A2a receptor - ADORA2A; nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta – NFKBIZ; Bcl2 modifying factor – BMF; peptidase inhibitor 3, skin-derived - (SKALP) ; pleiomorphic adenoma gene-like 2 - PLAGL2; mitogen-activated protein kinase kinase kinase 8 - MAP3K8; hypothetical protein LOC285286 - LOC285286; IBR domain containing 2 - IBRDC2; chemokine (C-C motif) ligand 4 - CCL4; EH-domain containing 1 EHD1; nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) - NFKB2; solute carrier family 39 (zinc transporter), member 8 - SLC39A8; reticulon 2 - RTN2; nibrin – NBN; orosomucoid 1 /// orosomucoid 2 - ORM1 /// ORM2; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 - SLC11A2; RNA binding motif, single stranded interacting protein 1 - RBMS1; thrombospondin 1 - THBS1; nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) - NFKB2; hypothetical protein LOC253842 - LOC253842; interleukin-1 receptor-associated kinase 3 - IRAK3; immediate early response 5 - IER5; EH-domain containing 1 - EHD1; CDNA clone IMAGE:30408657; nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha – NFKBIA; EH-domain containing 1 - EHD1; hypoxia-inducible protein 2 - HIG2; prostaglandin E synthase – PTGES; pleiomorphic adenoma gene-like 2 - PLAGL2; IBR domain containing 2 - IBRDC2; CDNA FLJ13601 fis, clone PLACE1010069; thrombospondin 1 - THBS1; antizyme inhibitor 1 - AZIN1; ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1 - ATP6V1C1; stannin – SNN; immediate early response 3 - IER3; ATG7 autophagy related 7 homolog (S. cerevisiae) - ATG7; v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian) – RELB; G protein-coupled receptor 157 - GPR157; oligodendrocyte transcription factor 1 /// similar to oligodendrocyte transcription factor 1 /// similar to oligodendrocyte transcription factor 1 - OLIG1;/// LOC728598 ///; LOC732056 – 6355; Thrombospondin 1 - THBS1

The TNFα genes from which the TNFα signature was derived included: C-type lectin domain family 4, member D - CLEC4D; DENN/MADD domain containing 4A - DENND4A; phosphoinositide-3-kinase adaptor protein 1 - PIK3AP1; interferon induced

with helicase C domain 1 - IFIH1; SAM domain, SH3 domain and nuclear localization signals 1 - SAMSN1; guanine nucleotide binding protein (G protein), gamma 2 - GNG2; Hypothetical protein LOC149478 - LOC149478; CDNA FLJ32866 fis, clone TESTI2003718; hypothetical protein LOC389072 - LOC389072; LIM domain kinase 2 - LIMK2; RNA binding motif, single stranded interacting protein 1 - RBMS1; hypothetical protein LOC731424 - LOC731424; cytoskeleton-associated protein 4 - CKAP4; acidic (leucine-rich) nuclear phosphoprotein 32 family, member A - ANP32A; solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 - SLC7A5; influenza virus NS1A binding protein - IVNS1ABP; nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha – NFKBIA; chloride intracellular channel 4 - CLIC4; fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus) - FSCN1; interferon gamma receptor 2 (interferon gamma transducer 1) - IFNGR2; myristoylated alanine-rich protein kinase C substrate – MARCKS; early growth response 1 - EGR1; antizyme inhibitor 1 - AZIN1; LIM domain kinase 2 - LIMK2; guanylate binding protein 1, interferon-inducible, 67kDa /// guanylate binding protein 1, interferon-inducible, 67kDa - GBP1; tumor necrosis factor, alpha-induced protein 2 - TNFAIP2; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor - ICAM1; tumor necrosis factor, alpha-induced protein 3 - TNFAIP3; signal-regulatory protein alpha – SIRPA; nibrin – NBN; EPM2A (laforin) interacting protein 1 - EPM2AIP1; pleiomorphic adenoma gene-like 2 - PLAGL2; NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa - NDUFV2; ninjurin 1 - NINJ1; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 - SLC11A2; presenilin 1 (Alzheimer disease 3) - PSEN1; pleckstrin – PLEK; fasciculation and elongation protein zeta 1 (zygin I) - FEZ1; peptidase inhibitor 3, skin-derived (SKALP); nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon – NFKBIE; purinergic receptor P2X, ligand-gated ion channel, 4 - P2RX4; chemokine (C-C motif) ligand 4 - CCL4; GTP cyclohydrolase 1 (dopa-responsive dystonia) - GCH1; CD83 molecule - CD83; human immunodeficiency virus type I enhancer binding protein 1 - HIVEP1; Nedd4 binding protein 1 - N4BP1; nuclear factor (erythroid-derived 2)-like 3 - NFE2L3; transcription factor-like 5 (basic helix-loop-helix) - TCFL5; prostaglandin E receptor 4 (subtype EP4) - PTGER4; polo-like kinase 3 (Drosophila) - PLK3; adenosine A2a receptor - ADORA2A;

mitogen-activated protein kinase kinase kinase 8 - MAP3K8; orosomucoid 1 - ORM1; orosomucoid 1 /// orosomucoid 2 - ORM1 /// ORM2; chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine; CCL3 /// CCL3L1 /// CCL3L3 /// LOC728830 /// LOC730422; CD40 molecule, TNF receptor superfamily member 5 - CD40; v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian) – RELB; butyrophilin, subfamily 2, member A2 - BTN2A2; metal-regulatory transcription factor 1 - MTF1; activin A receptor, type IIA -ACVR2A; plasminogen activator, urokinase – PLAU; TNF receptor-associated factor 1 - TRAF1; tumor necrosis factor, alpha-induced protein 6 - TNFAIP6; influenza virus NS1A binding protein - IVNS1ABP; platelet-activating factor receptor – PTAFR; immunoglobulin superfamily, member 6 - IGSF6; hypothetical protein FLJ23556 - FLJ23556; transcription factor EC – TFEC; potassium inwardly-rectifying channel, subfamily J, member 2 - KCNJ2; purinergic receptor P2X, ligand-gated ion channel, 7 P2RX7 – 6811; egf-like module containing, mucin-like, hormone receptor-like 1 - EMR1; tumor necrosis factor (TNF superfamily, member 2) – TNF; TNFAIP3 interacting protein 1 - TNIP1; LIM and senescent cell antigen-like domains 1 - LIMS1; acyl-CoA synthetase long-chain family member 1 - ACSL1; nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) - NFKB2; presenilin 1 (Alzheimer disease 3) - PSEN1; CASP8 and FADD-like apoptosis regulato – CFLAR; EH-domain containing 1 - EHD1; nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) - NFKB1; solute carrier family 39 (zinc transporter), member 8 - SLC39A8; CASP8 and FADD-like apoptosis regulator /// CASP8 and FADD-like apoptosis regulator – CFLAR; receptor-interacting serine-threonine kinase 2 - RIPK2; nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) - NFKB2; serpin peptidase inhibitor, clade B (ovalbumin), member 9 - SERPINB9; complement component 3a receptor 1 - C3AR1; CASP8 and FADD-like apoptosis regulator – CFLAR; villin-like – VILL; G protein-coupled receptor 35 - GPR35; prostaglandin E synthase – PTGES; baculoviral IAP repeat-containing 3 - BIRC3; CASP8 and FADD-like apoptosis regulator – CFLAR; LIM domain kinase 2 - LIMK2; leukocyte-associated immunoglobulin-like receptor 1 - LAIR1; fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus) - FSCN1; kynurenine 3-monooxygenase (kynurenine 3-

hydroxylase) – KMO; phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) - PDE4B; Fc fragment of IgA, receptor for – FCAR; CASP8 and FADD-like apoptosis regulator – CFLAR; chemokine (C-C motif) receptor-like 2 /// similar to chemokine (C-C motif) receptor-like 2 - CCRL2 /// LOC727811; platelet-activating factor receptor /// platelet-activating factor receptor – PTAFR; plasminogen activator, urokinase /// plasminogen activator, urokinase – PLAU; CASP8 and FADD-like apoptosis regulator – CFLAR; antizyme inhibitor 1 - AZIN1; RAB6 interacting protein 1 - RAB6IP1; interleukin 1 receptor antagonist - IL1RN; transcription factor 7-like 2 (T-cell specific, HMG-box) - TCF7L2; SEC24 related gene family, member A (S. cerevisiae) - SEC24A; Myristoylated alanine-rich protein kinase C substrate – MARCKS; IBR domain containing 3 - IBRDC3; membrane-associated ring finger (C3HC4); G0/G1switch 2 - G0S2; CDNA FLJ13601 fis, clone PLACE1010069; CDC42 effector protein (Rho GTPase binding) 2 - CDC42EP2; CASP8 and FADD-like apoptosis regulator – CFLAR; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor - ICAM1; Dmx-like 2 - DMXL2; glycerol kinase – GK; NLR family, pyrin domain containing 3 - NLRP3; transcription factor 7-like 2 (T-cell specific, HMG-box) - TCF7L2; CD44 molecule (Indian blood group) - CD44; interleukin 1 receptor antagonist - IL1RN; superoxide dismutase 2, mitochondrial - SOD2; CD58 molecule - CD58; nibrin – NBN; kynureninase (L-kynurenine hydrolase) – KYNU; LIM domain kinase 2 - LIMK2; bromodomain adjacent to zinc finger domain, 1A - BAZ1A; stannin – SNN; damage-regulated autophagy modulator – DRAM; pleckstrin homology domain containing, family F (with FYVE domain) member 2 - PLEKHF2; SLAM family member 7 - SLAMF7; solute carrier family 15, member 3 - SLC15A3; C-type lectin domain family 4, member E - CLEC4E; solute carrier family 39 (zinc transporter), member 8 - SLC39A8; proline-serine-threonine phosphatase interacting protein 2 - PSTPIP2; interleukin-1 receptor-associated kinase 3 - IRAK3; solute carrier family 2 (facilitated glucose transporter), member 6 - SLC2A6; SAM domain, SH3 domain and nuclear localization signals 1 - SAMSN1; Jun dimerization protein p21SNFT – SNFT; ureidopropionase, beta - UPB1; apolipoprotein L, 3 - APOL3; FLJ12886; free fatty acid receptor 2 - FFAR2; free fatty acid receptor 3 /// G protein-coupled receptor 42 /// similar to Free fatty acid receptor 3 (G-protein coupled receptor 41) - FFAR3; UDP-

Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5 - B4GALT5; adducin 3 (gamma) /// chloride ; EH-domain containing 1 - EHD1; pleckstrin homology domain containing, family F (with FYVE domain) member 2 - PLEKHF2; SLAM family member 7 - SLAMF7; C-type lectin domain family 4, member E - CLEC4E; chromosome 15 open reading frame 48 - C15orf48; G protein-coupled receptor 84 - GPR84; CD274 molecule - CD274 ureidopropionase, beta - UPB1; solute carrier family 35, member B - SLC35B2; GRAM domain containing 1A - GRAMD1A; tumor protein p53 inducible nuclear protein 2 - TP53INP2; tubulin tyrosine ligase – TTL; guanine nucleotide binding protein (G protein), gamma 2 - GNG2; major facilitator superfamily domain containing 2 - MFSD2; Homo sapiens, clone IMAGE:5547644; Cdc42 GTPase-activating protein – CDGAP; TRAF-interacting protein with a forkhead-associated domain – TIFA; dehydrogenase/reductase (SDR family) member 13 - DHRS13; Splicing factor 3a, subunit 2, 66kDa - SF3A2; ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1 - ATP6V1C1; Bcl2 modifying factor BMF; metal-regulatory transcription factor 1 - MTF1; Early growth response 1 - EGR1; EPM2A (laforin) interacting protein 1 - EPM2AIP1; hypothetical protein MGC7036 - MGC7036; IBR domain containing 2 - IBRDC2; oligodendrocyte transcription factor 1 /// similar to oligodendrocyte transcription factor 1 /// similar to oligodendrocyte transcription factor 1 - OLIG1; ureidopropionase, beta - UPB1; Mitogen-activated protein kinase 10 - MAPK10; Baculoviral IAP repeat-containing 3 - BIRC3; Full length insert cDNA clone YX74D05; Formin-like 3 - FMNL3; interleukin 4 induced 1 - IL4I1; guanylate binding protein 1, interferon-inducible, 67kDa - GBP1; interleukin-1 receptor-associated kinase 2 - IRAK2; zinc finger CCCH-type containing 12C - ZC3H12C; Homo sapiens, clone IMAGE:; Transcription factor 7-like 2 (T-cell specific, HMG-box) - TCF7L2; SLAM family member 7 - SLAMF7; TNF receptor-associated factor 1 - TRAF1; CDNA clone IMAGE:6254031; Mitogen-activated protein kinase kinase kinase 8 - MAP3K8; chromosome 8 open reading frame 38 - C8orf38; IBR domain containing 2 - IBRDC2; CDNA clone IMAGE:5270500; Hypothetical gene supported by BC008048 - LOC440934; IBR domain containing 2 - IBRDC2; dedicator of cytokinesis 4 - DOCK4; Nedd4 binding protein 1 - N4BP1; peptidase inhibitor 3, skin-derived (SKALP) - PI3

The IL4 genes from which the IL4 signature was derived included: the genes listed and annotated on figures 11-104

The IL10 genes from which the IL10 signature was derived included: the genes listed and annotated on figures 105-158.

The IL13 gene from which the IL13 signature was derived included: the genes listed and annotated on figures 159-234.

Results: In agreement with the results described in Example 1d, the IFNα/β-inducible gene signature score of DM and PM patients in this set of patients was able to predict disease stability, improvement, and relapse. Figure 2a shows that the IFNα/β-inducible gene signature of DM and PM patients is higher in those with active disease relative to those that are improving. Figure 2b provides the IFNα/β-inducible gene signature of individual DM patients in paired samples, one obtained during active disease and one obtained during disease improvement. The IFNα/β-inducible gene signature of DM patients decreased as the DM patients exhibited disease improvement. Figure 3 provides the IFNα/β-inducible gene signature in whole blood of three other DM patients that showed clinical improvement over the course of two visits with a physician. For each of the three patients ((a), (b), and (c)) the IFNα/β-inducible gene signature deceased as the patient clinically improved. This correlation of cytokine gene signature score with clinical improvement was not observed for other cytokine gene signatures (TNFα, IL1β, IL4, IL10, or IL13). Figure 4 provides changes in the IFNα/β-inducible gene signature of a DM patient. The IFNα/β-inducible gene signature increases as the patient's condition worsens clinically and decreases as the patient's condition improves clinically. Figure 5 furthers show correlation of IFNα/β-inducible gene signature and serum CK level in a PM patient. Figures 6 and 7 show correlation of clinical disease, serum CK activity, and IFNα/β-inducible gene signature in a DM patient. Figure 6 provides the tight correlation between the IFNα/β-inducible gene signature and serum CK activity. Figure 7 further correlates the IFNα/β-inducible gene signature and clinical disease course of the patient.

Example 2b: TNF-α, IL-1β, GM-CSF, IL-10, and IL-13 signaling pathways are activated in DM and PM patients, but not correlated with disease activity

Similar to as described in Example 1d, the whole genome array approach was again used to evaluate the potential effects of cytokines, TNF-α, IL-1β, IL-10, IL-13 and

GM-CSF, that might play a role in DM and PM pathogenesis. Figure 388a shows the composite cytokine-inducible gene signature scores for TNF-α, IL-1β, IL-10, IL-13 and GM-CSF, respectively, in WB of 36 healthy normal controls, and in DM and PM patients with low and high disease activity (patients discussed in Examples 1b – 1d). The cytokine-inducible genes signature scores of type 1 IFN, GM-CSF, IL-10, IL-13, IL-1β, and TNF-α were calculated as described (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008;Volume 2009, Article ID 374312, doi:10.4061/2009/374312; Yao, Y, Jallal J, et al. Neutralization of IFN-α/β–Inducible Genes and Downstream Effect in a Phase I Trial of an Anti–IFN-α Monoclonal Antibody in SLE. Accepted by Arthritis Rheum.). The DM and PM patients were classified into type I IFN-inducible gene signature weak, moderate, and high scores as described (Yao, Y, Jallal J, et al. Development of Potential Pharmacodynamic and Diagnostic Markers for Anti-IFN-α Monoclonal Antibody Trials in Systemic Lupus Erythematosus. Human Genomics and Proteomics. 2008; Volume 2009, Article ID 374312, doi:10.4061/2009/374312). Between the controls and the patients with either low or high disease activity, all differences between TNF-α, IL-1β, IL-10, IL-13 and GM-CSF inducible gene signature scores in WB were statistically significant, after adjustment for multiple comparisons (Table 8). This suggested that all of these cytokine signaling pathways were activated in the blood of these patients. TaqMan QRT-PCR also confirmed the overexpression of mRNAs of these cytokines in the muscle biopsies of PM, and to a lesser degree, DM patients (not shown). However, none of these cytokine-inducible gene signature scores showed any statistically significant difference between patients with low and high disease activity (Table 8). Furthermore, for 18 patients with changes in disease activity during the study, none of these cytokine-inducible gene signature scores changed in the concordant direction (Figure 388b). For the 3 patients for whom the level of disease activity never changed throughout their treatment, no significant changes in these cytokine-inducible gene signature scores were observed (Figure 388c).

Figure 389 shows the cytokine-inducible gene signature scores of all 24 patients stratified by high disease and low disease activity. Suppression of type 1 IFN-inducible

genes was universal for patients who showed improvement in disease activity while it was not the case for the TNF-α, IL-1β, IL-10, IL-13 and GM-CSF inducible gene signatures.

Example 3: IFNα/β-inducible gene signature is overexpressed in IBM patient muscle and whole blood samples

It was also determined that the IFNα/β-inducible gene signature is overexpressed in IBM patient muscle and whole blood samples.

Total RNA extraction and microarray processing: Total RNA was extracted from PAXgene blood and muscle biopsies using the PAXgene Blood RNA kit and the Qiagen RNeasy Fibrous Tissue Mini (Hilden, Germany), respectively. RNA purity and concentration were determined spectrophotometrically (260/280 > 1.9). RNA quality was assessed on an Agilent 2100 Bioanalyzer using the RNA 6000 Nano LabChip®.

Generation of biotin-labeled amplified cRNA, from 2ug of total RNA, was accomplished with the Affymetrix GeneChip® One-Cycle cDNA Synthesis kit and the Affymetrix GeneChip® IVT Labeling kit. Concentration and purity of the cRNA product were determined spectrophotometrically. Twenty micrograms of each biotin-labeled cRNA was fragmented for hybridization on Affymetrix Human Genome U133 Plus 2.0 GeneChip® arrays. Fragmented cRNA was prepared for hybridization as outlined in the Affymetrix GeneChip® manual. Hybridization was conducted overnight in a model 320 rotating hybridization oven set at 45°C. All GeneChip® wash and staining procedures were performed on an Affymetrix Model 450 Fluidics station. Arrays were scanned on an Affymetrix GeneChip® Scanner 3000. Data capture and initial array quality assessment were performed with the GeneChip Operating Software (GCOS) tool.

Calculation of gene signature using static list of 21 genes: The 21 genes within this list were identified by their prevalence and magnitude of overexpression in Myositis patients as compared to those of normal controls. It includes a standard list of the same 21 genes (i.e. 21 probes that map to 21 unique genes) for each Myositis patient. These 21 genes were DNAPTP6; EPSTI1; HERC5; IFI27; IFI44; IFI44L; IFI6; IFIT1; IFIT3; ISG15; LAMP3; LY6E; MX1; OAS1; OAS2; OAS3; PLSCR1; RSAD2; RTP4; SIGLEC1; and USP18. The fold change is calculated between Myositis patients at day 0 (predose) and the average of 24 normal healthy controls. The median of these 21 fold

change values is then computed for each Myositis patient and this value is used as the IFN-α/β-inducible gene signature score.

Calculation of gene signature using the dynamic list of 25 genes: For each patient, a dynamic list of the top 25 genes (determined by fold change value) is selected from a set of 807 probes previously found to be IFN-α/β–inducible and neutralized by MEDI-545. See Figures 235-381 These 25 genes are chosen by their fold change magnitude and all represent a unique known gene (for genes that are represented by multiple probes, the one that showed the highest fold change was used for the purpose). The fold change is calculated between Myositis patients at day 0 (predose) and the average of 24 normal healthy controls. The median of these 25 fold change values is then computed for each Myositis patient and this value is used as the IFN-α/β-inducible gene signature score.

Results: Table 1 shows that the IFNα/β-inducible gene signature is overexpressed in IBM patient muscle whether calculated using a static list of 21 genes or a dynamic list of 25 genes. Figure 8 provides a scatter plot which illustrates the overexpression of the IFNα/β-inducible gene signature in muscle tissue of the individual IBM patients shown in

Table 1.

Table 1: Overexpression of IFN-α/β-inducible gene signature in IBM patient muscle specimens

Sample	ID	IFNab.med.fc (25 genes)	IFNab.med.fc (21 genes)
IBM	MA45_GEIM18	29.49	4.48
IBM	MA45_GEIM127	16.56	3.37
IBM vs PM	MA45_GEIM323	26.09	7.07
IBM	MA45_GEIM335	15.24	3.57
IBM	MA45_GEIM354	27.11	5.49
IBM-HIV	MA45_GEIM358	6.74	3.13
IBM	MA45_GEIM363	58.73	7.14
IBM	MA45_GEIM366	8.14	2.86
IBM	MA45_GEIM372	53.50	11.16
IBM	MA45_GEIM373	21.65	4.85
IBM	MA45_GEIM374	33.71	5.47
IBM	MA45_GEIM377	48.42	6.20
IBM	MA45_GEIM380	25.23	4.24
IBM	MA45_GEIM397	10.00	3.01

Whole blood of IBM patients was also examined to determine whether overexpression of the IFNα/β-inducible gene signature could be detected. Using a dynamic list of 25 genes to detect the IFNα/β-inducible gene signature in the samples, overexpression of the IFNα/β-inducible gene signature could be detected in IBM whole blood. See Figure 9a for the IFNα/β-inducible gene signature scores of 9 IBM patient whole blood samples and Figure 9b for a scatter plot illustrating the IFNα/β-inducible gene signature score of the individual IBM patients.

Example 4: The IFNα/β-inducible gene signature is more elevated in muscle of $Jo1^-$ than $Jo1^+$ DM patients

Overexpression of the IFNα/β-inducible gene signature is greater in muscle of $Jo1^-$ than $Jo1^+$ DM patients.

Total RNA extraction and microarray processing: Total RNA was extracted from PAXgene muscle biopsies using the the Qiagen RNeasy Fibrous Tissue Mini (Hilden, Germany). RNA purity and concentration were determined spectrophotometrically (260/280 > 1.9). RNA quality was assessed on an Agilent 2100 Bioanalyzer using the RNA 6000 Nano LabChip®.

Generation of biotin-labeled amplified cRNA, from 2ug of total RNA, was accomplished with the Affymetrix GeneChip® One-Cycle cDNA Synthesis kit and the Affymetrix GeneChip® IVT Labeling kit. Concentration and purity of the cRNA product were determined spectrophotometrically. Twenty micrograms of each biotin-labeled cRNA was fragmented for hybridization on Affymetrix Human Genome U133 Plus 2.0 GeneChip® arrays. Fragmented cRNA was prepared for hybridization as outlined in the Affymetrix GeneChip® manual. Hybridization was conducted overnight in a model 320 rotating hybridization oven set at 45°C. All GeneChip® wash and staining procedures were performed on an Affymetrix Model 450 Fluidics station. Arrays were scanned on an Affymetrix GeneChip® Scanner 3000. Data capture and initial array quality assessment were performed with the GeneChip Operating Software (GCOS) tool.

Calculation of gene signature using static list of 19 genes: The 19 genes within this list were identified by their prevalence and magnitude of overexpression in Myositis patients as compared to those of normal controls. The same 19 genes (i.e. 19 probes that map to 19 unique genes) were used for each myositis patient. The 19 genes included

EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, RSAD2, RTP4, SIGLEC1, and USP18. The fold change is calculated between myositis patients at day 0 (predose) and the average of 24 normal healthy controls. The median of these 19 fold change values is then computed for each

Results: Figure 10a provides the median-fold overexpression of the each of the 19 genes included in the IFNα/β-inducible gene signature and the overall median-fold change in IFNα/β-inducible gene signature for each of 10 IBM patient muscle samples. Figure 10b provides a scatter plot which illustrates the overexpression of the IFNα/β-inducible gene signature in muscle tissue of each individual IBM patient shown in Figure 10a. While the IFNα/β-inducible gene signature was over-expressed in muscle samples of both the $Jo1^-$ and $Jo1^+$ patients, overexpression was greater in muscle samples of $Jo1^-$ patients.

Example 5: miRNAs are differentially regulated in myositis patient muscle tissue relative to healthy donor muscle tissue

miRNA levels in muscle tissue were measured in samples obtained from 8 healthy donors, 11 DM patients, and 10 IBM patients.

Sample processing: Muscle tissue samples were processed with the *mir*Vana miRNA Isolation Kit (Ambion, Inc., Austin, TX) following the manufacturers suggested protocol. Concentration and purity (260/280 nm) of each sample was determined spectrophotometrically. Sample quality was assessed by Agilent 2100 Bioanalyzer (Agilent Technologies, Inc., Santa Clara, CA) analysis.

Multiplex RT for TaqMan Array Human MicroRNA Panel (Applied Biosystems, Foster City, CA): Processed RNA samples were normalized to a concentration of 25 ng/μL. 4 μL of each normalized RNA sample was transferred to individual wells of an eight-tube microtube strip (4 μL x 8) that had been placed on ice. 5 μL ice cold RT master mix was added to well containing the 4 μL of normalized RNA. Each 5 μL RT master mix contained 0.2 μL 100 mM dNTPs, 2.0 μL MultiScribe Reverse Transcriptase (50 U/mL), 1.0 μL 10X Reverse Transcription Buffer, 0.125 μL RNase Inhibitor (20 U/μL), and 1.675 μL Nuclease-free water that had been prepared on ice. A 1 μL volume of a Multiplex RT human primer pool (one of each of primer pools #1-8) was added to a corresponding microtube (microtubes 1-8)), resulting in a total of eight independent RT

reactions per RNA sample. The microtubes were capped, mixed gently and centrifuged briefly. All reaction samples were then incubated on ice for at least 5 minutes prior to conducting the cDNA synthesis protocol.

The cDNA synthesis procedure was conducted in a Bio-Rad (Hercules, CA) Tetrad thermal cycler using the following profile: 16°C for 30 minutes, 42°C for 30 minutes, 85°C for 5 minutes, 4°C-hold. After completion of the cDNA synthesis reaction, all sample volumes (10 μL) were transferred to individual 1.5 mL microcentrifuge tubes and diluted 62.5-fold by adding 615 μL nuclease-free water. All samples were kept on ice until further processing.

TaqMan Low-Density Array: In preparation for analysis on the Human MicroRNA Panel TaqMan Low-Density Array (TLDA) (Applied Biosystems, Foster City, CA), 50 μL diluted RT reaction and 50 μL TaqMan Universal PCR Master Mix (2X) (Applied Biosystems, Foster City, CA) were combined in individual 1.5 mL microcentrifuge tubes. The sample tubes were capped, mixed gently and centrifuged briefly. Standard procedures for loading the array were followed and the array was run on a 7900HT Fast Real-Time PCR System (Applied Biosystems, Foster City, CA). Data analysis of the resulting Ct values was conducted with SDSv2.2.2 software (Applied Biosystems, Foster City, CA).

Results: miRNAs were differentially regulated in muscle of both DM and IBM patients. See Tables 2-5. Unique detector Ids, miRNA ids, and sequences are provided in Figure sheets

Table 2: Differentially up-regulated miRNAs in DM patient muscle specimens

Detector	p value	fold change
hsa-miR-21-4373090	0.042	2.141
hsa-miR-34b-4373037	0.046	34.091
hsa-miR-382-4373019	0.024	2.07

Table 3: Differentially down-regulated miRNAs in DM patient muscle specimens

Detector	p value	fold change
hsa-miR-1-4373161	0.022	0.413
hsa-miR-100-4373160	0.023	0.47
hsa-miR-101-4373159	0	0.381
hsa-miR-128b-4373170	0.012	0.287

hsa-miR-133a-4373142	0	0.225
hsa-miR-133b-4373172	0.006	0.471
hsa-miR-181c-4373115	0.019	0.407
hsa-miR-186-4373112	0.012	0.468
hsa-miR-193b-4373185	0.004	0.294
hsa-miR-22-4373079	0.007	0.445
hsa-miR-23a-4373074	0.008	0.494
hsa-miR-23b-4373073	0.016	0.374
hsa-miR-26b-4373069	0.038	0.491
hsa-miR-27a-4373287	0.008	0.384
hsa-miR-27b-4373068	0.013	0.253
hsa-miR-296-4373066	0.002	0.327
hsa-miR-29a-4373065	0.002	0.435
hsa-miR-29c-4373289	0	0.399
hsa-miR-30a-3p-4373062	0.029	0.402
hsa-miR-30a-5p-4373061	0.01	0.398
hsa-miR-30b-4373290	0.005	0.407
hsa-miR-30c-4373060	0.006	0.344
hsa-miR-30d-4373059	0.004	0.395
hsa-miR-30e-3p-4373057	0.011	0.331
hsa-miR-30e-5p-4373058	0.032	0.36
hsa-miR-324-5p-4373052	0.002	0.446
hsa-miR-328-4373049	0.032	0.436
hsa-miR-331-4373046	0.025	0.471
hsa-miR-340-4373041	0	0.445
hsa-miR-361-4373035	0.001	0.371
hsa-miR-365-4373194	0	0.304
hsa-miR-378-4373024	0.004	0.227
hsa-miR-422a-4373200	0.004	0.306
hsa-miR-423-4373015	0.031	0.416
hsa-miR-489-4373214	0.015	0.307
hsa-miR-491-4373216	0	0.384
hsa-miR-504-4373229	0.031	0.293
hsa-miR-518e-4373265	0.033	0.236
hsa-miR-594-4380958	0.047	0.442
hsa-miR-99a-4373008	0.016	0.445

Table 4: Differentially up-regulated miRNAs in IBM patient muscle specimens

Detector	**p value**	**fold change**
hsa-miR-127-4373147	0.001343696	2.383908732
hsa-miR-132-4373143	0.016749924	2.309908878
hsa-miR-146a-4373132	4.77E-05	6.948265587

hsa-miR-155-4373124	0.018655052	12.97376751
hsa-miR-21-4373090	0.000174951	2.970268559
hsa-miR-214-4373085	0.012834402	2.089563254
hsa-miR-221-4373077	0.000213444	4.590059735
hsa-miR-222-4373076	5.61E-05	2.156256092
hsa-miR-299-5p-4373188	0.002824631	3.814890525
hsa-miR-31-4373190	0.011811928	4.216344588
hsa-miR-323-4373054	0.005094215	4.026315243
hsa-miR-34a-4373278	0.026043587	3.074758212
hsa-miR-34b-4373037	0.006396276	47.2379796
hsa-miR-376a-4378104	0.027686874	2.592096707
hsa-miR-382-4373019	6.05E-05	3.002877696
hsa-miR-411-4381013	0.002347682	2.735004685
hsa-miR-432-4373280	0.009111595	4.007329367
hsa-miR-433-4373205	0.001574922	2.996897264
hsa-miR-511-4373236	0.000664051	4.444594072

Table 5: Differentially down-regulated miRNAs in IBM patient muscle specimens

Detector	**p value**	**fold change**
hsa-let-7a-4373169	0.000261495	0.461940063
hsa-let-7d-4373166	0.000519994	0.449301892
hsa-let-7f-4373164	0.004942999	0.275220876
hsa-let-7g-4373163	0.003108841	0.479827561
hsa-miR-1-4373161	0.0089026	0.151102573
hsa-miR-101-4373159	4.99E-06	0.242569835
hsa-miR-126-4373269	0.042276687	0.45132497
hsa-miR-128b-4373170	0.014270087	0.160708669
hsa-miR-133a-4373142	5.99E-05	0.200538744
hsa-miR-133b-4373172	2.25E-08	0.238646208
hsa-miR-181c-4373115	0.019419918	0.420494392
hsa-miR-186-4373112	0.016570765	0.488720432
hsa-miR-190-4373110	0.011508084	0.366253183
hsa-miR-193b-4373185	0.005790023	0.19249679
hsa-miR-196b-4373103	0.024105127	0.375328485
hsa-miR-197-4373102	0.022613224	0.479233993
hsa-miR-19a-4373099	0.042678905	0.45412976
hsa-miR-20a-4373286	0.009776077	0.4466972
hsa-miR-22-4373079	0.004224752	0.263087054
hsa-miR-23b-4373073	0.0146826	0.359600816
hsa-miR-26a-4373070	0.005930571	0.39550998
hsa-miR-26b-4373069	0.033096249	0.443882937
hsa-miR-27b-4373068	0.015743098	0.297783418
hsa-miR-296-4373066	0.001194699	0.298589928

hsa-miR-29a-4373065	0.001349097	0.336664818
hsa-miR-29c-4373289	2.52E-09	0.238818173
hsa-miR-30a-3p-4373062	0.017730482	0.229143827
hsa-miR-30a-5p-4373061	0.006268296	0.257975023
hsa-miR-30b-4373290	0.004246722	0.274619234
hsa-miR-30c-4373060	0.005198547	0.281971024
hsa-miR-30d-4373059	0.002285223	0.241803139
hsa-miR-30e-3p-4373057	0.010367212	0.2350075
hsa-miR-30e-5p-4373058	0.020271038	0.244720048
hsa-miR-32-4373056	0.019282796	0.385941654
hsa-miR-328-4373049	0.022423378	0.370315868
hsa-miR-331-4373046	0.016552922	0.372139854
hsa-miR-340-4373041	5.05E-05	0.441742765
hsa-miR-345-4373039	0.04317298	0.422795116
hsa-miR-361-4373035	0.002496089	0.377110989
hsa-miR-365-4373194	0.000215304	0.21743854
hsa-miR-374-4373028	0.042460027	0.4973205
hsa-miR-378-4373024	0.003719421	0.233224009
hsa-miR-422a-4373200	0.003828686	0.171239493
hsa-miR-423-4373015	0.022144073	0.35633136
hsa-miR-486-4378096	0.01445536	0.345595073
hsa-miR-491-4373216	6.63E-06	0.34787378
hsa-miR-504-4373229	0.027141237	0.237911164
hsa-miR-518e-4373265	0.030022387	0.147803021
hsa-miR-594-4380958	0.022205513	0.250995551
hsa-miR-616-4380992	0.043443863	0.235726158
hsa-miR-92-4373013	0.041324118	0.347364092
hsa-miR-95-4373011	0.00098202	0.187541196
hsa-miR-98-4373009	0.004874227	0.322319097
hsa-miR-99a-4373008	0.026616112	0.499299362

Owing to this differential regulation, miRNAs may be useful in the diagnosis, prognosis, treatment, and/or stratification of myositis patients.

WE CLAIM:

1. A method of treating a patient having a type I IFN or an IFNα-mediated disease or disorder comprising:

administering an agent that binds to and modulates type I IFN or IFNα activity;

wherein the patient comprises a differentially regulated miRNA marker profile; and

wherein the agent neutralizes the diff erentially regulated miRNA marker profile of the patient.

2. The method of claim 1 further comprising detecting neutralization of the differentially regulated miRNA marker profile of the patient.

3. The method of claim 1 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 2 or 4.

4. The method of claim 3 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 2 or 4.

5. The method of claim 4 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 2 or 4.

6. The method of claim 5 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 2 or 4.

7. The method of claim 6 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 2 or 4.

8. The method of claim 3 wherein the at least one of the miRNAs is detected by the detector hsa-miR-34b-4373037.

9. The method of claim 1 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

10. The method of claim 9 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

11. The method of claim 10 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

12. The method of claim 11 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

13. The method of claim 12 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

14. The method of claim 9 wherein the at least one of the miRNAs is detected by the detector hsa-miR-1-4373161.

15. The method of claim 3 wherein the differentially regulated miRNA marker profile further comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

16. The method of claim 15 wherein the down-regulated expression or activity is of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

17. The method of claim 16 wherein the down-regulated expression or activity is of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

18. The method of claim 17 wherein the down-regulated expression or activity is of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

19. The method of claim 18 wherein the down-regulated expression or activity is of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

20. The method of claim 15 wherein the at least one of the miRNAs detected by the detectors identified in Tables 3 or 5 is hsa-miR-1-4373161.

21. The method of claim 1 wherein the agent is a biologic agent.

22. The method of claim 21 wherein the agent is an antibody.

23. The method of claim 22 wherein the antibody is MEDI-545.

24. The method of claim 22 wherein the antibody is specific for one or more type I IFN or IFNα subtype but is not MEDI-545.

25. The method of claim 1 wherein the administering the agent alleviates one or more symptoms of the disease or disorder.

26. The method of claim 22 wherein the antibody is administered at a dose between approximately .03 and 30 mg/kg.

27. The method of claim 26 wherein the antibody is administered at a dose between 0.3 and 3 mg/kg.

28. The method of claim 27 wherein the antibody is administered at a dose between .03 and 1 mg/kg.

29. The method of any one of claims 21 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 10%.

30. The method of claim 29 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 20%.

31. The method of claim 30 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 30%.

32. The method of claim 31 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 40%.

33. The method of claim 32 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 50%.

34. The method of claim 1 wherein the disease or disorder is one of lupus, psoriasis, vasculitis, sarcoidosis, Sjogren's syndrome, or myositis.

35. The method of claim 34 wherein the disease or disorder is myositis.

36. The method of claim 1 wherein the patient further comprises up-regulated expression or activity of at least IFNα subtypes 1, 2, 8, and 14.

37. The method of claim 2 wherein the differentially regulated miRNA marker profile is detected in whole blood of the patient.

38. The method of claim 2 wherein the differentially regulated miRNA marker profile is detected in muscle tissue of the patient.

39. The method of claim 1 wherein the differentially regulated miRNA marker profile is strong or moderate.

40. A method of neutralizing a differentially regulated miRNA marker profile in a patient in need thereof, comprising:

administering an agent that binds to and modulates type I IFN or IFNα activity to the patient;

wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient.

41. The method of claim 40 further comprising detecting neutralization of the differentially regulated miRNA marker profile of the patient.

42. The method of claim 40 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 2 or 4.

43. The method of claim 42 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 2 or 4.

44. The method of claim 43 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 2 or 4.

45. The method of claim 44 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 2 or 4.

46. The method of claim 45 wherein the differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 2 or 4.

47. The method of claim 42 wherein the at least one of the miRNAs is detected by the detector hsa-miR-34b-4373037.

48. The method of claim 40 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

49. The method of claim 48 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

50. The method of claim 49 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

51. The method of claim 50 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

52. The method of claim 51 wherein the differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

53. The method of claim 48 wherein the at least one of the miRNAs is detected by the detector hsa-miR-1-4373161.

54. The method of claim 42 wherein the differentially regulated miRNA marker profile further comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

55. The method of claim 54 wherein the down-regulated expression or activity is of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

56. The method of claim 55 wherein the down-regulated expression or activity is of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

57. The method of claim 56 wherein the down-regulated expression or activity is of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

58. The method of claim 57 wherein the down-regulated expression or activity is of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

59. The method of claim 54 wherein the at least one of the miRNAs detected by the detectors identified in Tables 3 or 5 is hsa-miR-1-4373161.

60. The method of claim 40 wherein the agent is a biologic agent.

61. The method of claim 60 wherein the agent is an antibody.

62. The method of claim 61 wherein the antibody is MEDI-545.

63. The method of claim 61 wherein the antibody is specific for one or more type I IFN or IFNα subtype but is not MEDI-545.

64. The method of claim 40 wherein the administering the agent alleviates one or more symptoms of the disease or disorder.

65. The method of claim 61 wherein the antibody is administered at a dose between approximately .03 and 30 mg/kg.

66. The method of claim 65 wherein the antibody is administered at a dose between 0.3 and 3 mg/kg.

67. The method of claim 66 wherein the antibody is administered at a dose between .03 and 1 mg/kg.

68. The method of claim 40 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 10%.

69. The method of claim 68 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 20%.

70. The method of claim 69 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 30%.

71. The method of claim 70 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 40%.

72. The method of claim 71 wherein the agent neutralizes the differentially regulated miRNA marker profile of the patient by at least 50%.

73. The method of claim 40 wherein the patient has been diagnosed with one of lupus, psoriasis, vasculitis, sarcoidosis, Sjogren's syndrome, or myositis.

74. The method of claim 73 wherein the patient has been diagnosed with myositis.

75. The method of claim 40 wherein the patient further comprises up-regulated expression or activity of at least IFNα subtypes 1, 2, 8, and 14.

76. The method of claim 41 wherein the differentially regulated miRNA marker profile is detected in whole blood of the patient.

77. The method of claim 41 wherein the differentially regulated miRNA marker profile is detected in muscle tissue of the patient.

78. The method of claim 40 wherein the differentially regulated miRNA marker profile is strong or moderate.

79. A method of monitoring or prognosing an inflammatory disease progression of a patient comprising:

obtaining a first differentially regulated miRNA marker profile in a first sample from a patient.

80. The method of claim 79 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 2 or 4.

81. The method of claim 80 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 2 or 4.

82. The method of claim 81 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 2 or 4.

83. The method of claim 82 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 2 or 4.

84. The method of claim 83 wherein the first differentially regulated miRNA marker profile comprises up-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 2 or 4.

85. The method of claim 80 wherein the at least one of the miRNAs is detected by the detector hsa-miR-34b-4373037.

86. The method of claim 79 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

87. The method of claim 86 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

88. The method of claim 87 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

89. The method of claim 88 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

90. The method of claim 89 wherein the first differentially regulated miRNA marker profile comprises down-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

91. The method of claim 86 wherein the at least one of the miRNAs is detected by the detector hsa-miR-1-4373161.

92. The method of claim 80 wherein the first differentially regulated miRNA marker profile further comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

93. The method of claim 92 wherein the down-regulated expression or activity is of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

94. The method of claim 93 wherein the down-regulated expression or activity is of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

95. The method of claim 94 wherein the down-regulated expression or activity is of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

96. The method of claim 95 wherein the down-regulated expression or activity is of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

97. The method of claim 92 wherein the at least one of the miRNAs detected by the detectors identified in Tables 3 or 5 is hsa-miR-1-4373161.

98. The method of claim 79 wherein the first first differentially regulated miRNA marker profile is a strong profile and the patient prognosis is disease progression.

99. The method of claim 98 wherein the strong profile comprises a differential expression of the miRNAs of at least 10-fold that of a healthy individual.

100. The method of claim 98 wherein the autoimmune disease is myositis.

101. The method of claim 79 wherein the first IFNα-inducible PD marker expression profile is a weak profile and the patient prognosis is disease regression.

102. The method of claim 101 wherein the weak profile comprises a differential expression of the miRNAs no more than 2-fold that of a healthy individual.

103. The method of claim 98 wherein the strong profile indicates to a physician to change disease treatment.

104. The method of claim 79 further comprising:

obtaining a second differentially regulated miRNA marker profile in a second sample from a patient;

wherein an increase in number or level of miRNA markers in the second relative to the first profile prognoses disease progression; or

wherein a decrease in number or level of miRNA markers in the second relative to the first profile prognoses disease regression.

105. A method of monitoring autoimmune or inflammatory disease progression of a patient receiving treatment with a therapeutic agent comprising:

obtaining a first miRNA profile in a first sample from the patient;

administering a therapeutic agent ;

obtaining a second miRNA profile in a second sample from the patient; and

comparing the first and the second miRNA profiles,

wherein a variance in the first and the second miRNA profiles indicates a level of efficacy of the therapeutic agent.

106. The method of claim 105 wherein the first miRNA profile comprises up-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 2 or 4.

107. The method of claim 106 wherein the first miRNA profile comprises up-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 2 or 4.

108. The method of claim 107 wherein the first miRNA profile comprises up-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 2 or 4.

109. The method of claim 108 wherein the first miRNA marker profile comprises up-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 2 or 4.

110. The method of claim 109 wherein the first miRNA profile comprises up-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 2 or 4.

111. The method of claim 106 wherein the at least one of the miRNAs is detected by the detector hsa-miR-34b-4373037.

112. The method of claim 105 wherein the first miRNA profile comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

113. The method of claim 112 wherein the first miRNA profile comprises down-regulated expression or activity of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

114. The method of claim 113 wherein the first miRNA profile comprises down-regulated expression or activity of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

115. The method of claim 114 wherein the first miRNA profile comprises down-regulated expression or activity of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

116. The method of claim 115 wherein the first miRNA profile comprises down-regulated expression or activity of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

117. The method of claim 112 wherein the at least one of the miRNAs is detected by the detector hsa-miR-1-4373161.

118. The method of claim 106 wherein the first miRNA profile further comprises down-regulated expression or activity of at least one of the miRNAs detected by the detectors identified in Tables 3 or 5.

119. The method of claim 118 wherein the down-regulated expression or activity is of at least two of the miRNAs detected by the detectors identified in Tables 3 or 5.

120. The method of claim 119 wherein the down-regulated expression or activity is of at least five of the miRNAs detected by the detectors identified in Tables 3 or 5.

121. The method of claim 120 wherein the down-regulated expression or activity is of at least ten of the miRNAs detected by the detectors identified in Tables 3 or 5.

122. The method of claim 121 wherein the down-regulated expression or activity is of at least fifteen of the miRNAs detected by the detectors identified in Tables 3 or 5.

123. The method of claim 118 wherein the at least one of the miRNAs detected by the detectors identified in Tables 3 or 5 is hsa-miR-1-4373161.

124. The method of claim 105 wherein the autoimmune or inflammatory disease is lupus, idiopathic inflammatory myositis, Sjogren's syndrome, vasculitis, sarcoidosis, or psoriasis.

125. The method of claim 124 wherein the autoimmune disease is idiopathic inflammatory myositis.

126. The method of claim 105 wherein the therapeutic agent is a small molecule or a biologic agent.

127. The method of claim 126 wherein the biologic agent is an antibody.

128. The method of claim 127 wherein the antibody is MEDI-545.

129. The method of claim 105 wherein the first miRNA profile is obtained prior to administration of the therapeutic agent.

130. The method of claim 105 wherein the first miRNA profile is obtained at the time of administration of the therapeutic agent.

131. The method of claim 105 wherein the first and the second sample are whole blood, muscle, or serum.

132. The method of claim 105 further comprising obtaining a third miRNA profile in a third sample from the patient.

133. The method of claim 132 further comprising obtaining a fourth miRNA profile in a fourth sample from the patient.

134. The method of claim 133 further comprising obtaining a fifth miRNA profile in a fifth sample from the patient.

135. The method of claim 134 further comprising obtaining a sixth miRNA profile in a sixth sample from the patient.

136. The method of claim 105 wherein the second sample is obtained at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following administration of the therapeutic agent.

137. The method of claim 132 wherein the third sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the second sample.

138. The method of claim 133 wherein the fourth sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the third sample.

139. The method of claim 134 wherein the fifth sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the fourth sample.

140. The method of claim 105 wherein variance is a decrease in differential miRNA levels of the patient relative to healthy levels.

141. The method of claim 105 wherein variance is an increase in differential miRNA levels of the patient relative to healthy levels.

142. The method of claim 141 wherein the increase in differential miRNA levels indicates poor disease prognosis or disease will flare.

143. The method of claim 141 wherein the increase in differential miRNA levels of the patients indicates a change in treatment of the patient.

144. A method of treating a myositis patient comprising:

administering an agent that binds to and modulates type I IFN or IFNα activity;

wherein the patient comprises a type I IFN or IFNα-inducible PD marker expression profile;

and wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient.

145. The method of claim 144 further comprising detecting neutralization of the type I IFN or IFNα-inducible PD marker expression profile of the patient.

146. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes MX1, LY6E, IFI27, OAS1 IFIT1, IFI6, IFI44L, ISG15, LAMP3, OASL, RSAD2, and IFI44.

147. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes LAMP3, SIGLEC1, DNAPTP6, IFIT2, ETV7, RTP4, SERPING1, HERC5, XAF1, MX1, EPSTI1, OAS2, OAS1, OAS3, IFIT3, IFI6, USP18, RSAD2, IFI44, LY6E, ISG15, and IFI27.

148. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, RSAD2, RTP4, SIGLEC1, and USP18

149. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes DNAPTP6, EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, PLSCR1, RSAD2, RTP4, SIGLEC1, and USP18.

150. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes SAMD9L, IFI6, IFI44, IFIT2, OAS1, IFI27, OAS3, IFI44L, HERC5, IFIT1, EPSTI1, ISG15, SERPING1, OASL, GBP1, and MX1.

151. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI6, RSAD2, IFI44, IFI44L, IFI27, MX1, IFIT1, ISG15, LAMP3, OAS3, OAS1, EPSTI1, IFIT3, OAS2, SIGLEC1, and USP18.

152. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI6, RSAD2, IFI44, IFI44L, and IFI27.

153. The method of claim 144 wherein the agent is a biologic agent.

154. The method of claim 153 wherein the agent is an antibody.

155. The method of claim 154 wherein the antibody is MEDI-545.

156. The method of claim 154 wherein the antibody is specific for one or more type I IFN or IFNα subtype but is not MEDI-545.

157. The method of claim 144 wherein the administering the agent alleviates one or more myositis symptoms.

158. The method of claim 154 wherein the antibody is administered at a dose between approximately .03 and 30 mg/kg.

159. The method of claim 158 wherein the antibody is administered at a dose between 0.3 and 3 mg/kg.

160. The method of claim 159 wherein the antibody is administered at a dose between .03 and 1 mg/kg.

161. The method of any one of claims 153-155 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 10%.

162. The method of claim 144 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 20%.

163. The method of claim 162 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 30%.

164. The method of claim 163 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 40%.

165. The method of claim 164 wherein the agent neutralizes the type I IFN or IFNα-inducible PD marker expression profile of the patient by at least 50%.

166. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of at least IFNα subtypes 1, 2, 8, and 14.

167. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises transcripts of PD marker genes.

168. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises polypeptides expressed from PD marker genes.

169. A method of monitoring or prognosing myositis disease progression of a patient comprising:

obtaining a first IFNα-inducible PD marker expression profile in a first sample from a patient.

170. The method of claim 169 wherein the first IFNα-inducible PD marker expression profile is a strong profile and the patient prognosis is myositis disease progression.

171. The method of claim 170 wherein the first IFNα-inducible PD marker expression profile comprises overexpression or activity of genes EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, RSAD2, RTP4, SIGLEC1, and USP18.

172. The method of claim 169 wherein the first IFNα-inducible PD marker expression profile is a weak profile and the patient prognosis is myositis disease regression.

173. The method of claim 169 further comprising:

obtaining a second IFNα-inducible PD marker expression profile in a second sample from the patient;

wherein an increase in number or level of type I IFN or IFNα inducible PD markers in the second relative to the first expression profile prognoses myositis disease progression; or

wherein a decrease in number or level of type I IFN or IFNα inducible PD markers in the second relative to the first expression profile prognoses myositis disease regression.

174. A method of monitoring myositis disease progression of a patient receiving treatment with a therapeutic agent comprising:

obtaining a first IFNα-inducible PD marker expression profile in a first sample from the patient;

administering a therapeutic agent;

obtaining a second IFNα-inducible PD marker expression profile in a second sample from the patient; and

comparing the first and the second IFNα-inducible PD marker expression profiles,

wherein a variance in the first and the second IFNα-inducible PD marker expression profiles indicates a level of efficacy of the therapeutic agent.

175. The method of claim 174 wherein the first type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes profile comprises overexpression or activity of genes EPSTI1, HERC5, IFI27, IFI44, IFI44L, IFI6, IFIT1, IFIT3, ISG15, LAMP3, LY6E, MX1, OAS1, OAS2, OAS3, RSAD2, RTP4, SIGLEC1, and USP18.

176. The method of claim 174 wherein the variance is a decrease in up-regulated expression of activity levels of the genes.

177. The method of claim 174 wherein the therapeutic agent is a small molecule or a biologic agent.

178. The method of claim 177 wherein the therapeutic agent is biologic agent that binds to and modulates IFNα activity

179. The method of claim 178 wherein the biologic agent is an antibody.

180. The method of claim 179 wherein the antibody is MEDI-545.

181. The method of claim 179 wherein the antibody binds to at least one IFNα subtype but is not MEDI-545.

182. The method of claim 174 wherein the first IFNα-inducible PD marker expression profile is obtained prior to administration of the therapeutic agent.

183. The method of claim 174 wherein the first IFNα-inducible PD marker expression profile is obtained at the time of administration of the therapeutic agent.

184. The method of claim 174 wherein the first and the second sample are whole blood, muscle, or serum.

185. The method of claim 174 further comprising obtaining a third IFNα-inducible PD marker expression profile in a third sample from the patient.

186. The method of claim 185 further comprising obtaining a fourth IFNα-inducible PD marker expression profile in a fourth sample from the patient.

187. The method of claim 186 further comprising obtaining a fifth IFNα-inducible PD marker expression profile in a fifth sample from the patient.

188. The method of claim 187 further comprising obtaining a sixth IFNα-inducible PD marker expression profile in a sixth sample from the patient.

189. The method of claim 174 wherein the second sample is obtained at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following administration of the therapeutic agent.

190. The method of claim 185 wherein the third sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the second sample.

191. The method of 186 wherein the fourth sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the third sample.

192. The method of claim 187 wherein the fifth sample is obtained at least 2 days, at least 5 days, at least one week, at least 2 weeks, at least three weeks, at least one month or at least two months following obtaining the fourth sample.

193. The method of claim 174 wherein variance is a decrease in up-regulated expression or activity of the gene.

194. The method of claim 193 wherein the decrease is at least 10%, at least 20%, at least 25%, at least 30%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%.

195. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI27, RSAD2, IFI44L, IFI44, OAS1, IFIT1, ISG15, OAS3, HERC5, MX1, ESPTI1, IFIT3, and IFI6.

196. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L, RSAD2, IFI27, and IFI44.

197. The method of claim 144 wherein the type I IFN or IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L and RSAD2.

198. The method of claim 169 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI27, RSAD2, IFI44L, IFI44, OAS1, IFIT1, ISG15, OAS3, HERC5, MX1, ESPTI1, IFIT3, and IFI6.

199. The method of claim 169 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L, RSAD2, IFI27, and IFI44.

200. The method of claim 169 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L and RSAD2.

201. The method of claim 174 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI27, RSAD2, IFI44L, IFI44, OAS1, IFIT1, ISG15, OAS3, HERC5, MX1, ESPTI1, IFIT3, and IFI6.

202. The method of claim 174 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L, RSAD2, IFI27, and IFI44.

203. The method of claim 174 wherein the first IFNα-inducible PD marker expression profile comprises up-regulated expression or activity of genes IFI44L and RSAD2.

204. The method of claim 1 wherein the patient has a strong type I IFN or IFNα-inducible gene signature score.

205. The method of claim 1 wherein the patient has a moderate type I IFN or IFNα-inducible gene signature score.

206. The method of claim 204 wherein the strong score is greater than or equal to 10.

207. The method of claim 205 wherein the moderate score is greater than or equal to 4 but less than 10.

208. The method of claim 35 or 74 wherein the myositis is DM or PM.

209. The method of claim 144 wherein the myositis patient is a DM or PM patient.

210. The method of claim 144 wherein the myositis patient comprises a MITAX score greater than 6.

211. The method of claim 144 wherein the type I IFN or IFNα-inducible gene signature score is strong.

212. The method of claim 144 wherein the type I IFN or IFNα-inducible gene signature score is moderate.

213. The method of claim 211 wherein the score is greater than or equal to 10.

214. The method of claim 212 wherein the score is greater than or equal to 4 but less than 10.

215. The method of claim 174 wherein the first IFNα-inducible PD marker expression profile comprises a strong type I IFN or IFNα-inducible gene signature score.

216. The method of claim 215 wherein the strong score is a score greater than or equal to 10.

217. The method of claim 174 wherein the first IFNα-inducible PD marker expression profile comprises a moderate type I IFN or IFNα-inducible gene signature score.

218. The method of claim 217 wherein the moderate score is a score greater than or equal to 4 but less than 10.

DEMANDE OU BREVET VOLUMINEUX

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Figure 1

a

Gene#Title	Gene#Symbol	Avg normal	Avg DM	DM Fold Change
interferon, alpha-inducible protein 6	IFI6	25.10	4132.22	164.62
chemokine (C-X-C motif) ligand 11	CXCL11	7.15	774.10	108.24
radical S-adenosyl methionine domain containing 2	RSAD2	24.42	2575.56	105.49
chemokine (C-X-C motif) ligand 10	CXCL10	10.95	1014.40	92.68
ISG15 ubiquitin-like modifier	ISG15	147.43	13142.96	89.15
interferon-induced protein with tetratricopeptide repeats 3	IFIT3	42.12	3624.43	86.06
2',5'-oligoadenylate synthetase 1, 40/46kDa	OAS1	12.28	992.19	80.80
myosin, heavy chain 3, skeletal muscle, embryonic	MYH3	50.80	3957.71	77.90
epithelial stromal interaction 1 (breast)	EPSTI1	7.94	506.64	63.83
2',5'-oligoadenylate synthetase 1, 40/46kDa	OAS1	22.89	1412.26	61.69
---	---	165.30	9922.67	60.03
interferon-induced protein 44	IFI44	14.40	816.24	56.67
hect domain and RLD 6	HERC6	8.34	471.25	56.51
chemokine (C-X-C motif) ligand 11	CXCL11	7.85	417.86	53.22
myosin binding protein H	MYBPH	13.37	693.49	51.87
proteasome (prosome, macropain) subunit, beta type, 8 (lar	PSMB8	17.37	855.90	49.29
radical S-adenosyl methionine domain containing 2	RSAD2	93.82	4239.56	45.19
ubiquitin specific peptidase 18 /// similar to ubiquitin specifi	USP18 /// LOC	10.35	457.21	44.18
interferon-induced protein with tetratricopeptide repeats 2	IFIT2	74.01	3174.49	42.89
interferon-induced protein with tetratricopeptide repeats 2	IFIT2	8.57	326.61	38.11
hypothetical protein LOC129607	LOC129607	93.94	3504.76	37.31
myxovirus (influenza virus) resistance 1, interferon-inducibl	MX1	97.31	3612.28	37.12
hect domain and RLD 5	HERC5	30.72	1104.68	35.96
interferon-induced protein 44-like	IFI44L	40.09	1310.67	32.68
DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	DDX58	23.93	768.85	32.12
signal transducer and activator of transcription 1, 91kDa	STAT1	27.32	852.60	31.21
interferon stimulated exonuclease gene 20kDa	ISG20	8.83	247.19	28.00
---	---	11.12	298.55	26.85
signal transducer and activator of transcription 1, 91kDa	STAT1	51.62	1352.92	26.21
2'-5'-oligoadenylate synthetase 2, 69/71kDa	OAS2	14.35	369.21	25.73
signal transducer and activator of transcription 1, 91kDa	STAT1	72.40	1780.05	24.58
2'-5'-oligoadenylate synthetase 3, 100kDa	OAS3	29.06	707.86	24.36
tumor necrosis factor (ligand) superfamily, member 13b	TNFSF13B	13.59	309.13	22.74
myxovirus (influenza virus) resistance 2 (mouse)	MX2	17.71	389.12	21.97
receptor (chemosensory) transporter protein 4	RTP4	8.82	187.24	21.23
complement component 4A (Rodgers blood group) /// complemer	C4A /// C4B	14.07	291.31	20.71
interferon-induced protein 35	IFI35	14.10	289.59	20.54
interferon-induced protein with tetratricopeptide repeats 1	IFIT1	577.07	11242.91	19.48
signal transducer and activator of transcription 1, 91kDa	STAT1	43.66	831.46	19.04
2'-5'-oligoadenylate synthetase-like	OASL	6.77	128.45	18.96
---	---	29.41	541.19	18.40
tripartite motif-containing 14	TRIM14	8.21	148.48	18.09
tribbles homolog 3 (Drosophila)	TRIB3	9.83	177.66	18.08
guanylate binding protein 1, interferon-inducible, 67kDa ///	GBP1	89.94	1555.44	17.29
interferon induced with helicase C domain 1	IFIH1	54.92	946.03	17.23
proteasome (prosome, macropain) subunit, beta type, 9 (lar	PSMB9	23.36	378.70	16.21
periostin, osteoblast specific factor	POSTN	162.34	2570.73	15.84
retinoic acid receptor responder (tazarotene induced) 3	RARRES3	71.51	1115.29	15.60
phosphoinositide-3-kinase adaptor protein 1	PIK3AP1	6.55	101.62	15.51
interferon-stimulated transcription factor 3, gamma 48kDa	ISGF3G	58.47	884.26	15.12
sterile alpha motif domain containing 9	SAMD9	25.36	347.00	13.68

b

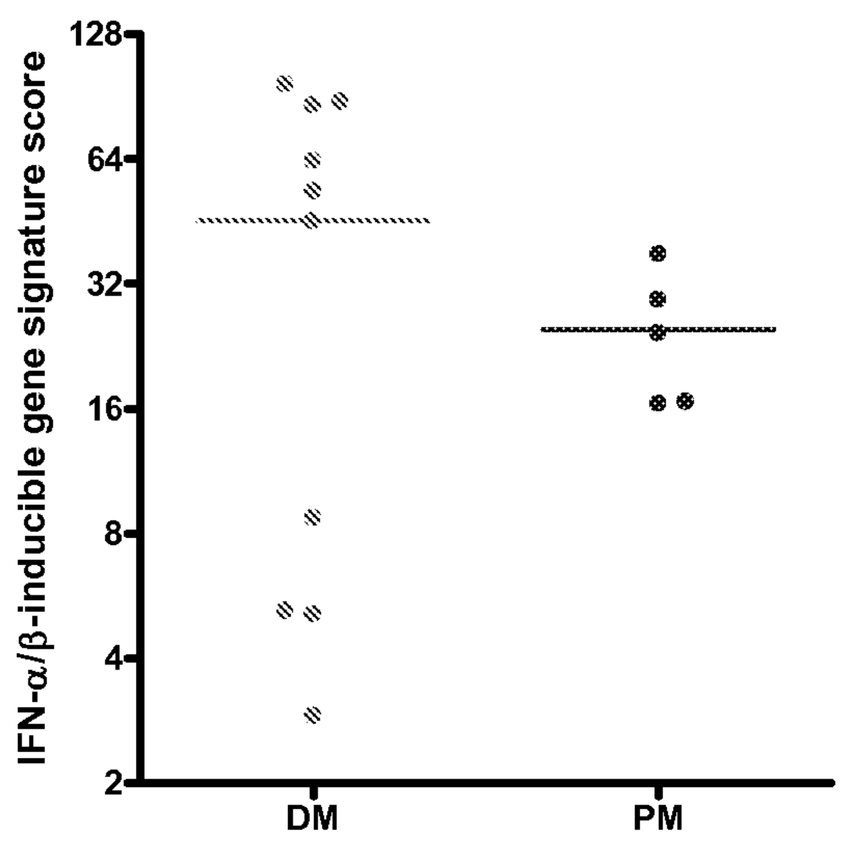


Figure 2

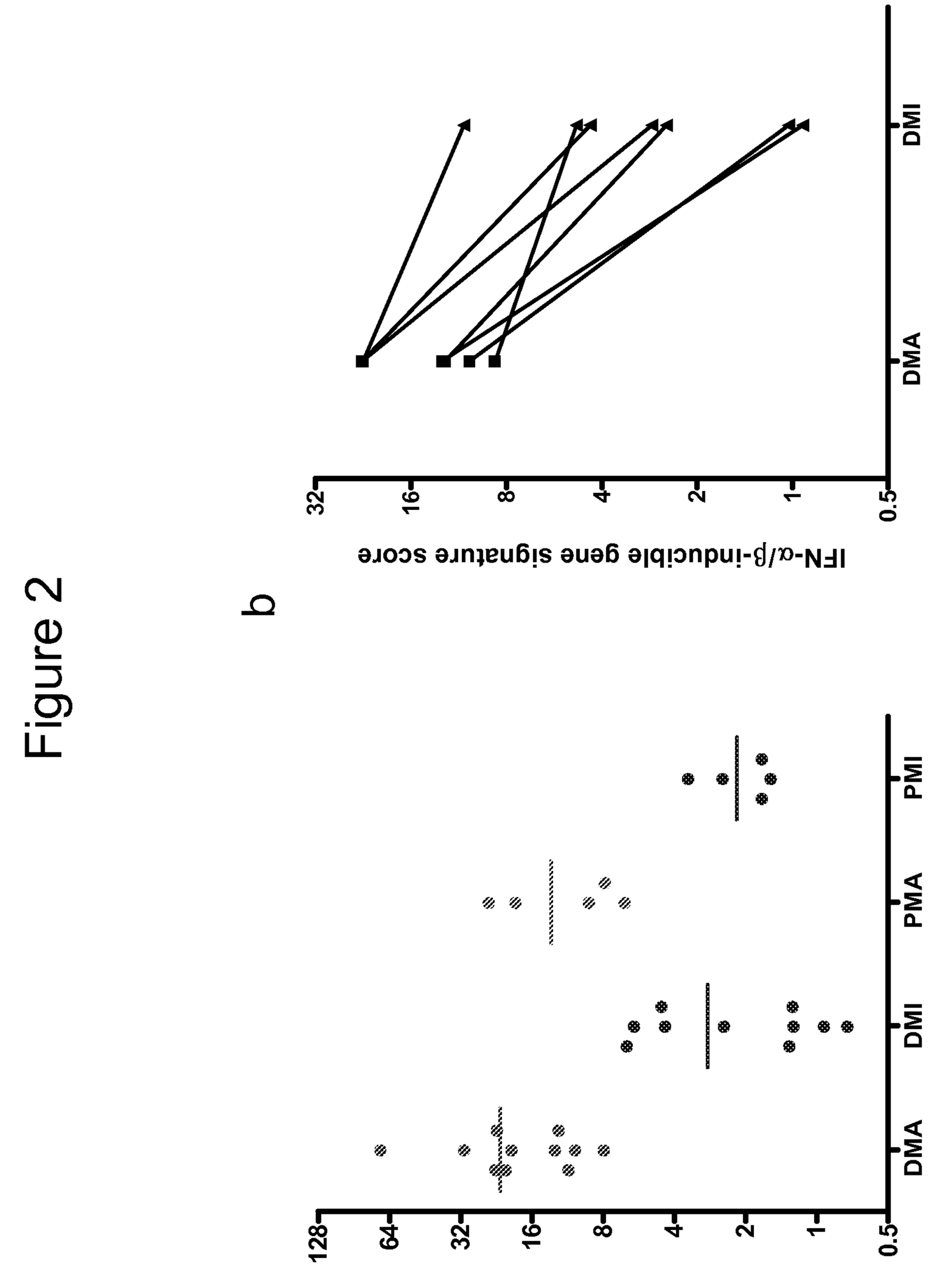
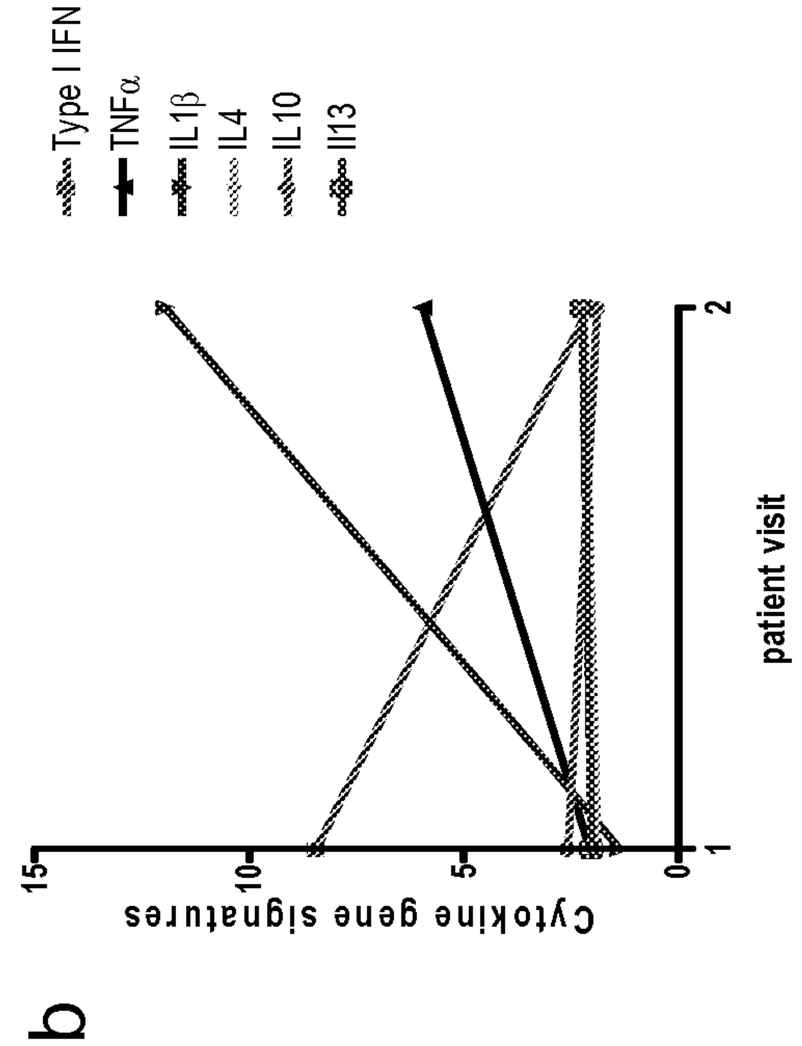
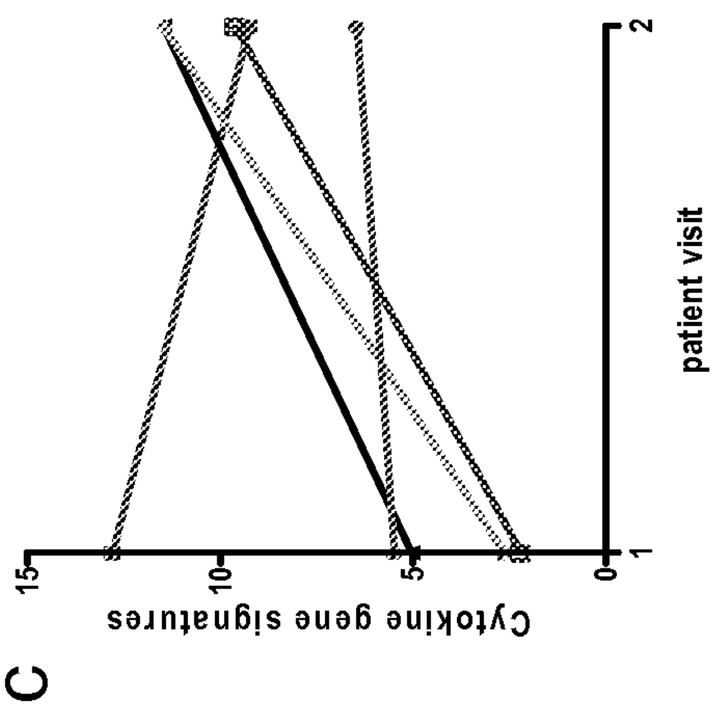

a
IFN-α/β-inducible signature score
128
64
32
16
8
4
2
1
0.5
DMA
DMI
PMA
PMI
b
IFN-α/β-inducible gene signature score
32
16
8
4
2
1
0.5
DMA
DMI

Figure 3


Type I IFN
TNFα
IL1β
IL4
IL10
Il13
Cytokine gene signatures
15
10
5
0
1
2
patient visit
b


Type I IFN
TNFα
IL1β
IL4
IL10
Il13
Cytokine gene signatures
15
10
5
0
1
2
patient visit
C

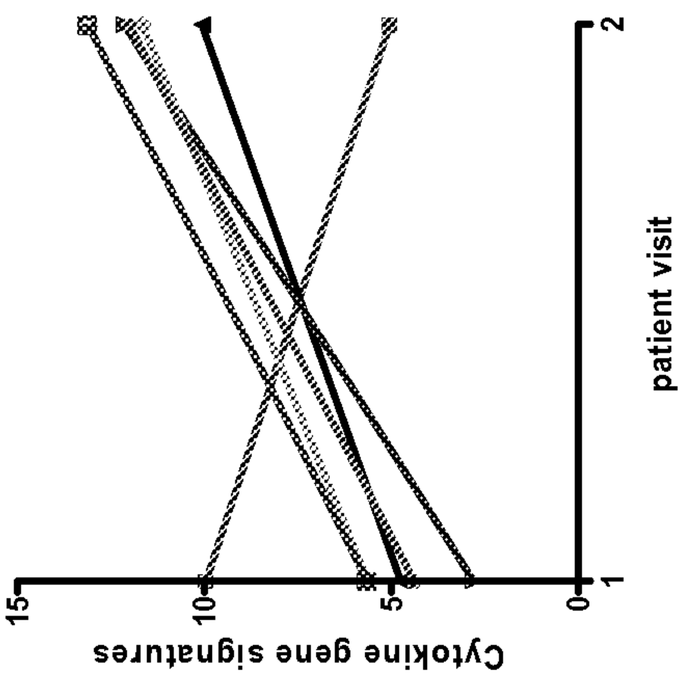

Type I IFN
TNFα
IL1β
IL4
IL10
Il13
Cytokine gene signatures
15
10
5
0
1
2
patient visit
a

Figure 4

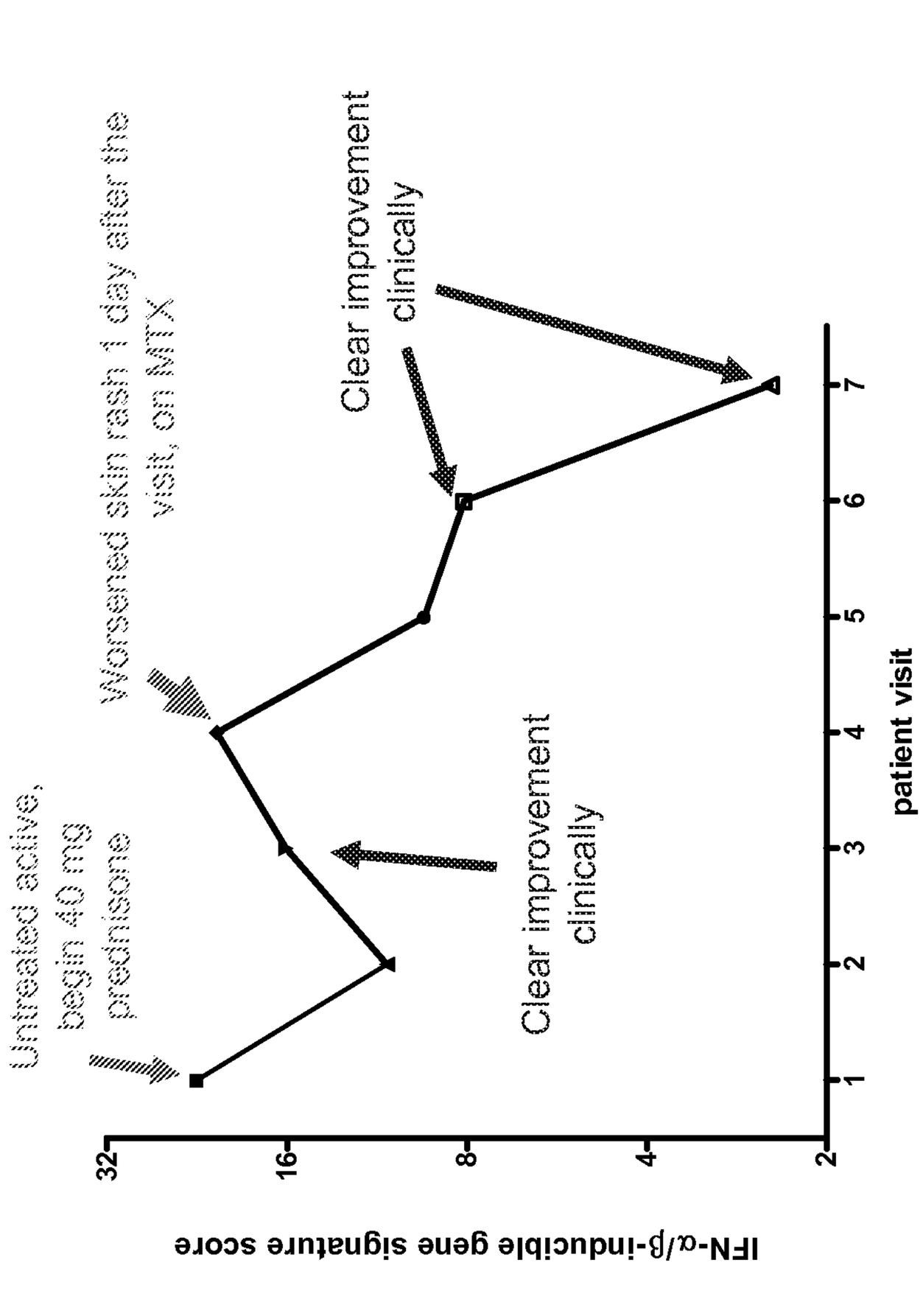

IFN-α/β-inducible gene signature score
32
16
8
4
2
1
2
3
4
5
6
7
patient visit
Untreated active, begin 40 mg prednisone
Worsened skin rash 1 day after the visit, on MTX
Clear improvement clinically
Clear improvement clinically

Figure 5

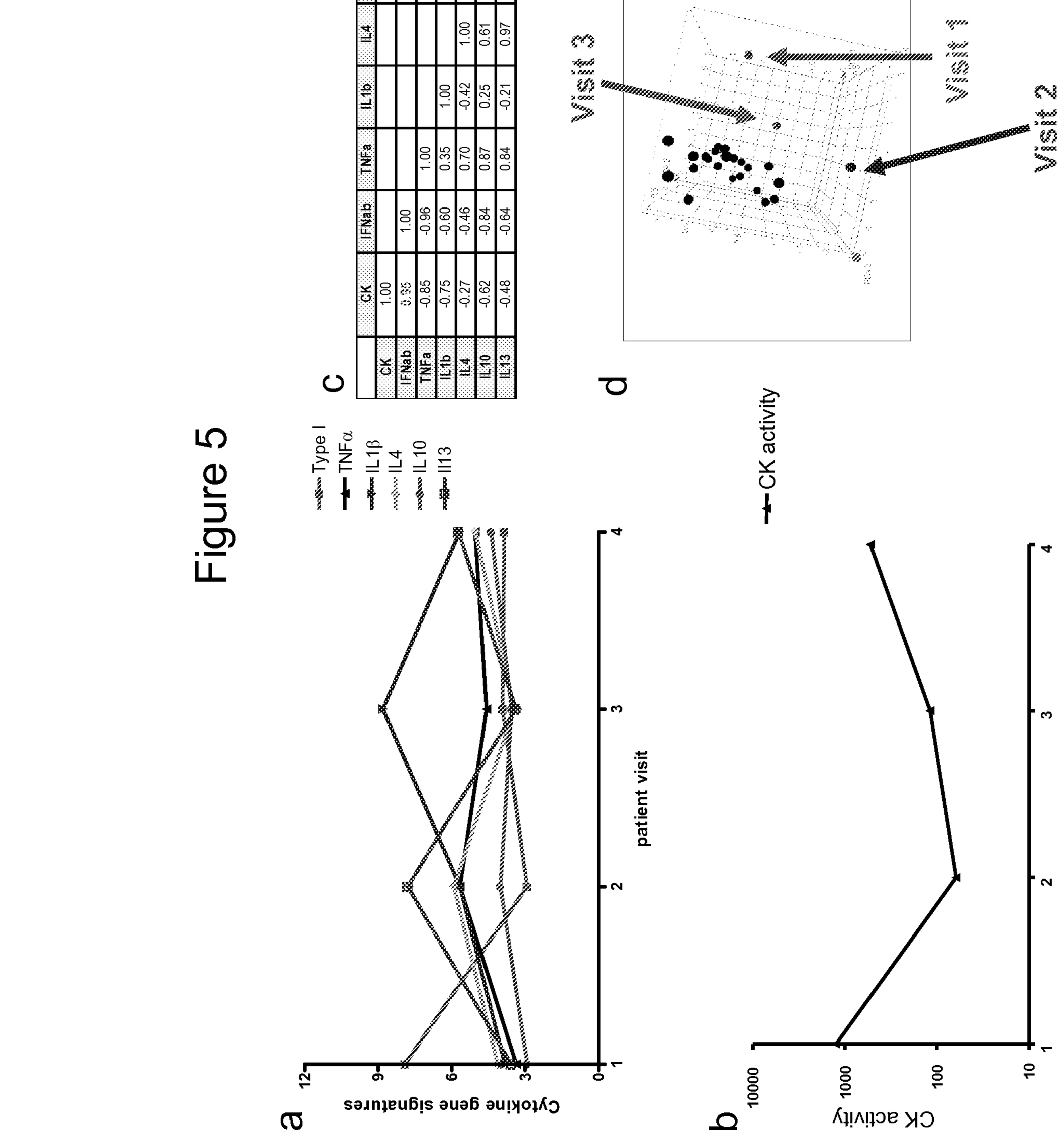
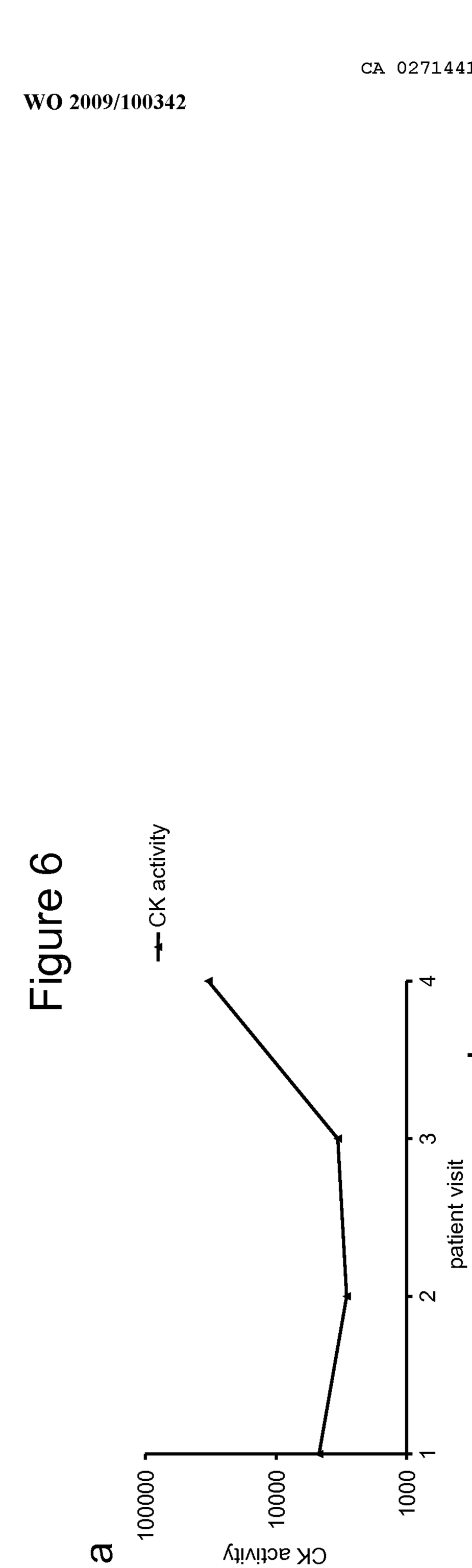
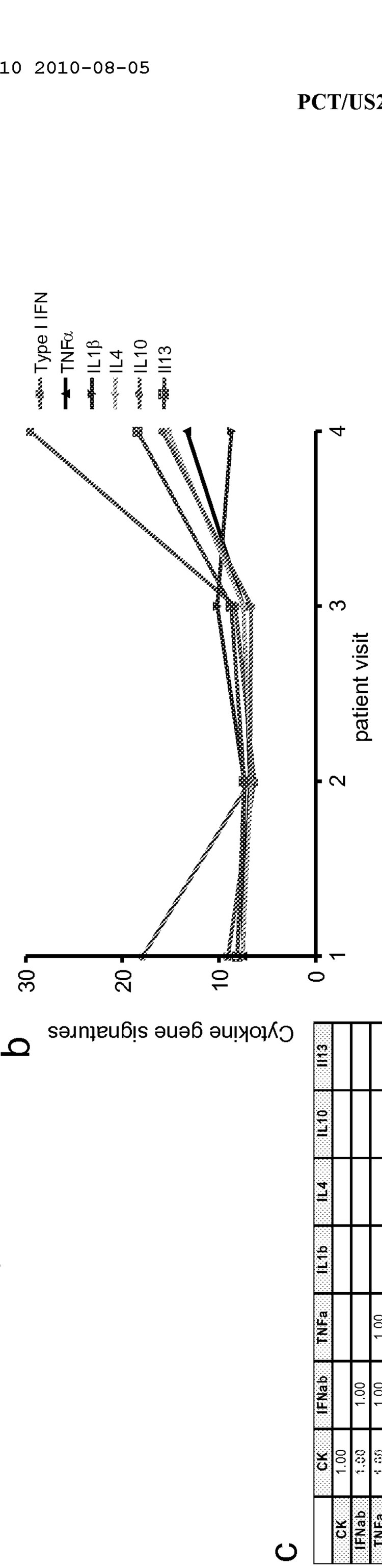

a
Cytokine gene signatures
12
9
6
3
0
1
2
3
4
patient visit
Type I
TNFα
IL1β
IL4
IL10
Il13
b
CK activity
10000
1000
100
10
1
2
3
4
patient visit
c
CK IFNab TNFa IL1b IL4
CK 1.00
IFNab 0.35 1.00
TNFa -0.85 -0.96 1.00
IL1b -0.75 -0.60 0.35 1.00
IL4 -0.27 -0.46 0.70 -0.42 1.00
IL10 -0.62 -0.84 0.87 0.25 0.61
Il13 -0.48 -0.64 0.84 -0.21 0.97
d
Visit 3
Visit 1
Visit 2

Figure 6





c

	CK	IFNab	TNFa	IL1b	IL4	IL10	Il13
CK	1.00						
IFNab	1.00	1.00					
TNFa	1.00	1.00	1.00				
IL1b	0.12	0.16	0.18	1.00			
IL4	1.00	1.00	1.00	0.17	1.00		
IL10	0.50	0.52	0.51	-0.36	0.51	1.00	
IL13	0.39	1.00	1.00	0.22	1.00	0.46	1.00

Figure 7

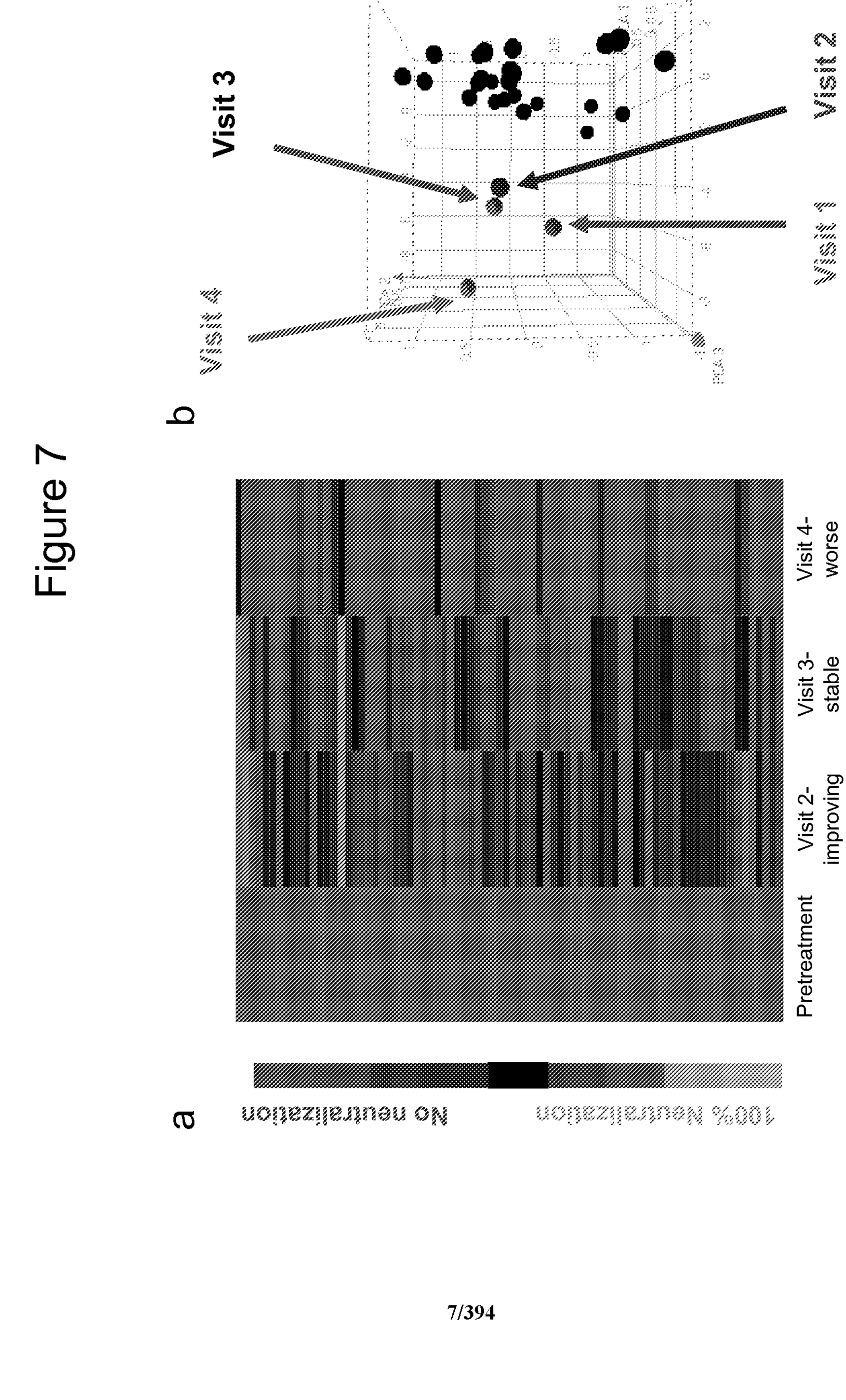

a
No neutralization
100% Neutralization
Pretreatment
Visit 2- improving
Visit 3- stable
Visit 4- worse
b
Visit 1
Visit 3
Visit 2

Figure 8

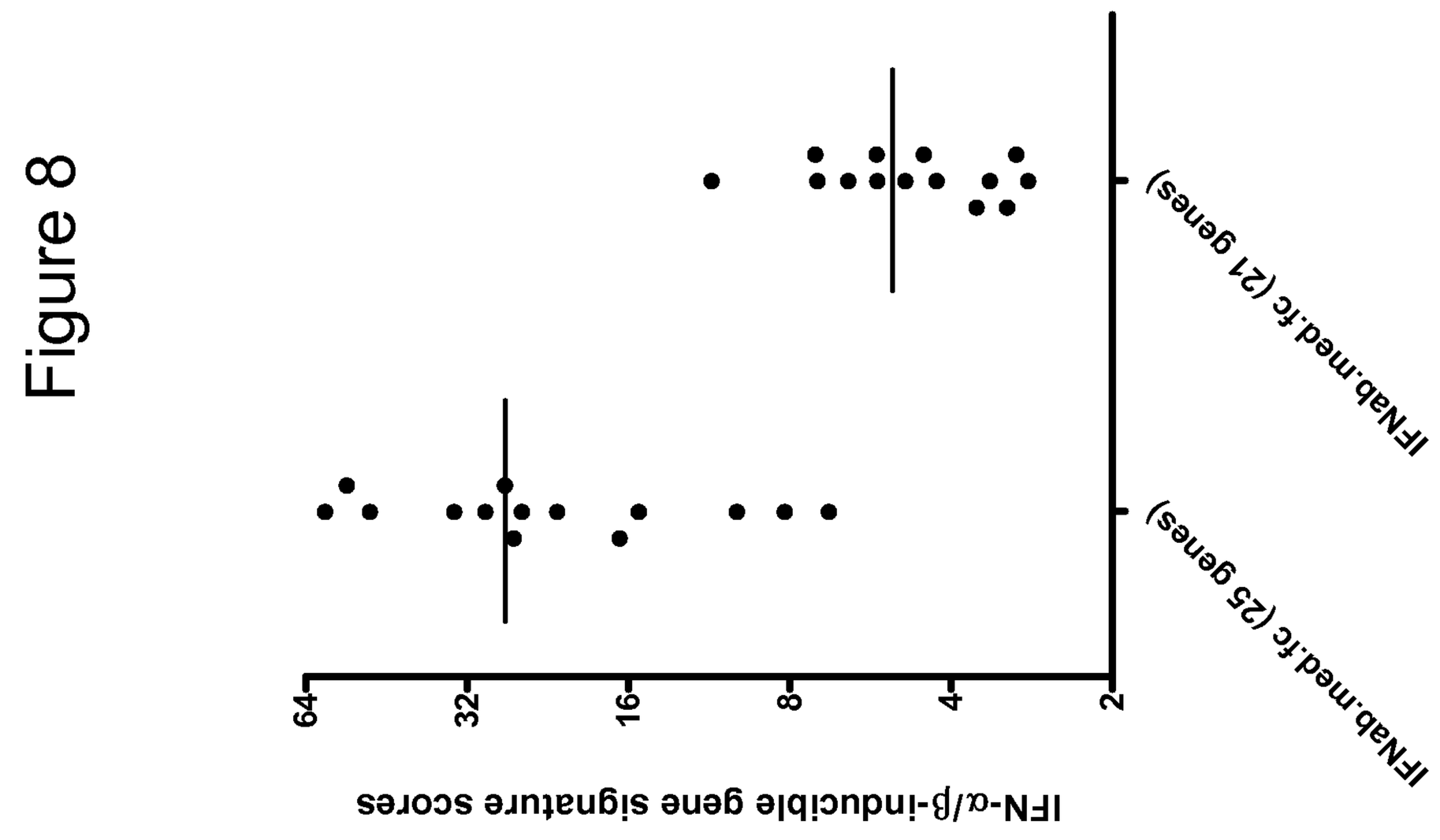
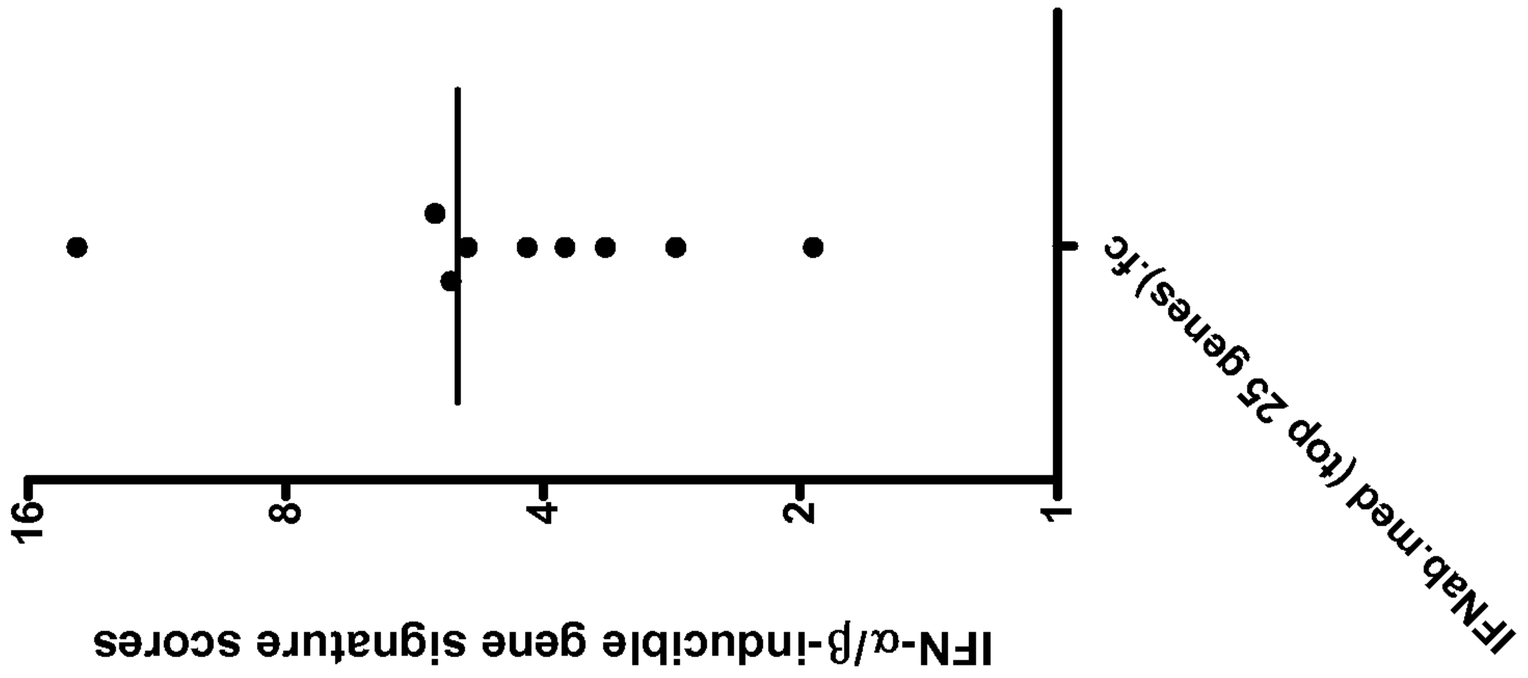

IFNab.med.fc (21 genes)
IFNab.med.fc (25 genes)
64
32
16
8
4
2
IFN-α/β-inducible gene signature scores

Figure 9

b



a

Sample ID	Donor ID	Generalized Code	IFNab.med.fc
MA44_BGE_23v1	23	IM-IBM	13.989
MA44_BGE_40v3	40	IM-IBM	1.923
MA44_BGE_49v2	49	IM-IBM-Probable	4.887
MA44_BGE_97v2	97	IM-IBM	4.158
MA44_BGE_100v2	100	IM-IBM-Probable	5.105
MA44_BGE_118v2	118	IM-IBM-HIV	5.332
MA44_BGE_131v1	131	IM-IBM	3.368
MA44_BGE_137v1	137	IM-IBM	2.787
MA44_BGE_139v1	139	IM-IBM	3.754

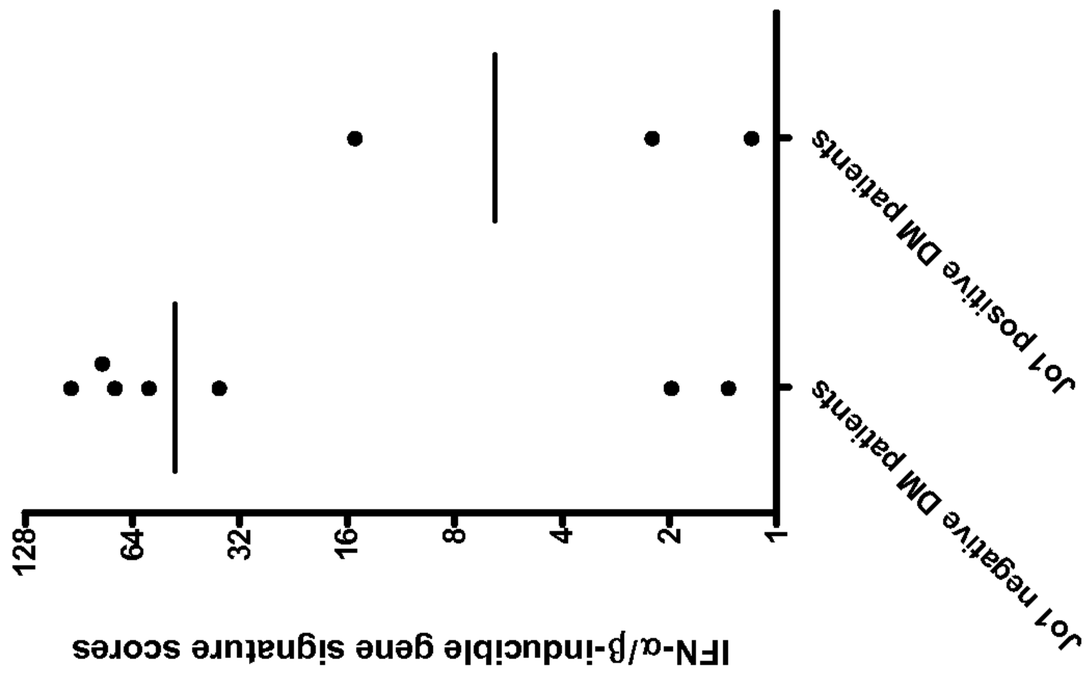
Figure 10

a

sample	Condition
MA45_GEIM12	DM
MA45_GEIM272	DM
MA45_GEIM369	DM
MA45_GEIM376	DM
MA45_GEIM382	DM
MA45_GEIM383	DM
MA45_GEIM389	DM
MA45_GEIM315	DM-Jo1
MA45_GEIM349	DM-Jo1
MA45_GEIM351	DM-Jo1

	Medium fold change																								
	SIGLEC1	USP18	ISG15	LAMP3	LY6E	MX1	OAS1	OAS2	OAS3	RSAD2	RTP4	EPSTI1	HERC5	IFI27	IFI44	IFI44L	IFI6	IFIT1	IFIT3	ISG20	MX2	OAS1	OAS2	OAS3	RSAD2	RTP4
MA45_GEIM12	1.68	84.04	222.47	1.64	15.76	61.75	177.16	34.44	24.39	244.72	42.42	82.59	57.16	6.36	9.00	56.75	373.93	63.16	253.74	2.14	61.75	177.16	34.44	24.39	244.72	42.42
MA45_GEIM272	3.49	141.20	192.34	19.83	29.46	96.87	247.17	71.12	62.38	285.89	54.43	114.87	85.74	43.31	26.59	62.35	298.22	56.39	219.25	1.98	96.87	247.17	71.12	62.38	285.89	54.43
MA45_GEIM369	14.62	89.27	184.59	13.53	41.55	105.54	94.39	96.84	75.59	279.16	33.58	190.77	97.57	24.79	18.15	104.22	345.48	45.90	174.99	1.88	105.54	94.39	96.84	75.59	279.16	33.58
MA45_GEIM376	-1.01	1.96	1.88	-1.04	1.54	1.27	-1.02	1.09	1.36	2.91	1.09	1.26	1.77	1.08	-1.03	2.22	1.76	1.98	2.17	-1.03	1.27	-1.02	1.09	1.36	2.91	1.09
MA45_GEIM382	3.16	95.59	222.33	4.64	23.96	77.18	253.34	61.97	41.53	241.14	40.14	104.00	87.94	22.81	12.86	90.35	417.80	62.96	222.76	6.26	77.18	253.34	61.97	41.53	241.14	40.14
MA45_GEIM383	3.94	41.53	110.40	17.46	18.27	36.66	99.16	36.34	34.76	131.75	19.82	70.99	35.80	13.38	4.08	53.20	216.44	29.09	88.72	1.92	36.66	99.16	36.34	34.76	131.75	19.82
MA45_GEIM389	1.11	1.97	5.73	1.32	2.06	1.96	1.31	1.12	1.37	3.65	2.54	12.87	-1.15	2.04	-1.01	-1.22	21.79	1.08	12.84	1.01	1.96	1.31	1.12	1.37	3.65	2.54
MA45_GEIM315	7.74	7.48	26.21	15.11	7.78	13.43	36.03	32.70	10.51	32.63	16.27	115.08	11.89	10.33	14.38	44.19	40.16	4.99	40.07	2.06	13.43	36.03	32.70	10.51	32.63	16.27
MA45_GEIM349	-1.01	-1.06	4.24	-1.03	2.22	1.94	5.60	3.49	2.14	2.10	1.29	4.30	1.00	3.02	1.07	5.30	6.26	4.08	6.01	-1.03	1.94	5.60	3.49	2.14	2.10	1.29
MA45_GEIM351	-1.05	1.02	2.55	1.01	1.92	-2.07	1.36	-2.24	-1.31	-2.58	2.12	2.95	-1.20	1.68	1.17	-3.14	2.23	1.58	1.92	1.01	-2.07	1.36	-2.24	-1.31	-2.58	2.12

b



probe UniGene.ID Gene.Title Gene.Symbol
Gene.Ontology.Biological.Process
Gene.Ontology.Cellular.Component
Gene.Ontology.Molecular.Function Pathway Entrez.Gene

223710_at Hs.131342 chemokine (C-C motif) ligand 26 CCL26 6935
// chemotaxis // traceable author statement /// 6954 // inflammatory
response // traceable author statement /// 7165 // signal transduction
// non-traceable author statement /// 7267 // cell-cell signaling //
traceable author statement /// 50896 // response to stimulus //
inferred from electronic annotation /// 6935 // chemotaxis // inferred
from electronic annotation /// 6954 // inflammatory response //
inferred from electronic annotation /// 6955 // immune response //
inferred from electronic annotation /// 6955 // immune response //
traceable author statement 5615 // extracellular space // inferred
from electronic annotation /// 5576 // extracellular region // inferred
from electronic annotation /// 5615 // extracellular space // not
recorded 8009 // chemokine activity // traceable author statement
/// 5125 // cytokine activity // inferred from electronic annotation
/// 8009 // chemokine activity // inferred from electronic annotation
--- 10344

221029_s_at Hs.306051 wingless-type MMTV integration site family,
member 5B /// wingless-type MMTV integration site family, member 5B
WNT5B 7223 // frizzled-2 signaling pathway // inferred from
electronic annotation /// 7275 // development // inferred from
electronic annotation /// 16055 // Wnt receptor signaling pathway //
inferred from electronic annotation 5576 // extracellular region //
inferred from electronic annotation 4871 // signal transducer activity
// inferred from electronic annotation Wnt_signaling // GenMAPP
81029

202468_s_at Hs.58488 catenin (cadherin-associated protein), alpha-
like 1 CTNNAL1 6915 // apoptosis // not recorded /// 7155 //
cell adhesion // inferred from electronic annotation 15629 // actin
cytoskeleton // inferred from electronic annotation /// 5856 //
cytoskeleton // inferred from electronic annotation 5198 //
structural molecule activity // inferred from electronic annotation ///
45296 // cadherin binding // inferred from electronic annotation ---
8727

223939_at Hs.279575 succinate receptor 1 SUCNR1 7165 //
signal transduction // inferred from electronic annotation /// 7186 //
G-protein coupled receptor protein signaling pathway // inferred from
electronic annotation 16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // non-traceable author
statement /// 16021 // integral to membrane // inferred from electronic
annotation 1584 // rhodopsin-like receptor activity // inferred from
electronic annotation /// 4872 // receptor activity // inferred from
electronic annotation /// 16526 // G-protein coupled receptor activity,
unknown ligand // non-traceable author statement /// 45028 //
purinergic nucleotide receptor activity, G-protein coupled // inferred
from electronic annotation /// 4871 // signal transducer activity //
inferred from electronic annotation /// 4930 // G-protein coupled
receptor activity // inferred from electronic annotation
GPCRDB_Class_A_Rhodopsin-like // GenMAPP 56670

Figure 11

213638_at Hs.436996 phosphatase and actin regulator 1 PHACTR1 --- --- 3779 // actin binding // inferred from electronic annotation /// 4864 // protein phosphatase inhibitor activity // inferred from electronic annotation --- 221692

223377_x_at Hs.8257 cytokine inducible SH2-containing protein CISH 1558 // regulation of cell growth // non-traceable author statement /// 7242 // intracellular signaling cascade // non-traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- --- --- 1154

205249_at Hs.1395 early growth response 2 (Krox-20 homolog, Drosophila) EGR2 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7420 // brain development // traceable author statement /// 7422 // peripheral nervous system development // traceable author statement /// 7638 // mechanosensory behavior // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from direct assay /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 1959

204438_at Hs.75182 mannose receptor, C type 1 /// mannose receptor, C type 1-like 1 MRC1 /// MRC1L1 6898 // receptor mediated endocytosis // traceable author statement /// 6907 // pinocytosis // not recorded /// 6897 // endocytosis // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5529 // sugar binding // inferred from electronic annotation /// 5537 // mannose binding // traceable author statement /// 4872 // receptor activity // inferred from electronic annotation --- 414308 /// 4360
217771_at Hs.494337 golgi phosphoprotein 2 GOLPH2 --- 5795 // Golgi stack // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5794 // Golgi apparatus // traceable author statement --- --- 51280

205698_s_at Hs.463978 mitogen-activated protein kinase kinase 6 MAP2K6 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6975 // DNA damage induced protein phosphorylation // traceable author statement /// 7050 // cell cycle arrest // traceable author statement /// 7165 // signal transduction // traceable author statement --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation

Figure 12

/// 4708 // MAP kinase kinase activity // traceable author statement /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation Integrin-mediated_cell_adhesion_KEGG // GenMAPP /// MAPK_Cascade // GenMAPP 5608

201042_at Hs.517033 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) TGM2 7186 // G-protein coupled receptor protein signaling pathway // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred from sequence or structural similarity /// 45785 // positive regulation of cell adhesion // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred from electronic annotation 5578 // extracellular matrix (sensu Metazoa) // inferred from sequence or structural similarity /// 5829 // cytosol // inferred from sequence or structural similarity /// 16020 // membrane // inferred from sequence or structural similarity 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from sequence or structural similarity /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5525 // GTP binding // inferred from sequence or structural similarity /// 8415 // acyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation Complement and coagulation cascades // KEGG /// Huntington's disease // KEGG 7052

205699_at --- --- --- --- --- --- --- ---

229569_at Hs.49329 CDNA clone IMAGE:5263455 --- --- --- --- --- ---

205990_s_at Hs.643085 wingless-type MMTV integration site family, member 5A WNT5A 7165 // signal transduction // traceable author statement /// 7223 // frizzled-2 signaling pathway // inferred from electronic annotation /// 7267 // cell-cell signaling // traceable author statement /// 9653 // morphogenesis // traceable author statement /// 7275 // development // inferred from electronic annotation /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation 5615 // extracellular space // traceable author statement /// 5625 // soluble fraction // traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 5102 // receptor binding // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4871 // signal transducer activity // traceable author statement Wnt_signaling // GenMAPP 7474

232045_at Hs.436996 phosphatase and actin regulator 1 PHACTR1 --- --- 3779 // actin binding // inferred from electronic annotation /// 4864 // protein phosphatase inhibitor activity // inferred from electronic annotation --- 221692

Figure 13

221223_x_at Hs.8257 cytokine inducible SH2-containing protein CISH 1558 // regulation of cell growth // non-traceable author statement /// 7242 // intracellular signaling cascade // non-traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- --- --- 1154

223961_s_at Hs.8257 cytokine inducible SH2-containing protein CISH 1558 // regulation of cell growth // non-traceable author statement /// 7242 // intracellular signaling cascade // non-traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- --- --- 1154

224802_at Hs.525093 Nedd4 family interacting protein 2 NDFIP2 --- 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 54602

221170_at Hs.287388 histamine receptor H4 HRH4 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4969 // histamine receptor activity // non-traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation GPCRDB_Other // GenMAPP /// GPCRDB_Other // GenMAPP 59340

229116_at Hs.555917 CDNA clone IMAGE:30721737 --- --- --- --- --- ---

223537_s_at Hs.306051 wingless-type MMTV integration site family, member 5B WNT5B 7223 // frizzled-2 signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation 5576 // extracellular region // inferred from electronic annotation 4871 // signal transducer activity // inferred from electronic annotation Wnt_signaling // GenMAPP 81029

216268_s_at Hs.224012 jagged 1 (Alagille syndrome) JAG1 1525 // angiogenesis // non-traceable author statement /// 1709 // cell fate determination // non-traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 7219 // Notch signaling pathway // non-traceable author statement /// 7275 // development // non-traceable author statement /// 7399 // nervous

Figure 14

system development // non-traceable author statement /// 30097 // hemopoiesis // non-traceable author statement /// 30216 // keratinocyte differentiation // non-traceable author statement /// 30334 // regulation of cell migration // non-traceable author statement /// 42127 // regulation of cell proliferation // non-traceable author statement /// 45445 // myoblast differentiation // non-traceable author statement /// 45446 // endothelial cell differentiation // non-traceable author statement /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5112 // Notch binding // non-traceable author statement /// 5198 // structural molecule activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 8083 // growth factor activity // non-traceable author statement --- 182

210001_s_at Hs.50640 suppressor of cytokine signaling 1 SOCS1 1558 // regulation of cell growth // inferred from electronic annotation /// 1932 // regulation of protein amino acid phosphorylation // inferred from sequence or structural similarity /// 6512 // ubiquitin cycle // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // inferred from sequence or structural similarity /// 42518 // negative regulation of tyrosine phosphorylation of Stat3 protein // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // non-traceable author statement /// 46627 // negative regulation of insulin receptor signaling pathway // inferred from sequence or structural similarity /// 9968 // negative regulation of signal transduction // inferred from electronic annotation 5737 // cytoplasm // traceable author statement 4860 // protein kinase inhibitor activity // traceable author statement /// 5159 // insulin-like growth factor receptor binding // inferred from physical interaction /// 19901 // protein kinase binding // inferred from physical interaction /// 19210 // kinase inhibitor activity // inferred from sequence or structural similarity --- 8651

223625_at Hs.85603 family with sequence similarity 126, member A FAM126A --- --- 4871 // signal transducer activity // non-traceable author statement --- 84668

228915_at Hs.129452 dachshund homolog 1 (Drosophila) DACH1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7456 // eye development (sensu Endopterygota) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction --- 1602

Figure 15

221724_s_at Hs.504657 C-type lectin domain family 4, member A CLEC4A 6955 // immune response // inferred from electronic annotation /// 7155 // cell adhesion // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 19735 // antimicrobial humoral response (sensu Vertebrata) // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation /// 9653 // morphogenesis // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4888 // transmembrane receptor activity // traceable author statement /// 5529 // sugar binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // traceable author statement --- 50856

219298_at Hs.22242 enoyl Coenzyme A hydratase domain containing 3 ECHDC3 8152 // metabolism // inferred from electronic annotation --- 3824 // catalytic activity // inferred from electronic annotation --- 79746

212094_at Hs.147492 paternally expressed 10 PEG10 --- --- 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation --- 23089

219947_at Hs.504657 C-type lectin domain family 4, member A CLEC4A 6955 // immune response // inferred from electronic annotation /// 7155 // cell adhesion // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 19735 // antimicrobial humoral response (sensu Vertebrata) // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation /// 9653 // morphogenesis // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4888 // transmembrane receptor activity // traceable author statement /// 5529 // sugar binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // traceable author statement --- 50856

212741_at Hs.183109 monoamine oxidase A MAOA 6118 // electron transport // inferred from electronic annotation /// 6584 //

Figure 16

catecholamine metabolism // inferred from electronic annotation /// 7610 // behavior // traceable author statement /// 42135 // neurotransmitter catabolism // inferred from electronic annotation /// 6576 // biogenic amine metabolism // traceable author statement 5739 // mitochondrion // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // not recorded 8131 // amine oxidase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 8131 // amine oxidase activity // not recorded Biogenic_Amine_Synthesis // GenMAPP /// Glycine, serine and threonine metabolism // KEGG /// Arginine and proline metabolism // KEGG /// Histidine metabolism // KEGG /// Tyrosine metabolism // KEGG /// Phenylalanine metabolism // KEGG /// Tryptophan metabolism // KEGG 4128

243606_at Hs.595933 Transcribed locus --- --- --- --- --- ---

229506_at Hs.592572 CDNA clone IMAGE:5263177 --- --- --- --- --- ---

1556314_a_at Hs.224794 (clone 1NIB-4) normalized cDNA library sequence --- --- --- --- --- ---

219179_at Hs.48950 dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis) DACT1 7275 // development // inferred from electronic annotation /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation --- --- 51339

204388_s_at Hs.183109 monoamine oxidase A MAOA 6118 // electron transport // inferred from electronic annotation /// 6584 // catecholamine metabolism // inferred from electronic annotation /// 7610 // behavior // traceable author statement /// 42135 // neurotransmitter catabolism // inferred from electronic annotation /// 6576 // biogenic amine metabolism // traceable author statement 5739 // mitochondrion // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // not recorded 8131 // amine oxidase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 8131 // amine oxidase activity // not recorded Biogenic_Amine_Synthesis // GenMAPP /// Glycine, serine and threonine metabolism // KEGG /// Arginine and proline metabolism // KEGG /// Histidine metabolism // KEGG /// Tyrosine metabolism // KEGG /// Phenylalanine metabolism // KEGG /// Tryptophan metabolism // KEGG 4128

226397_s_at Hs.484678 TBC1 domain family, member 7 TBC1D7 --- --- 5096 // GTPase activator activity // inferred from electronic annotation --- 51256

1556097_at Hs.459142 MRNA; cDNA DKFZp686A11113 (from clone DKFZp686A11113) --- --- --- --- --- ---

Figure 17

231183_s_at Hs.224012 Jagged 1 (Alagille syndrome) JAG1 1525 // angiogenesis // non-traceable author statement /// 1709 // cell fate determination // non-traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 7219 // Notch signaling pathway // non-traceable author statement /// 7275 // development // non-traceable author statement /// 7399 // nervous system development // non-traceable author statement /// 30097 // hemopoiesis // non-traceable author statement /// 30216 // keratinocyte differentiation // non-traceable author statement /// 30334 // regulation of cell migration // non-traceable author statement /// 42127 // regulation of cell proliferation // non-traceable author statement /// 45445 // myoblast differentiation // non-traceable author statement /// 45446 // endothelial cell differentiation // non-traceable author statement /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5112 // Notch binding // non-traceable author statement /// 5198 // structural molecule activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 8083 // growth factor activity // non-traceable author statement --- 182

1555326_a_at Hs.591852 ADAM metallopeptidase domain 9 (meltrin gamma) ADAM9 6508 // proteolysis // inferred from electronic annotation /// 7243 // protein kinase cascade // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement 4222 // metalloendopeptidase activity // inferred from electronic annotation /// 5178 // integrin binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 17124 // SH3 domain binding // inferred from physical interaction /// 19901 // protein kinase binding // traceable author statement /// 46872 // metal ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // traceable author statement /// 8237 // metallopeptidase activity // non-traceable author statement --- 8754

209099_x_at Hs.224012 jagged 1 (Alagille syndrome) JAG1 1525 // angiogenesis // non-traceable author statement /// 1709 // cell fate determination // non-traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 7219 // Notch signaling pathway // non-traceable author statement /// 7275 // development // non-traceable author statement /// 7399 // nervous system development // non-traceable author statement /// 30097 // hemopoiesis // non-traceable author statement /// 30216 // keratinocyte differentiation // non-traceable author statement /// 30334 //

Figure 18

regulation of cell migration // non-traceable author statement /// 42127 // regulation of cell proliferation // non-traceable author statement /// 45445 // myoblast differentiation // non-traceable author statement /// 45446 // endothelial cell differentiation // non-traceable author statement /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5112 // Notch binding // non-traceable author statement /// 5198 // structural molecule activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 8083 // growth factor activity // non-traceable author statement --- 182

228457_at Hs.592572 CDNA clone IMAGE:5263177 --- --- --- --- --- ---

225776_at Hs.505729 CDNA FLJ39093 fis, clone NT2RP7020112 --- 5975 // carbohydrate metabolism // traceable author statement /// 6486 // protein amino acid glycosylation // traceable author statement /// 42355 // L-fucose catabolism // non-traceable author statement /// 6396 // RNA processing // traceable author statement /// 6445 // regulation of translation // traceable author statement 5624 // membrane fraction // traceable author statement /// 5795 // Golgi stack // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation 8107 // galactoside 2-alpha-L-fucosyltransferase activity // traceable author statement /// 8417 // fucosyltransferase activity // traceable author statement /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement Blood group glycolipid biosynthesis - lactoseries // KEGG /// Blood group glycolipid biosynthesis - // KEGG /// Globoside metabolism // KEGG /// Glycan structures - biosynthesis 2 // KEGG 2523

235030_at Hs.130195 family with sequence similarity 55, member C FAM55C --- --- --- --- 91775

203464_s_at Hs.515176 epsin 2 EPN2 6897 // endocytosis // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- 8289 // lipid binding // inferred from electronic annotation --- 22905

1552875_a_at Hs.309158 CD200 receptor 1 CD200R1 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 131450

Figure 19

1553222_at Hs.168439 oxoeicosanoid (OXE) receptor 1 OXER1 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // non-traceable author statement /// 30817 // regulation of cAMP biosynthesis // inferred from direct assay /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 50646 // 5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid binding // non-traceable author statement /// 50647 // 5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic acid binding // non-traceable author statement /// 50648 // 5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetraenoic acid binding // non-traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // non-traceable author statement --- 165140

221385_s_at Hs.533926 free fatty acid receptor 3 /// G protein-coupled receptor 42 /// similar to Free fatty acid receptor 3 (G-protein coupled receptor 41) FFAR3 /// GPR42 /// LOC731823 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // traceable author statement GPCRDB_Class_A_Rhodopsin-like2 // GenMAPP 2865 /// 2866 /// 654110

218718_at Hs.570855 platelet derived growth factor C PDGFC 7417 // central nervous system development // traceable author statement 16020 // membrane // inferred from electronic annotation /// 5576 // extracellular region // non-traceable author statement 8083 // growth factor activity // inferred from electronic annotation /// 8083 // growth factor activity // traceable author statement --- 56034
209544_at Hs.103755 receptor-interacting serine-threonine kinase 2 RIPK2 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6954 // inflammatory response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 42981 // regulation of apoptosis // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from expression pattern /// 6915 // apoptosis // inferred from electronic annotation /// 6915 // apoptosis // traceable author statement 5622 // intracellular // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // traceable author statement /// 4871 // signal transducer activity // inferred from expression pattern ///

Figure 20

5515 // protein binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 30274 // LIM domain binding // inferred from physical interaction /// 50700 // CARD domain binding // inferred from physical interaction /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // traceable author statement mTOR signaling pathway // KEGG /// Wnt signaling pathway // KEGG /// Dorso-ventral axis formation // KEGG /// Hedgehog signaling pathway // KEGG /// TGF-beta signaling pathway // KEGG /// Axon guidance // KEGG /// VEGF signaling pathway // KEGG /// Focal adhesion // KEGG /// Adherens junction // KEGG /// Tight junction // KEGG /// Gap junction // KEGG /// B cell receptor signaling pathway // KEGG /// Fc epsilon RI signaling pathway // KEGG /// Long-term potentiation // KEGG /// Long-term depression // KEGG /// Regulation of actin cytoskeleton // KEGG /// Insulin signaling pathway // KEGG /// Alzheimer's disease // KEGG 8767

232406_at Hs.224012 Jagged 1 (Alagille syndrome) JAG1 1525 // angiogenesis // non-traceable author statement /// 1709 // cell fate determination // non-traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 7219 // Notch signaling pathway // non-traceable author statement /// 7275 // development // non-traceable author statement /// 7399 // nervous system development // non-traceable author statement /// 30097 // hemopoiesis // non-traceable author statement /// 30216 // keratinocyte differentiation // non-traceable author statement /// 30334 // regulation of cell migration // non-traceable author statement /// 42127 // regulation of cell proliferation // non-traceable author statement /// 45445 // myoblast differentiation // non-traceable author statement /// 45446 // endothelial cell differentiation // non-traceable author statement /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5112 // Notch binding // non-traceable author statement /// 5198 // structural molecule activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 8083 // growth factor activity // non-traceable author statement --- 182

1553395_a_at Hs.309158 CD200 receptor 1 CD200R1 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 131450

220049_s_at Hs.532279 programmed cell death 1 ligand 2 PDCD1LG2 6955 // immune response // non-traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 //

Figure 21

integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 80380

231396_s_at Hs.85603 family with sequence similarity 126, member A FAM126A --- --- 4871 // signal transducer activity // non-traceable author statement --- 84668

213425_at Hs.643085 wingless-type MMTV integration site family, member 5A /// wingless-type MMTV integration site family, member 5A WNT5A 7165 // signal transduction // traceable author statement /// 7223 // frizzled-2 signaling pathway // inferred from electronic annotation /// 7267 // cell-cell signaling // traceable author statement /// 9653 // morphogenesis // traceable author statement /// 7275 // development // inferred from electronic annotation /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation 5615 // extracellular space // traceable author statement /// 5625 // soluble fraction // traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 5102 // receptor binding // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation --- 7474

231972_at Hs.484678 TBC1 domain family, member 7 TBC1D7 --- --- 5096 // GTPase activator activity // inferred from electronic annotation --- 51256

232530_at Hs.382865 phospholipase D1, phosphatidylcholine-specific PLD1 --- --- --- --- 652226

222891_s_at Hs.370549 B-cell CLL/lymphoma 11A (zinc finger protein) BCL11A 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 30097 // hemopoiesis // non-traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 53335

226416_at Hs.20000 three prime histone mRNA exonuclease 1 THEX1 --- 5622 // intracellular // inferred from electronic annotation 287 // magnesium ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 8408 // 3'-5' exonuclease activity // inferred from direct assay /// 16787 // hydrolase activity // inferred from electronic annotation /// 4518 // nuclease activity // inferred from electronic annotation /// 4527 // exonuclease activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 90459

217540_at Hs.598134 Transcribed locus --- --- --- --- --- ---

221463_at Hs.247838 chemokine (C-C motif) ligand 24 CCL24 6935 // chemotaxis // traceable author statement /// 6954 // inflammatory response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7267 // cell-cell signaling //

Figure 22

traceable author statement /// 50896 // response to stimulus // inferred from electronic annotation /// 6935 // chemotaxis // inferred from electronic annotation /// 6954 // inflammatory response // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation /// 6955 // immune response // traceable author statement 5615 // extracellular space // inferred from electronic annotation /// 5576 // extracellular region // inferred from electronic annotation 8009 // chemokine activity // traceable author statement /// 5125 // cytokine activity // inferred from electronic annotation /// 8009 // chemokine activity // inferred from electronic annotation --- 6369

220014_at Hs.157461 proline rich 16 PRR16 --- --- --- --- 51334

215561_s_at Hs.557403 interleukin 1 receptor, type I IL1R1 6954 // inflammatory response // not recorded /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 6955 // immune response // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4888 // transmembrane receptor activity // traceable author statement /// 4909 // interleukin-1, Type I, activating receptor activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 4872 // receptor activity // inferred from electronic annotation /// 4888 // transmembrane receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // inferred from electronic annotation /// 4909 // interleukin-1, Type I, activating receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // traceable author statement /// 4908 // interleukin-1 receptor activity // traceable author statement Hypertrophy_model // GenMAPP 3554

225778_at Hs.648783 fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group) FUT1 5975 // carbohydrate metabolism // traceable author statement /// 6486 // protein amino acid glycosylation // traceable author statement /// 42355 // L-fucose catabolism // non-traceable author statement /// 6396 // RNA processing // traceable author statement /// 6445 // regulation of translation // traceable author statement 5624 // membrane fraction // traceable author statement /// 5795 // Golgi stack // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation 8107 // galactoside 2-alpha-L-fucosyltransferase activity // traceable author statement /// 8417 // fucosyltransferase activity // traceable author statement /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement Blood group glycolipid biosynthesis - lactoseries // KEGG /// Blood group glycolipid biosynthesis - // KEGG /// Globoside metabolism // KEGG /// Glycan structures - biosynthesis 2 // KEGG 2523

Figure 23

231852_at Hs.20000 Three prime histone mRNA exonuclease 1 THEX1 --- 5622 // intracellular // inferred from electronic annotation 287 // magnesium ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 8408 // 3'-5' exonuclease activity // inferred from direct assay /// 16787 // hydrolase activity // inferred from electronic annotation /// 4518 // nuclease activity // inferred from electronic annotation /// 4527 // exonuclease activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 90459

238439_at Hs.217484 ankyrin repeat domain 22 ANKRD22 --- --- --- --- 118932

229810_at Hs.391527 Transcribed locus --- --- --- --- ---

225646_at Hs.128065 cathepsin C CTSC 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 6508 // proteolysis // not recorded 5764 // lysosome // traceable author statement /// 5764 // lysosome // inferred from electronic annotation 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4214 // dipeptidyl-peptidase I activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1075

243011_at Hs.130195 family with sequence similarity 55, member C FAM55C --- --- --- --- 91775

211003_x_at Hs.517033 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) TGM2 7186 // G-protein coupled receptor protein signaling pathway // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred from sequence or structural similarity /// 45785 // positive regulation of cell adhesion // inferred from sequence or structural similarity /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from mutant phenotype /// 18153 // isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine // inferred from direct assay /// 18149 // peptide cross-linking // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 12501 // programmed cell death // traceable author statement /// 19933 // cAMP-mediated signaling // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // non-traceable author statement 5578 // extracellular matrix (sensu Metazoa) // inferred from sequence or structural similarity /// 5829 // cytosol // inferred from sequence or structural similarity /// 16020 // membrane // inferred from sequence or structural similarity /// 5622 // intracellular // non-traceable author statement 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from sequence or structural similarity /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5525 // GTP binding // inferred from sequence or structural similarity /// 8415 // acyltransferase activity // inferred from electronic annotation ///

Figure 24

16740 // transferase activity // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // traceable author statement /// 3924 // GTPase activity // traceable author statement /// 5524 // ATP binding // traceable author statement /// 5525 // GTP binding // traceable author statement Complement and coagulation cascades // KEGG /// Huntington's disease // KEGG 7052

228108_at Hs.592572 CDNA clone IMAGE:5263177 --- --- --- --- --- ---

223304_at Hs.446021 solute carrier family 37 (glycerol-3-phosphate transporter), member 3 SLC37A3 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 84255

228565_at Hs.547779 mixed lineage kinase 4 KIAA1804 7257 // activation of JNK activity // inferred from sequence or structural similarity /// 46777 // protein amino acid autophosphorylation // inferred from sequence or structural similarity /// 6468 // protein amino acid phosphorylation // inferred from sequence or structural similarity /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from sequence or structural similarity /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 42803 // protein homodimerization activity // inferred from sequence or structural similarity /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation --- 84451

219497_s_at Hs.370549 B-cell CLL/lymphoma 11A (zinc finger protein) BCL11A 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 30097 // hemopoiesis // non-traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 53335

224799_at Hs.525093 Nedd4 family interacting protein 2 NDFIP2 --- 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 54602

202948_at Hs.557403 interleukin 1 receptor, type I IL1R1 6954 // inflammatory response // not recorded /// 7166 // cell surface receptor linked signal transduction // traceable author statement ///

Figure 25

6955 // immune response // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4888 // transmembrane receptor activity // traceable author statement /// 4909 // interleukin-1, Type I, activating receptor activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 4872 // receptor activity // inferred from electronic annotation /// 4888 // transmembrane receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // inferred from electronic annotation /// 4909 // interleukin-1, Type I, activating receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // traceable author statement /// 4908 // interleukin-1 receptor activity // traceable author statement
Hypertrophy_model // GenMAPP 3554
219886_at Hs.444135 leucine-rich repeats and IQ motif containing 2
LRRIQ2 --- --- --- --- 79598
224399_at Hs.532279 programmed cell death 1 ligand 2 /// programmed cell death 1 ligand 2 PDCD1LG2 6955 // immune response // non-traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 80380
231227_at Hs.643085 Wingless-type MMTV integration site family, member 5A WNT5A --- --- --- --- ---
225567_at Hs.530791 MRNA; cDNA DKFZp762E1314 (from clone DKFZp762E1314) --- --- --- --- --- 388114
212658_at Hs.79299 lipoma HMGIC fusion partner-like 2 LHFPL2 --- --- --- --- 10184
203463_s_at Hs.515176 epsin 2 EPN2 6897 // endocytosis // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- 8289 // lipid binding // inferred from electronic annotation --- 22905
219525_at Hs.232054 hypothetical protein FLJ10847 FLJ10847 6855 // multidrug transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 15238 // drug transporter activity // inferred from electronic annotation /// 15297 // antiporter activity // inferred from electronic annotation ---
55244
226844_at Hs.651275 MOB1, Mps One Binder kinase activator-like 2B (yeast) MOBKL2B --- --- 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 79817
205471_s_at Hs.129452 dachshund homolog 1 (Drosophila) DACH1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7456 // eye development (sensu Endopterygota) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction --- 1602
202381_at Hs.591852 ADAM metallopeptidase domain 9 (meltrin gamma)
ADAM9 6508 // proteolysis // inferred from electronic annotation /// 7243 // protein kinase cascade // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 //

Figure 26

integral to membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement 4222 // metalloendopeptidase activity // inferred from electronic annotation /// 5178 // integrin binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 17124 // SH3 domain binding // inferred from physical interaction /// 19901 // protein kinase binding // traceable author statement /// 46872 // metal ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // traceable author statement /// 8237 // metallopeptidase activity // non-traceable author statement --- 8754

231431_s_at Hs.530791 MRNA; cDNA DKFZp762E1314 (from clone DKFZp762E1314) --- --- --- --- --- 388114 /// 649557

203560_at Hs.78619 gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase) GGH 6541 // glutamine metabolism // inferred from electronic annotation 5764 // lysosome // inferred from electronic annotation 8238 // exopeptidase activity // traceable author statement /// 8464 // gamma-glutamyl hydrolase activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 8464 // gamma-glutamyl hydrolase activity // inferred from electronic annotation Folate biosynthesis // KEGG 8836

203685_at Hs.150749 B-cell CLL/lymphoma 2 BCL2 74 // regulation of progression through cell cycle // traceable author statement /// 1836 // release of cytochrome c from mitochondria // non-traceable author statement /// 6916 // anti-apoptosis // inferred from direct assay /// 6959 // humoral immune response // traceable author statement /// 8285 // negative regulation of cell proliferation // traceable author statement /// 42981 // regulation of apoptosis // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5739 // mitochondrion // inferred from electronic annotation /// 5741 // mitochondrial outer membrane // inferred from direct assay /// 5741 // mitochondrial outer membrane // traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // traceable author statement Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP /// Apoptosis_KEGG // GenMAPP /// Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP /// Apoptosis_KEGG // GenMAPP 596

201482_at Hs.518374 quiescin Q6 QSCN6 74 // regulation of progression through cell cycle // traceable author statement /// 1558 // regulation of cell growth // non-traceable author statement /// 6118 // electron transport // inferred from electronic annotation /// 8285 // negative regulation of cell proliferation // traceable author statement --- --- --- 5768

232614_at Hs.150749 B-cell CLL/lymphoma 2 BCL2 74 // regulation of progression through cell cycle // traceable author statement ///

Figure 27

1836 // release of cytochrome c from mitochondria // non-traceable author statement /// 6916 // anti-apoptosis // inferred from direct assay /// 6959 // humoral immune response // traceable author statement /// 8285 // negative regulation of cell proliferation // traceable author statement /// 42981 // regulation of apoptosis // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5739 // mitochondrion // inferred from electronic annotation /// 5741 // mitochondrial outer membrane // inferred from direct assay /// 5741 // mitochondrial outer membrane // traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // traceable author statement Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP /// Apoptosis_KEGG // GenMAPP /// Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP /// Apoptosis_KEGG // GenMAPP 596

222719_s_at Hs.570855 platelet derived growth factor C PDGFC 7417 // central nervous system development // traceable author statement 16020 // membrane // inferred from electronic annotation /// 5576 // extracellular region // non-traceable author statement 8083 // growth factor activity // inferred from electronic annotation /// 8083 // growth factor activity // traceable author statement --- 56034

210347_s_at Hs.370549 B-cell CLL/lymphoma 11A (zinc finger protein) BCL11A 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 30097 // hemopoiesis // non-traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation ---- 53335

235885_at Hs.591281 purinergic receptor P2Y, G-protein coupled, 12 P2RY12 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7599 // hemostasis // non-traceable author statement 16020 // membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 45028 // purinergic nucleotide receptor activity, G-protein coupled // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation GPCRDB_Class_A_Rhodopsin-like // GenMAPP 64805

212797_at Hs.485195 sortilin 1 SORT1 1503 // ossification // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6886 // intracellular protein transport // inferred from electronic annotation /// 6897 // endocytosis // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development //

Figure 28

inferred from electronic annotation 5764 // lysosome // inferred from electronic annotation /// 5768 // endosome // non-traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation
4872 // receptor activity // inferred from electronic annotation /// 8565 // protein transporter activity // inferred from electronic annotation /// 16492 // neurotensin receptor activity, G-protein coupled // non-traceable author statement --- 6272
219498_s_at Hs.370549 B-cell CLL/lymphoma 11A (zinc finger protein)
BCL11A 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 30097 // hemopoiesis // non-traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 53335
222071_s_at Hs.127648 solute carrier organic anion transporter family, member 4C1 SLCO4C1 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 353189
211668_s_at Hs.77274 plasminogen activator, urokinase /// plasminogen activator, urokinase PLAU 6508 // proteolysis // inferred from electronic annotation /// 6508 // proteolysis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7596 // blood coagulation // inferred from electronic annotation /// 42730 // fibrinolysis // inferred from electronic annotation /// 7596 // blood coagulation // not recorded 5615 // extracellular space // not recorded 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8243 // plasminogen activator activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Wnt_signaling // GenMAPP /// Blood_Clotting_Cascade // GenMAPP /// Wnt_signaling // GenMAPP /// Blood_Clotting_Cascade // GenMAPP /// Complement and coagulation cascades // KEGG 5328
216243_s_at Hs.81134 interleukin 1 receptor antagonist IL1RN 6954 // inflammatory response // not recorded /// 6955 // immune response // inferred from electronic annotation /// 6955 // immune response // non-traceable author statement 5615 // extracellular space // traceable author statement /// 5622 // intracellular // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation /// 5622 // intracellular // not recorded 5152 // interleukin-1 receptor antagonist activity // traceable author statement /// 5149 // interleukin-1 receptor binding // inferred from electronic annotation /// 5152 // interleukin-1 receptor antagonist activity // inferred from electronic annotation --- 3557
209545_s_at Hs.103755 receptor-interacting serine-threonine kinase 2
RIPK2 6468 // protein amino acid phosphorylation // inferred from

Figure 29

electronic annotation /// 6954 // inflammatory response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 42981 // regulation of apoptosis // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from expression pattern /// 6915 // apoptosis // inferred from electronic annotation /// 6915 // apoptosis // traceable author statement 5622 // intracellular // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // traceable author statement /// 4871 // signal transducer activity // inferred from expression pattern /// 5515 // protein binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 30274 // LIM domain binding // inferred from physical interaction /// 50700 // CARD domain binding // inferred from physical interaction /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // traceable author statement mTOR signaling pathway // KEGG /// Wnt signaling pathway // KEGG /// Dorso-ventral axis formation // KEGG /// Hedgehog signaling pathway // KEGG /// TGF-beta signaling pathway // KEGG /// Axon guidance // KEGG /// VEGF signaling pathway // KEGG /// Focal adhesion // KEGG /// Adherens junction // KEGG /// Tight junction // KEGG /// Gap junction // KEGG /// B cell receptor signaling pathway // KEGG /// Fc epsilon RI signaling pathway // KEGG /// Long-term potentiation // KEGG /// Long-term depression // KEGG /// Regulation of actin cytoskeleton // KEGG /// Insulin signaling pathway // KEGG /// Alzheimer's disease // KEGG 8767

212659_s_at Hs.81134 interleukin 1 receptor antagonist IL1RN 6954 // inflammatory response // not recorded /// 6955 // immune response // inferred from electronic annotation /// 6955 // immune response // non-traceable author statement 5615 // extracellular space // traceable author statement /// 5622 // intracellular // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation /// 5622 // intracellular // not recorded 5152 // interleukin-1 receptor antagonist activity // traceable author statement /// 5149 // interleukin-1 receptor binding // inferred from electronic annotation /// 5152 // interleukin-1 receptor antagonist activity // inferred from electronic annotation --- 3557

239196_at Hs.217484 ankyrin repeat domain 22 ANKRD22 --- --- --- --- 118932

242230_at Hs.434961 ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310

227475_at Hs.591352 forkhead box Q1 FOXQ1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 94234

Figure 30

1559078_at Hs.370549 B-cell CLL/lymphoma 11A (zinc finger protein) BCL11A 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 30097 // hemopoiesis // non-traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 53335

205220_at Hs.458425 G protein-coupled receptor 109B /// G protein-coupled receptor 109B GPR109B 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 45028 // purinergic nucleotide receptor activity, G-protein coupled // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // traceable author statement GPCRDB_Class_A_Rhodopsin-like2 // GenMAPP 8843

235236_at Hs.586174 Dedicator of cytokinesis 2 DOCK2 30036 // actin cytoskeleton organization and biogenesis // traceable author statement /// 48247 // lymphocyte chemotaxis // inferred from sequence or structural similarity 5856 // cytoskeleton // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 5515 // protein binding // inferred from physical interaction /// 5525 // GTP binding // inferred from electronic annotation /// 30676 // Rac guanyl-nucleotide exchange factor activity // inferred from direct assay /// 42608 // T cell receptor binding // inferred from direct assay /// 51020 // GTPase binding // inferred from electronic annotation /// 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation /// 5488 // binding // inferred from electronic annotation --- 1794

224009_x_at Hs.179608 dehydrogenase/reductase (SDR family) member 9 DHRS9 8152 // metabolism // inferred from electronic annotation /// 8209 // androgen metabolism // inferred from direct assay /// 30855 // epithelial cell differentiation // non-traceable author statement /// 42448 // progesterone metabolism // inferred from direct assay /// 42572 // retinol metabolism // non-traceable author statement /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from direct assay /// 8209 // androgen metabolism // inferred from sequence or structural similarity /// 30855 // epithelial cell differentiation // inferred from sequence or structural similarity /// 42572 // retinol metabolism // inferred from sequence or structural similarity /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from sequence or structural similarity 5792 // microsome // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 30176 // integral to endoplasmic reticulum membrane // inferred from direct assay /// 5792 // microsome // inferred from sequence or structural similarity /// 30176 // integral to endoplasmic reticulum membrane //

Figure 31

inferred from sequence or structural similarity 4022 // alcohol dehydrogenase activity // inferred from direct assay /// 4745 // retinol dehydrogenase activity // inferred from direct assay /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 16854 // racemase and epimerase activity // non-traceable author statement /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from direct assay /// 4022 // alcohol dehydrogenase activity // inferred from sequence or structural similarity /// 4745 // retinol dehydrogenase activity // inferred from sequence or structural similarity /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from sequence or structural similarity --- 10170
227792_at Hs.530899 Hypothetical protein LOC162073 LOC162073 --- --- --- --- 162073
234657_at Hs.545095 CDNA: FLJ23521 fis, clone LNG04928 --- --- --- --- ---
206760_s_at Hs.465778 Fc fragment of IgE, low affinity II, receptor for (CD23) FCER2 --- 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5057 // receptor signaling protein activity // not recorded /// 5178 // integrin binding // traceable author statement /// 5529 // sugar binding // inferred from electronic annotation /// 19863 // IgE binding // inferred from electronic annotation --- 2208
205479_s_at Hs.77274 plasminogen activator, urokinase PLAU 6508 // proteolysis // inferred from electronic annotation /// 6508 // proteolysis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7596 // blood coagulation // inferred from electronic annotation /// 42730 // fibrinolysis // inferred from electronic annotation /// 7596 // blood coagulation // not recorded 5615 // extracellular space // not recorded 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8243 // plasminogen activator activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Wnt_signaling // GenMAPP /// Blood_Clotting_Cascade // GenMAPP /// Wnt_signaling // GenMAPP /// Blood_Clotting_Cascade // GenMAPP /// Complement and coagulation cascades // KEGG 5328
1569040_s_at Hs.105323 similar to protein immuno-reactive with anti-PTH polyclonal antibodies FLJ40330 --- --- --- --- 645784 /// 648184
201554_x_at Hs.477892 glycogenin 1 GYG1 5978 // glycogen biosynthesis // inferred from electronic annotation /// 16051 // carbohydrate biosynthesis // inferred from electronic annotation --- 8466 // glycogenin glucosyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16758 // transferase activity, transferring hexosyl groups // inferred from electronic annotation /// 8466 // glycogenin glucosyltransferase activity // not recorded Glycogen_Metabolism // GenMAPP /// Glycogen_Metabolism // GenMAPP 2992
228785_at Hs.59757 Zinc finger protein 281 ZNF281 122 // negative regulation of transcription from RNA polymerase II promoter //

Figure 32

traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5665 // DNA-directed RNA polymerase II, core complex // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3704 // specific RNA polymerase II transcription factor activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 23528
226175_at Hs.31704 tetratricopeptide repeat domain 9C TTC9C ---
--- 5488 // binding // inferred from electronic annotation
--- 283237
1555250_a_at Hs.131683 cytoplasmic polyadenylation element binding protein 3 CPEB3 --- --- 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 22849
231412_at Hs.651324 hypothetical gene supported by BX538329
DKFZp686L14188 --- --- --- --- 441366
211275_s_at Hs.477892 glycogenin 1 GYG1 5978 // glycogen biosynthesis // inferred from electronic annotation /// 16051 // carbohydrate biosynthesis // inferred from electronic annotation ---
8466 // glycogenin glucosyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16758 // transferase activity, transferring hexosyl groups // inferred from electronic annotation /// 8466 // glycogenin glucosyltransferase activity // not recorded
Glycogen_Metabolism // GenMAPP /// Glycogen_Metabolism // GenMAPP 2992
201718_s_at Hs.486470 erythrocyte membrane protein band 4.1-like 2
EPB41L2 30866 // cortical actin cytoskeleton organization and biogenesis // inferred from electronic annotation 5737 // cytoplasm // inferred from electronic annotation /// 5856 // cytoskeleton // inferred from electronic annotation /// 5886 // plasma membrane // traceable author statement /// 8091 // spectrin // traceable author statement /// 16020 // membrane // inferred from electronic annotation
3779 // actin binding // inferred from electronic annotation /// 5198 // structural molecule activity // inferred from electronic annotation /// 5200 // structural constituent of cytoskeleton // not recorded /// 5488 // binding // inferred from electronic annotation /// 8092 // cytoskeletal protein binding // inferred from electronic annotation --- 2037
204777_s_at Hs.80395 mal, T-cell differentiation protein MAL 1766 // lipid raft polarization // traceable author statement /// 6917 // induction of apoptosis // non-traceable author statement /// 7165 // signal transduction // traceable author statement /// 7417 // central nervous system development // traceable author statement /// 7516 // hemocyte development (sensu Arthropoda) // traceable author statement /// 30154 // cell differentiation // traceable author statement /// 42552 // myelination // non-traceable author statement /// 42552 // myelination // traceable author statement /// 45176 // apical protein localization // traceable author statement 5624 // membrane fraction // traceable author statement /// 5626 // insoluble fraction // traceable author statement /// 5768 // endosome // traceable author statement /// 5783 // endoplasmic reticulum // inferred from direct assay /// 5887 // integral to plasma membrane // traceable author

Figure 33

statement /// 16020 // membrane // inferred from electronic annotation /// 16324 // apical plasma membrane // traceable author statement /// 45121 // lipid raft // inferred from direct assay /// 16021 // integral to membrane // inferred from electronic annotation 8289 // lipid binding // traceable author statement /// 15267 // channel or pore class transporter activity // traceable author statement /// 16505 // apoptotic protease activator activity // non-traceable author statement /// 19911 // structural constituent of myelin sheath // inferred from direct assay --- 4118
226498_at Hs.507621 Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) FLT1 1525 // angiogenesis // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7169 // transmembrane receptor protein tyrosine kinase signaling pathway // traceable author statement /// 7565 // pregnancy // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 30154 // cell differentiation // inferred from electronic annotation /// 7169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5615 // extracellular space // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4872 // receptor activity // traceable author statement /// 5021 // vascular endothelial growth factor receptor activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4714 // transmembrane receptor protein tyrosine kinase activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 5021 // vascular endothelial growth factor receptor activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 4714 // transmembrane receptor protein tyrosine kinase activity // traceable author statement --- 2321
1569666_s_at Hs.446021 Solute carrier family 37 (glycerol-3-phosphate transporter), member 3 SLC37A3 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 84255
212657_s_at Hs.81134 interleukin 1 receptor antagonist IL1RN 6954 // inflammatory response // not recorded /// 6955 // immune response // inferred from electronic annotation /// 6955 // immune response // non-traceable author statement 5615 // extracellular space // traceable author statement /// 5622 // intracellular // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation /// 5622 // intracellular // not recorded 5152 // interleukin-1 receptor antagonist activity // traceable author statement /// 5149 // interleukin-1 receptor binding // inferred from electronic annotation /// 5152 // interleukin-1 receptor antagonist activity // inferred from electronic annotation --- 3557

Figure 34

1555728_a_at Hs.325960 membrane-spanning 4-domains, subfamily A, member 4 MS4A4A 7165 // signal transduction // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 51338
230354_at Hs.135108 Transcribed locus --- --- --- --- --- ---
229568_at Hs.651275 MOB1, Mps One Binder kinase activator-like 2B (yeast) MOBKL2B --- --- 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 79817
209298_s_at Hs.160324 intersectin 1 (SH3 domain protein) ITSN1 35023 // regulation of Rho protein signal transduction // inferred from electronic annotation /// 48488 // synaptic vesicle endocytosis // traceable author statement /// 6897 // endocytosis // inferred from electronic annotation 5622 // intracellular // inferred from electronic annotation 5089 // Rho guanyl-nucleotide exchange factor activity // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5509 // calcium ion binding // inferred from electronic annotation /// 5085 // guanyl-nucleotide exchange factor activity // non-traceable author statement --- 6453
1559065_a_at Hs.220649 C-type lectin superfamily 4, member G CLEC4G --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5529 // sugar binding // inferred from electronic annotation --- 339390
205933_at Hs.435458 SET binding protein 1 SETBP1 --- 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation --- 26040
221169_s_at Hs.287388 histamine receptor H4 HRH4 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4969 // histamine receptor activity // non-traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation GPCRDB_Other // GenMAPP /// GPCRDB_Other // GenMAPP 59340
224836_at Hs.516994 tumor protein p53 inducible nuclear protein 2 TP53INP2 --- 5634 // nucleus // inferred from electronic annotation --- --- 58476
244570_at --- --- --- --- --- --- --- ---
223952_x_at Hs.179608 dehydrogenase/reductase (SDR family) member 9 DHRS9 8152 // metabolism // inferred from electronic annotation /// 8209 // androgen metabolism // inferred from direct assay /// 30855 // epithelial cell differentiation // non-traceable author statement /// 42448 // progesterone metabolism // inferred from direct assay /// 42572 // retinol metabolism // non-traceable author statement /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from direct assay /// 8209 // androgen metabolism // inferred from sequence or structural similarity /// 30855 // epithelial cell differentiation // inferred

Figure 35

from sequence or structural similarity /// 42572 // retinol metabolism // inferred from sequence or structural similarity /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from sequence or structural similarity 5792 // microsome // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 30176 // integral to endoplasmic reticulum membrane // inferred from direct assay /// 5792 // microsome // inferred from sequence or structural similarity /// 30176 // integral to endoplasmic reticulum membrane // inferred from sequence or structural similarity 4022 // alcohol dehydrogenase activity // inferred from direct assay /// 4745 // retinol dehydrogenase activity // inferred from direct assay /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 16854 // racemase and epimerase activity // non-traceable author statement /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from direct assay /// 4022 // alcohol dehydrogenase activity // inferred from sequence or structural similarity /// 4745 // retinol dehydrogenase activity // inferred from sequence or structural similarity /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from sequence or structural similarity --- 10170
202972_s_at Hs.97270 family with sequence similarity 13, member A1 FAM13A1 --- --- --- --- 10144
211573_x_at Hs.517033 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) TGM2 7186 // G-protein coupled receptor protein signaling pathway // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred from sequence or structural similarity /// 45785 // positive regulation of cell adhesion // inferred from sequence or structural similarity /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from mutant phenotype /// 18153 // isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine // inferred from direct assay /// 18149 // peptide cross-linking // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 12501 // programmed cell death // traceable author statement /// 19933 // cAMP-mediated signaling // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // non-traceable author statement 5578 // extracellular matrix (sensu Metazoa) // inferred from sequence or structural similarity /// 5829 // cytosol // inferred from sequence or structural similarity /// 16020 // membrane // inferred from sequence or structural similarity /// 5622 // intracellular // non-traceable author statement 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from sequence or structural similarity /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5525 // GTP binding // inferred from sequence or structural similarity /// 8415 // acyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // traceable author statement /// 3924 // GTPase activity // traceable author statement /// 5524 // ATP binding // traceable author statement /// 5525 // GTP binding // traceable author statement Complement and coagulation cascades // KEGG /// Huntington's disease // KEGG 7052

Figure 36

204067_at Hs.558403 sulfite oxidase SUOX 6118 // electron transport // inferred from electronic annotation /// 9087 // methionine catabolism // not recorded 5739 // mitochondrion // inferred from electronic annotation 5506 // iron ion binding // inferred from electronic annotation /// 8482 // sulfite oxidase activity // traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 30151 // molybdenum ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 8482 // sulfite oxidase activity // inferred from electronic annotation Sulfur metabolism // KEGG 6821
243179_at Hs.408455 CDNA FLJ33993 fis, clone DFNES2007757 ---
--- --- --- --- ---
205228_at Hs.645521 RNA binding motif, single stranded interacting protein 2 RBMS2 6396 // RNA processing // traceable author statement /// 6445 // regulation of translation // traceable author statement
5634 // nucleus // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation --- 5939
231042_s_at Hs.643629 Transcribed locus --- --- --- --- ---

206759_at Hs.465778 Fc fragment of IgE, low affinity II, receptor for (CD23) FCER2 --- 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5057 // receptor signaling protein activity // not recorded /// 5178 // integrin binding // traceable author statement /// 5529 // sugar binding // inferred from electronic annotation /// 19863 // IgE binding // inferred from electronic annotation --- 2208
215968_at Hs.130195 Family with sequence similarity 55, member C FAM55C --- --- --- --- 91775
210612_s_at Hs.434494 synaptojanin 2 SYNJ2 --- --- 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 4439 // phosphoinositide 5-phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 4437 // inositol or phosphatidylinositol phosphatase activity // inferred from electronic annotation --- 8871
206756_at Hs.129955 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7 CHST7 5976 // polysaccharide metabolism // traceable author statement /// 6044 // N-acetylglucosamine metabolism // inferred from direct assay /// 6790 // sulfur metabolism // inferred from direct assay /// 30206 // chondroitin sulfate biosynthesis // inferred from direct assay /// 5975 // carbohydrate metabolism // inferred from electronic annotation 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // traceable author statement /// 31228 // intrinsic to Golgi membrane // inferred from sequence or structural similarity /// 16021 // integral to membrane // inferred from electronic annotation 1517 // N-acetylglucosamine 6-O-sulfotransferase activity // inferred from direct assay /// 8459 // chondroitin 6-sulfotransferase activity // inferred

Figure 37

from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 8146 // sulfotransferase activity // inferred from electronic annotation --- 56548
212173_at Hs.470907 adenylate kinase 2 AK2 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // inferred from electronic annotation 5739 // mitochondrion // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4017 // adenylate kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4017 // adenylate kinase activity // inferred from electronic annotation /// 16776 // phosphotransferase activity, phosphate group as acceptor // inferred from electronic annotation /// 19201 // nucleotide kinase activity // inferred from electronic annotation Purine metabolism // KEGG 204
222343_at Hs.469658 BCL2-like 11 (apoptosis facilitator) BCL2L11 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 43065 // positive regulation of apoptosis // inferred from electronic annotation 5624 // membrane fraction // traceable author statement /// 16020 // membrane // inferred from electronic annotation 5515 // protein binding // inferred from physical interaction Apoptosis // GenMAPP /// Apoptosis // GenMAPP 10018
227478_at --- hypothetical protein LOC284262 LOC284262 --- --- --- --- 284262
235558_at Hs.648783 Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group) FUT1 5975 // carbohydrate metabolism // traceable author statement /// 6486 // protein amino acid glycosylation // traceable author statement /// 42355 // L-fucose catabolism // non-traceable author statement /// 6396 // RNA processing // traceable author statement /// 6445 // regulation of translation // traceable author statement 5624 // membrane fraction // traceable author statement /// 5795 // Golgi stack // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation 8107 // galactoside 2-alpha-L-fucosyltransferase activity // traceable author statement /// 8417 // fucosyltransferase activity // traceable author statement /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement Blood group glycolipid biosynthesis - lactoseries // KEGG /// Blood group glycolipid biosynthesis - // KEGG /// Globoside metabolism // KEGG /// Glycan structures - biosynthesis 2 // KEGG 2523
231234_at Hs.128065 cathepsin C CTSC 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 6508 // proteolysis // not recorded 5764 // lysosome // traceable author statement /// 5764 // lysosome // inferred from electronic annotation 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4214 // dipeptidyl-peptidase I activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred

Figure 38

from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1075
225647_s_at Hs.128065 cathepsin C CTSC 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 6508 // proteolysis // not recorded 5764 // lysosome // traceable author statement /// 5764 // lysosome // inferred from electronic annotation 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4214 // dipeptidyl-peptidase I activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1075
216950_s_at Hs.77424 Fc fragment of IgG, high affinity Ia, receptor (CD64) FCGR1A 6911 // phagocytosis, engulfment // traceable author statement /// 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6955 // immune response // non-traceable author statement 5887 // integral to plasma membrane // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5886 // plasma membrane // non-traceable author statement 4872 // receptor activity // inferred from electronic annotation /// 5057 // receptor signaling protein activity // traceable author statement /// 19864 // IgG binding // inferred from electronic annotation /// 19763 // immunoglobulin receptor activity // non-traceable author statement --- 2209
228486_at Hs.573495 solute carrier family 44, member 1 SLC44A1 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 23446
205773_at Hs.131683 cytoplasmic polyadenylation element binding protein 3 CPEB3 --- --- 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 22849
235898_at Hs.446292 Transcribed locus, strongly similar to XP_515434.1 hypothetical protein XP_515434 [Pan troglodytes] --- --- --- --- ---
227954_at Hs.530899 hypothetical protein LOC162073 LOC162073 --- --- --- --- 162073
1554607_at Hs.632794 connector enhancer of kinase suppressor of Ras 2 CNKSR2 9966 // regulation of signal transduction // inferred from electronic annotation 5737 // cytoplasm // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 5515 // protein binding // inferred from electronic annotation --- 22866
214511_x_at Hs.534956 Fc fragment of IgG, high affinity Ib, receptor (CD64) FCGR1B 6911 // phagocytosis, engulfment // traceable author statement /// 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6955 // immune response // non-traceable author statement 5887 // integral to plasma membrane // not recorded /// 16020 // membrane // inferred from electronic annotation /// 5886 // plasma membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5057 // receptor signaling protein activity // traceable author statement /// 19864 // IgG binding

Figure 39

// inferred from electronic annotation /// 19763 // immunoglobulin receptor activity // non-traceable author statement --- 2209 /// 440607 /// 652758
205258_at Hs.1735 inhibin, beta B (activin AB beta polypeptide) INHBB 1541 // ovarian follicle development // non-traceable author statement /// 6952 // defense response // traceable author statement /// 9605 // response to external stimulus // inferred from direct assay /// 30154 // cell differentiation // non-traceable author statement /// 40007 // growth // inferred from electronic annotation /// 46881 // positive regulation of follicle-stimulating hormone secretion // inferred from physical interaction /// 46882 // negative regulation of follicle-stimulating hormone secretion // inferred from physical interaction /// 48178 // negative regulation of hepatocyte growth factor biosynthesis // inferred from direct assay 5576 // extracellular region // traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 5125 // cytokine activity // traceable author statement /// 5179 // hormone activity // traceable author statement /// 8083 // growth factor activity // inferred from electronic annotation /// 42803 // protein homodimerization activity // inferred from physical interaction /// 46789 // host cell surface receptor binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5179 // hormone activity // inferred from electronic annotation /// 5102 // receptor binding // non-traceable author statement --- 3625
1568593_a_at Hs.380350 nudix (nucleoside diphosphate linked moiety X)-type motif 16 pseudogene NUDT16P --- --- --- --- 152195
232628_at Hs.97270 Family with sequence similarity 13, member A1 FAM13A1 --- --- --- --- 10144
206513_at Hs.281898 absent in melanoma 2 AIM2 6955 // immune response // traceable author statement /// 6955 // immune response // inferred from electronic annotation --- --- --- 9447
1555536_at Hs.162963 anthrax toxin receptor 2 ANTXR2 --- 5783 // endoplasmic reticulum // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 46872 // metal ion binding // inferred from electronic annotation --- 118429
218854_at --- squamous cell carcinoma antigen recognized by T cells 2 SART2 --- 5783 // endoplasmic reticulum // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 29940
206576_s_at Hs.512682 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) CEACAM1 1525 // angiogenesis // non-traceable author statement /// 7156 // homophilic cell adhesion // non-traceable author statement /// 7229 // integrin-mediated signaling pathway // non-traceable author statement /// 7565 // pregnancy // traceable author statement /// 16477 // cell migration // non-traceable author statement 5624 // membrane fraction // traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 634

Figure 40

239108_at Hs.298851 Male sterility domain containing 1 MLSTD1 --- --- --- --- 55711
226706_at --- hypothetical protein FLJ23867 FLJ23867 --- --- --- --- 200058
226456_at Hs.347524 chromosome 16 open reading frame 75 C16orf75 --- --- 3676 // nucleic acid binding // inferred from electronic annotation --- 116028
223241_at Hs.584900 sorting nexin 8 SNX8 7242 // intracellular signaling cascade // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation --- 5515 // protein binding // inferred from electronic annotation /// 35091 // phosphoinositide binding // inferred from electronic annotation --- 29886
243969_at Hs.510281 solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 SLC24A4 6811 // ion transport // inferred from electronic annotation /// 6813 // potassium ion transport // inferred from electronic annotation /// 6814 // sodium ion transport // inferred from electronic annotation /// 6816 // calcium ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5509 // calcium ion binding // inferred from electronic annotation /// 15293 // symporter activity // inferred from electronic annotation /// 15297 // antiporter activity // inferred from electronic annotation /// 30955 // potassium ion binding // inferred from electronic annotation /// 31402 // sodium ion binding // inferred from electronic annotation --- 123041
208536_s_at Hs.469658 BCL2-like 11 (apoptosis facilitator) BCL2L11 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 43065 // positive regulation of apoptosis // inferred from electronic annotation 5624 // membrane fraction // traceable author statement /// 16020 // membrane // inferred from electronic annotation 5515 // protein binding // inferred from physical interaction Apoptosis // GenMAPP /// Apoptosis // GenMAPP 10018
218979_at Hs.284137 RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae) RMI1 --- --- 3676 // nucleic acid binding // inferred from electronic annotation --- 80010
235918_x_at --- --- --- --- --- --- --- ---
232232_s_at Hs.520319 solute carrier family 22 (organic cation transporter), member 16 SLC22A16 7338 // fertilization (sensu Metazoa) // inferred from mutant phenotype /// 30317 // sperm motility // inferred from mutant phenotype /// 7286 // spermatid development // inferred from sequence or structural similarity /// 15695 // organic cation transport // inferred from sequence or structural similarity /// 15879 // carnitine transport // inferred from sequence or structural similarity /// 15695 // organic cation transport // inferred from direct assay /// 15879 // carnitine transport // inferred from direct assay /// 46717 // acid secretion // inferred from direct assay /// 6810 // transport // inferred from electronic annotation /// 7286 // spermatid development // non-traceable author statement 16021 // integral to membrane // inferred from sequence or structural similarity /// 5886 // plasma membrane // inferred from direct assay /// 16021 // integral to membrane // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 15226 //

Figure 41

carnitine transporter activity // inferred from sequence or structural similarity /// 15226 // carnitine transporter activity // inferred from direct assay /// 5215 // transporter activity // inferred from electronic annotation /// 15075 // ion transporter activity // non-traceable author statement --- 85413
219799_s_at Hs.179608 dehydrogenase/reductase (SDR family) member 9 DHRS9 8152 // metabolism // inferred from electronic annotation /// 8209 // androgen metabolism // inferred from direct assay /// 30855 // epithelial cell differentiation // non-traceable author statement /// 42448 // progesterone metabolism // inferred from direct assay /// 42572 // retinol metabolism // non-traceable author statement /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from direct assay /// 8209 // androgen metabolism // inferred from sequence or structural similarity /// 30855 // epithelial cell differentiation // inferred from sequence or structural similarity /// 42572 // retinol metabolism // inferred from sequence or structural similarity /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from sequence or structural similarity 5792 // microsome // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 30176 // integral to endoplasmic reticulum membrane // inferred from direct assay /// 5792 // microsome // inferred from sequence or structural similarity /// 30176 // integral to endoplasmic reticulum membrane // inferred from sequence or structural similarity 4022 // alcohol dehydrogenase activity // inferred from direct assay /// 4745 // retinol dehydrogenase activity // inferred from direct assay /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 16854 // racemase and epimerase activity // non-traceable author statement /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from direct assay /// 4022 // alcohol dehydrogenase activity // inferred from sequence or structural similarity /// 4745 // retinol dehydrogenase activity // inferred from sequence or structural similarity /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from sequence or structural similarity --- 10170
227514_at Hs.648523 CDNA clone IMAGE:4402981 --- --- --- --- --- 162073
242388_x_at --- --- --- --- --- --- --- ---
1554835_a_at Hs.208267 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 B3GNT5 7417 // central nervous system development // inferred from direct assay /// 6486 // protein amino acid glycosylation // inferred from electronic annotation /// 6486 // protein amino acid glycosylation // traceable author statement /// 9247 // glycolipid biosynthesis // traceable author statement 5622 // intracellular // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation 8457 // beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,3-acetylglucosaminyltransferase activity // inferred from direct assay /// 8378 // galactosyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation --- 84002
231771_at Hs.511757 gap junction protein, beta 6 (connexin 30) GJB6 7154 // cell communication // inferred from electronic annotation /// 7605 // sensory perception of sound // traceable author statement /// 7605 // sensory perception of sound // inferred from electronic annotation 5922 // connexon complex // inferred from electronic annotation /// 16020 // membrane // inferred from electronic

Figure 42

annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5921 // gap junction // inferred from electronic annotation 15285 // connexon channel activity // inferred from electronic annotation Calcium_regulation_in_cardiac_cells // GenMAPP 10804
224863_at Hs.269782 Guanine nucleotide binding protein (G protein), q polypeptide GNAQ 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7596 // blood coagulation // traceable author statement 5737 // cytoplasm // traceable author statement /// 5834 // heterotrimeric G-protein complex // not recorded /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 2776
227239_at Hs.85603 family with sequence similarity 126, member A FAM126A --- --- 4871 // signal transducer activity // non-traceable author statement --- 84668
235889_at Hs.618649 Transcribed locus --- --- --- --- --- ---
220162_s_at Hs.647176 caspase recruitment domain family, member 9 CARD9 42981 // regulation of apoptosis // inferred from electronic annotation 5622 // intracellular // inferred from electronic annotation 5515 // protein binding // inferred from electronic annotation --- 64170
231793_s_at Hs.144114 calcium/calmodulin-dependent protein kinase (CaM kinase) II delta CAMK2D 1558 // regulation of cell growth // non-traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // non-traceable author statement 5954 // calcium- and calmodulin-dependent protein kinase complex // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // non-traceable author statement /// 5516 // calmodulin binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 5524 // ATP binding // non-traceable author statement /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation Calcium_regulation_in_cardiac_cells // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP 817
225622_at Hs.266175 phosphoprotein associated with glycosphingolipid microdomains 1 PAG1 6955 // immune response //

Figure 43

inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 55824
235278_at Hs.570367 chromosome 20 open reading frame 133 C20orf133 --- --- --- --- 140733
209297_at Hs.160324 intersectin 1 (SH3 domain protein) ITSN1 35023 // regulation of Rho protein signal transduction // inferred from electronic annotation /// 48488 // synaptic vesicle endocytosis // traceable author statement /// 6897 // endocytosis // inferred from electronic annotation 5622 // intracellular // inferred from electronic annotation 5089 // Rho guanyl-nucleotide exchange factor activity // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5509 // calcium ion binding // inferred from electronic annotation /// 5085 // guanyl-nucleotide exchange factor activity // non-traceable author statement --- 6453
216504_s_at Hs.288034 Solute carrier family 39 (zinc transporter), member 8 SLC39A8 30001 // metal ion transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 46873 // metal ion transporter activity // inferred from electronic annotation --- 64116
222619_at Hs.59757 zinc finger protein 281 ZNF281 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5665 // DNA-directed RNA polymerase II, core complex // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3704 // specific RNA polymerase II transcription factor activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 23528
216015_s_at Hs.159483 NLR family, pyrin domain containing 3 NLRP3 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // non-traceable author statement /// 6952 // defense response // traceable author statement /// 6954 // inflammatory response // inferred from mutant phenotype /// 7165 // signal transduction // non-traceable author statement /// 7605 // sensory perception of sound // inferred from electronic annotation /// 9595 // detection of biotic stimulus // traceable author statement /// 51259 // protein oligomerization // traceable author statement 5737 // cytoplasm // traceable author statement 42834 // peptidoglycan binding // traceable author statement --- 114548
229070_at Hs.126409 chromosome 6 open reading frame 105 C6orf105 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 84830
1552542_s_at Hs.529984 T-cell activation GTPase activating protein TAGAP --- --- 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation --- 117289
223713_at Hs.154628 radial spokehead-like 2 RSHL2 --- --- --- --- 83861
209921_at Hs.390594 solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 SLC7A11 6461 // protein complex assembly // not recorded /// 6810 // transport // inferred from

Figure 44

electronic annotation /// 6865 // amino acid transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 15327 // cystine:glutamate antiporter activity // traceable author statement /// 15359 // amino acid permease activity // inferred from electronic annotation /// 5279 // amino acid-polyamine transporter activity // inferred from electronic annotation /// 15171 // amino acid transporter activity // inferred from electronic annotation --- 23657
215573_at Hs.502302 Catalase CAT 6118 // electron transport // inferred from electronic annotation /// 6979 // response to oxidative stress // inferred from electronic annotation /// 42744 // hydrogen peroxide catabolism // inferred from electronic annotation 5777 // peroxisome // inferred from electronic annotation 4096 // catalase activity // traceable author statement /// 5506 // iron ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4096 // catalase activity // inferred from electronic annotation /// 4601 // peroxidase activity // inferred from electronic annotation Tryptophan metabolism // KEGG /// Methane metabolism // KEGG /// Amyotrophic lateral sclerosis (ALS) // KEGG 847
224861_at Hs.269782 Guanine nucleotide binding protein (G protein), q polypeptide GNAQ 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7596 // blood coagulation // traceable author statement 5737 // cytoplasm // traceable author statement /// 5834 // heterotrimeric G-protein complex // not recorded /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 2776
202973_x_at Hs.97270 family with sequence similarity 13, member A1 FAM13A1 --- --- --- --- 10144
220615_s_at Hs.298851 male sterility domain containing 1 MLSTD1 --- --- --- --- 55711
34187_at Hs.645521 RNA binding motif, single stranded interacting protein 2 RBMS2 6396 // RNA processing // traceable author statement /// 6445 // regulation of translation // traceable author statement 5634 // nucleus // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation --- 5939
222154_s_at Hs.120323 DNA polymerase-transactivated protein 6 DNAPTP6 --- --- --- --- 26010
204925_at Hs.187667 cystinosis, nephropathic CTNS 6520 // amino acid metabolism // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 15811 // L-cystine transport // traceable author statement 5765 // lysosomal membrane //

Figure 45

traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 5764 // lysosome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // not recorded 15184 // L-cystine transporter activity // traceable author statement --- 1497
1569624_at Hs.382630 Homo sapiens, clone IMAGE:4248008, mRNA --- --- --- --- ---
207596_at --- --- --- --- --- --- --- ---
232210_at Hs.150749 B-cell CLL/lymphoma 2 BCL2 74 // regulation of progression through cell cycle // traceable author statement /// 1836 // release of cytochrome c from mitochondria // non-traceable author statement /// 6916 // anti-apoptosis // inferred from direct assay /// 6959 // humoral immune response // traceable author statement /// 8285 // negative regulation of cell proliferation // traceable author statement /// 42981 // regulation of apoptosis // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5739 // mitochondrion // inferred from electronic annotation /// 5741 // mitochondrial outer membrane // inferred from direct assay /// 5741 // mitochondrial outer membrane // traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // traceable author statement Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP /// Apoptosis_KEGG // GenMAPP /// Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP /// Apoptosis_KEGG // GenMAPP 596
218880_at Hs.220971 FOS-like antigen 2 FOSL2 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 8219 // cell death // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 2355
203627_at Hs.592020 Insulin-like growth factor 1 receptor IGF1R 74 // regulation of progression through cell cycle // traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 7165 // signal transduction // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 8286 // insulin receptor signaling pathway // traceable author statement /// 46777 // protein amino acid autophosphorylation // inferred from direct assay /// 48009 // insulin-like growth factor receptor signaling pathway // inferred from direct assay /// 51262 // protein tetramerization // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // Unknown /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral

Figure 46

to membrane // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 5006 // epidermal growth factor receptor activity // inferred from electronic annotation /// 5010 // insulin-like growth factor receptor activity // inferred from direct assay /// 5520 // insulin-like growth factor binding // inferred from direct assay /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 43548 // phosphoinositide 3-kinase binding // inferred from physical interaction /// 43560 // insulin receptor substrate binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 4713 // protein-tyrosine kinase activity // inferred from direct assay /// 4672 // protein kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4714 // transmembrane receptor protein tyrosine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 5010 // insulin-like growth factor receptor activity // traceable author statement --- 3480
211810_s_at Hs.513439 galactosylceramidase GALC 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6683 // galactosylceramide catabolism // inferred from electronic annotation 5764 // lysosome // traceable author statement 4336 // galactosylceramidase activity // inferred from electronic annotation /// 16798 // hydrolase activity, acting on glycosyl bonds // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 2581
1560679_at Hs.516245 hypothetical protein LOC151438 LOC151438 --- --- --- --- 151438
232744_x_at Hs.434961 Ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310
229373_at Hs.457403 Transcribed locus --- --- --- --- --- ---
219607_s_at Hs.325960 membrane-spanning 4-domains, subfamily A, member 4 MS4A4A 7165 // signal transduction // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 51338
235920_at Hs.594098 Transcribed locus --- --- --- --- --- ---
236404_at Hs.434961 Ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310
1569189_at Hs.31704 tetratricopeptide repeat domain 9C TTC9C --- --- 5488 // binding // inferred from electronic annotation --- 283237
211372_s_at Hs.25333 interleukin 1 receptor, type II IL1R2 6955 // immune response // traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor

Figure 47

activity // inferred from electronic annotation /// 4910 // interleukin-1, Type II, blocking receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // traceable author statement --- 7850
223158_s_at Hs.197071 NIMA (never in mitosis gene a)-related kinase 6 NEK6 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from mutant phenotype 5634 // nucleus // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from mutant phenotype /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 10783
228790_at Hs.154652 chromosome 8 open reading frame 72 C8orf72 --- --- --- --- 90362
209999_x_at Hs.50640 suppressor of cytokine signaling 1 SOCS1 1558 // regulation of cell growth // inferred from electronic annotation /// 1932 // regulation of protein amino acid phosphorylation // inferred from sequence or structural similarity /// 6512 // ubiquitin cycle // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // inferred from sequence or structural similarity /// 42518 // negative regulation of tyrosine phosphorylation of Stat3 protein // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // non-traceable author statement /// 46627 // negative regulation of insulin receptor signaling pathway // inferred from sequence or structural similarity /// 9968 // negative regulation of signal transduction // inferred from electronic annotation 5737 // cytoplasm // traceable author statement 4860 // protein kinase inhibitor activity // traceable author statement /// 5159 // insulin-like growth factor receptor binding // inferred from physical interaction /// 19901 // protein kinase binding // inferred from physical interaction /// 19210 // kinase inhibitor activity // inferred from sequence or structural similarity --- 8651
229723_at Hs.529984 T-cell activation GTPase activating protein TAGAP --- --- 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation --- 117289
238363_at Hs.502302 Catalase CAT 6118 // electron transport // inferred from electronic annotation /// 6979 // response to oxidative stress // inferred from electronic annotation /// 42744 // hydrogen peroxide catabolism // inferred from electronic annotation 5777 // peroxisome // inferred from electronic annotation 4096 // catalase activity // traceable author statement /// 5506 // iron ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4096 // catalase

Figure 48

activity // inferred from electronic annotation /// 4601 // peroxidase activity // inferred from electronic annotation Tryptophan metabolism // KEGG /// Methane metabolism // KEGG /// Amyotrophic lateral sclerosis (ALS) // KEGG 847
205403_at Hs.25333 interleukin 1 receptor, type II IL1R2 6955 // immune response // traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4910 // interleukin-1, Type II, blocking receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // traceable author statement --- 7850
225612_s_at Hs.208267 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 B3GNT5 6486 // protein amino acid glycosylation // inferred from electronic annotation /// 7417 // central nervous system development // inferred from direct assay /// 6486 // protein amino acid glycosylation // traceable author statement /// 9247 // glycolipid biosynthesis // traceable author statement 16020 // membrane // inferred from electronic annotation /// 5622 // intracellular // inferred from direct assay 8378 // galactosyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 8457 // beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,3-acetylglucosaminyltransferase activity // inferred from direct assay --- 84002
203305_at Hs.335513 coagulation factor XIII, A1 polypeptide F13A1 7596 // blood coagulation // traceable author statement /// 18149 // peptide cross-linking // inferred from electronic annotation /// 7596 // blood coagulation // inferred from electronic annotation 5576 // extracellular region // traceable author statement 3810 // protein-glutamine gamma-glutamyltransferase activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 8415 // acyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation
Complement and coagulation cascades // KEGG /// Huntington's disease // KEGG 2162
218401_s_at Hs.59757 zinc finger protein 281 ZNF281 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5665 // DNA-directed RNA polymerase II, core complex // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3704 // specific RNA polymerase II transcription factor activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 23528
205095_s_at Hs.463074 ATPase, H+ transporting, lysosomal V0 subunit a1 ATP6V0A1 6811 // ion transport // inferred from electronic

Figure 49

annotation /// 15992 // proton transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 15078 // hydrogen ion transporter activity // inferred from electronic annotation Oxidative phosphorylation // KEGG /// ATP synthesis // KEGG /// Photosynthesis // KEGG /// Flagellar assembly // KEGG /// Type III secretion system // KEGG /// Epithelial cell signaling in Helicobacter pylori // KEGG 535
213030_s_at Hs.497626 plexin A2 PLXNA2 7275 // development // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 5362
214738_s_at Hs.7200 NIMA (never in mitosis gene a)- related kinase 9 NEK9 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7067 // mitosis // inferred from electronic annotation /// 51301 // cell division // inferred from electronic annotation --- 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 91754
201487_at Hs.128065 cathepsin C CTSC 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 6508 // proteolysis // not recorded 5764 // lysosome // traceable author statement /// 5764 // lysosome // inferred from electronic annotation 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4214 // dipeptidyl-peptidase I activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1075
224862_at Hs.269782 Guanine nucleotide binding protein (G protein), q polypeptide GNAQ 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7596 // blood coagulation // traceable author statement 5737 // cytoplasm // traceable author statement /// 5834 // heterotrimeric G-protein complex // not recorded /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 2776
226931_at Hs.401954 transmembrane and tetratricopeptide repeat containing 1 TMTC1 --- --- 5488 // binding // inferred from

Figure 50

electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation --- 653626 /// 83857
203060_s_at Hs.524491 3'-phosphoadenosine 5'-phosphosulfate synthase 2 PAPSS2 103 // sulfate assimilation // inferred from electronic annotation /// 1501 // skeletal development // inferred from sequence or structural similarity /// 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // not recorded /// 1501 // skeletal development // traceable author statement 5622 // intracellular // inferred from sequence or structural similarity 166 // nucleotide binding // inferred from electronic annotation /// 4020 // adenylylsulfate kinase activity // inferred from electronic annotation /// 4781 // sulfate adenylyltransferase (ATP) activity // inferred from sequence or structural similarity /// 5524 // ATP binding // inferred from sequence or structural similarity /// 16779 // nucleotidyltransferase activity // inferred from sequence or structural similarity /// 16740 // transferase activity // inferred from sequence or structural similarity /// 3824 // catalytic activity // inferred from electronic annotation /// 4781 // sulfate adenylyltransferase (ATP) activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16772 // transferase activity, transferring phosphorus-containing groups // inferred from electronic annotation /// 16779 // nucleotidyltransferase activity // inferred from electronic annotation Purine metabolism // KEGG /// Selenoamino acid metabolism // KEGG /// Sulfur metabolism // KEGG /// Purine metabolism // KEGG /// Selenoamino acid metabolism // KEGG /// Sulfur metabolism // KEGG 9060
36566_at Hs.187667 cystinosis, nephropathic CTNS 6520 // amino acid metabolism // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 15811 // L-cystine transport // traceable author statement 5765 // lysosomal membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 5764 // lysosome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // not recorded 15184 // L-cystine transporter activity // traceable author statement --- 1497
205016_at Hs.170009 transforming growth factor, alpha TGFA 74 // regulation of progression through cell cycle // inferred from electronic annotation /// 7267 // cell-cell signaling // not recorded /// 8283 // cell proliferation // traceable author statement /// 8283 // cell proliferation // inferred from electronic annotation 5615 // extracellular space // not recorded /// 5625 // soluble fraction // not recorded /// 5886 // plasma membrane // non-traceable author statement /// 5887 // integral to plasma membrane // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4713 // protein-tyrosine kinase activity // traceable author statement /// 4871 // signal transducer activity // traceable author statement /// 5155 // epidermal growth factor receptor activating ligand activity // not recorded /// 5515 // protein binding // traceable author statement /// 8083 // growth factor activity // inferred from electronic annotation --- 7039

Figure 51

1567101_at Hs.129452 Dachshund homolog 1 (Drosophila) DACH1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7456 // eye development (sensu Endopterygota) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction --- 1602
209498_at Hs.512682 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) CEACAM1 1525 // angiogenesis // non-traceable author statement /// 7156 // homophilic cell adhesion // non-traceable author statement /// 7229 // integrin-mediated signaling pathway // non-traceable author statement /// 7565 // pregnancy // traceable author statement /// 16477 // cell migration // non-traceable author statement 5624 // membrane fraction // traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 634
230179_at Hs.593631 hypothetical protein LOC285812 LOC285812 --- --- --- --- 285812
202615_at Hs.269782 Guanine nucleotide binding protein (G protein), q polypeptide GNAQ 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7596 // blood coagulation // traceable author statement 5737 // cytoplasm // traceable author statement /// 5834 // heterotrimeric G-protein complex // not recorded /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 2776
210715_s_at Hs.31439 serine peptidase inhibitor, Kunitz type, 2 SPINT2 6928 // cell motility // traceable author statement 5576 // extracellular region // traceable author statement /// 5625 // soluble fraction // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4867 // serine-type endopeptidase inhibitor activity // traceable author statement /// 4866 // endopeptidase inhibitor activity // inferred from electronic annotation /// 4867 // serine-type endopeptidase inhibitor activity // inferred from electronic annotation /// 4866 // endopeptidase inhibitor activity // traceable author statement --- 10653
228555_at Hs.144114 Calcium/calmodulin-dependent protein kinase (CaM kinase) II delta CAMK2D 1558 // regulation of cell growth // non-traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // non-traceable author statement 5954 // calcium- and calmodulin-dependent protein kinase complex

Figure 52

// traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // non-traceable author statement /// 5516 // calmodulin binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 5524 // ATP binding // non-traceable author statement /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
Calcium_regulation_in_cardiac_cells // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP 817
223461_at Hs.484678 TBC1 domain family, member 7 TBC1D7 --- --- 5096 // GTPase activator activity // inferred from electronic annotation --- 51256
223834_at Hs.521989 CD274 molecule CD274 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 8283 // cell proliferation // traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 29126
1552263_at Hs.431850 mitogen-activated protein kinase 1 MAPK1 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 6950 // response to stress // traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7268 // synaptic transmission // traceable author statement --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
MAPK_Cascade // GenMAPP /// S1P_Signaling // GenMAPP 5594
224994_at Hs.144114 calcium/calmodulin-dependent protein kinase (CaM kinase) II delta CAMK2D 1558 // regulation of cell growth // non-traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // non-traceable author statement
5954 // calcium- and calmodulin-dependent protein kinase complex // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // non-traceable author statement /// 5516 // calmodulin binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from

Figure 53

electronic annotation /// 5524 // ATP binding // non-traceable author statement /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
Calcium_regulation_in_cardiac_cells // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP 817
212807_s_at Hs.485195 sortilin 1 SORT1 1503 // ossification // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6886 // intracellular protein transport // inferred from electronic annotation /// 6897 // endocytosis // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5764 // lysosome // inferred from electronic annotation /// 5768 // endosome // non-traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation
4872 // receptor activity // inferred from electronic annotation /// 8565 // protein transporter activity // inferred from electronic annotation /// 16492 // neurotensin receptor activity, G-protein coupled // non-traceable author statement --- 6272
205472_s_at Hs.129452 dachshund homolog 1 (Drosophila) DACH1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7456 // eye development (sensu Endopterygota) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction --- 1602
220358_at Hs.62919 Jun dimerization protein p21SNFT SNFT 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement /// 9613 // response to pest, pathogen or parasite // traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3700 // transcription factor activity // traceable author statement /// 3714 // transcription corepressor activity // traceable author statement ---
55509
228231_at Hs.594383 MRNA; cDNA DKFZp761E1721 (from clone DKFZp761E1721) --- --- --- --- --- ---
1560224_at Hs.300887 AT hook containing transcription factor 1
AHCTF1 --- --- --- --- 25909
219821_s_at Hs.484686 glucose-fructose oxidoreductase domain containing 1 GFOD1 6118 // electron transport // inferred from

Figure 54

electronic annotation /// 8152 // metabolism // inferred from electronic annotation --- 16491 // oxidoreductase activity // inferred from electronic annotation --- 54438
215268_at --- hypothetical LOC643314 KIAA0754 --- --- --- --- 643314
204417_at Hs.513439 galactosylceramidase GALC 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6683 // galactosylceramide catabolism // inferred from electronic annotation 5764 // lysosome // traceable author statement 4336 // galactosylceramidase activity // inferred from electronic annotation /// 16798 // hydrolase activity, acting on glycosyl bonds // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 2581
211478_s_at Hs.368912 dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2) DPP4 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4177 // aminopeptidase activity // inferred from electronic annotation /// 4274 // dipeptidyl-peptidase IV activity // traceable author statement /// 4287 // prolyl oligopeptidase activity // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 4274 // dipeptidyl-peptidase IV activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8236 // serine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1803
205409_at Hs.220971 FOS-like antigen 2 FOSL2 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 8219 // cell death // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 2355
237953_at Hs.368912 Dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2) DPP4 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4177 // aminopeptidase activity // inferred from electronic annotation /// 4274 // dipeptidyl-peptidase IV activity // traceable author statement /// 4287 // prolyl oligopeptidase activity // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 4274 // dipeptidyl-peptidase IV activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8236 // serine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1803

Figure 55

207075_at Hs.159483 NLR family, pyrin domain containing 3 NLRP3 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // non-traceable author statement /// 6952 // defense response // traceable author statement /// 6954 // inflammatory response // inferred from mutant phenotype /// 7165 // signal transduction // non-traceable author statement /// 7605 // sensory perception of sound // inferred from electronic annotation /// 9595 // detection of biotic stimulus // traceable author statement /// 51259 // protein oligomerization // traceable author statement 5737 // cytoplasm // traceable author statement 42834 // peptidoglycan binding // traceable author statement --- 114548
214438_at Hs.74870 H2.0-like homeobox 1 (Drosophila) HLX1 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // not recorded /// 7275 // development // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3677 // DNA binding // not recorded --- 3142
238452_at Hs.517422 Fc receptor-like B FCRLB --- --- 4872 // receptor activity // inferred from electronic annotation --- 127943
225707_at Hs.516468 ADP-ribosylation-like factor 6 interacting protein 6 ARL6IP6 --- --- --- --- 151188
212172_at Hs.470907 adenylate kinase 2 AK2 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // inferred from electronic annotation 5739 // mitochondrion // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4017 // adenylate kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4017 // adenylate kinase activity // inferred from electronic annotation /// 16776 // phosphotransferase activity, phosphate group as acceptor // inferred from electronic annotation /// 19201 // nucleotide kinase activity // inferred from electronic annotation Purine metabolism // KEGG 204
224818_at Hs.485195 sortilin 1 SORT1 1503 // ossification // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6886 // intracellular protein transport // inferred from electronic annotation /// 6897 // endocytosis // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5764 // lysosome // inferred from electronic annotation /// 5768 // endosome // non-traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 8565 // protein transporter activity // inferred from electronic

Figure 56

annotation /// 16492 // neurotensin receptor activity, G-protein coupled // non-traceable author statement --- 6272
1568619_s_at Hs.648523 CDNA clone IMAGE:4402981 --- --- --- --- --- 162073
203233_at Hs.513457 interleukin 4 receptor IL4R 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6955 // immune response // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4896 // hematopoietin/interferon-class (D200-domain) cytokine receptor activity // inferred from electronic annotation /// 4913 // interleukin-4 receptor activity // traceable author statement /// 5057 // receptor signaling protein activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction Inflammatory_Response_Pathway // GenMAPP 3566
230523_at --- --- --- --- --- --- --- ---
203434_s_at Hs.307734 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase) MME 6508 // proteolysis // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 6508 // proteolysis // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4245 // neprilysin activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Hematopoietic cell lineage // KEGG /// Alzheimer's disease // KEGG 4311
239488_at Hs.634885 CDNA FLJ30948 fis, clone FEBRA2007900 --- --- --- --- ---
227458_at --- --- --- --- --- --- --- ---
219869_s_at Hs.288034 solute carrier family 39 (zinc transporter), member 8 SLC39A8 30001 // metal ion transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 46873 // metal ion transporter activity // inferred from electronic annotation --- 64116
203397_s_at Hs.170986 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3) GALNT3 5975 // carbohydrate metabolism // non-traceable author statement 5624 // membrane fraction // traceable author statement /// 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4653 // polypeptide N-acetylgalactosaminyltransferase activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5529 // sugar binding // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 30145 // manganese ion binding // inferred from electronic annotation /// 4653 // polypeptide N-

Figure 57

acetylgalactosaminyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation O-Glycan biosynthesis // KEGG /// Glycan structures - biosynthesis 1 // KEGG 2591
217678_at Hs.390594 solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 SLC7A11 6461 // protein complex assembly // not recorded /// 6810 // transport // inferred from electronic annotation /// 6865 // amino acid transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 15327 // cystine:glutamate antiporter activity // traceable author statement /// 15359 // amino acid permease activity // inferred from electronic annotation /// 5279 // amino acid-polyamine transporter activity // inferred from electronic annotation /// 15171 // amino acid transporter activity // inferred from electronic annotation --- 23657
204470_at Hs.789 chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) CXCL1 6935 // chemotaxis // traceable author statement /// 6954 // inflammatory response // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 7242 // intracellular signaling cascade // traceable author statement /// 7399 // nervous system development // traceable author statement /// 8283 // cell proliferation // traceable author statement /// 8285 // negative regulation of cell proliferation // traceable author statement /// 30036 // actin cytoskeleton organization and biogenesis // traceable author statement /// 6954 // inflammatory response // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement 5615 // extracellular space // traceable author statement /// 5576 // extracellular region // inferred from electronic annotation /// 5615 // extracellular space // inferred from electronic annotation 8009 // chemokine activity // traceable author statement /// 8047 // enzyme activator activity // traceable author statement /// 8083 // growth factor activity // inferred from electronic annotation /// 5125 // cytokine activity // inferred from electronic annotation /// 8009 // chemokine activity // inferred from electronic annotation /// 5102 // receptor binding // traceable author statement --- 2919
212828_at Hs.434494 synaptojanin 2 SYNJ2 --- --- 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 4439 // phosphoinositide 5-phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 4437 // inositol or phosphatidylinositol phosphatase activity // inferred from electronic annotation --- 8871
229970_at --- --- --- --- --- --- --- ---
225436_at Hs.459072 hypothetical protein from EUROIMAGE 588495 LOC58489 --- --- 3824 // catalytic activity // inferred from electronic annotation --- 58489
36564_at Hs.591504 IBR domain containing 3 IBRDC3 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation ---
127544

Figure 58

243578_at Hs.44780 Glycosyltransferase-like domain containing 1 GTDC1 9058 // biosynthesis // inferred from electronic annotation --- 16740 // transferase activity // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation --- 79712
212092_at Hs.147492 paternally expressed 10 PEG10 --- --- 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation --- 23089
203435_s_at Hs.307734 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase) MME 6508 // proteolysis // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 6508 // proteolysis // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4245 // neprilysin activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Hematopoietic cell lineage // KEGG /// Alzheimer's disease // KEGG 4311
201169_s_at Hs.171825 basic helix-loop-helix domain containing, class B, 2 BHLHB2 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // non-traceable author statement /// 3677 // DNA binding // inferred from electronic annotation /// 30528 // transcription regulator activity // inferred from electronic annotation --- 8553
205934_at Hs.153322 phospholipase C-like 1 PLCL1 6629 // lipid metabolism // inferred from electronic annotation /// 7242 // intracellular signaling cascade // traceable author statement /// 7165 // signal transduction // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- 4435 // phosphoinositide phospholipase C activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 4629 // phospholipase C activity // inferred from electronic annotation /// 4629 // phospholipase C activity // traceable author statement --- 5334
207358_x_at Hs.580782 microtubule-actin crosslinking factor 1 MACF1 7050 // cell cycle arrest // inferred from electronic annotation /// 5975 // carbohydrate metabolism // inferred from electronic annotation 5737 // cytoplasm // inferred from direct assay /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 5856 // cytoskeleton // inferred from sequence or structural similarity /// 5856 // cytoskeleton // non-traceable author statement /// 5856 // cytoskeleton // inferred from electronic annotation 3779 // actin binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion

Figure 59

binding // inferred from sequence or structural similarity /// 5509 // calcium ion binding // non-traceable author statement /// 8017 // microtubule binding // inferred from sequence or structural similarity /// 8017 // microtubule binding // non-traceable author statement /// 51015 // actin filament binding // non-traceable author statement /// 3779 // actin binding // inferred from direct assay /// 4553 // hydrolase activity, hydrolyzing O-glycosyl compounds // inferred from electronic annotation --- 23499
1565804_at Hs.434961 Ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310
212175_s_at Hs.470907 adenylate kinase 2 AK2 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // inferred from electronic annotation 5739 // mitochondrion // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4017 // adenylate kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4017 // adenylate kinase activity // inferred from electronic annotation /// 16776 // phosphotransferase activity, phosphate group as acceptor // inferred from electronic annotation /// 19201 // nucleotide kinase activity // inferred from electronic annotation Purine metabolism // KEGG 204
1569665_at Hs.446021 Solute carrier family 37 (glycerol-3-phosphate transporter), member 3 SLC37A3 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 84255
225626_at Hs.266175 phosphoprotein associated with glycosphingolipid microdomains 1 PAG1 6955 // immune response // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 55824
225019_at Hs.144114 calcium/calmodulin-dependent protein kinase (CaM kinase) II delta CAMK2D 1558 // regulation of cell growth // non-traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // non-traceable author statement 5954 // calcium- and calmodulin-dependent protein kinase complex // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // non-traceable author statement /// 5516 // calmodulin binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 5524 // ATP binding // non-traceable author statement /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation Calcium_regulation_in_cardiac_cells // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP ///

Figure 60

Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP 817 202445_s_at Hs.487360 Notch homolog 2 (Drosophila) NOTCH2 1709 // cell fate determination // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 6917 // induction of apoptosis // traceable author statement /// 7050 // cell cycle arrest // inferred from direct assay /// 7219 // Notch signaling pathway // inferred from sequence or structural similarity /// 7399 // nervous system development // non-traceable author statement /// 8285 // negative regulation of cell proliferation // inferred from direct assay /// 9887 // organ morphogenesis // inferred from expression pattern /// 16049 // cell growth // inferred from direct assay /// 19827 // stem cell maintenance // traceable author statement /// 30097 // hemopoiesis // traceable author statement /// 30154 // cell differentiation // inferred from electronic annotation /// 46579 // positive regulation of Ras protein signal transduction // inferred from direct assay /// 50793 // regulation of development // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7275 // development // non-traceable author statement 5634 // nucleus // inferred from direct assay /// 5887 // integral to plasma membrane // inferred from direct assay /// 9986 // cell surface // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 3706 // ligand-regulated transcription factor activity // traceable author statement /// 4872 // receptor activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // non-traceable author statement /// 46982 // protein heterodimerization activity // non-traceable author statement /// 4872 // receptor activity // inferred from electronic annotation --- 4853 223159_s_at Hs.197071 NIMA (never in mitosis gene a)-related kinase 6 NEK6 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from mutant phenotype 5634 // nucleus // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from mutant phenotype /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 10783 231426_at Hs.567760 Chromosome 9 open reading frame 71 C9orf71 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 169693

Figure 61

209267_s_at Hs.288034 solute carrier family 39 (zinc transporter), member 8 SLC39A8 30001 // metal ion transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 46873 // metal ion transporter activity // inferred from electronic annotation --- 64116
234156_at Hs.501928 Microtubule associated monoxygenase, calponin and LIM domain containing 2 MICAL2 6118 // electron transport // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation 5856 // cytoskeleton // inferred from electronic annotation 8270 // zinc ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 9645
227354_at Hs.266175 phosphoprotein associated with glycosphingolipid microdomains 1 PAG1 6955 // immune response // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 55824 /// 653745
210187_at Hs.471933 FK506 binding protein 1A, 12kDa FKBP1A 6457 // protein folding // inferred from electronic annotation /// 6457 // protein folding // non-traceable author statement /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from mutant phenotype /// 7242 // intracellular signaling cascade // non-traceable author statement /// 7399 // nervous system development // non-traceable author statement /// 46907 // intracellular transport // non-traceable author statement 5737 // cytoplasm // inferred from direct assay 3755 // peptidyl-prolyl cis-trans isomerase activity // inferred from electronic annotation /// 4872 // receptor activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 16853 // isomerase activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from mutant phenotype /// 8022 // protein C-terminus binding // inferred from physical interaction /// 46982 // protein heterodimerization activity // inferred from physical interaction /// 42803 // protein homodimerization activity // inferred from direct assay /// 5515 // protein binding // inferred from electronic annotation Calcium signaling pathway // KEGG 2280
229847_at Hs.431850 Mitogen-activated protein kinase 1 MAPK1 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 6950 // response to stress // traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7268 // synaptic transmission // traceable author statement --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation MAPK_Cascade // GenMAPP /// S1P_Signaling // GenMAPP 5594
209392_at Hs.190977 ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) ENPP2 6796 // phosphate metabolism // traceable author statement /// 6928 // cell motility //

Figure 62

traceable author statement /// 6935 // chemotaxis // non-traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 9117 // nucleotide metabolism // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 3676 // nucleic acid binding // inferred from electronic annotation /// 4519 // endonuclease activity // inferred from electronic annotation /// 4528 // phosphodiesterase I activity // traceable author statement /// 4551 // nucleotide diphosphatase activity // traceable author statement /// 8134 // transcription factor binding // traceable author statement /// 16787 // hydrolase activity // traceable author statement /// 3824 // catalytic activity // inferred from electronic annotation /// 4551 // nucleotide diphosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 5168
214467_at Hs.513440 G protein-coupled receptor 65 GPR65 6915 // apoptosis // traceable author statement /// 6955 // immune response // traceable author statement /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 7275 // development // traceable author statement /// 6915 // apoptosis // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // traceable author statement GPCRDB_Class_A_Rhodopsin-like2 // GenMAPP 8477
205743_at Hs.56045 SH3 and cysteine rich domain STAC 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement 5625 // soluble fraction // traceable author statement 8270 // zinc ion binding // inferred from electronic annotation /// 19992 // diacylglycerol binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 6769
1570021_at Hs.558004 homeobox C14 LOC360030 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6350 // transcription // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 360030
200670_at Hs.437638 X-box binding protein 1 XBP1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6955 // immune response // traceable author statement 5634 // nucleus // inferred from electronic annotation 3700

Figure 63

```
// transcription factor activity // traceable author statement ///
43565 // sequence-specific DNA binding // inferred from electronic
annotation /// 46983 // protein dimerization activity // inferred from
electronic annotation /// 3677 // DNA binding // inferred from
electronic annotation /// 3677 // DNA binding // traceable author
statement   ---   7494
213624_at   Hs.486357   sphingomyelin phosphodiesterase, acid-like 3A
      SMPDL3A     5975 // carbohydrate metabolism // inferred from
electronic annotation   5576 // extracellular region // non-traceable
author statement  5515 // protein binding // inferred from physical
interaction /// 16798 // hydrolase activity, acting on glycosyl bonds
// inferred from electronic annotation /// 16787 // hydrolase activity
// inferred from electronic annotation    ---   10924
200878_at   Hs.468410   endothelial PAS domain protein 1    EPAS1 1525
// angiogenesis // inferred from electronic annotation /// 1666 //
response to hypoxia // inferred from direct assay /// 6355 //
regulation of transcription, DNA-dependent // inferred from electronic
annotation /// 6366 // transcription from RNA polymerase II promoter //
traceable author statement /// 7165 // signal transduction // traceable
author statement /// 30154 // cell differentiation // inferred from
electronic annotation /// 6350 // transcription // inferred from
electronic annotation /// 7165 // signal transduction // inferred from
electronic annotation /// 7275 // development // inferred from
electronic annotation /// 45449 // regulation of transcription //
inferred from electronic annotation 5634 // nucleus // inferred from
electronic annotation   3705 // RNA polymerase II transcription factor
activity, enhancer binding // traceable author statement /// 3713 //
transcription coactivator activity // traceable author statement ///
4871 // signal transducer activity // inferred from electronic
annotation /// 5515 // protein binding // inferred from physical
interaction /// 35035 // histone acetyltransferase binding // inferred
from physical interaction /// 3677 // DNA binding // inferred from
electronic annotation /// 3700 // transcription factor activity //
inferred from electronic annotation /// 30528 // transcription
regulator activity // inferred from electronic annotation   ---   2034
203716_s_at Hs.368912   dipeptidyl-peptidase 4 (CD26, adenosine
deaminase complexing protein 2)     DPP4  6508 // proteolysis //
inferred from electronic annotation /// 6955 // immune response //
traceable author statement    16020 // membrane // inferred from
electronic annotation /// 16021 // integral to membrane // inferred
from electronic annotation    4177 // aminopeptidase activity //
inferred from electronic annotation /// 4274 // dipeptidyl-peptidase IV
activity // traceable author statement /// 4287 // prolyl
oligopeptidase activity // inferred from electronic annotation /// 3824
// catalytic activity // inferred from electronic annotation /// 4252
// serine-type endopeptidase activity // inferred from electronic
annotation /// 4274 // dipeptidyl-peptidase IV activity // inferred
from electronic annotation /// 8233 // peptidase activity // inferred
from electronic annotation /// 8236 // serine-type peptidase activity
// inferred from electronic annotation /// 16787 // hydrolase activity
// inferred from electronic annotation    ---   1803
228485_s_at Hs.573495   solute carrier family 44, member 1  SLC44A1
      6810 // transport // inferred from electronic annotation    16020
// membrane // inferred from electronic annotation /// 16021 //
integral to membrane // inferred from electronic annotation ---   ---
      23446
```

Figure 64

209850_s_at Hs.343380 CDC42 effector protein (Rho GTPase binding) 2 CDC42EP2 7015 // actin filament organization // non-traceable author statement /// 8360 // regulation of cell shape // inferred from direct assay /// 30838 // positive regulation of actin filament polymerization // inferred from direct assay /// 31274 // positive regulation of pseudopodium formation // inferred from direct assay /// 31334 // positive regulation of protein complex assembly // traceable author statement /// 8360 // regulation of cell shape // inferred from electronic annotation 5737 // cytoplasm // inferred from direct assay /// 5856 // cytoskeleton // inferred from electronic annotation /// 16020 // membrane // inferred from direct assay 5515 // protein binding // inferred from physical interaction /// 17049 // GTP-Rho binding // inferred from physical interaction --- 10435
1552264_a_at Hs.431850 mitogen-activated protein kinase 1 MAPK1 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 6950 // response to stress // traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7268 // synaptic transmission // traceable author statement --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation MAPK_Cascade // GenMAPP /// S1P_Signaling // GenMAPP 5594
220104_at Hs.133512 zinc finger CCCH-type, antiviral 1 ZC3HAV1 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3676 // nucleic acid binding // inferred from electronic annotation /// 3950 // NAD+ ADP-ribosyltransferase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 56829
237710_at Hs.156135 Transcribed locus --- --- --- --- --- ---
227367_at Hs.311187 solute carrier organic anion transporter family, member 3A1 SLCO3A1 6811 // ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 28232
35254_at Hs.5148 TRAF-type zinc finger domain containing 1 TRAFD1 --- --- 8270 // zinc ion binding // inferred from electronic annotation --- 10906
225557_at Hs.370950 AXIN1 up-regulated 1 AXUD1 6915 // apoptosis // non-traceable author statement /// 6915 // apoptosis // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation --- --- 64651
211889_x_at Hs.512682 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) CEACAM1 1525 // angiogenesis // non-traceable author statement /// 7156 // homophilic cell adhesion //

Figure 65

non-traceable author statement /// 7229 // integrin-mediated signaling pathway // non-traceable author statement /// 7565 // pregnancy // traceable author statement /// 16477 // cell migration // non-traceable author statement 5624 // membrane fraction // traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 634
235439_at Hs.648783 Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group) FUT1 5975 // carbohydrate metabolism // traceable author statement /// 6486 // protein amino acid glycosylation // traceable author statement /// 42355 // L-fucose catabolism // non-traceable author statement /// 6396 // RNA processing // traceable author statement /// 6445 // regulation of translation // traceable author statement 5624 // membrane fraction // traceable author statement /// 5795 // Golgi stack // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation 8107 // galactoside 2-alpha-L-fucosyltransferase activity // traceable author statement /// 8417 // fucosyltransferase activity // traceable author statement /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement Blood group glycolipid biosynthesis - lactoseries // KEGG /// Blood group glycolipid biosynthesis - // KEGG /// Globoside metabolism // KEGG /// Glycan structures - biosynthesis 2 // KEGG 2523
213497_at Hs.23361 ankyrin repeat and BTB (POZ) domain containing 2 ABTB2 1558 // regulation of cell growth // non-traceable author statement /// 6334 // nucleosome assembly // inferred from electronic annotation /// 7001 // chromosome organization and biogenesis (sensu Eukaryota) // inferred from electronic annotation 786 // nucleosome // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation --- 25841
226207_at Hs.530315 hypothetical protein FLJ39378 FLJ39378 --- --- 3824 // catalytic activity // inferred from electronic annotation --- 353116
212500_at Hs.99821 chromosome 10 open reading frame 22 C10orf22 --- --- --- --- 84890
225524_at Hs.162963 anthrax toxin receptor 2 ANTXR2 --- 5783 // endoplasmic reticulum // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 46872 // metal ion binding // inferred from electronic annotation --- 118429
241091_at Hs.527515 Transcribed locus --- --- --- --- --- ---
200884_at Hs.173724 creatine kinase, brain CKB --- 5737 // cytoplasm // not recorded 4111 // creatine kinase activity // traceable author statement /// 4111 // creatine kinase activity //

Figure 66

inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16772 // transferase activity, transferring phosphorus-containing groups // inferred from electronic annotation Urea cycle and metabolism of amino groups // KEGG /// Arginine and proline metabolism // KEGG 1152
213038_at Hs.591504 IBR domain containing 3 IBRDC3 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation ---
127544
227067_x_at --- Notch homolog 2 (Drosophila) N-terminal like
NOTCH2NL --- --- 5509 // calcium ion binding // inferred from electronic annotation --- 388677
223551_at Hs.486354 protein kinase (cAMP-dependent, catalytic) inhibitor beta PKIB 6469 // negative regulation of protein kinase activity // inferred from electronic annotation --- 4862 // cAMP-dependent protein kinase inhibitor activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 4860 // protein kinase inhibitor activity // inferred from electronic annotation Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 5570
36553_at Hs.533514 acetylserotonin O-methyltransferase-like ASMTL
30187 // melatonin biosynthesis // traceable author statement --- 8171 // O-methyltransferase activity // inferred from electronic annotation /// 8757 // S-adenosylmethionine-dependent methyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 17096 // acetylserotonin O-methyltransferase activity // non-traceable author statement /// 8168 // methyltransferase activity // inferred from electronic annotation --- 8623
211883_x_at Hs.512682 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) CEACAM1 1525 // angiogenesis // non-traceable author statement /// 7156 // homophilic cell adhesion // non-traceable author statement /// 7229 // integrin-mediated signaling pathway // non-traceable author statement /// 7565 // pregnancy // traceable author statement /// 16477 // cell migration // non-traceable author statement 5624 // membrane fraction // traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 634
219938_s_at Hs.567384 proline-serine-threonine phosphatase interacting protein 2 PSTPIP2 --- --- --- --- 9050
236439_at Hs.478588 B-cell CLL/lymphoma 6 (zinc finger protein 51)
BCL6 122 // negative regulation of transcription from RNA polymerase II promoter // not recorded /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6954 // inflammatory response // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 119 // mediator complex // not recorded /// 5634 // nucleus // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred

Figure 67

from electronic annotation /// 3700 // transcription factor activity // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation --- 604
212383_at Hs.463074 ATPase, H+ transporting, lysosomal V0 subunit a1 ATP6V0A1 6811 // ion transport // inferred from electronic annotation /// 15992 // proton transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation
16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation
15078 // hydrogen ion transporter activity // inferred from electronic annotation Oxidative phosphorylation // KEGG /// ATP synthesis // KEGG /// Photosynthesis // KEGG /// Flagellar assembly // KEGG /// Type III secretion system // KEGG /// Epithelial cell signaling in Helicobacter pylori // KEGG 535
208633_s_at Hs.580782 microtubule-actin crosslinking factor 1 MACF1
7050 // cell cycle arrest // inferred from electronic annotation /// 5975 // carbohydrate metabolism // inferred from electronic annotation 5737 // cytoplasm // inferred from direct assay /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 5856 // cytoskeleton // inferred from sequence or structural similarity /// 5856 // cytoskeleton // non-traceable author statement /// 5856 // cytoskeleton // inferred from electronic annotation 3779 // actin binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5509 // calcium ion binding // non-traceable author statement /// 8017 // microtubule binding // inferred from sequence or structural similarity /// 8017 // microtubule binding // non-traceable author statement /// 51015 // actin filament binding // non-traceable author statement /// 3779 // actin binding // inferred from direct assay /// 4553 // hydrolase activity, hydrolyzing O-glycosyl compounds // inferred from electronic annotation --- 23499
211426_x_at Hs.269782 guanine nucleotide binding protein (G protein), q polypeptide GNAQ 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7596 // blood coagulation // traceable author statement
5737 // cytoplasm // traceable author statement /// 5834 // heterotrimeric G-protein complex // not recorded /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 2776
1557543_at Hs.487360 Notch homolog 2 (Drosophila) NOTCH2 1709 // cell fate determination // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author

Figure 68

statement /// 6916 // anti-apoptosis // traceable author statement /// 6917 // induction of apoptosis // traceable author statement /// 7050 // cell cycle arrest // inferred from direct assay /// 7219 // Notch signaling pathway // inferred from sequence or structural similarity /// 7399 // nervous system development // non-traceable author statement /// 8285 // negative regulation of cell proliferation // inferred from direct assay /// 9887 // organ morphogenesis // inferred from expression pattern /// 16049 // cell growth // inferred from direct assay /// 19827 // stem cell maintenance // traceable author statement /// 30097 // hemopoiesis // traceable author statement /// 30154 // cell differentiation // inferred from electronic annotation /// 46579 // positive regulation of Ras protein signal transduction // inferred from direct assay /// 50793 // regulation of development // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7275 // development // non-traceable author statement 5634 // nucleus // inferred from direct assay /// 5887 // integral to plasma membrane // inferred from direct assay /// 9986 // cell surface // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 3706 // ligand-regulated transcription factor activity // traceable author statement /// 4872 // receptor activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // non-traceable author statement /// 46982 // protein heterodimerization activity // non-traceable author statement /// 4872 // receptor activity // inferred from electronic annotation --- 4853
222530_s_at Hs.472119 McKusick-Kaufman syndrome MKKS 6457 // protein folding // traceable author statement /// 7507 // heart development // traceable author statement /// 7601 // visual perception // inferred from electronic annotation /// 8406 // gonad development // traceable author statement /// 50896 // response to stimulus // inferred from electronic annotation /// 6457 // protein folding // inferred from electronic annotation /// 44267 // cellular protein metabolism // inferred from electronic annotation --- 166 // nucleotide binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 51082 // unfolded protein binding // traceable author statement /// 5515 // protein binding // inferred from electronic annotation /// 51082 // unfolded protein binding // inferred from electronic annotation --- 8195
201594_s_at Hs.464595 protein phosphatase 4, regulatory subunit 1 PPP4R1 7165 // signal transduction // non-traceable author statement 5625 // soluble fraction // non-traceable author statement 5488 // binding // inferred from electronic annotation /// 30362 // protein phosphatase type 4 regulator activity // non-traceable author statement --- 9989
218983_at Hs.631730 complement component 1, r subcomponent-like C1RL 6508 // proteolysis // inferred from electronic annotation --- 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 3815 // complement component C1r activity // inferred from electronic annotation --- 51279
215966_x_at --- glycerol kinase 3 pseudogene GK3P 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic

Figure 69

annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation --- 2713
228573_at Hs.632957 Full-length cDNA clone CS0DD001YA12 of Neuroblastoma Cot 50-normalized of Homo sapiens (human) --- --- --- --- --- ---
208967_s_at Hs.470907 adenylate kinase 2 AK2 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // inferred from electronic annotation 5739 // mitochondrion // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4017 // adenylate kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4017 // adenylate kinase activity // inferred from electronic annotation /// 16776 // phosphotransferase activity, phosphate group as acceptor // inferred from electronic annotation /// 19201 // nucleotide kinase activity // inferred from electronic annotation Purine metabolism // KEGG 204
218499_at Hs.444247 serine/threonine protein kinase MST4 RP6-213H19.1 6468 // protein amino acid phosphorylation // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 42981 // regulation of apoptosis // inferred from direct assay /// 6915 // apoptosis // inferred from electronic annotation 5795 // Golgi stack // inferred from electronic annotation /// 5794 // Golgi apparatus // inferred from physical interaction 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from direct assay /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from direct assay /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 4672 // protein kinase activity // inferred from direct assay /// 16301 // kinase activity // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 51765
240690_at Hs.29068 Homolog of rat pragma of Rnd2 DKFZp761P0423 6468 // protein amino acid phosphorylation // inferred from electronic annotation --- 4672 // protein kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation --- 157285
211597_s_at Hs.121443 homeodomain-only protein /// homeodomain-only protein HOP 6355 // regulation of transcription, DNA-dependent //

Figure 70

inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 6350 // transcription // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 84525
210756_s_at Hs.487360 Notch homolog 2 (Drosophila) /// Notch homolog 2 (Drosophila) NOTCH2 1709 // cell fate determination // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 6917 // induction of apoptosis // traceable author statement /// 7050 // cell cycle arrest // inferred from direct assay /// 7219 // Notch signaling pathway // inferred from sequence or structural similarity /// 7399 // nervous system development // non-traceable author statement /// 8285 // negative regulation of cell proliferation // inferred from direct assay /// 9887 // organ morphogenesis // inferred from expression pattern /// 16049 // cell growth // inferred from direct assay /// 19827 // stem cell maintenance // traceable author statement /// 30097 // hemopoiesis // traceable author statement /// 30154 // cell differentiation // inferred from electronic annotation /// 46579 // positive regulation of Ras protein signal transduction // inferred from direct assay /// 50793 // regulation of development // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7275 // development // non-traceable author statement 5634 // nucleus // inferred from direct assay /// 5887 // integral to plasma membrane // inferred from direct assay /// 9986 // cell surface // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 3706 // ligand-regulated transcription factor activity // traceable author statement /// 4872 // receptor activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // non-traceable author statement /// 46982 // protein heterodimerization activity // non-traceable author statement /// 4872 // receptor activity // inferred from electronic annotation --- 4853
214681_at Hs.1466 glycerol kinase GK 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
Glycerolipid metabolism // KEGG 2710
203574_at Hs.79334 nuclear factor, interleukin 3 regulated NFIL3
6355 // regulation of transcription, DNA-dependent // inferred

Figure 71

from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement /// 6955 // immune response // traceable author statement 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 3714 // transcription corepressor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3677 // DNA binding // traceable author statement --- 4783
228298_at Hs.560100 family with sequence similarity 113, member B FAM113B --- --- --- --- 91523
1568870_at Hs.385530 CDNA clone IMAGE:4818211 --- --- --- --- --- ---
225214_at Hs.213470 Proteasome (prosome, macropain) subunit, beta type, 7 PSMB7 6511 // ubiquitin-dependent protein catabolism // inferred from electronic annotation 5829 // cytosol // inferred from electronic annotation /// 5839 // proteasome core complex (sensu Eukaryota) // inferred from electronic annotation /// 43234 // protein complex // inferred from electronic annotation /// 502 // proteasome complex (sensu Eukaryota) // traceable author statement 4298 // threonine endopeptidase activity // inferred from electronic annotation /// 4175 // endopeptidase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation Proteasome_Degradation // GenMAPP /// Proteasome_Degradation // GenMAPP /// Proteasome_Degradation // GenMAPP /// Proteasome_Degradation // GenMAPP /// Proteasome // KEGG 5695
212502_at Hs.99821 chromosome 10 open reading frame 22 C10orf22 --- --- --- --- 84890
203628_at Hs.592020 insulin-like growth factor 1 receptor IGF1R 74 // regulation of progression through cell cycle // traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 7165 // signal transduction // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 8286 // insulin receptor signaling pathway // traceable author statement /// 46777 // protein amino acid autophosphorylation // inferred from direct assay /// 48009 // insulin-like growth factor receptor signaling pathway // inferred from direct assay /// 51262 // protein tetramerization // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // Unknown /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 5006 // epidermal growth factor receptor activity // inferred from electronic annotation /// 5010 // insulin-like growth factor receptor activity // inferred from direct assay /// 5520 // insulin-like growth factor binding // inferred from direct assay /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 43548 // phosphoinositide 3-kinase binding // inferred from physical interaction /// 43560 // insulin

Figure 72

receptor substrate binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 4713 // protein-tyrosine kinase activity // inferred from direct assay /// 4672 // protein kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4714 // transmembrane receptor protein tyrosine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 5010 // insulin-like growth factor receptor activity // traceable author statement --- 3480

238429_at Hs.293842 transmembrane protein 71 TMEM71 --- --- --- --- 137835

218115_at Hs.26516 ASF1 anti-silencing function 1 homolog B (S. cerevisiae) ASF1B --- --- --- --- 55723

1553096_s_at Hs.469658 BCL2-like 11 (apoptosis facilitator) BCL2L11 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 43065 // positive regulation of apoptosis // inferred from electronic annotation 5624 // membrane fraction // traceable author statement /// 16020 // membrane // inferred from electronic annotation 5515 // protein binding // inferred from physical interaction Apoptosis // GenMAPP /// Apoptosis // GenMAPP 10018

243568_at Hs.580782 Microtubule-actin crosslinking factor 1 MACF1 7050 // cell cycle arrest // inferred from electronic annotation 5737 // cytoplasm // inferred from direct assay /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 5856 // cytoskeleton // inferred from sequence or structural similarity /// 5856 // cytoskeleton // non-traceable author statement /// 5856 // cytoskeleton // inferred from electronic annotation 3779 // actin binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5509 // calcium ion binding // non-traceable author statement /// 8017 // microtubule binding // inferred from sequence or structural similarity /// 8017 // microtubule binding // non-traceable author statement /// 51015 // actin filament binding // non-traceable author statement /// 3779 // actin binding // inferred from direct assay --- 23499

205101_at Hs.126714 class II, major histocompatibility complex, transactivator CIITA 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 9596 // detection of pest, pathogen or parasite // traceable author statement /// 42829 // defense response to pathogen // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation /// 6350 // transcription // inferred from electronic annotation /// 6952 // defense response // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 3677 // DNA binding // traceable author statement /// 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 3713 // transcription coactivator activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 30528 // transcription regulator activity // inferred from electronic annotation /// 43130 // ubiquitin binding // inferred from physical interaction --- 4261

232231_at Hs.535845 runt-related transcription factor 2 RUNX2 1503 // ossification // traceable author statement /// 6350 // transcription

Figure 73

```
// inferred from electronic annotation /// 6355 // regulation of
transcription, DNA-dependent // inferred from electronic annotation
      5634 // nucleus // inferred from electronic annotation      3700
// transcription factor activity // inferred from electronic annotation
/// 3700 // transcription factor activity // non-traceable author
statement /// 3702 // RNA polymerase II transcription factor activity
// traceable author statement /// 5515 // protein binding // inferred
from physical interaction /// 5524 // ATP binding // inferred from
electronic annotation /// 3677 // DNA binding // inferred from
electronic annotation   TGF_Beta_Signaling_Pathway // GenMAPP     860
203887_s_at Hs.2030     thrombomodulin    THBD  7596 // blood
coagulation // traceable author statement /// 7596 // blood coagulation
// inferred from electronic annotation    5887 // integral to plasma
membrane // traceable author statement /// 16020 // membrane //
inferred from electronic annotation /// 16021 // integral to membrane
// inferred from electronic annotation    4888 // transmembrane
receptor activity // inferred from electronic annotation /// 5509 //
calcium ion binding // traceable author statement /// 5529 // sugar
binding // inferred from electronic annotation /// 4872 // receptor
activity // inferred from electronic annotation /// 5509 // calcium ion
binding // inferred from electronic annotation /// 4872 // receptor
activity // traceable author statement    ---    7056
227345_at   Hs.213467   tumor necrosis factor receptor superfamily,
member 10d, decoy with truncated death domain   TNFRSF10D   6915 //
apoptosis // inferred from electronic annotation /// 6916 // anti-
apoptosis // traceable author statement /// 7165 // signal transduction
// traceable author statement 16020 // membrane // inferred from
electronic annotation /// 16021 // integral to membrane // inferred
from electronic annotation    4888 // transmembrane receptor activity
// traceable author statement /// 4872 // receptor activity // inferred
from electronic annotation    ---    8793
212174_at   Hs.470907   adenylate kinase 2      AK2   6139 //
nucleobase, nucleoside, nucleotide and nucleic acid metabolism //
inferred from electronic annotation 5739 // mitochondrion // inferred
from electronic annotation    166 // nucleotide binding // inferred
from electronic annotation /// 4017 // adenylate kinase activity //
traceable author statement /// 5524 // ATP binding // inferred from
electronic annotation /// 16301 // kinase activity // inferred from
electronic annotation /// 16740 // transferase activity // inferred
from electronic annotation /// 4017 // adenylate kinase activity //
inferred from electronic annotation /// 16776 // phosphotransferase
activity, phosphate group as acceptor // inferred from electronic
annotation /// 19201 // nucleotide kinase activity // inferred from
electronic annotation   Purine metabolism // KEGG     204
200769_s_at Hs.516157   methionine adenosyltransferase II, alpha  MAT2A
      6730 // one-carbon compound metabolism // inferred from
electronic annotation   ---    166 // nucleotide binding // inferred
from electronic annotation /// 287 // magnesium ion binding // inferred
from electronic annotation /// 4478 // methionine adenosyltransferase
activity // traceable author statement /// 5524 // ATP binding //
inferred from electronic annotation /// 16740 // transferase activity
// inferred from electronic annotation /// 30955 // potassium ion
binding // inferred from electronic annotation /// 4478 // methionine
adenosyltransferase activity // inferred from electronic annotation ///
46872 // metal ion binding // inferred from electronic annotation ---
      4144
```

Figure 74

236475_at Hs.501928 Microtubule associated monoxygenase, calponin and LIM domain containing 2 MICAL2 6118 // electron transport // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation 5856 // cytoskeleton // inferred from electronic annotation 8270 // zinc ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 9645
205996_s_at Hs.470907 adenylate kinase 2 AK2 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // inferred from electronic annotation 5739 // mitochondrion // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4017 // adenylate kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4017 // adenylate kinase activity // inferred from electronic annotation /// 16776 // phosphotransferase activity, phosphate group as acceptor // inferred from electronic annotation /// 19201 // nucleotide kinase activity // inferred from electronic annotation Purine metabolism // KEGG 204
209357_at Hs.82071 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 CITED2 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // not recorded 3700 // transcription factor activity // traceable author statement /// 5515 // protein binding // non-traceable author statement /// 30528 // transcription regulator activity // inferred from electronic annotation --- 10370
227620_at --- --- --- --- --- --- --- ---
239574_at Hs.22242 Enoyl Coenzyme A hydratase domain containing 3 ECHDC3 8152 // metabolism // inferred from electronic annotation --- 3824 // catalytic activity // inferred from electronic annotation --- 79746
1558837_a_at Hs.424184 Plasminogen-like B1 PLGLB1 --- --- --- --- 112597
226679_at Hs.4866 solute carrier family 26, member 11 SLC26A11 6810 // transport // inferred from electronic annotation 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 284129
201118_at Hs.464071 phosphogluconate dehydrogenase /// phosphogluconate dehydrogenase /// UDP-glucose dehydrogenase /// UDP-glucose dehydrogenase PGD /// UGDH 9051 // pentose-phosphate shunt, oxidative branch // traceable author statement /// 6098 // pentose-phosphate shunt // inferred from electronic annotation /// 9051 // pentose-phosphate shunt, oxidative branch // inferred from electronic annotation --- 4616 // phosphogluconate dehydrogenase (decarboxylating) activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 16491 // oxidoreductase activity // inferred from electronic annotation ///

Figure 75

50661 // NADP binding // inferred from electronic annotation
Pentose_Phosphate_Pathway // GenMAPP /// Pentose phosphate pathway // KEGG /// Pentose phosphate pathway // KEGG /// Glutathione metabolism // KEGG 5226
202760_s_at Hs.591908 A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 protein AKAP2 /// PALM2-AKAP2 8360 // regulation of cell shape // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 16301 // kinase activity // inferred from electronic annotation /// 19899 // enzyme binding // non-traceable author statement G_Protein_Signaling // GenMAPP /// G_Protein_Signaling // GenMAPP /// G_Protein_Signaling // GenMAPP 11217 /// 445815
201719_s_at Hs.486470 erythrocyte membrane protein band 4.1-like 2
EPB41L2 30866 // cortical actin cytoskeleton organization and biogenesis // inferred from electronic annotation 5737 // cytoplasm // inferred from electronic annotation /// 5856 // cytoskeleton // inferred from electronic annotation /// 5886 // plasma membrane // traceable author statement /// 8091 // spectrin // traceable author statement /// 16020 // membrane // inferred from electronic annotation
3779 // actin binding // inferred from electronic annotation /// 5198 // structural molecule activity // inferred from electronic annotation /// 5200 // structural constituent of cytoskeleton // not recorded /// 5488 // binding // inferred from electronic annotation /// 8092 // cytoskeletal protein binding // inferred from electronic annotation --- 2037
206637_at Hs.2465 purinergic receptor P2Y, G-protein coupled, 14
P2RY14 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // non-traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 45028 // purinergic nucleotide receptor activity, G-protein coupled // inferred from electronic annotation /// 45029 // UDP-activated nucleotide receptor activity // non-traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation
GPCRDB_Class_A_Rhodopsin-like // GenMAPP 9934
210889_s_at Hs.352642 Fc fragment of IgG, low affinity IIb, receptor (CD32) FCGR2B 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6457 // protein folding // inferred from electronic annotation /// 6986 // response to unfolded protein // inferred from electronic annotation /// 6986 // response to unfolded protein // traceable author statement /// 6955 // immune response // non-traceable author statement /// 6955 // immune response // not recorded 5886 // plasma membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement 4872 // receptor activity // inferred from electronic annotation /// 19864 // IgG binding // inferred from electronic annotation /// 166 // nucleotide binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from

Figure 76

electronic annotation /// 4888 // transmembrane receptor activity // non-traceable author statement /// 5057 // receptor signaling protein activity // not recorded --- 2213
208351_s_at Hs.431850 mitogen-activated protein kinase 1 MAPK1 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 6950 // response to stress // traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7268 // synaptic transmission // traceable author statement --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
MAPK_Cascade // GenMAPP /// S1P_Signaling // GenMAPP 5594
203759_at Hs.591947 ST3 beta-galactoside alpha-2,3-sialyltransferase 4 ST3GAL4 6486 // protein amino acid glycosylation // inferred from electronic annotation 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 30173 // integral to Golgi membrane // inferred from electronic annotation 3836 // beta-galactoside alpha-2,3-sialyltransferase activity // traceable author statement /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 8373 // sialyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 3836 // beta-galactoside alpha-2,3-sialyltransferase activity // inferred from electronic annotation O-Glycan biosynthesis // KEGG /// Keratan sulfate biosynthesis // KEGG /// Blood group glycolipid biosynthesis - lactoseries // KEGG /// Globoside metabolism // KEGG /// Ganglioside biosynthesis // KEGG /// Glycan structures - biosynthesis 1 // KEGG /// Glycan structures - biosynthesis 2 // KEGG 6484
1558836_at Hs.424184 Plasminogen-like B1 PLGLB1 --- --- --- --- 112597
201170_s_at Hs.171825 basic helix-loop-helix domain containing, class B, 2 BHLHB2 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation
5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // non-traceable author statement /// 3677 // DNA binding // inferred from electronic annotation /// 30528 // transcription regulator activity // inferred from electronic annotation
--- 8553
218881_s_at Hs.220971 FOS-like antigen 2 FOSL2 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 8219 // cell death // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // traceable author

Figure 77

statement /// 5634 // nucleus // inferred from electronic annotation
3700 // transcription factor activity // traceable author
statement /// 43565 // sequence-specific DNA binding // inferred from
electronic annotation /// 46983 // protein dimerization activity //
inferred from electronic annotation /// 3677 // DNA binding // inferred
from electronic annotation --- 2355
220059_at Hs.435579 BCR downstream signaling 1 BRDG1 6886 //
intracellular protein transport // traceable author statement /// 6944
// membrane fusion // traceable author statement /// 6959 // humoral
immune response // not recorded /// 7242 // intracellular signaling
cascade // inferred from electronic annotation /// 7165 // signal
transduction // traceable author statement --- --- --- 26228
224407_s_at Hs.444247 serine/threonine protein kinase MST4 ///
serine/threonine protein kinase MST4 RP6-213H19.1 6468 //
protein amino acid phosphorylation // inferred from direct assay ///
6468 // protein amino acid phosphorylation // inferred from electronic
annotation /// 42981 // regulation of apoptosis // inferred from direct
assay /// 6915 // apoptosis // inferred from electronic annotation
5795 // Golgi stack // inferred from electronic annotation ///
5794 // Golgi apparatus // inferred from physical interaction 166
// nucleotide binding // inferred from electronic annotation /// 287 //
magnesium ion binding // inferred from direct assay /// 4672 // protein
kinase activity // inferred from electronic annotation /// 4674 //
protein serine/threonine kinase activity // inferred from electronic
annotation /// 4713 // protein-tyrosine kinase activity // inferred
from electronic annotation /// 5524 // ATP binding // inferred from
direct assay /// 5524 // ATP binding // inferred from electronic
annotation /// 16740 // transferase activity // inferred from
electronic annotation /// 42802 // identical protein binding //
inferred from physical interaction /// 5515 // protein binding //
inferred from physical interaction /// 4672 // protein kinase activity
// inferred from direct assay /// 16301 // kinase activity // inferred
from electronic annotation /// 287 // magnesium ion binding // inferred
from electronic annotation /// 46872 // metal ion binding // inferred
from electronic annotation --- 51765
203717_at Hs.368912 dipeptidyl-peptidase 4 (CD26, adenosine
deaminase complexing protein 2) DPP4 6508 // proteolysis //
inferred from electronic annotation /// 6955 // immune response //
traceable author statement 16020 // membrane // inferred from
electronic annotation /// 16021 // integral to membrane // inferred
from electronic annotation 4177 // aminopeptidase activity //
inferred from electronic annotation /// 4274 // dipeptidyl-peptidase IV
activity // traceable author statement /// 4287 // prolyl
oligopeptidase activity // inferred from electronic annotation /// 3824
// catalytic activity // inferred from electronic annotation /// 4252
// serine-type endopeptidase activity // inferred from electronic
annotation /// 4274 // dipeptidyl-peptidase IV activity // inferred
from electronic annotation /// 8233 // peptidase activity // inferred
from electronic annotation /// 8236 // serine-type peptidase activity
// inferred from electronic annotation /// 16787 // hydrolase activity
// inferred from electronic annotation --- 1803
237112_at Hs.200230 Family with sequence similarity 102, member B
FAM102B --- --- --- --- 284611
226694_at Hs.591908 A kinase (PRKA) anchor protein 2 /// PALM2-
AKAP2 protein AKAP2 /// PALM2-AKAP2 8360 // regulation of cell
shape // inferred from electronic annotation 16020 // membrane //
inferred from electronic annotation 16301 // kinase activity //

Figure 78

inferred from electronic annotation /// 19899 // enzyme binding // non-traceable author statement G_Protein_Signaling // GenMAPP /// G_Protein_Signaling // GenMAPP /// G_Protein_Signaling // GenMAPP /// G_Protein_Signaling // GenMAPP 11217 /// 445815
215977_x_at Hs.1466 glycerol kinase GK 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
Glycerolipid metabolism // KEGG 2710
202716_at Hs.417549 protein tyrosine phosphatase, non-receptor type 1 PTPN1 6470 // protein amino acid dephosphorylation // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement 5625 // soluble fraction // not recorded /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5737 // cytoplasm // not recorded 4725 // protein tyrosine phosphatase activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation /// 4725 // protein tyrosine phosphatase activity // inferred from electronic annotation Cell adhesion molecules (CAMs) // KEGG /// Adherens junction // KEGG /// Jak-STAT signaling pathway // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Leukocyte transendothelial migration // KEGG /// Insulin signaling pathway // KEGG /// Adipocytokine signaling pathway // KEGG /// Type I diabetes mellitus // KEGG /// Epithelial cell signaling in Helicobacter pylori // KEGG 5770
226322_at Hs.401954 transmembrane and tetratricopeptide repeat containing 1 TMTC1 --- --- 5488 // binding // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation --- 653626 /// 83857
207387_s_at Hs.1466 glycerol kinase GK 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
Glycerolipid metabolism // KEGG 2710
239249_at Hs.478588 B-cell CLL/lymphoma 6 (zinc finger protein 51) BCL6 122 // negative regulation of transcription from RNA

Figure 79

polymerase II promoter // not recorded /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6954 // inflammatory response // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 119 // mediator complex // not recorded /// 5634 // nucleus // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation --- 604
221572_s_at Hs.631925 solute carrier family 26, member 6 SLC26A6 6810 // transport // inferred from electronic annotation /// 7156 // homophilic cell adhesion // inferred from electronic annotation /// 7218 // neuropeptide signaling pathway // inferred from electronic annotation /// 8272 // sulfate transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 5198 // structural molecule activity // inferred from electronic annotation /// 5215 // transporter activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 8271 // sulfate porter activity // inferred from electronic annotation --- 65010
216316_x_at Hs.1466 glycerol kinase /// glycerol kinase 3 pseudogene GK /// GK3P 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation Glycerolipid metabolism // KEGG 2710 /// 2713
207980_s_at Hs.82071 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 CITED2 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // not recorded 3700 // transcription factor activity // traceable author statement /// 5515 // protein binding // non-traceable

Figure 80

author statement /// 30528 // transcription regulator activity // inferred from electronic annotation --- 10370
1552541_at Hs.529984 T-cell activation GTPase activating protein TAGAP --- --- 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation --- 117289
202837_at Hs.5148 TRAF-type zinc finger domain containing 1 TRAFD1 --- --- 8270 // zinc ion binding // inferred from electronic annotation --- 10906
238050_at --- --- --- --- --- --- --- ---
208634_s_at Hs.580782 microtubule-actin crosslinking factor 1 MACF1 7050 // cell cycle arrest // inferred from electronic annotation /// 5975 // carbohydrate metabolism // inferred from electronic annotation 5737 // cytoplasm // inferred from direct assay /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 5856 // cytoskeleton // inferred from sequence or structural similarity /// 5856 // cytoskeleton // non-traceable author statement /// 5856 // cytoskeleton // inferred from electronic annotation 3779 // actin binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5509 // calcium ion binding // non-traceable author statement /// 8017 // microtubule binding // inferred from sequence or structural similarity /// 8017 // microtubule binding // non-traceable author statement /// 51015 // actin filament binding // non-traceable author statement /// 3779 // actin binding // inferred from direct assay /// 4553 // hydrolase activity, hydrolyzing O-glycosyl compounds // inferred from electronic annotation --- 23499
224739_at Hs.530381 pim-3 oncogene PIM3 6468 // protein amino acid phosphorylation // inferred from electronic annotation --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation --- 415116
239647_at Hs.292375 carbohydrate (chondroitin 4) sulfotransferase 13 CHST13 5975 // carbohydrate metabolism // inferred from electronic annotation /// 30206 // chondroitin sulfate biosynthesis // inferred from direct assay 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 1537 // N-acetylgalactosamine 4-O-sulfotransferase activity // inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 47756 // chondroitin 4-sulfotransferase activity // inferred from direct assay /// 47756 // chondroitin 4-sulfotransferase activity // inferred from electronic annotation --- 166012
1554867_a_at Hs.157461 proline rich 16 PRR16 --- --- --- --- 51334
236802_at Hs.434961 Ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310

Figure 81

203641_s_at Hs.470457 COBL-like 1 COBLL1 --- --- --- ---
22837
236198_at Hs.124554 Transcribed locus --- --- --- --- ---

243052_at Hs.632401 MOB1, Mps One Binder kinase activator-like 2C
(yeast) MOBKL2C --- --- 16301 // kinase activity //
inferred from electronic annotation /// 8270 // zinc ion binding //
inferred from electronic annotation /// 46872 // metal ion binding //
inferred from electronic annotation --- 148932
203234_at Hs.488240 uridine phosphorylase 1 UPP1 9116 //
nucleoside metabolism // inferred from electronic annotation /// 9166
// nucleotide catabolism // inferred from electronic annotation ///
6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism
// traceable author statement 5737 // cytoplasm // inferred from
electronic annotation 4850 // uridine phosphorylase activity //
traceable author statement /// 16757 // transferase activity,
transferring glycosyl groups // inferred from electronic annotation ///
3824 // catalytic activity // inferred from electronic annotation ///
4850 // uridine phosphorylase activity // inferred from electronic
annotation /// 16740 // transferase activity // inferred from
electronic annotation Pyrimidine metabolism // KEGG 7378
243358_at Hs.595494 insulin-like growth factor 1 receptor IGF1R
--- --- --- --- 145815
1553407_at Hs.580782 microtubule-actin crosslinking factor 1 MACF1
7050 // cell cycle arrest // inferred from electronic annotation
5737 // cytoplasm // inferred from direct assay /// 5737 //
cytoplasm // inferred from sequence or structural similarity /// 5856
// cytoskeleton // inferred from sequence or structural similarity ///
5856 // cytoskeleton // non-traceable author statement /// 5856 //
cytoskeleton // inferred from electronic annotation 3779 // actin
binding // inferred from electronic annotation /// 5509 // calcium ion
binding // inferred from electronic annotation /// 5509 // calcium ion
binding // inferred from sequence or structural similarity /// 5509 //
calcium ion binding // non-traceable author statement /// 8017 //
microtubule binding // inferred from sequence or structural similarity
/// 8017 // microtubule binding // non-traceable author statement ///
51015 // actin filament binding // non-traceable author statement ///
3779 // actin binding // inferred from direct assay --- 23499
225262_at Hs.220971 FOS-like antigen 2 FOSL2 6357 //
regulation of transcription from RNA polymerase II promoter //
traceable author statement /// 8219 // cell death // traceable author
statement /// 6355 // regulation of transcription, DNA-dependent //
inferred from electronic annotation 5634 // nucleus // traceable author
statement /// 5634 // nucleus // inferred from electronic annotation
3700 // transcription factor activity // traceable author
statement /// 43565 // sequence-specific DNA binding // inferred from
electronic annotation /// 46983 // protein dimerization activity //
inferred from electronic annotation /// 3677 // DNA binding // inferred
from electronic annotation --- 2355
217974_at Hs.438641 transmembrane 7 superfamily member 3
TM7SF3 --- 16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from
electronic annotation --- --- 51768
202759_s_at Hs.591908 A kinase (PRKA) anchor protein 2 /// PALM2-
AKAP2 protein AKAP2 /// PALM2-AKAP2 8360 // regulation of cell
shape // inferred from electronic annotation 16020 // membrane //
inferred from electronic annotation 16301 // kinase activity //

Figure 82

inferred from electronic annotation /// 19899 // enzyme binding // non-traceable author statement G_Protein_Signaling // GenMAPP /// G_Protein_Signaling // GenMAPP /// G_Protein_Signaling // GenMAPP /// G_Protein_Signaling // GenMAPP 11217 /// 445815
207693_at Hs.614033 calcium channel, voltage-dependent, beta 4 subunit CACNB4 6811 // ion transport // inferred from electronic annotation /// 6816 // calcium ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6810 // transport // traceable author statement 5624 // membrane fraction // not recorded /// 5891 // voltage-gated calcium channel complex // traceable author statement 5245 // voltage-gated calcium channel activity // inferred from electronic annotation /// 5245 // voltage-gated calcium channel activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5216 // ion channel activity // inferred from electronic annotation /// 5244 // voltage-gated ion channel activity // inferred from electronic annotation /// 5262 // calcium channel activity // inferred from electronic annotation --- 785
244115_at Hs.85603 family with sequence similarity 126, member A FAM126A --- --- 4871 // signal transducer activity // non-traceable author statement --- 84668
203665_at Hs.517581 heme oxygenase (decycling) 1 HMOX1 6788 // heme oxidation // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from mutant phenotype 5624 // membrane fraction // traceable author statement /// 5783 // endoplasmic reticulum // traceable author statement /// 5792 // microsome // inferred from electronic annotation /// 5783 // endoplasmic reticulum // inferred from electronic annotation 4392 // heme oxygenase (decyclizing) activity // traceable author statement /// 4871 // signal transducer activity // inferred from mutant phenotype /// 5506 // iron ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4392 // heme oxygenase (decyclizing) activity // inferred from electronic annotation Porphyrin and chlorophyll metabolism // KEGG 3162
205270_s_at Hs.304475 lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) LCP2 6955 // immune response // traceable author statement /// 7169 // transmembrane receptor protein tyrosine kinase signaling pathway // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // traceable author statement --- 3937
222701_s_at Hs.436913 coiled-coil-helix-coiled-coil-helix domain containing 7 CHCHD7 --- --- --- --- 79145
227697_at Hs.527973 suppressor of cytokine signaling 3 SOCS3 1558 // regulation of cell growth // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation --- 4860 // protein kinase inhibitor activity // traceable author statement --- 9021

Figure 83

219669_at Hs.232165 CD177 molecule CD177 --- --- --- --- 57126
229776_at Hs.311187 solute carrier organic anion transporter family, member 3A1 SLCO3A1 6811 // ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 28232
225799_at --- hypothetical protein MGC4677 MGC4677 --- --- --- 112597 /// 541471
215222_x_at Hs.580782 microtubule-actin crosslinking factor 1 MACF1 7050 // cell cycle arrest // inferred from electronic annotation /// 5975 // carbohydrate metabolism // inferred from electronic annotation 5737 // cytoplasm // inferred from direct assay /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 5856 // cytoskeleton // inferred from sequence or structural similarity /// 5856 // cytoskeleton // non-traceable author statement /// 5856 // cytoskeleton // inferred from electronic annotation 3779 // actin binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5509 // calcium ion binding // non-traceable author statement /// 8017 // microtubule binding // inferred from sequence or structural similarity /// 8017 // microtubule binding // non-traceable author statement /// 51015 // actin filament binding // non-traceable author statement /// 3779 // actin binding // inferred from direct assay /// 4553 // hydrolase activity, hydrolyzing O-glycosyl compounds // inferred from electronic annotation --- 23499
227193_at Hs.375762 CDNA FLJ37631 fis, clone BRCOC2015944 --- --- --- --- ---
229221_at Hs.125503 Mitogen-activated protein kinase 10 MAPK10 --- --- --- --- ---
226430_at --- hypothetical protein LOC253981 LOC253981 --- --- --- --- 253981
214766_s_at Hs.300887 AT hook containing transcription factor 1 AHCTF1 --- --- --- --- 25909
242106_at Hs.431850 Mitogen-activated protein kinase 1 MAPK1 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 6950 // response to stress // traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7268 // synaptic transmission // traceable author statement --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation MAPK_Cascade // GenMAPP /// S1P_Signaling // GenMAPP 5594
205965_at Hs.509964 basic leucine zipper transcription factor, ATF-like BATF 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent //

Figure 84

inferred from electronic annotation /// 19735 // antimicrobial humoral response (sensu Vertebrata) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 3677 // DNA binding // inferred from electronic annotation --- 10538
219229_at Hs.311187 solute carrier organic anion transporter family, member 3A1 SLCO3A1 6811 // ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 28232
224102_at Hs.591281 purinergic receptor P2Y, G-protein coupled, 12 P2RY12 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7599 // hemostasis // non-traceable author statement 16020 // membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 45028 // purinergic nucleotide receptor activity, G-protein coupled // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation GPCRDB_Class_A_Rhodopsin-like // GenMAPP 64805
212377_s_at Hs.487360 Notch homolog 2 (Drosophila) NOTCH2 1709 // cell fate determination // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 6917 // induction of apoptosis // traceable author statement /// 7050 // cell cycle arrest // inferred from direct assay /// 7219 // Notch signaling pathway // inferred from sequence or structural similarity /// 7399 // nervous system development // non-traceable author statement /// 8285 // negative regulation of cell proliferation // inferred from direct assay /// 9887 // organ morphogenesis // inferred from expression pattern /// 16049 // cell growth // inferred from direct assay /// 19827 // stem cell maintenance // traceable author statement /// 30097 // hemopoiesis // traceable author statement /// 30154 // cell differentiation // inferred from electronic annotation /// 46579 // positive regulation of Ras protein signal transduction // inferred from direct assay /// 50793 // regulation of development // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7275 // development // non-traceable author statement 5634 // nucleus // inferred from direct assay /// 5887 // integral to plasma membrane // inferred from direct assay /// 9986 // cell surface // inferred from direct assay /// 16020 // membrane // inferred from electronic

Figure 85

annotation /// 16021 // integral to membrane // inferred from electronic annotation 3706 // ligand-regulated transcription factor activity // traceable author statement /// 4872 // receptor activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // non-traceable author statement /// 46982 // protein heterodimerization activity // non-traceable author statement /// 4872 // receptor activity // inferred from electronic annotation --- 4853
217762_s_at Hs.99528 RAB31, member RAS oncogene family RAB31 7264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 5525 // GTP binding // inferred from electronic annotation --- 11031
204601_at Hs.511839 Nedd4 binding protein 1 N4BP1 --- 5634 // nucleus // inferred from electronic annotation --- --- 9683
217763_s_at Hs.99528 RAB31, member RAS oncogene family RAB31 7264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 5525 // GTP binding // inferred from electronic annotation --- 11031
202443_x_at Hs.487360 Notch homolog 2 (Drosophila) NOTCH2 1709 // cell fate determination // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 6917 // induction of apoptosis // traceable author statement /// 7050 // cell cycle arrest // inferred from direct assay /// 7219 // Notch signaling pathway // inferred from sequence or structural similarity /// 7399 // nervous system development // non-traceable author statement /// 8285 // negative regulation of cell proliferation // inferred from direct assay /// 9887 // organ morphogenesis // inferred from expression pattern /// 16049 // cell growth // inferred from direct assay /// 19827 // stem cell maintenance // traceable author statement /// 30097 // hemopoiesis // traceable author statement /// 30154 // cell differentiation // inferred from electronic annotation /// 46579 // positive regulation of Ras protein signal transduction // inferred from direct assay /// 50793 // regulation of development // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7275 // development // non-traceable author statement 5634 // nucleus // inferred from direct assay /// 5887 // integral to plasma membrane // inferred from direct assay /// 9986 // cell surface // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 3706 // ligand-regulated transcription factor activity // traceable author statement /// 4872 // receptor activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // non-traceable author statement /// 46982 // protein heterodimerization

Figure 86

activity // non-traceable author statement /// 4872 // receptor activity // inferred from electronic annotation --- 4853
226273_at Hs.166486 chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) CLCN5 --- --- --- --- 158563
214014_at Hs.343380 CDC42 effector protein (Rho GTPase binding) 2 CDC42EP2 7015 // actin filament organization // non-traceable author statement /// 8360 // regulation of cell shape // inferred from direct assay /// 30838 // positive regulation of actin filament polymerization // inferred from direct assay /// 31274 // positive regulation of pseudopodium formation // inferred from direct assay /// 31334 // positive regulation of protein complex assembly // traceable author statement /// 8360 // regulation of cell shape // inferred from electronic annotation 5737 // cytoplasm // inferred from direct assay /// 5856 // cytoskeleton // inferred from electronic annotation /// 16020 // membrane // inferred from direct assay 5515 // protein binding // inferred from physical interaction /// 17049 // GTP-Rho binding // inferred from physical interaction --- 10435
203231_s_at Hs.434961 ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310
205307_s_at Hs.409081 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) KMO 6118 // electron transport // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation /// 8152 // metabolism // traceable author statement --- 4497 // monooxygenase activity // inferred from electronic annotation /// 4502 // kynurenine 3-monooxygenase activity // traceable author statement /// 4502 // kynurenine 3-monooxygenase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation Tryptophan metabolism // KEGG 8564
227606_s_at Hs.16229 STAM binding protein-like 1 STAMBPL1 6512 // ubiquitin cycle // inferred from electronic annotation --- 4221 // ubiquitin thiolesterase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 57559
221959_at Hs.154652 chromosome 8 open reading frame 72 C8orf72 --- --- --- --- 90362
204490_s_at Hs.502328 CD44 molecule (Indian blood group) CD44 7155 // cell adhesion // inferred from electronic annotation /// 7160 // cell-matrix adhesion // non-traceable author statement /// 16337 // cell-cell adhesion // non-traceable author statement 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5518 // collagen binding // non-traceable author statement /// 5540 // hyaluronic acid binding // inferred from electronic annotation /// 5540 // hyaluronic acid binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from electronic annotation --- 960

Figure 87

203232_s_at Hs.434961 ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310
207277_at Hs.278694 CD209 molecule CD209 6897 // endocytosis // inferred from electronic annotation /// 7155 // cell adhesion // inferred from electronic annotation /// 7159 // leukocyte adhesion // non-traceable author statement /// 7242 // intracellular signaling cascade // non-traceable author statement /// 9405 // pathogenesis // non-traceable author statement /// 9988 // cell-cell recognition // traceable author statement /// 19048 // virus-host interaction // traceable author statement /// 19062 // virion attachment to host cell surface receptor // traceable author statement /// 19079 // viral genome replication // non-traceable author statement /// 19882 // antigen presentation // non-traceable author statement /// 30333 // antigen processing // non-traceable author statement /// 46795 // intracellular virion transport // traceable author statement /// 46800 // enhancement of virulence // traceable author statement /// 46968 // peptide antigen transport // non-traceable author statement /// 6955 // immune response // inferred from electronic annotation /// 7157 // heterophilic cell adhesion // traceable author statement 16020 // membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 5529 // sugar binding // non-traceable author statement /// 5537 // mannose binding // traceable author statement /// 42607 // exogenous peptide antigen binding // non-traceable author statement /// 46790 // virion binding // traceable author statement /// 5529 // sugar binding // inferred from electronic annotation /// 5537 // mannose binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 30835
212271_at Hs.431850 mitogen-activated protein kinase 1 MAPK1 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 6950 // response to stress // traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7268 // synaptic transmission // traceable author statement --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation MAPK_Cascade // GenMAPP /// S1P_Signaling // GenMAPP 5594
228938_at Hs.551713 Myelin basic protein MBP 6955 // immune response // traceable author statement /// 7268 // synaptic transmission // traceable author statement /// 7417 // central nervous system development // traceable author statement /// 8366 // nerve ensheathment // traceable author statement --- 19911 //

Figure 88

structural constituent of myelin sheath // inferred from electronic annotation /// 5198 // structural molecule activity // inferred from electronic annotation MAPK_Cascade // GenMAPP 4155
241501_at Hs.531807 Rho GTPase activating protein 25 ARHGAP25 --- --- 5096 // GTPase activator activity // inferred from electronic annotation --- 9938
227523_s_at Hs.304362 PHD finger protein 20-like 1 PHF20L1 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation --- 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation --- 51105
244578_at Hs.304475 lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) LCP2 6955 // immune response // traceable author statement /// 7169 // transmembrane receptor protein tyrosine kinase signaling pathway // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // traceable author statement --- 3937
228372_at Hs.385493 chromosome 10 open reading frame 128 C10orf128 --- --- --- --- 170371
204562_at Hs.401013 interferon regulatory factor 4 IRF4 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 42110 // T cell activation // inferred from sequence or structural similarity /// 42110 // T cell activation // non-traceable author statement /// 45082 // positive regulation of interleukin-10 biosynthesis // inferred from direct assay /// 45082 // positive regulation of interleukin-10 biosynthesis // inferred from sequence or structural similarity /// 45086 // positive regulation of interleukin-2 biosynthesis // inferred from direct assay /// 45086 // positive regulation of interleukin-2 biosynthesis // inferred from sequence or structural similarity /// 45368 // positive regulation of interleukin-13 biosynthesis // inferred from direct assay /// 45368 // positive regulation of interleukin-13 biosynthesis // inferred from sequence or structural similarity /// 45404 // positive regulation of interleukin-4 biosynthesis // inferred from direct assay /// 45404 // positive regulation of interleukin-4 biosynthesis // inferred from sequence or structural similarity /// 45622 // regulation of T-helper cell differentiation // inferred from sequence or structural similarity /// 45622 // regulation of T-helper cell differentiation // non-traceable author statement /// 45941 // positive regulation of transcription // inferred from direct assay /// 45941 // positive regulation of transcription // inferred from sequence or structural similarity 5634 // nucleus // Unknown /// 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // inferred from sequence or structural similarity /// 5634 // nucleus // non-traceable author statement 3700 // transcription factor activity // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from sequence or structural similarity /// 3700 // transcription factor activity // non-traceable author statement /// 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 8134 // transcription factor binding // inferred from sequence or structural similarity /// 8134 // transcription factor binding // non-traceable author statement /// 16563 // transcriptional

Figure 89

activator activity // inferred from direct assay /// 16563 // transcriptional activator activity // inferred from sequence or structural similarity /// 3677 // DNA binding // inferred from electronic annotation Apoptosis // GenMAPP /// Apoptosis // GenMAPP 3662
205654_at Hs.1012 complement component 4 binding protein, alpha C4BPA 6958 // complement activation, classical pathway // inferred from electronic annotation /// 45087 // innate immune response // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation 5615 // extracellular space // not recorded /// 5576 // extracellular region // non-traceable author statement --- --- 722
201012_at Hs.494173 annexin A1 ANXA1 6629 // lipid metabolism // traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 6928 // cell motility // traceable author statement /// 6954 // inflammatory response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 7165 // signal transduction // traceable author statement 5737 // cytoplasm // traceable author statement 4859 // phospholipase inhibitor activity // inferred from electronic annotation /// 5102 // receptor binding // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // traceable author statement /// 5544 // calcium-dependent phospholipid binding // inferred from electronic annotation /// 19834 // phospholipase A2 inhibitor activity // inferred from electronic annotation /// 4859 // phospholipase inhibitor activity // traceable author statement /// 5543 // phospholipid binding // traceable author statement Prostaglandin_synthesis_regulation // GenMAPP 301
230343_at Hs.28773 Transcribed locus --- --- --- --- --- ---
226891_at Hs.478741 chromosome 3 open reading frame 21 C3orf21 --- --- --- --- 152002
208771_s_at Hs.524648 leukotriene A4 hydrolase LTA4H 6508 // proteolysis // inferred from electronic annotation /// 6954 // inflammatory response // inferred from sequence or structural similarity /// 6954 // inflammatory response // non-traceable author statement /// 19370 // leukotriene biosynthesis // inferred from sequence or structural similarity /// 19370 // leukotriene biosynthesis // traceable author statement /// 19370 // leukotriene biosynthesis // inferred from electronic annotation --- 4179 // membrane alanyl aminopeptidase activity // inferred from electronic annotation /// 4301 // epoxide hydrolase activity // inferred from sequence or structural similarity /// 4301 // epoxide hydrolase activity // traceable author statement /// 8233 // peptidase activity // inferred from sequence or structural similarity /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from sequence or structural similarity /// 8270 // zinc ion binding // traceable author statement /// 46872 // metal ion binding // inferred from electronic annotation /// 4463 // leukotriene-A4 hydrolase activity // inferred from sequence or structural similarity /// 3824 // catalytic activity // inferred from electronic annotation /// 4463 // leukotriene-A4 hydrolase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4463 // leukotriene-A4 hydrolase activity // traceable

Figure 90

author statement /// 8233 // peptidase activity // traceable author statement Eicosanoid_Synthesis // GenMAPP /// Arachidonic acid metabolism // KEGG 4048

202877_s_at Hs.97199 CD93 molecule /// CD93 molecule CD93 6909 // phagocytosis // non-traceable author statement /// 16337 // cell-cell adhesion // inferred from direct assay /// 42116 // macrophage activation // non-traceable author statement /// 7596 // blood coagulation // inferred from electronic annotation /// 7155 // cell adhesion // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // Unknown /// 16021 // integral to membrane // inferred from electronic annotation 1849 // complement component C1q binding // inferred from direct assay /// 4872 // receptor activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 5529 // sugar binding // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation --- 22918
214693_x_at Hs.512037 calcitonin/calcitonin-related polypeptide, alpha /// calcitonin-related polypeptide, beta /// neuroblastoma breakpoint family, member 14 /// DKFZP564O0823 protein /// neuroblastoma breakpoint family, member 1 /// par-3 partitioning defective 3 homolog B (C. elegans) /// KIAA1245 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 9 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 8 /// similar to CG10522-PA /// hypothetical protein LOC728980 /// hypothetical protein LOC730476 CALCA /// CALCB /// NBPF14 /// DKFZP564O0823 /// NBPF1 /// PARD3B /// KIAA1245 /// NBPF11 /// NBPF15 /// NBPF20 /// NBPF9 /// NBPF10 /// NBPF8 /// LOC728936 /// LOC728980 /// LOC730476 --- --- 5509 // calcium ion binding // inferred from electronic annotation --- 149013 /// 200030 /// 25832 /// 284565 /// 400818 /// 440670 /// 440673 /// 440675 /// 55672 /// 641559 /// 644291 /// 644474 /// 652874
232599_at Hs.292097 exocyst complex component 6 EXOC6 6904 // vesicle docking during exocytosis // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6887 // exocytosis // inferred from electronic annotation 145 // exocyst // inferred from electronic annotation --- --- 54536
1569053_at --- adaptor-related protein complex 3, mu 2 subunit AP3M2 6886 // intracellular protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation 5795 // Golgi stack // inferred from electronic annotation /// 30119 // membrane coat adaptor complex // traceable author statement /// 30125 // clathrin vesicle coat // inferred from electronic annotation --- --- 10947
222775_s_at Hs.433439 mitochondrial ribosomal protein L35 MRPL35 6412 // protein biosynthesis // non-traceable author statement 5739 // mitochondrion // inferred from electronic annotation /// 5761 // mitochondrial ribosome // non-traceable author statement /// 30529 // ribonucleoprotein complex // inferred from electronic annotation 3735 // structural constituent of ribosome // non-traceable

Figure 91

author statement /// 45182 // translation regulator activity // non-traceable author statement --- 51318
227607_at Hs.16229 STAM binding protein-like 1 STAMBPL1 6512 // ubiquitin cycle // inferred from electronic annotation --- 4221 // ubiquitin thiolesterase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 57559
211719_x_at Hs.203717 fibronectin 1 /// fibronectin 1 FN1 6953 // acute-phase response // inferred from electronic annotation /// 7155 // cell adhesion // non-traceable author statement /// 7169 // transmembrane receptor protein tyrosine kinase signaling pathway // non-traceable author statement /// 8152 // metabolism // inferred from electronic annotation /// 9611 // response to wounding // non-traceable author statement /// 16477 // cell migration // non-traceable author statement /// 7155 // cell adhesion // inferred from electronic annotation 5576 // extracellular region // inferred from electronic annotation /// 5578 // extracellular matrix (sensu Metazoa) // non-traceable author statement /// 5793 // ER-Golgi intermediate compartment // inferred from direct assay /// 5576 // extracellular region // non-traceable author statement 5201 // extracellular matrix structural constituent // non-traceable author statement /// 5518 // collagen binding // non-traceable author statement /// 8201 // heparin binding // non-traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8201 // heparin binding // inferred from electronic annotation
Inflammatory_Response_Pathway // GenMAPP 2335
212299_at Hs.7200 NIMA (never in mitosis gene a)- related kinase 9 NEK9 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7067 // mitosis // inferred from electronic annotation /// 51301 // cell division // inferred from electronic annotation --- 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 91754
1553030_a_at Hs.558403 sulfite oxidase SUOX 6118 // electron transport // inferred from electronic annotation /// 9087 // methionine catabolism // not recorded 5739 // mitochondrion // inferred from electronic annotation 5506 // iron ion binding // inferred from electronic annotation /// 8482 // sulfite oxidase activity // traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 30151 // molybdenum ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 8482 // sulfite oxidase activity // inferred from electronic annotation Sulfur metabolism // KEGG 6821

Figure 92

242743_at Hs.513457 Interleukin 4 receptor IL4R 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6955 // immune response // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4896 // hematopoietin/interferon-class (D200-domain) cytokine receptor activity // inferred from electronic annotation /// 4913 // interleukin-4 receptor activity // traceable author statement /// 5057 // receptor signaling protein activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction Inflammatory_Response_Pathway // GenMAPP 3566
213120_at Hs.620701 KIAA0701 protein KIAA0701 --- --- ---
--- 23074
234050_at Hs.529984 T-cell activation GTPase activating protein
TAGAP --- --- 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation --- 117289
210839_s_at Hs.190977 ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) ENPP2 6796 // phosphate metabolism // traceable author statement /// 6928 // cell motility // traceable author statement /// 6935 // chemotaxis // non-traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 9117 // nucleotide metabolism // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 3676 // nucleic acid binding // inferred from electronic annotation /// 4519 // endonuclease activity // inferred from electronic annotation /// 4528 // phosphodiesterase I activity // traceable author statement /// 4551 // nucleotide diphosphatase activity // traceable author statement /// 8134 // transcription factor binding // traceable author statement /// 16787 // hydrolase activity // traceable author statement /// 3824 // catalytic activity // inferred from electronic annotation /// 4551 // nucleotide diphosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 5168
203058_s_at Hs.524491 3'-phosphoadenosine 5'-phosphosulfate synthase 2 PAPSS2 103 // sulfate assimilation // inferred from electronic annotation /// 1501 // skeletal development // inferred from sequence or structural similarity /// 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // not recorded /// 1501 // skeletal development // traceable author statement 5622 // intracellular // inferred from sequence or structural similarity 166 // nucleotide binding // inferred from electronic annotation /// 4020 // adenylylsulfate kinase activity // inferred from electronic annotation /// 4781 // sulfate adenylyltransferase (ATP) activity // inferred from sequence or structural similarity /// 5524 // ATP binding // inferred from sequence or structural similarity /// 16779 // nucleotidyltransferase activity // inferred from sequence or structural similarity /// 16740 // transferase activity // inferred from sequence or structural similarity /// 3824 // catalytic activity // inferred from electronic annotation /// 4781 // sulfate adenylyltransferase (ATP) activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase

Figure 93

activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16772 // transferase activity, transferring phosphorus-containing groups // inferred from electronic annotation /// 16779 // nucleotidyltransferase activity // inferred from electronic annotation Purine metabolism // KEGG /// Selenoamino acid metabolism // KEGG /// Sulfur metabolism // KEGG /// Purine metabolism // KEGG /// Selenoamino acid metabolism // KEGG /// Sulfur metabolism // KEGG 9060
233690_at Hs.149261 Runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) RUNX1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 7275 // development // traceable author statement /// 45944 // positive regulation of transcription from RNA polymerase II promoter // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // non-traceable author statement /// 16563 // transcriptional activator activity // inferred from direct assay /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 3677 // DNA binding // non-traceable author statement --- 861
204669_s_at Hs.589884 ring finger protein 24 RNF24 --- --- 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 11237
235359_at Hs.478815 leucine rich repeat containing 33 LRRC33 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 375387
1552516_a_at Hs.532363 homeodomain interacting protein kinase 1 HIPK1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation --- 204851
206148_at Hs.632790 interleukin 3 receptor, alpha (low affinity) IL3RA 6468 // protein amino acid phosphorylation // not recorded /// 7275 // development // not recorded 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4896 // hematopoietin/interferon-class (D200-domain) cytokine receptor activity // inferred from electronic annotation /// 4912 // interleukin-3

Figure 94

receptor activity // traceable author statement /// 5057 // receptor signaling protein activity // not recorded --- 3563
1557905_s_at Hs.502328 CD44 molecule (Indian blood group) /// mitogen-activated protein kinase 10 CD44 /// MAPK10 7155 // cell adhesion // inferred from electronic annotation /// 7160 // cell-matrix adhesion // non-traceable author statement /// 16337 // cell-cell adhesion // non-traceable author statement 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5518 // collagen binding // non-traceable author statement /// 5540 // hyaluronic acid binding // inferred from electronic annotation /// 5540 // hyaluronic acid binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from electronic annotation --- 960
236345_at Hs.520757 Thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A) TBXAS1 1516 // prostaglandin biosynthesis // inferred from electronic annotation /// 6118 // electron transport // inferred from electronic annotation /// 6633 // fatty acid biosynthesis // inferred from electronic annotation /// 7596 // blood coagulation // not recorded /// 8610 // lipid biosynthesis // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4796 // thromboxane-A synthase activity // inferred from electronic annotation /// 5506 // iron ion binding // inferred from electronic annotation /// 16712 // oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen // inferred from electronic annotation /// 16853 // isomerase activity // inferred from electronic annotation /// 20037 // heme binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4497 // monooxygenase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation Eicosanoid_Synthesis // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP /// Eicosanoid_Synthesis // GenMAPP /// Eicosanoid_Synthesis // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP /// Arachidonic acid metabolism // KEGG 6916
213734_at --- --- --- 7242 // intracellular signaling cascade // inferred from electronic annotation --- --- --- 55884
243860_at Hs.434961 Ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310
224595_at Hs.573495 solute carrier family 44, member 1 SLC44A1 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 23446
210706_s_at Hs.589884 ring finger protein 24 RNF24 --- --- 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 11237

Figure 95

226542_at Hs.547576 Full-length cDNA clone CS0DJ002YF02 of T cells (Jurkat cell line) Cot 10-normalized of Homo sapiens (human) --- --- --- --- --- ---
228758_at Hs.478588 B-cell CLL/lymphoma 6 (zinc finger protein 51) BCL6 122 // negative regulation of transcription from RNA polymerase II promoter // not recorded /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // traceable author statement /// 6954 // inflammatory response // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 119 // mediator complex // not recorded /// 5634 // nucleus // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation --- 604
209835_x_at Hs.502328 CD44 molecule (Indian blood group) CD44 7155 // cell adhesion // inferred from electronic annotation /// 7160 // cell-matrix adhesion // non-traceable author statement /// 16337 // cell-cell adhesion // non-traceable author statement 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5518 // collagen binding // non-traceable author statement /// 5540 // hyaluronic acid binding // inferred from electronic annotation /// 5540 // hyaluronic acid binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from electronic annotation --- 960
211974_x_at Hs.479396 recombining binding protein suppressor of hairless (Drosophila) RBPSUH 6310 // DNA recombination // non-traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // not recorded /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 45892 // negative regulation of transcription, DNA-dependent // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from direct assay /// 5634 // nucleus // non-traceable author statement /// 5730 // nucleolus // inferred from direct assay /// 5634 // nucleus // inferred from electronic annotation 150 // recombinase activity // non-traceable author statement /// 3700 // transcription factor activity // traceable author statement /// 3702 // RNA polymerase II transcription factor activity // not recorded /// 5515 // protein binding // inferred from physical interaction /// 3677 // DNA binding // inferred from electronic annotation /// 3677 // DNA binding // traceable author statement /// 3677 // DNA binding // non-traceable author statement --- 3516
240593_x_at Hs.144114 Calcium/calmodulin-dependent protein kinase (CaM kinase) II delta CAMK2D 1558 // regulation of cell growth // non-traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 //

Figure 96

protein amino acid phosphorylation // non-traceable author statement
5954 // calcium- and calmodulin-dependent protein kinase complex // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // non-traceable author statement /// 5516 // calmodulin binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 5524 // ATP binding // non-traceable author statement /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4685 // calcium- and calmodulin-dependent protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
Calcium_regulation_in_cardiac_cells // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP /// Smooth_muscle_contraction // GenMAPP 817
223412_at Hs.63841 kelch repeat and BTB (POZ) domain containing 7
KBTBD7 --- --- 5515 // protein binding // inferred from electronic annotation --- 84078
225115_at Hs.397465 Homeodomain interacting protein kinase 2 HIPK2
74 // regulation of progression through cell cycle // non-traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 8629 // induction of apoptosis by intracellular signals // non-traceable author statement /// 19048 // virus-host interaction // non-traceable author statement /// 30511 // positive regulation of transforming growth factor beta receptor signaling pathway // inferred from mutant phenotype /// 46330 // positive regulation of JNK cascade // inferred from mutant phenotype 5634 // nucleus // inferred from direct assay /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 16604 // nuclear body // traceable author statement /// 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3714 // transcription corepressor activity // traceable author statement /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 46790 // virion binding // inferred from physical interaction /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 4672 // protein kinase activity // traceable author statement --- 28996
201631_s_at Hs.591785 immediate early response 3 IER3 6915 // apoptosis // traceable author statement /// 6916 // anti-apoptosis // non-traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 9653 // morphogenesis // traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 8870

Figure 97

219394_at Hs.464217 phosphatidylglycerophosphate synthase 1 PGS1 8152 // metabolism // inferred from electronic annotation /// 8654 // phospholipid biosynthesis // inferred from sequence or structural similarity 5739 // mitochondrion // inferred from sequence or structural similarity 3824 // catalytic activity // inferred from electronic annotation /// 8444 // CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity // inferred from sequence or structural similarity --- 9489
219431_at Hs.368631 Rho GTPase activating protein 10 ARHGAP10 7010 // cytoskeleton organization and biogenesis // inferred from sequence or structural similarity --- 5100 // Rho GTPase activator activity // inferred from sequence or structural similarity /// 5515 // protein binding // inferred from sequence or structural similarity /// 5096 // GTPase activator activity // inferred from electronic annotation --- 79658
212014_x_at Hs.502328 CD44 molecule (Indian blood group) CD44 7155 // cell adhesion // inferred from electronic annotation /// 7160 // cell-matrix adhesion // non-traceable author statement /// 16337 // cell-cell adhesion // non-traceable author statement 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5518 // collagen binding // non-traceable author statement /// 5540 // hyaluronic acid binding // inferred from electronic annotation /// 5540 // hyaluronic acid binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from electronic annotation --- 960
205273_s_at Hs.528300 pitrilysin metallopeptidase 1 PITRM1 --- --- 8047 // enzyme activator activity // traceable author statement /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation --- 10531
210916_s_at Hs.502328 CD44 molecule (Indian blood group) /// mitogen-activated protein kinase 10 CD44 /// MAPK10 7155 // cell adhesion // inferred from electronic annotation /// 7160 // cell-matrix adhesion // non-traceable author statement /// 16337 // cell-cell adhesion // non-traceable author statement 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5518 // collagen binding // non-traceable author statement /// 5540 // hyaluronic acid binding // inferred from electronic annotation /// 5540 // hyaluronic acid binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from electronic annotation --- 960
202382_s_at Hs.633853 glucosamine-6-phosphate deaminase 1 GNPDA1 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6043 // glucosamine catabolism // traceable author statement /// 6044 // N-acetylglucosamine metabolism // inferred from electronic annotation /// 6091 // generation of precursor metabolites and energy // traceable author statement /// 7338 // fertilization (sensu Metazoa) // traceable author statement --- 4342 // glucosamine-6-phosphate deaminase activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation /// 4342 // glucosamine-6-phosphate deaminase activity //

Figure 98

inferred from electronic annotation Aminosugars metabolism // KEGG
10007
226056_at Hs.477278 Cdc42 GTPase-activating protein CDGAP ---
--- --- --- 57514
200768_s_at Hs.516157 methionine adenosyltransferase II, alpha MAT2A
6730 // one-carbon compound metabolism // inferred from
electronic annotation --- 166 // nucleotide binding // inferred
from electronic annotation /// 287 // magnesium ion binding // inferred
from electronic annotation /// 4478 // methionine adenosyltransferase
activity // traceable author statement /// 5524 // ATP binding //
inferred from electronic annotation /// 16740 // transferase activity
// inferred from electronic annotation /// 30955 // potassium ion
binding // inferred from electronic annotation /// 4478 // methionine
adenosyltransferase activity // inferred from electronic annotation ///
46872 // metal ion binding // inferred from electronic annotation ---
4144
207253_s_at Hs.440219 ubinuclein 1 UBN1 --- 5634 // nucleus
// inferred from electronic annotation --- --- 29855
203410_at --- adaptor-related protein complex 3, mu 2 subunit AP3M2
6886 // intracellular protein transport // inferred from
electronic annotation /// 6810 // transport // inferred from electronic
annotation /// 15031 // protein transport // inferred from electronic
annotation 5795 // Golgi stack // inferred from electronic annotation
/// 30119 // membrane coat adaptor complex // traceable author
statement /// 30125 // clathrin vesicle coat // inferred from
electronic annotation --- --- 10947
205928_at Hs.631623 zinc finger protein 443 ZNF443 6350 //
transcription // inferred from electronic annotation /// 6355 //
regulation of transcription, DNA-dependent // inferred from electronic
annotation /// 6917 // induction of apoptosis // traceable author
statement /// 6950 // response to stress // traceable author statement
5634 // nucleus // inferred from electronic annotation /// 5622
// intracellular // inferred from electronic annotation 3677 // DNA
binding // inferred from electronic annotation /// 8270 // zinc ion
binding // inferred from electronic annotation /// 46872 // metal ion
binding // inferred from electronic annotation /// 3676 // nucleic acid
binding // inferred from electronic annotation --- 10224
218795_at Hs.562154 acid phosphatase 6, lysophosphatidic ACP6
--- --- 3993 // acid phosphatase activity // inferred from
electronic annotation /// 16787 // hydrolase activity // inferred from
electronic annotation --- 51205
225305_at Hs.578109 solute carrier family 25, member 29 SLC25A29
6810 // transport // inferred from electronic annotation 5739
// mitochondrion // inferred from electronic annotation /// 5743 //
mitochondrial inner membrane // inferred from electronic annotation ///
16020 // membrane // inferred from electronic annotation /// 16021 //
integral to membrane // inferred from electronic annotation 5215 //
transporter activity // inferred from electronic annotation /// 5488 //
binding // inferred from electronic annotation --- 123096
206363_at Hs.134859 v-maf musculoaponeurotic fibrosarcoma oncogene
homolog (avian) MAF 6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-
dependent // inferred from electronic annotation /// 6366 //
transcription from RNA polymerase II promoter // traceable author
statement 785 // chromatin // traceable author statement /// 5634 //
nucleus // inferred from electronic annotation 3702 // RNA polymerase
II transcription factor activity // traceable author statement ///

Figure 99

43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 4094
1557527_at Hs.149261 Runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) RUNX1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 7275 // development // traceable author statement /// 45944 // positive regulation of transcription from RNA polymerase II promoter // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // non-traceable author statement /// 16563 // transcriptional activator activity // inferred from direct assay /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 3677 // DNA binding // non-traceable author statement --- 861
212226_s_at Hs.405156 phosphatidic acid phosphatase type 2B PPAP2B 6629 // lipid metabolism // non-traceable author statement /// 8354 // germ cell migration // traceable author statement 16020 // membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 4721 // phosphoprotein phosphatase activity // traceable author statement /// 8195 // phosphatidate phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Glycerolipid metabolism // KEGG /// Glycerophospholipid metabolism // KEGG /// Glycosphingolipid metabolism // KEGG 8613
203771_s_at Hs.488143 biliverdin reductase A BLVRA 6118 // electron transport // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation --- 4074 // biliverdin reductase activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4074 // biliverdin reductase activity // inferred from electronic annotation Porphyrin and chlorophyll metabolism // KEGG 644
215813_s_at Hs.201978 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) PTGS1 1516 // prostaglandin biosynthesis // inferred from electronic annotation /// 1516 // prostaglandin biosynthesis // inferred from sequence or structural similarity /// 6629 // lipid metabolism // non-traceable author statement /// 6633 // fatty acid biosynthesis // inferred from electronic annotation /// 7582 // physiological process // traceable author statement /// 8217 // blood pressure regulation // inferred from sequence or structural similarity /// 30216 // keratinocyte differentiation // inferred from sequence or structural similarity /// 8610 // lipid biosynthesis // inferred from electronic annotation 5634 // nucleus // inferred from sequence or structural similarity /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 5792 // microsome // inferred from sequence or structural similarity /// 16020 // membrane // inferred from electronic annotation 4601

Figure 100

// peroxidase activity // inferred from electronic annotation /// 4666 // prostaglandin-endoperoxide synthase activity // traceable author statement /// 5506 // iron ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 16702 // oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4666 // prostaglandin-endoperoxide synthase activity // inferred from electronic annotation Eicosanoid_Synthesis // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP /// Arachidonic acid metabolism // KEGG 5742

214894_x_at Hs.580782 microtubule-actin crosslinking factor 1 MACF1 7050 // cell cycle arrest // inferred from electronic annotation /// 5975 // carbohydrate metabolism // inferred from electronic annotation 5737 // cytoplasm // inferred from direct assay /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 5856 // cytoskeleton // inferred from sequence or structural similarity /// 5856 // cytoskeleton // non-traceable author statement /// 5856 // cytoskeleton // inferred from electronic annotation 3779 // actin binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5509 // calcium ion binding // non-traceable author statement /// 8017 // microtubule binding // inferred from sequence or structural similarity /// 8017 // microtubule binding // non-traceable author statement /// 51015 // actin filament binding // non-traceable author statement /// 3779 // actin binding // inferred from direct assay /// 4553 // hydrolase activity, hydrolyzing O-glycosyl compounds // inferred from electronic annotation --- 23499

244556_at Hs.304475 Lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) LCP2 6955 // immune response // traceable author statement /// 7169 // transmembrane receptor protein tyrosine kinase signaling pathway // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // traceable author statement --- 3937

212158_at Hs.1501 syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) SDC2 --- 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 8092 // cytoskeletal protein binding // inferred from electronic annotation --- 6383

1556332_at Hs.634213 CDNA FLJ38412 fis, clone FEBRA2009385 --- --- --- --- ---

210264_at Hs.239891 G protein-coupled receptor 35 GPR35 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation

Figure 101

/// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // traceable author statement GPCRDB_Class_A_Rhodopsin-like // GenMAPP 2859
233011_at Hs.494173 Annexin A1 ANXA1 6629 // lipid metabolism // traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 6928 // cell motility // traceable author statement /// 6954 // inflammatory response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 7165 // signal transduction // traceable author statement 5737 // cytoplasm // traceable author statement 4859 // phospholipase inhibitor activity // inferred from electronic annotation /// 5102 // receptor binding // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // traceable author statement /// 5544 // calcium-dependent phospholipid binding // inferred from electronic annotation /// 19834 // phospholipase A2 inhibitor activity // inferred from electronic annotation /// 4859 // phospholipase inhibitor activity // traceable author statement /// 5543 // phospholipid binding // traceable author statement
Prostaglandin_synthesis_regulation // GenMAPP 301
238983_at Hs.590923 NOL1/NOP2/Sun domain family, member 7 NSUN7
--- --- --- Cell_cycle_KEGG // GenMAPP /// Cell_cycle_KEGG // GenMAPP /// G1_to_S_cell_cycle_Reactome // GenMAPP /// G1_to_S_cell_cycle_Reactome // GenMAPP 79730
224596_at Hs.573495 solute carrier family 44, member 1 SLC44A1
6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- ---
23446
209184_s_at Hs.442344 insulin receptor substrate 2 IRS2 6006 // glucose metabolism // traceable author statement /// 7165 // signal transduction // traceable author statement /// 8284 // positive regulation of cell proliferation // not recorded /// 7165 // signal transduction // inferred from electronic annotation --- 4871 // signal transducer activity // traceable author statement /// 5158 // insulin receptor binding // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation --- 8660
209930_s_at Hs.75643 nuclear factor (erythroid-derived 2), 45kDa
NFE2 6350 // transcription // inferred from electronic annotation /// 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 7275 // development // traceable author statement /// 7599 // hemostasis // traceable author statement /// 8015 // circulation // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 3713 // transcription coactivator activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 4778
222477_s_at Hs.438641 transmembrane 7 superfamily member 3
TM7SF3 --- 16020 // membrane // inferred from electronic

Figure 102

annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 51768
219748_at Hs.164797 triggering receptor expressed on myeloid cells-like 2 TREML2 --- --- --- --- 79865
1554472_a_at Hs.304362 PHD finger protein 20-like 1 PHF20L1 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation --- 3676 // nucleic acid binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation --- 51105
1556211_a_at Hs.567501 Androgen-induced 1 AIG1 --- --- --- --- 644480
236114_at Hs.149261 Runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) RUNX1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 7275 // development // traceable author statement /// 45944 // positive regulation of transcription from RNA polymerase II promoter // inferred from direct assay /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // non-traceable author statement /// 16563 // transcriptional activator activity // inferred from direct assay /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 3677 // DNA binding // non-traceable author statement --- 861
239301_at Hs.610104 Transcribed locus --- --- --- --- --- ---
1562031_at Hs.591081 Janus kinase 2 (a protein tyrosine kinase) JAK2 74 // regulation of progression through cell cycle // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // traceable author statement /// 6928 // cell motility // traceable author statement /// 7242 // intracellular signaling cascade // traceable author statement /// 7259 // JAK-STAT cascade // traceable author statement /// 7498 // mesoderm development // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation 5856 // cytoskeleton // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // traceable author statement /// 4718 // Janus kinase activity // inferred from electronic annotation /// 5102 // receptor binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 42169 // SH2 domain binding // inferred from physical interaction /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4672 // protein kinase activity // non-traceable author statement --- 3717

Figure 103

205052_at Hs.175905 AU RNA binding protein/enoyl-Coenzyme A hydratase AUH 6402 // mRNA catabolism // traceable author statement /// 8152 // metabolism // inferred from electronic annotation /// 9083 // branched chain family amino acid catabolism // inferred from electronic annotation 5739 // mitochondrion // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation /// 3730 // mRNA 3'-UTR binding // traceable author statement /// 4300 // enoyl-CoA hydratase activity // traceable author statement /// 4490 // methylglutaconyl-CoA hydratase activity // inferred from electronic annotation /// 16829 // lyase activity // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation --- 549
201760_s_at Hs.506985 WD repeat and SOCS box-containing 2 WSB2 7242 // intracellular signaling cascade // inferred from electronic annotation --- --- --- 55884
32069_at Hs.511839 Nedd4 binding protein 1 N4BP1 --- 5634 // nucleus // inferred from electronic annotation --- --- 9683
229327_s_at Hs.643995 Transcribed locus --- --- --- --- --- ---
228410_at Hs.496982 GRB2-associated binding protein 3 GAB3 --- --- --- --- 139716
229686_at Hs.111377 purinergic receptor P2Y, G-protein coupled, 8 P2RY8 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 45028 // purinergic nucleotide receptor activity, G-protein coupled // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation --- 286530
232472_at Hs.159430 Fibronectin type III domain containing 3B FNDC3B --- --- --- --- 64778
220918_at --- chromosome 21 open reading frame 96 C21orf96 --- --- --- --- 80215

Figure 104

probe UniGene.ID Gene.Title Gene.Symbol
Gene.Ontology.Biological.Process
Gene.Ontology.Cellular.Component
Gene.Ontology.Molecular.Function Pathway Entrez.Gene

209392_at Hs.190977 ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin) ENPP2 6796 // phosphate
metabolism // traceable author statement /// 6928 // cell motility //
traceable author statement /// 6935 // chemotaxis // non-traceable
author statement /// 7186 // G-protein coupled receptor protein
signaling pathway // traceable author statement /// 9117 // nucleotide
metabolism // inferred from electronic annotation 5886 // plasma
membrane // traceable author statement /// 5887 // integral to plasma
membrane // traceable author statement /// 16020 // membrane //
inferred from electronic annotation /// 16021 // integral to membrane
// inferred from electronic annotation 3676 // nucleic acid binding
// inferred from electronic annotation /// 4519 // endonuclease
activity // inferred from electronic annotation /// 4528 //
phosphodiesterase I activity // traceable author statement /// 4551 //
nucleotide diphosphatase activity // traceable author statement ///
8134 // transcription factor binding // traceable author statement ///
16787 // hydrolase activity // traceable author statement /// 3824 //
catalytic activity // inferred from electronic annotation /// 4551 //
nucleotide diphosphatase activity // inferred from electronic
annotation /// 16787 // hydrolase activity // inferred from electronic
annotation --- 5168
210839_s_at Hs.190977 ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin) ENPP2 6796 // phosphate
metabolism // traceable author statement /// 6928 // cell motility //
traceable author statement /// 6935 // chemotaxis // non-traceable
author statement /// 7186 // G-protein coupled receptor protein
signaling pathway // traceable author statement /// 9117 // nucleotide
metabolism // inferred from electronic annotation 5886 // plasma
membrane // traceable author statement /// 5887 // integral to plasma
membrane // traceable author statement /// 16020 // membrane //
inferred from electronic annotation /// 16021 // integral to membrane
// inferred from electronic annotation 3676 // nucleic acid binding
// inferred from electronic annotation /// 4519 // endonuclease
activity // inferred from electronic annotation /// 4528 //
phosphodiesterase I activity // traceable author statement /// 4551 //
nucleotide diphosphatase activity // traceable author statement ///
8134 // transcription factor binding // traceable author statement ///
16787 // hydrolase activity // traceable author statement /// 3824 //
catalytic activity // inferred from electronic annotation /// 4551 //
nucleotide diphosphatase activity // inferred from electronic
annotation /// 16787 // hydrolase activity // inferred from electronic
annotation --- 5168
204271_s_at Hs.82002 endothelin receptor type B EDNRB 7194 //
negative regulation of adenylate cyclase activity // traceable author
statement /// 7200 // G-protein signaling, coupled to IP3 second
messenger (phospholipase C activating) // traceable author statement
/// 7399 // nervous system development // traceable author statement
/// 7605 // sensory perception of sound // inferred from electronic
annotation /// 7165 // signal transduction // inferred from electronic
annotation /// 7186 // G-protein coupled receptor protein signaling
pathway // inferred from electronic annotation /// 7166 // cell surface
receptor linked signal transduction // traceable author statement 5886

Figure 105

// plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4962 // endothelin receptor activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4962 // endothelin receptor activity // inferred from electronic annotation Prostaglandin_synthesis_regulation // GenMAPP /// GPCRDB_Class_A_Rhodopsin-like // GenMAPP /// Peptide_GPCRs // GenMAPP 1910
201109_s_at Hs.164226 thrombospondin 1 THBS1 6928 // cell motility // not recorded /// 7155 // cell adhesion // inferred from electronic annotation /// 7275 // development // traceable author statement /// 7399 // nervous system development // not recorded /// 7596 // blood coagulation // not recorded 5576 // extracellular region // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 4866 // endopeptidase inhibitor activity // traceable author statement /// 4871 // signal transducer activity // traceable author statement /// 5198 // structural molecule activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8201 // heparin binding // inferred from electronic annotation TGF_Beta_Signaling_Pathway // GenMAPP /// Inflammatory_Response_Pathway // GenMAPP 7057
206701_x_at Hs.82002 endothelin receptor type B EDNRB 7194 // negative regulation of adenylate cyclase activity // traceable author statement /// 7200 // G-protein signaling, coupled to IP3 second messenger (phospholipase C activating) // traceable author statement /// 7399 // nervous system development // traceable author statement /// 7605 // sensory perception of sound // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7166 // cell surface receptor linked signal transduction // traceable author statement 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4962 // endothelin receptor activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4962 // endothelin receptor activity // inferred from electronic annotation Prostaglandin_synthesis_regulation // GenMAPP /// GPCRDB_Class_A_Rhodopsin-like // GenMAPP /// Peptide_GPCRs // GenMAPP 1910
202087_s_at Hs.418123 cathepsin L CTSL 6508 // proteolysis // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5764 // lysosome // non-traceable author statement /// 5764 // lysosome // inferred from electronic annotation /// 5764 // lysosome // not recorded 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4217 // cathepsin L activity // traceable author statement /// 4217 //

Figure 106

cathepsin L activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation
Antigen processing and presentation // KEGG 1514
204273_at Hs.82002 endothelin receptor type B EDNRB 7194 // negative regulation of adenylate cyclase activity // traceable author statement /// 7200 // G-protein signaling, coupled to IP3 second messenger (phospholipase C activating) // traceable author statement /// 7399 // nervous system development // traceable author statement /// 7605 // sensory perception of sound // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7166 // cell surface receptor linked signal transduction // traceable author statement 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4962 // endothelin receptor activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4962 // endothelin receptor activity // inferred from electronic annotation Prostaglandin_synthesis_regulation // GenMAPP /// GPCRDB_Class_A_Rhodopsin-like // GenMAPP /// Peptide_GPCRs // GenMAPP 1910
213060_s_at Hs.514840 chitinase 3-like 2 /// chitinase 3-like 2
CHI3L2 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6032 // chitin catabolism // inferred from electronic annotation 5615 // extracellular space // traceable author statement 3824 // catalytic activity // inferred from electronic annotation /// 4568 // chitinase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4553 // hydrolase activity, hydrolyzing O-glycosyl compounds // inferred from electronic annotation --- 1117
203913_s_at Hs.77348 hydroxyprostaglandin dehydrogenase 15-(NAD)
HPGD 6629 // lipid metabolism // inferred from electronic annotation /// 6631 // fatty acid metabolism // inferred from electronic annotation /// 6693 // prostaglandin metabolism // traceable author statement /// 7179 // transforming growth factor beta receptor signaling pathway // inferred from direct assay /// 7565 // pregnancy // inferred from direct assay /// 7567 // parturition // inferred from direct assay /// 8152 // metabolism // inferred from electronic annotation /// 19372 // lipoxygenase pathway // traceable author statement /// 45786 // negative regulation of progression through cell cycle // inferred from direct assay /// 6693 // prostaglandin metabolism // inferred from electronic annotation 5829 // cytosol // traceable author statement 4667 // prostaglandin-D synthase activity // not recorded /// 4957 // prostaglandin E receptor activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // non-traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 42803 // protein homodimerization activity // traceable author statement /// 51287 //

Figure 107

NAD binding // inferred from direct assay /// 3824 // catalytic activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // inferred from electronic annotation Prostaglandin_synthesis_regulation // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP 3248
219911_s_at Hs.235782 solute carrier organic anion transporter family, member 4A1 SLCO4A1 6811 // ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 28231
225016_at Hs.293274 adenomatosis polyposis coli down-regulated 1 APCDD1 --- --- --- --- 147495
212298_at Hs.131704 neuropilin 1 NRP1 1525 // angiogenesis // inferred from electronic annotation /// 7155 // cell adhesion // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 7399 // nervous system development // inferred from electronic annotation /// 7411 // axon guidance // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 9887 // organ morphogenesis // traceable author statement /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5624 // membrane fraction // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5021 // vascular endothelial growth factor receptor activity // traceable author statement --- 8829
1555728_a_at Hs.325960 membrane-spanning 4-domains, subfamily A, member 4 MS4A4A 7165 // signal transduction // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 51338
241981_at Hs.268874 family with sequence similarity 20, member A FAM20A --- --- --- --- 54757
227697_at Hs.527973 suppressor of cytokine signaling 3 SOCS3 1558 // regulation of cell growth // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation --- 4860 // protein kinase inhibitor activity // traceable author statement --- 9021

201110_s_at Hs.164226 thrombospondin 1 THBS1 6928 // cell motility // not recorded /// 7155 // cell adhesion // inferred from electronic annotation /// 7275 // development // traceable author statement /// 7399 // nervous system development // not recorded /// 7596 // blood coagulation // not recorded 5576 // extracellular region // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 4866 // endopeptidase inhibitor activity // traceable author statement /// 4871 // signal transducer activity // traceable author statement /// 5198 // structural molecule activity //

Figure 108

inferred from electronic annotation /// 5509 // calcium ion binding //
inferred from electronic annotation /// 5515 // protein binding //
inferred from electronic annotation /// 8201 // heparin binding //
inferred from electronic annotation TGF_Beta_Signaling_Pathway //
GenMAPP /// Inflammatory_Response_Pathway // GenMAPP 7057
1563445_x_at --- cathepsin L-like 3 CTSLL3 --- ---
--- --- 1518
219607_s_at Hs.325960 membrane-spanning 4-domains, subfamily A,
member 4 MS4A4A 7165 // signal transduction // inferred from
electronic annotation 16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from
electronic annotation 4872 // receptor activity // inferred from
electronic annotation --- 51338
209875_s_at Hs.313 secreted phosphoprotein 1 (osteopontin, bone
sialoprotein I, early T-lymphocyte activation 1) SPP1 1503 //
ossification // inferred from electronic annotation /// 1503 //
ossification // traceable author statement /// 6916 // anti-apoptosis
// inferred from sequence or structural similarity /// 7155 // cell
adhesion // inferred from electronic annotation /// 7160 // cell-matrix
adhesion // non-traceable author statement /// 7267 // cell-cell
signaling // traceable author statement /// 30502 // negative
regulation of bone mineralization // non-traceable author statement ///
30595 // immune cell chemotaxis // traceable author statement /// 42088
// T-helper 1 type immune response // traceable author statement ///
42102 // positive regulation of T cell proliferation // traceable
author statement /// 45637 // regulation of myeloid cell
differentiation // traceable author statement /// 50930 // induction of
positive chemotaxis // traceable author statement /// 6954 //
inflammatory response // traceable author statement 5578 //
extracellular matrix (sensu Metazoa) // traceable author statement ///
5615 // extracellular space // inferred from electronic annotation ///
5576 // extracellular region // traceable author statement 5125 //
cytokine activity // inferred from sequence or structural similarity
/// 5178 // integrin binding // non-traceable author statement /// 5515
// protein binding // inferred from electronic annotation /// 8083 //
growth factor activity // traceable author statement /// 5125 //
cytokine activity // inferred from electronic annotation
TGF_Beta_Signaling_Pathway // GenMAPP 6696
203149_at --- poliovirus receptor-related 2 (herpesvirus entry
mediator B) PVRL2 --- 5886 // plasma membrane // traceable author
statement /// 16021 // integral to membrane // inferred from electronic
annotation /// 16020 // membrane // inferred from electronic annotation
15026 // coreceptor activity // traceable author statement ///
4872 // receptor activity // inferred from electronic annotation ---
5819
216950_s_at Hs.77424 Fc fragment of IgG, high affinity Ia, receptor
(CD64) FCGR1A 6911 // phagocytosis, engulfment // traceable
author statement /// 6955 // immune response // traceable author
statement /// 7165 // signal transduction // traceable author statement
/// 6955 // immune response // non-traceable author statement 5887
// integral to plasma membrane // not recorded /// 16020 // membrane //
inferred from electronic annotation /// 16021 // integral to membrane
// inferred from electronic annotation /// 5886 // plasma membrane //
non-traceable author statement 4872 // receptor activity //
inferred from electronic annotation /// 5057 // receptor signaling
protein activity // traceable author statement /// 19864 // IgG binding

Figure 109

// inferred from electronic annotation /// 19763 // immunoglobulin receptor activity // non-traceable author statement --- 2209 202800_at Hs.481918 solute carrier family 1 (glial high affinity glutamate transporter), member 3 SLC1A3 1504 // neurotransmitter uptake // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 6835 // dicarboxylic acid transport // inferred from electronic annotation /// 7268 // synaptic transmission // traceable author statement /// 15813 // L-glutamate transport // traceable author statement 5624 // membrane fraction // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5313 // L-glutamate transporter activity // traceable author statement /// 15293 // symporter activity // inferred from electronic annotation /// 17153 // sodium:dicarboxylate symporter activity // inferred from electronic annotation --- 6507
220491_at Hs.8821 hepcidin antimicrobial peptide HAMP 6805 // xenobiotic metabolism // inferred from electronic annotation /// 6879 // iron ion homeostasis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 42742 // defense response to bacteria // inferred from electronic annotation /// 42828 // response to pathogen // inferred from electronic annotation /// 50832 // defense response to fungi // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 5179 // hormone activity // inferred from electronic annotation --- 57817
211330_s_at Hs.233325 hemochromatosis HFE 6461 // protein complex assembly // traceable author statement /// 6811 // ion transport // inferred from electronic annotation /// 6826 // iron ion transport // traceable author statement /// 6879 // iron ion homeostasis // traceable author statement /// 6898 // receptor mediated endocytosis // traceable author statement /// 19882 // antigen presentation // inferred from electronic annotation /// 19883 // antigen presentation, endogenous antigen // inferred from electronic annotation /// 19885 // antigen processing, endogenous antigen via MHC class I // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6826 // iron ion transport // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation 5737 // cytoplasm // traceable author statement /// 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 42612 // MHC class I protein complex // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5506 // iron ion binding // inferred from electronic annotation /// 30106 // MHC class I receptor activity // inferred from electronic annotation --- 3077
231823_s_at Hs.285666 SH3 and PX domains 2B SH3PXD2B 7242 // intracellular signaling cascade // inferred from electronic annotation --- 5515 // protein binding // inferred from electronic annotation /// 35091 // phosphoinositide binding // inferred from electronic annotation --- 285590
227297_at Hs.113157 integrin, alpha 9 ITGA9 7155 // cell adhesion // traceable author statement /// 7229 // integrin-mediated signaling pathway // inferred from electronic annotation /// 7155 // cell adhesion // inferred from electronic annotation 8305 // integrin complex // traceable author statement /// 16020 // membrane // inferred

Figure 110

from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 8305 // integrin complex // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation Integrin-mediated_cell_adhesion_KEGG // GenMAPP /// Integrin-mediated_cell_adhesion_KEGG // GenMAPP 3680
214511_x_at Hs.534956 Fc fragment of IgG, high affinity Ib, receptor (CD64) FCGR1B 6911 // phagocytosis, engulfment // traceable author statement /// 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6955 // immune response // non-traceable author statement 5887 // integral to plasma membrane // not recorded /// 16020 // membrane // inferred from electronic annotation /// 5886 // plasma membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5057 // receptor signaling protein activity // traceable author statement /// 19864 // IgG binding // inferred from electronic annotation /// 19763 // immunoglobulin receptor activity // non-traceable author statement --- 2209 /// 440607 /// 652758
207053_at Hs.468274 solute carrier family 8 (sodium/calcium exchanger), member 1 SLC8A1 6811 // ion transport // inferred from electronic annotation /// 6814 // sodium ion transport // traceable author statement /// 6816 // calcium ion transport // traceable author statement /// 6936 // muscle contraction // traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6814 // sodium ion transport // inferred from electronic annotation /// 6816 // calcium ion transport // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5432 // calcium:sodium antiporter activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5516 // calmodulin binding // inferred from electronic annotation /// 15081 // sodium ion transporter activity // traceable author statement /// 15085 // calcium ion transporter activity // traceable author statement /// 15297 // antiporter activity // inferred from electronic annotation /// 31402 // sodium ion binding // inferred from electronic annotation
Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 6546
211548_s_at Hs.77348 hydroxyprostaglandin dehydrogenase 15-(NAD)
HPGD 6629 // lipid metabolism // inferred from electronic annotation /// 6631 // fatty acid metabolism // inferred from electronic annotation /// 6693 // prostaglandin metabolism // traceable author statement /// 7179 // transforming growth factor beta receptor signaling pathway // inferred from direct assay /// 7565 // pregnancy // inferred from direct assay /// 7567 // parturition // inferred from direct assay /// 8152 // metabolism // inferred from electronic annotation /// 19372 // lipoxygenase pathway // traceable author statement /// 45786 // negative regulation of progression through cell cycle // inferred from direct assay /// 6693 // prostaglandin metabolism // inferred from electronic annotation 5829 // cytosol // traceable author statement 4667 // prostaglandin-D synthase activity

Figure 111

// not recorded /// 4957 // prostaglandin E receptor activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // non-traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 42803 // protein homodimerization activity // traceable author statement /// 51287 // NAD binding // inferred from direct assay /// 3824 // catalytic activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // inferred from electronic annotation Prostaglandin_synthesis_regulation // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP 3248
221245_s_at Hs.17631 frizzled homolog 5 (Drosophila) /// frizzled homolog 5 (Drosophila) FZD5 --- --- --- --- 81561
215049_x_at Hs.504641 CD163 molecule CD163 19735 // antimicrobial humoral response (sensu Vertebrata) // traceable author statement 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation 5044 // scavenger receptor activity // non-traceable author statement /// 5044 // scavenger receptor activity // traceable author statement /// 5044 // scavenger receptor activity // inferred from electronic annotation --- 9332
203914_x_at Hs.77348 hydroxyprostaglandin dehydrogenase 15-(NAD) HPGD 6629 // lipid metabolism // inferred from electronic annotation /// 6631 // fatty acid metabolism // inferred from electronic annotation /// 6693 // prostaglandin metabolism // traceable author statement /// 7179 // transforming growth factor beta receptor signaling pathway // inferred from direct assay /// 7565 // pregnancy // inferred from direct assay /// 7567 // parturition // inferred from direct assay /// 8152 // metabolism // inferred from electronic annotation /// 19372 // lipoxygenase pathway // traceable author statement /// 45786 // negative regulation of progression through cell cycle // inferred from direct assay /// 6693 // prostaglandin metabolism // inferred from electronic annotation 5829 // cytosol // traceable author statement 4667 // prostaglandin-D synthase activity // not recorded /// 4957 // prostaglandin E receptor activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // non-traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 42803 // protein homodimerization activity // traceable author statement /// 51287 // NAD binding // inferred from direct assay /// 3824 // catalytic activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // inferred from electronic annotation Prostaglandin_synthesis_regulation // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP 3248
239519_at Hs.131704 Neuropilin 1 NRP1 1525 // angiogenesis // inferred from electronic annotation /// 7155 // cell adhesion // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 7399 // nervous system development // inferred from electronic annotation /// 7411 // axon guidance // traceable author statement /// 8284 // positive regulation of cell proliferation

Figure 112

// traceable author statement /// 9887 // organ morphogenesis // traceable author statement /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5624 // membrane fraction // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5021 // vascular endothelial growth factor receptor activity // traceable author statement --- 8829
203645_s_at Hs.504641 CD163 molecule CD163 19735 // antimicrobial humoral response (sensu Vertebrata) // traceable author statement 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation 5044 // scavenger receptor activity // non-traceable author statement /// 5044 // scavenger receptor activity // traceable author statement /// 5044 // scavenger receptor activity // inferred from electronic annotation --- 9332
226804_at Hs.268874 family with sequence similarity 20, member A FAM20A --- --- --- --- 54757
234985_at --- --- --- --- --- --- --- ---
241752_at Hs.468274 solute carrier family 8 (sodium/calcium exchanger), member 1 SLC8A1 6811 // ion transport // inferred from electronic annotation /// 6814 // sodium ion transport // traceable author statement /// 6816 // calcium ion transport // traceable author statement /// 6936 // muscle contraction // traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6814 // sodium ion transport // inferred from electronic annotation /// 6816 // calcium ion transport // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5432 // calcium:sodium antiporter activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5516 // calmodulin binding // inferred from electronic annotation /// 15081 // sodium ion transporter activity // traceable author statement /// 15085 // calcium ion transporter activity // traceable author statement /// 15297 // antiporter activity // inferred from electronic annotation /// 31402 // sodium ion binding // inferred from electronic annotation Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 6546
225959_s_at Hs.427284 zinc and ring finger 1 ZNRF1 6512 // ubiquitin cycle // inferred from electronic annotation --- 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 84937
222866_s_at Hs.509966 chromosome 14 open reading frame 58 C14orf58 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 55640
242945_at Hs.268874 family with sequence similarity 20, member A FAM20A --- --- --- --- 54757
212158_at Hs.1501 syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) SDC2 --- 5887 // integral

Figure 113

to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 8092 // cytoskeletal protein binding // inferred from electronic annotation --- 6383
211269_s_at Hs.231367 interleukin 2 receptor, alpha IL2RA 74 // regulation of progression through cell cycle // not recorded /// 6915 // apoptosis // traceable author statement /// 6955 // immune response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 8283 // cell proliferation // traceable author statement 5886 // plasma membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4911 // interleukin-2 receptor activity // traceable author statement Inflammatory_Response_Pathway // GenMAPP /// Inflammatory_Response_Pathway // GenMAPP 3559
225418_at --- poliovirus receptor-related 2 (herpesvirus entry mediator B) PVRL2 --- --- --- --- 643722
221042_s_at Hs.301478 calmin (calponin-like, transmembrane) CLMN --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 3779 // actin binding // inferred from electronic annotation --- 79789
235754_at Hs.233325 hemochromatosis HFE 6461 // protein complex assembly // traceable author statement /// 6811 // ion transport // inferred from electronic annotation /// 6826 // iron ion transport // traceable author statement /// 6879 // iron ion homeostasis // traceable author statement /// 6898 // receptor mediated endocytosis // traceable author statement /// 19882 // antigen presentation // inferred from electronic annotation /// 19883 // antigen presentation, endogenous antigen // inferred from electronic annotation /// 19885 // antigen processing, endogenous antigen via MHC class I // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6826 // iron ion transport // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation 5737 // cytoplasm // traceable author statement /// 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 42612 // MHC class I protein complex // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5506 // iron ion binding // inferred from electronic annotation /// 30106 // MHC class I receptor activity // inferred from electronic annotation --- 3077
1555628_a_at Hs.616365 hepatitis A virus cellular receptor 2 HAVCR2 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 84868
227478_at --- hypothetical protein LOC284262 LOC284262 --- --- --- --- 284262
228658_at --- chromosome 22 open reading frame 35 C22orf35 --- --- --- --- 150271
201108_s_at Hs.164226 thrombospondin 1 THBS1 6928 // cell motility // not recorded /// 7155 // cell adhesion // inferred from electronic annotation /// 7275 // development // traceable author statement /// 7399 // nervous system development // not recorded /// 7596 // blood coagulation // not recorded 5576 // extracellular region // non-

Figure 114

traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 4866 // endopeptidase inhibitor activity // traceable author statement /// 4871 // signal transducer activity // traceable author statement /// 5198 // structural molecule activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 8201 // heparin binding // inferred from electronic annotation TGF_Beta_Signaling_Pathway // GenMAPP /// Inflammatory_Response_Pathway // GenMAPP 7057
206341_at Hs.231367 interleukin 2 receptor, alpha IL2RA 74 // regulation of progression through cell cycle // not recorded /// 6915 // apoptosis // traceable author statement /// 6955 // immune response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 8283 // cell proliferation // traceable author statement 5886 // plasma membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4911 // interleukin-2 receptor activity // traceable author statement Inflammatory_Response_Pathway // GenMAPP /// Inflammatory_Response_Pathway // GenMAPP 3559
224397_s_at Hs.401954 transmembrane and tetratricopeptide repeat containing 1 /// transmembrane and tetratricopeptide repeat containing 1 TMTC1 --- --- 5488 // binding // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation --- 653626 /// 83857
229070_at Hs.126409 chromosome 6 open reading frame 105 C6orf105 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 84830
201538_s_at Hs.651126 dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) DUSP3 6470 // protein amino acid dephosphorylation // traceable author statement /// 6470 // protein amino acid dephosphorylation // inferred from electronic annotation --- 4725 // protein tyrosine phosphatase activity // traceable author statement /// 8138 // protein tyrosine/serine/threonine phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation Cell adhesion molecules (CAMs) // KEGG /// Adherens junction // KEGG /// Jak-STAT signaling pathway // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Leukocyte transendothelial migration // KEGG /// Insulin signaling pathway // KEGG /// Adipocytokine signaling pathway // KEGG /// Type I diabetes mellitus // KEGG /// Epithelial cell signaling in Helicobacter pylori // KEGG /// Calcium signaling pathway // KEGG /// Apoptosis // KEGG /// Wnt signaling pathway // KEGG /// TGF-beta signaling pathway // KEGG /// Axon guidance // KEGG /// VEGF signaling pathway // KEGG /// Focal adhesion // KEGG /// Tight junction // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Long-term potentiation // KEGG /// Long-term depression // KEGG /// Insulin signaling pathway // KEGG 1845
216233_at Hs.504641 CD163 molecule CD163 19735 // antimicrobial humoral response (sensu Vertebrata) // traceable author statement 5576 // extracellular region // non-traceable author statement /// 5887 //

Figure 115

integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation 5044 // scavenger receptor activity // non-traceable author statement /// 5044 // scavenger receptor activity // traceable author statement /// 5044 // scavenger receptor activity // inferred from electronic annotation --- 9332
218833_at Hs.444451 sterile alpha motif and leucine zipper containing kinase AZK ZAK 75 // cell cycle checkpoint // inferred from direct assay /// 77 // DNA damage checkpoint // inferred from mutant phenotype /// 186 // activation of MAPKK activity // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from direct assay /// 6950 // response to stress // non-traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7050 // cell cycle arrest // inferred from mutant phenotype /// 7243 // protein kinase cascade // inferred from direct assay /// 7257 // activation of JNK activity // inferred from direct assay /// 8219 // cell death // non-traceable author statement /// 8283 // cell proliferation // non-traceable author statement /// 9314 // response to radiation // inferred from direct assay /// 30154 // cell differentiation // non-traceable author statement /// 43065 // positive regulation of apoptosis // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation 5737 // cytoplasm // inferred from sequence or structural similarity 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from direct assay /// 4674 // protein serine/threonine kinase activity // inferred from direct assay /// 4709 // MAP kinase kinase kinase activity // inferred from direct assay /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 287 // magnesium ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 51776
203276_at Hs.89497 lamin B1 LMNB1 --- 5634 // nucleus // inferred from electronic annotation /// 5638 // lamin filament // traceable author statement /// 5882 // intermediate filament // inferred from electronic annotation 5198 // structural molecule activity // traceable author statement /// 5198 // structural molecule activity // inferred from electronic annotation --- 4001
242281_at --- --- --- --- --- --- --- ---
1553608_a_at Hs.536614 chromosome 21 open reading frame 109 C21orf109 --- --- --- --- 193629 /// 643720
201798_s_at Hs.500572 fer-1-like 3, myoferlin (C. elegans) FER1L3 6936 // muscle contraction // traceable author statement /// 8015 // circulation // traceable author statement 5635 // nuclear envelope // traceable author statement /// 5886 // plasma membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation --- --- 26509

Figure 116

202434_s_at Hs.154654 cytochrome P450, family 1, subfamily B, polypeptide 1 CYP1B1 1747 // eye development (sensu Mammalia) // traceable author statement /// 6118 // electron transport // inferred from electronic annotation /// 7601 // visual perception // traceable author statement 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5792 // microsome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 4497 // monooxygenase activity // inferred from electronic annotation /// 5506 // iron ion binding // inferred from electronic annotation /// 19825 // oxygen binding // traceable author statement /// 20037 // heme binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 50381 // unspecific monooxygenase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation --- 1545
232079_s_at --- poliovirus receptor-related 2 (herpesvirus entry mediator B) PVRL2 --- 5886 // plasma membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 15026 // coreceptor activity // traceable author statement --- 5819 /// 643722
206359_at Hs.527973 suppressor of cytokine signaling 3 SOCS3 1558 // regulation of cell growth // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation --- 4860 // protein kinase inhibitor activity // traceable author statement --- 9021

223383_at Hs.427284 zinc and ring finger 1 ZNRF1 6512 // ubiquitin cycle // inferred from electronic annotation --- 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 84937
229635_at Hs.235795 CDNA clone IMAGE:4800262 --- --- --- --- --- 643424
223567_at Hs.465642 sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B SEMA6B 7399 // nervous system development // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 10501
206486_at Hs.409523 lymphocyte-activation gene 3 LAG3 --- 5887 // integral to plasma membrane // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 3823 // antigen binding // traceable author statement /// 42289 // MHC class II protein binding // inferred from direct assay --- 3902
206991_s_at Hs.450802 chemokine (C-C motif) receptor 5 /// similar to C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5) (HIV-1 fusion coreceptor) (CHEMR13) (CD195 antigen) CCR5 /// LOC727797 6935 // chemotaxis // traceable author statement /// 6954 // inflammatory response // traceable author statement /// 6968 // cellular defense response // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author

Figure 117

statement /// 7204 // elevation of cytosolic calcium ion concentration // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 6412 // protein biosynthesis // inferred from electronic annotation /// 6414 // translational elongation // inferred from electronic annotation 5768 // endosome // traceable author statement /// 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 9986 // cell surface // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5737 // cytoplasm // traceable author statement /// 5737 // cytoplasm // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4435 // phosphoinositide phospholipase C activity // traceable author statement /// 15026 // coreceptor activity // traceable author statement /// 16493 // C-C chemokine receptor activity // non-traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 16493 // C-C chemokine receptor activity // inferred from electronic annotation /// 4950 // chemokine receptor activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 16493 // C-C chemokine receptor activity // inferred from direct assay /// 166 // nucleotide binding // inferred from electronic annotation /// 3746 // translation elongation factor activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation

GPCRDB_Class_A_Rhodopsin-like // GenMAPP /// Peptide_GPCRs // GenMAPP /// GPCRDB_Other // GenMAPP 1234 /// 653725

217933_s_at Hs.570791 leucine aminopeptidase 3 LAP3 6508 // proteolysis // non-traceable author statement /// 19538 // protein metabolism // inferred from electronic annotation /// 6508 // proteolysis // inferred from electronic annotation 5737 // cytoplasm // non-traceable author statement /// 5622 // intracellular // inferred from electronic annotation /// 5737 // cytoplasm // inferred from electronic annotation 287 // magnesium ion binding // non-traceable author statement /// 4178 // leucyl aminopeptidase activity // non-traceable author statement /// 8233 // peptidase activity // inferred from electronic annotation /// 8270 // zinc ion binding // non-traceable author statement /// 16804 // prolyl aminopeptidase activity // non-traceable author statement /// 30145 // manganese ion binding // non-traceable author statement /// 287 // magnesium ion binding // inferred from electronic annotation /// 4177 // aminopeptidase activity // inferred from electronic annotation /// 4178 // leucyl aminopeptidase activity // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 16804 // prolyl aminopeptidase activity // inferred from electronic annotation /// 30145 // manganese ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 51056

Figure 118

224916_at Hs.379754 transmembrane protein 173 TMEM173 --- --- --- --- 340061
219316_s_at Hs.509966 chromosome 14 open reading frame 58 C14orf58 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 55640
228955_at Hs.280387 Transcribed locus --- --- --- --- --- ---
223019_at Hs.522401 family with sequence similarity 129, member B FAM129B --- --- --- --- 64855
242218_at --- --- --- 122 // negative regulation of transcription from RNA polymerase II promoter // inferred from sequence or structural similarity /// 6006 // glucose metabolism // non-traceable author statement /// 6091 // generation of precursor metabolites and energy // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6629 // lipid metabolism // inferred from sequence or structural similarity /// 6635 // fatty acid beta-oxidation // inferred from sequence or structural similarity /// 6635 // fatty acid beta-oxidation // traceable author statement /// 6915 // apoptosis // inferred from mutant phenotype /// 7566 // embryo implantation // inferred from sequence or structural similarity /// 7566 // embryo implantation // traceable author statement /// 8203 // cholesterol metabolism // traceable author statement /// 8283 // cell proliferation // inferred from sequence or structural similarity /// 8283 // cell proliferation // traceable author statement /// 8366 // nerve ensheathment // inferred from sequence or structural similarity /// 8544 // epidermis development // inferred from sequence or structural similarity /// 9062 // fatty acid catabolism // traceable author statement /// 15758 // glucose transport // non-traceable author statement /// 15908 // fatty acid transport // inferred from sequence or structural similarity /// 45600 // positive regulation of fat cell differentiation // non-traceable author statement /// 46697 // decidualization // traceable author statement /// 50796 // regulation of insulin secretion // inferred from sequence or structural similarity /// 50875 // cellular physiological process // inferred from sequence or structural similarity /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6629 // lipid metabolism // traceable author statement 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // non-traceable author statement /// 3707 // steroid hormone receptor activity // traceable author statement /// 5504 // fatty acid binding // non-traceable author statement /// 8047 // enzyme activator activity // inferred from sequence or structural similarity /// 8270 // zinc ion binding // inferred from electronic annotation /// 16501 // prostacyclin receptor activity // inferred from sequence or structural similarity /// 16564 // transcriptional repressor activity // inferred from sequence or structural similarity /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 46965 // retinoid X receptor binding // inferred from sequence or structural similarity /// 46982 // protein heterodimerization activity // inferred from sequence or structural similarity /// 3677 // DNA binding // inferred from sequence or structural similarity /// 4879 // ligand-dependent nuclear receptor

Figure 119

activity // inferred from sequence or structural similarity /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 3707 // steroid hormone receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4879 // ligand-dependent nuclear receptor activity // inferred from electronic annotation Nuclear_Receptors // GenMAPP 5467
211864_s_at Hs.500572 fer-1-like 3, myoferlin (C. elegans) FER1L3 6936 // muscle contraction // traceable author statement /// 8015 // circulation // traceable author statement 5635 // nuclear envelope // traceable author statement /// 5886 // plasma membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation --- --- 26509
205376_at Hs.292075 inositol polyphosphate-4-phosphatase, type II, 105kDa INPP4B 7165 // signal transduction // traceable author statement --- 16316 // phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation /// 16316 // phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity // inferred from electronic annotation Inositol phosphate metabolism // KEGG /// Phosphatidylinositol signaling system // KEGG 8821
205933_at Hs.435458 SET binding protein 1 SETBP1 --- 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation --- 26040
216226_at Hs.369519 TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa TAF4B 6350 // transcription // inferred from electronic annotation /// 6352 // transcription initiation // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // non-traceable author statement /// 5669 // transcription factor TFIID complex // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from electronic annotation /// 16986 // transcription initiation factor activity // non-traceable author statement /// 51059 // NF-kappaB binding // inferred from physical interaction /// 16986 // transcription initiation factor activity // inferred from electronic annotation --- 6875
227168_at Hs.517502 hypothetical gene supported by AK098833 FLJ25967 --- --- --- --- 440823
1555326_a_at Hs.591852 ADAM metallopeptidase domain 9 (meltrin gamma) ADAM9 6508 // proteolysis // inferred from electronic annotation /// 7243 // protein kinase cascade // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement 4222 // metalloendopeptidase activity // inferred from electronic annotation /// 5178 // integrin binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 17124 // SH3 domain binding // inferred from physical interaction /// 19901 // protein kinase binding // traceable author statement /// 46872 // metal ion binding // inferred from electronic

Figure 120

annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // traceable author statement /// 8237 // metallopeptidase activity // non-traceable author statement --- 8754
209568_s_at Hs.497148 ral guanine nucleotide dissociation stimulator-like 1 RGL1 51056 // regulation of small GTPase mediated signal transduction // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7264 // small GTPase mediated signal transduction // inferred from electronic annotation /// 7264 // small GTPase mediated signal transduction // non-traceable author statement 5622 // intracellular // inferred from electronic annotation 5515 // protein binding // inferred from physical interaction /// 8321 // Ral guanyl-nucleotide exchange factor activity // non-traceable author statement /// 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation --- 23179
214647_s_at Hs.233325 hemochromatosis HFE 6461 // protein complex assembly // traceable author statement /// 6811 // ion transport // inferred from electronic annotation /// 6826 // iron ion transport // traceable author statement /// 6879 // iron ion homeostasis // traceable author statement /// 6898 // receptor mediated endocytosis // traceable author statement /// 19882 // antigen presentation // inferred from electronic annotation /// 19883 // antigen presentation, endogenous antigen // inferred from electronic annotation /// 19885 // antigen processing, endogenous antigen via MHC class I // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6826 // iron ion transport // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation 5737 // cytoplasm // traceable author statement /// 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 42612 // MHC class I protein complex // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5506 // iron ion binding // inferred from electronic annotation /// 30106 // MHC class I receptor activity // inferred from electronic annotation --- 3077
212843_at Hs.503878 neural cell adhesion molecule 1 NCAM1 7155 // cell adhesion // inferred from electronic annotation /// 7155 // cell adhesion // non-traceable author statement /// 7267 // cell-cell signaling // not recorded /// 7268 // synaptic transmission // not recorded /// 7399 // nervous system development // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 5515 // protein binding // inferred from electronic annotation --- 4684
207808_s_at Hs.64016 protein S (alpha) PROS1 7596 // blood coagulation // traceable author statement /// 7596 // blood coagulation // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 4866 // endopeptidase inhibitor

Figure 121

activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation --- 5627
223382_s_at Hs.427284 zinc and ring finger 1 ZNRF1 6512 // ubiquitin cycle // inferred from electronic annotation --- 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 84937
203355_s_at Hs.434255 pleckstrin and Sec7 domain containing 3 PSD3 --- 5622 // intracellular // inferred from electronic annotation 5086 // ARF guanyl-nucleotide exchange factor activity // inferred from electronic annotation /// 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation --- 23362
238546_at Hs.468274 solute carrier family 8 (sodium/calcium exchanger), member 1 SLC8A1 6811 // ion transport // inferred from electronic annotation /// 6814 // sodium ion transport // traceable author statement /// 6816 // calcium ion transport // traceable author statement /// 6936 // muscle contraction // traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6814 // sodium ion transport // inferred from electronic annotation /// 6816 // calcium ion transport // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5432 // calcium:sodium antiporter activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5516 // calmodulin binding // inferred from electronic annotation /// 15081 // sodium ion transporter activity // traceable author statement /// 15085 // calcium ion transporter activity // traceable author statement /// 15297 // antiporter activity // inferred from electronic annotation /// 31402 // sodium ion binding // inferred from electronic annotation Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 6546
210001_s_at Hs.50640 suppressor of cytokine signaling 1 SOCS1 1558 // regulation of cell growth // inferred from electronic annotation /// 1932 // regulation of protein amino acid phosphorylation // inferred from sequence or structural similarity /// 6512 // ubiquitin cycle // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // inferred from sequence or structural similarity /// 42518 // negative regulation of tyrosine phosphorylation of Stat3 protein // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // non-traceable author statement /// 46627 // negative regulation of insulin receptor signaling pathway // inferred from sequence or structural similarity /// 9968 // negative regulation of signal transduction // inferred from electronic annotation 5737 // cytoplasm // traceable author statement 4860 // protein kinase inhibitor activity // traceable author statement /// 5159 // insulin-like growth factor receptor binding // inferred from physical interaction /// 19901 // protein kinase binding // inferred from physical interaction /// 19210 // kinase inhibitor activity // inferred from sequence or structural similarity --- 8651

Figure 122

233587_s_at Hs.268774 signal-induced proliferation-associated 1 like 2 SIPA1L2 --- --- 5096 // GTPase activator activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation --- 57568
1553681_a_at Hs.2200 perforin 1 (pore forming protein) PRF1 6926 // virus-infected cell apoptosis // not recorded /// 6927 // transformed cell apoptosis // not recorded /// 6968 // cellular defense response // traceable author statement /// 9405 // pathogenesis // traceable author statement /// 19835 // cytolysis // inferred from electronic annotation /// 19836 // hemolysis of host red blood cells // not recorded /// 6915 // apoptosis // traceable author statement 5829 // cytosol // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5509 // calcium ion binding // inferred from electronic annotation Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP 5551
201537_s_at Hs.651126 dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) DUSP3 6470 // protein amino acid dephosphorylation // traceable author statement /// 6470 // protein amino acid dephosphorylation // inferred from electronic annotation --- 4725 // protein tyrosine phosphatase activity // traceable author statement /// 8138 // protein tyrosine/serine/threonine phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation Cell adhesion molecules (CAMs) // KEGG /// Adherens junction // KEGG /// Jak-STAT signaling pathway // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Leukocyte transendothelial migration // KEGG /// Insulin signaling pathway // KEGG /// Adipocytokine signaling pathway // KEGG /// Type I diabetes mellitus // KEGG /// Epithelial cell signaling in Helicobacter pylori // KEGG /// Calcium signaling pathway // KEGG /// Apoptosis // KEGG /// Wnt signaling pathway // KEGG /// TGF-beta signaling pathway // KEGG /// Axon guidance // KEGG /// VEGF signaling pathway // KEGG /// Focal adhesion // KEGG /// Tight junction // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Long-term potentiation // KEGG /// Long-term depression // KEGG /// Insulin signaling pathway // KEGG 1845
235020_at Hs.369519 TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa TAF4B 6350 // transcription // inferred from electronic annotation /// 6352 // transcription initiation // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // non-traceable author statement /// 5669 // transcription factor TFIID complex // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from electronic annotation /// 16986 // transcription initiation factor activity // non-traceable author statement /// 51059 // NF-kappaB binding // inferred from physical interaction /// 16986 // transcription initiation factor activity // inferred from electronic annotation --- 6875
207433_at Hs.193717 interleukin 10 IL10 6916 // anti-apoptosis // non-traceable author statement /// 7253 // cytoplasmic sequestering of NF-kappaB // non-traceable author statement /// 7267 // cell-cell

Figure 123

signaling // Unknown /// 30097 // hemopoiesis // traceable author statement /// 30183 // B cell differentiation // non-traceable author statement /// 30595 // immune cell chemotaxis // traceable author statement /// 42092 // T-helper 2 type immune response // traceable author statement /// 42100 // B cell proliferation // non-traceable author statement /// 42130 // negative regulation of T cell proliferation // non-traceable author statement /// 45019 // negative regulation of nitric oxide biosynthesis // inferred from sequence or structural similarity /// 45077 // negative regulation of interferon-gamma biosynthesis // inferred from sequence or structural similarity /// 45191 // regulation of isotype switching // non-traceable author statement /// 45347 // negative regulation of MHC class II biosynthesis // traceable author statement /// 45355 // negative regulation of interferon-alpha biosynthesis // non-traceable author statement /// 6955 // immune response // inferred from electronic annotation /// 6954 // inflammatory response // non-traceable author statement 5615 // extracellular space // inferred from electronic annotation /// 5576 // extracellular region // inferred from electronic annotation /// 5576 // extracellular region // non-traceable author statement 5125 // cytokine activity // inferred from electronic annotation /// 5141 // interleukin-10 receptor binding // non-traceable author statement /// 8083 // growth factor activity // non-traceable author statement --- 3586
210073_at Hs.408614 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1 ST8SIA1 5975 // carbohydrate metabolism // traceable author statement /// 6486 // protein amino acid glycosylation // inferred from electronic annotation /// 6688 // glycosphingolipid biosynthesis // traceable author statement 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 30173 // integral to Golgi membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 3828 // alpha-N-acetylneuraminate alpha-2,8-sialyltransferase activity // inferred from electronic annotation /// 8373 // sialyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 8373 // sialyltransferase activity // traceable author statement Blood group glycolipid biosynthesis - // KEGG /// Globoside metabolism // KEGG /// Ganglioside biosynthesis // KEGG /// Glycan structures - biosynthesis 2 // KEGG 6489
206974_at Hs.34526 chemokine (C-X-C motif) receptor 6 CXCR6 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 19079 // viral genome replication // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 15026 // coreceptor activity // traceable author statement /// 16493 // C-C chemokine receptor activity // inferred from electronic annotation /// 16494 // C-X-C chemokine receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4872 // receptor activity //

Figure 124

inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // traceable author statement
Peptide_GPCRs // GenMAPP 10663
238452_at Hs.517422 Fc receptor-like B FCRLB --- --- 4872 // receptor activity // inferred from electronic annotation --- 127943
235518_at Hs.468274 solute carrier family 8 (sodium/calcium exchanger), member 1 SLC8A1 6811 // ion transport // inferred from electronic annotation /// 6814 // sodium ion transport // traceable author statement /// 6816 // calcium ion transport // traceable author statement /// 6936 // muscle contraction // traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6814 // sodium ion transport // inferred from electronic annotation /// 6816 // calcium ion transport // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5432 // calcium:sodium antiporter activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5516 // calmodulin binding // inferred from electronic annotation /// 15081 // sodium ion transporter activity // traceable author statement /// 15085 // calcium ion transporter activity // traceable author statement /// 15297 // antiporter activity // inferred from electronic annotation /// 31402 // sodium ion binding // inferred from electronic annotation
Calcium_regulation_in_cardiac_cells // GenMAPP ///
Smooth_muscle_contraction // GenMAPP 6546
216260_at Hs.87889 Dicer1, Dcr-1 homolog (Drosophila) DICER1
6396 // RNA processing // inferred from electronic annotation /// 30423 // RNA interference, targeting of mRNA for destruction // inferred from expression pattern 5622 // intracellular // non-traceable author statement /// 5622 // intracellular // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 3725 // double-stranded RNA binding // inferred from direct assay /// 4519 // endonuclease activity // inferred from electronic annotation /// 4525 // ribonuclease III activity // inferred from direct assay /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 8026 // ATP-dependent helicase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3725 // double-stranded RNA binding // inferred from electronic annotation /// 4525 // ribonuclease III activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 4386 // helicase activity // inferred from electronic annotation /// 4518 // nuclease activity // inferred from electronic annotation
mRNA_processing_Reactome // GenMAPP /// mRNA_processing_Reactome // GenMAPP 23405
206360_s_at Hs.527973 suppressor of cytokine signaling 3 SOCS3 1558 // regulation of cell growth // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic

Figure 125

annotation --- 4860 // protein kinase inhibitor activity // traceable author statement --- 9021
221019_s_at Hs.464422 collectin sub-family member 12 /// collectin sub-family member 12 COLEC12 6910 // phagocytosis, recognition // inferred from sequence or structural similarity /// 9756 // carbohydrate mediated signaling // inferred from sequence or structural similarity /// 19733 // antibacterial humoral response (sensu Vertebrata) // inferred from sequence or structural similarity /// 19734 // antifungal humoral response (sensu Vertebrata) // inferred from sequence or structural similarity /// 45087 // innate immune response // inferred from sequence or structural similarity /// 45194 // oxidized low-density lipoprotein catabolism // inferred from sequence or structural similarity /// 51260 // protein homooligomerization // inferred from sequence or structural similarity /// 6910 // phagocytosis, recognition // inferred from direct assay /// 19733 // antibacterial humoral response (sensu Vertebrata) // inferred from direct assay /// 19734 // antifungal humoral response (sensu Vertebrata) // inferred from direct assay /// 6817 // phosphate transport // inferred from electronic annotation /// 45087 // innate immune response // traceable author statement /// 6952 // defense response // traceable author statement /// 9756 // carbohydrate mediated signaling // non-traceable author statement /// 45194 // oxidized low-density lipoprotein catabolism // non-traceable author statement /// 51260 // protein homooligomerization // non-traceable author statement 16020 // membrane // inferred from sequence or structural similarity /// 5737 // cytoplasm // inferred from electronic annotation /// 16020 // membrane // traceable author statement /// 16021 // integral to membrane // traceable author statement 5044 // scavenger receptor activity // inferred from sequence or structural similarity /// 5534 // galactose binding // inferred from sequence or structural similarity /// 8329 // pattern recognition receptor activity // inferred from sequence or structural similarity /// 30169 // low-density lipoprotein binding // inferred from sequence or structural similarity /// 8329 // pattern recognition receptor activity // inferred from direct assay /// 30169 // low-density lipoprotein binding // inferred from direct assay /// 4872 // receptor activity // inferred from electronic annotation /// 5529 // sugar binding // inferred from electronic annotation /// 5044 // scavenger receptor activity // traceable author statement /// 5534 // galactose binding // non-traceable author statement --- 81035
1556698_a_at Hs.605082 GPRIN family member 3 GPRIN3 --- --- --- --- 285513
201042_at Hs.517033 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) TGM2 7186 // G-protein coupled receptor protein signaling pathway // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred from sequence or structural similarity /// 45785 // positive regulation of cell adhesion // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred from electronic annotation 5578 // extracellular matrix (sensu Metazoa) // inferred from sequence or structural similarity /// 5829 // cytosol // inferred from sequence or structural similarity /// 16020 // membrane // inferred from sequence or structural similarity 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from sequence or structural similarity /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5525 // GTP binding // inferred from sequence or structural similarity /// 8415 // acyltransferase

Figure 126

activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation Complement and coagulation cascades // KEGG /// Huntington's disease // KEGG 7052
243221_at Hs.268874 Family with sequence similarity 20, member A FAM20A --- --- --- --- 54757
202435_s_at Hs.154654 cytochrome P450, family 1, subfamily B, polypeptide 1 CYP1B1 1747 // eye development (sensu Mammalia) // traceable author statement /// 6118 // electron transport // inferred from electronic annotation /// 7601 // visual perception // traceable author statement 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5792 // microsome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 4497 // monooxygenase activity // inferred from electronic annotation /// 5506 // iron ion binding // inferred from electronic annotation /// 19825 // oxygen binding // traceable author statement /// 20037 // heme binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 50381 // unspecific monooxygenase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation --- 1545
206363_at Hs.134859 v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) MAF 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement 785 // chromatin // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 4094
205011_at Hs.152944 loss of heterozygosity, 11, chromosomal region 2, gene A LOH11CR2A 7049 // cell cycle // inferred from electronic annotation /// 45786 // negative regulation of progression through cell cycle // inferred from electronic annotation --- --- --- 4013
229221_at Hs.125503 Mitogen-activated protein kinase 10 MAPK10 --- --- --- --- --- ---
210164_at Hs.1051 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) /// granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) GZMB 6508 // proteolysis // inferred from electronic annotation /// 6915 // apoptosis // traceable author statement /// 6922 // cleavage of lamin // inferred from direct assay /// 19835 // cytolysis // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation 1772 // immunological synapse // traceable author statement /// 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // not recorded 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 4278 // granzyme B activity // traceable author statement /// 8233 // peptidase activity // inferred from electronic annotation /// 4278 // granzyme B activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4252 // serine-type endopeptidase activity //

Figure 127

traceable author statement /// 8236 // serine-type peptidase activity // traceable author statement Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP /// Type I diabetes mellitus // KEGG 3002
235568_at --- chromosome 19 open reading frame 59 C19orf59 --- --- --- --- 199675
237322_at Hs.517502 Hypothetical gene supported by AK098833 FLJ25967 --- --- --- --- 150271
202945_at Hs.335084 folylpolyglutamate synthase FPGS 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // traceable author statement /// 6544 // glycine metabolism // inferred from sequence or structural similarity /// 6730 // one-carbon compound metabolism // inferred from electronic annotation /// 9058 // biosynthesis // inferred from electronic annotation /// 9116 // nucleoside metabolism // inferred from sequence or structural similarity /// 9396 // folic acid and derivative biosynthesis // inferred from electronic annotation /// 17144 // drug metabolism // inferred from sequence or structural similarity /// 42493 // response to drug // inferred from sequence or structural similarity /// 46655 // folic acid metabolism // inferred from sequence or structural similarity /// 46901 // tetrahydrofolylpolyglutamate biosynthesis // inferred from sequence or structural similarity 5739 // mitochondrion // inferred from sequence or structural similarity /// 5739 // mitochondrion // traceable author statement /// 5829 // cytosol // inferred from sequence or structural similarity /// 5829 // cytosol // traceable author statement /// 5739 // mitochondrion // inferred from electronic annotation /// 5737 // cytoplasm // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4326 // tetrahydrofolylpolyglutamate synthase activity // inferred from electronic annotation /// 4326 // tetrahydrofolylpolyglutamate synthase activity // inferred from sequence or structural similarity /// 4326 // tetrahydrofolylpolyglutamate synthase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16874 // ligase activity // inferred from electronic annotation Folate biosynthesis // KEGG 2356
235046_at Hs.176376 Transcribed locus --- --- --- --- --- ---
238613_at Hs.444451 sterile alpha motif and leucine zipper containing kinase AZK ZAK 75 // cell cycle checkpoint // inferred from direct assay /// 77 // DNA damage checkpoint // inferred from mutant phenotype /// 186 // activation of MAPKK activity // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from direct assay /// 6950 // response to stress // non-traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7050 // cell cycle arrest // inferred from mutant phenotype /// 7243 // protein kinase cascade // inferred from direct assay /// 7257 // activation of JNK activity // inferred from direct assay /// 8219 // cell death // non-traceable author statement /// 8283 // cell proliferation // non-traceable author statement /// 9314 // response to radiation // inferred from direct assay /// 30154 // cell differentiation // non-traceable author statement /// 43065 // positive regulation of apoptosis // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation 5737 // cytoplasm // inferred from sequence or structural similarity 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from direct assay /// 4674 // protein serine/threonine kinase activity // inferred

Figure 128

from direct assay /// 4709 // MAP kinase kinase kinase activity // inferred from direct assay /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 287 // magnesium ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 51776
227210_at Hs.593558 CDNA FLJ32568 fis, clone SPLEN2000098 --- --- --- --- --- ---
230966_at --- interleukin 4 induced 1 IL4I1 6118 // electron transport // inferred from electronic annotation --- 1716 // L-amino-acid oxidase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation --- 259307
210152_at --- leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4 LILRB4 6955 // immune response // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 6952 // defense response // not recorded 5886 // plasma membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 3823 // antigen binding // traceable author statement /// 4872 // receptor activity // traceable author statement /// 4872 // receptor activity // inferred from electronic annotation --- 11006
222689_at Hs.23862 phytoceramidase, alkaline PHCA 6412 // protein biosynthesis // inferred from electronic annotation /// 6672 // ceramide metabolism // inferred from electronic annotation 139 // Golgi membrane // inferred from electronic annotation /// 5622 // intracellular // inferred from electronic annotation /// 5789 // endoplasmic reticulum membrane // inferred from electronic annotation /// 5795 // Golgi stack // inferred from electronic annotation /// 5840 // ribosome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5783 // endoplasmic reticulum // inferred from electronic annotation 3735 // structural constituent of ribosome // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 16811 // hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides // inferred from electronic annotation --- 55331
214617_at Hs.2200 perforin 1 (pore forming protein) /// perforin 1 (pore forming protein) PRF1 6926 // virus-infected cell apoptosis // not recorded /// 6927 // transformed cell apoptosis // not recorded /// 6968 // cellular defense response // traceable author statement /// 9405 // pathogenesis // traceable author statement /// 19835 // cytolysis // inferred from electronic annotation /// 19836 // hemolysis of host red blood cells // not recorded /// 6915 // apoptosis // traceable author statement 5829 // cytosol // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5509 //

Figure 129

calcium ion binding // inferred from electronic annotation Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP 5551
213484_at Hs.66187 Clone 23700 mRNA sequence --- --- --- --- --- ---
224357_s_at Hs.325960 membrane-spanning 4-domains, subfamily A, member 4 /// membrane-spanning 4-domains, subfamily A, member 4 MS4A4A 7165 // signal transduction // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 51338
1554285_at Hs.616365 hepatitis A virus cellular receptor 2 HAVCR2 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 84868
210220_at Hs.142912 frizzled homolog 2 (Drosophila) FZD2 7164 // establishment of tissue polarity // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7166 // cell surface receptor linked signal transduction // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // traceable author statement /// 4926 // non-G-protein coupled 7TM receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation Wnt_signaling // GenMAPP /// Wnt_signaling // GenMAPP 2535
222757_s_at Hs.444451 sterile alpha motif and leucine zipper containing kinase AZK ZAK 75 // cell cycle checkpoint // inferred from direct assay /// 77 // DNA damage checkpoint // inferred from mutant phenotype /// 186 // activation of MAPKK activity // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from direct assay /// 6950 // response to stress // non-traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7050 // cell cycle arrest // inferred from mutant phenotype /// 7243 // protein kinase cascade // inferred from direct assay /// 7257 // activation of JNK activity // inferred from direct assay /// 8219 // cell death // non-traceable author statement /// 8283 // cell proliferation // non-traceable author statement /// 9314 // response to radiation // inferred from direct assay /// 30154 // cell differentiation // non-traceable author statement /// 43065 // positive regulation of apoptosis // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation 5737 // cytoplasm // inferred from sequence or structural similarity 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from direct assay /// 4674 // protein serine/threonine kinase activity // inferred from direct assay /// 4709 // MAP kinase kinase kinase activity // inferred from direct assay /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 5524 // ATP binding //

Figure 130

inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 287 // magnesium ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 51776
202464_s_at Hs.195471 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 PFKFB3 6003 // fructose 2,6-bisphosphate metabolism // inferred from electronic annotation /// 6003 // fructose 2,6-bisphosphate metabolism // non-traceable author statement /// 8152 // metabolism // inferred from electronic annotation --- 166 // nucleotide binding // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 3873 // 6-phosphofructo-2-kinase activity // inferred from electronic annotation /// 3873 // 6-phosphofructo-2-kinase activity // non-traceable author statement /// 4331 // fructose-2,6-bisphosphate 2-phosphatase activity // inferred from electronic annotation /// 4331 // fructose-2,6-bisphosphate 2-phosphatase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction Fructose and mannose metabolism // KEGG /// Fructose and mannose metabolism // KEGG 5209
210644_s_at Hs.572535 leukocyte-associated immunoglobulin-like receptor 1 LAIR1 --- --- 4872 // receptor activity // inferred from electronic annotation --- 3903
224929_at Hs.379754 transmembrane protein 173 TMEM173 --- --- --- --- 340061
218681_s_at Hs.303116 stromal cell-derived factor 2-like 1 SDF2L1 --- 16020 // membrane // inferred from electronic annotation /// 5783 // endoplasmic reticulum // inferred from electronic annotation 16787 // hydrolase activity // inferred from electronic annotation --- 23753
213926_s_at Hs.591619 HIV-1 Rev binding protein HRB 6406 // mRNA export from nucleus // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 43087 // regulation of GTPase activity // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5643 // nuclear pore // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 3267
230354_at Hs.135108 Transcribed locus --- --- --- --- --- ---
202068_s_at Hs.213289 low density lipoprotein receptor (familial hypercholesterolemia) LDLR 6493 // protein amino acid O-linked glycosylation // traceable author statement /// 6629 // lipid metabolism // traceable author statement /// 6869 // lipid transport //

Figure 131

inferred from electronic annotation /// 6897 // endocytosis // traceable author statement /// 8202 // steroid metabolism // inferred from electronic annotation /// 8203 // cholesterol metabolism // inferred from electronic annotation /// 6629 // lipid metabolism // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6897 // endocytosis // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 5905 // coated pit // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5886 // plasma membrane // traceable author statement 4872 // receptor activity // inferred from electronic annotation /// 4888 // transmembrane receptor activity // traceable author statement /// 5041 // low-density lipoprotein receptor activity // traceable author statement /// 5319 // lipid transporter activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 8034 // lipoprotein binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction Wnt_signaling // GenMAPP /// Statin_Pathway_PharmGKB // GenMAPP /// Wnt_signaling // GenMAPP /// Statin_Pathway_PharmGKB // GenMAPP 3949
208433_s_at Hs.576154 low density lipoprotein receptor-related protein 8, apolipoprotein e receptor LRP8 6508 // proteolysis // non-traceable author statement /// 6629 // lipid metabolism // inferred from sequence or structural similarity /// 6629 // lipid metabolism // non-traceable author statement /// 6897 // endocytosis // inferred from direct assay /// 6897 // endocytosis // inferred from sequence or structural similarity /// 7165 // signal transduction // inferred from sequence or structural similarity /// 7165 // signal transduction // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // non-traceable author statement /// 6897 // endocytosis // inferred from electronic annotation /// 6629 // lipid metabolism // traceable author statement 5886 // plasma membrane // inferred from sequence or structural similarity /// 5886 // plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // Unknown /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4888 // transmembrane receptor activity // inferred from sequence or structural similarity /// 4888 // transmembrane receptor activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 8034 // lipoprotein binding // Unknown /// 30227 // apolipoprotein E receptor activity // inferred from direct assay /// 30227 // apolipoprotein E receptor activity // inferred from sequence or structural similarity /// 30227 // apolipoprotein E receptor activity // traceable author statement --- 7804
201666_at Hs.522632 TIMP metallopeptidase inhibitor 1 TIMP1 7275 // development // not recorded /// 8284 // positive regulation of cell proliferation // traceable author statement /// 43249 // erythrocyte maturation // inferred from electronic annotation /// 51045 // negative regulation of membrane protein ectodomain proteolysis // inferred from direct assay 5578 // extracellular matrix (sensu Metazoa) // inferred from electronic annotation /// 5576 // extracellular region // non-traceable author statement 4857 // enzyme inhibitor activity // inferred from electronic annotation /// 8191 // metalloendopeptidase inhibitor activity // inferred from direct assay /// 8191 //

Figure 132

metalloendopeptidase inhibitor activity // inferred from electronic annotation MAPK_Cascade // GenMAPP /// MAPK_Cascade // GenMAPP /// Matrix_Metalloproteinases // GenMAPP /// Matrix_Metalloproteinases // GenMAPP 7076
200838_at Hs.520898 cathepsin B CTSB 6508 // proteolysis // traceable author statement /// 42981 // regulation of apoptosis // traceable author statement /// 50790 // regulation of enzyme activity // inferred from electronic annotation /// 6508 // proteolysis // inferred from electronic annotation 5622 // intracellular // traceable author statement /// 5764 // lysosome // inferred from electronic annotation /// 5764 // lysosome // not recorded 4213 // cathepsin B activity // traceable author statement /// 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4213 // cathepsin B activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Antigen processing and presentation // KEGG 1508
215975_x_at --- glycerol kinase GK 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
Glycerolipid metabolism // KEGG 2710
204438_at Hs.75182 mannose receptor, C type 1 /// mannose receptor, C type 1-like 1 MRC1 /// MRC1L1 6898 // receptor mediated endocytosis // traceable author statement /// 6907 // pinocytosis // not recorded /// 6897 // endocytosis // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5529 // sugar binding // inferred from electronic annotation /// 5537 // mannose binding // traceable author statement /// 4872 // receptor activity // inferred from electronic annotation --- 414308 /// 4360
235122_at Hs.403972 CDNA clone IMAGE:6254031 --- --- ---
--- --- ---
201466_s_at Hs.525704 jun oncogene JUN 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
228 // nuclear chromosome // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 8134 // transcription factor binding // inferred from physical interaction /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization

Figure 133

activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 3677 // DNA binding // traceable author statement Apoptosis // GenMAPP /// Apoptosis_GenMAPP // GenMAPP /// MAPK_Cascade // GenMAPP /// TGF_Beta_Signaling_Pathway // GenMAPP /// Wnt_signaling // GenMAPP /// Smooth_muscle_contraction // GenMAPP 3725
204935_at Hs.123352 protein tyrosine phosphatase, non-receptor type 2 PTPN2 6470 // protein amino acid dephosphorylation // inferred from electronic annotation /// 6470 // protein amino acid dephosphorylation // traceable author statement --- 4725 // protein tyrosine phosphatase activity // inferred from electronic annotation /// 4725 // protein tyrosine phosphatase activity // traceable author statement /// 4872 // receptor activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation Cell adhesion molecules (CAMs) // KEGG /// Adherens junction // KEGG /// Jak-STAT signaling pathway // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Leukocyte transendothelial migration // KEGG /// Insulin signaling pathway // KEGG /// Adipocytokine signaling pathway // KEGG /// Type I diabetes mellitus // KEGG /// Epithelial cell signaling in Helicobacter pylori // KEGG 5771
211329_x_at Hs.233325 hemochromatosis HFE 6461 // protein complex assembly // traceable author statement /// 6811 // ion transport // inferred from electronic annotation /// 6826 // iron ion transport // traceable author statement /// 6879 // iron ion homeostasis // traceable author statement /// 6898 // receptor mediated endocytosis // traceable author statement /// 19882 // antigen presentation // inferred from electronic annotation /// 19883 // antigen presentation, endogenous antigen // inferred from electronic annotation /// 19885 // antigen processing, endogenous antigen via MHC class I // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6826 // iron ion transport // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation 5737 // cytoplasm // traceable author statement /// 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 42612 // MHC class I protein complex // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5506 // iron ion binding // inferred from electronic annotation /// 30106 // MHC class I receptor activity // inferred from electronic annotation --- 3077
201013_s_at Hs.518774 phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase PAICS 6164 // purine nucleotide biosynthesis // inferred from electronic annotation /// 6189 // 'de novo' IMP biosynthesis // inferred from electronic annotation /// 9113 // purine base biosynthesis // traceable author statement 9320 // phosphoribosylaminoimidazole carboxylase complex // inferred from electronic annotation 4638 // phosphoribosylaminoimidazole carboxylase activity // inferred from electronic annotation /// 4639 // phosphoribosylaminoimidazolesuccinocarboxamide synthase activity // traceable author statement /// 16829 // lyase activity // inferred from electronic annotation /// 16874 // ligase activity // inferred from electronic annotation /// 42802 // identical protein binding //

Figure 134

inferred from physical interaction /// 3824 // catalytic activity // inferred from electronic annotation /// 4639 // phosphoribosylaminoimidazolesuccinocarboxamide synthase activity // inferred from electronic annotation /// 16831 // carboxy-lyase activity // inferred from electronic annotation Purine metabolism // KEGG /// Purine metabolism // KEGG 10606
202436_s_at Hs.154654 cytochrome P450, family 1, subfamily B, polypeptide 1 CYP1B1 1747 // eye development (sensu Mammalia) // traceable author statement /// 6118 // electron transport // inferred from electronic annotation /// 7601 // visual perception // traceable author statement 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5792 // microsome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 4497 // monooxygenase activity // inferred from electronic annotation /// 5506 // iron ion binding // inferred from electronic annotation /// 19825 // oxygen binding // traceable author statement /// 20037 // heme binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 50381 // unspecific monooxygenase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation --- 1545
213137_s_at Hs.123352 protein tyrosine phosphatase, non-receptor type 2 PTPN2 6470 // protein amino acid dephosphorylation // inferred from electronic annotation /// 6470 // protein amino acid dephosphorylation // traceable author statement --- 4725 // protein tyrosine phosphatase activity // inferred from electronic annotation /// 4725 // protein tyrosine phosphatase activity // traceable author statement /// 4872 // receptor activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation Cell adhesion molecules (CAMs) // KEGG /// Adherens junction // KEGG /// Jak-STAT signaling pathway // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Leukocyte transendothelial migration // KEGG /// Insulin signaling pathway // KEGG /// Adipocytokine signaling pathway // KEGG /// Type I diabetes mellitus // KEGG /// Epithelial cell signaling in Helicobacter pylori // KEGG 5771
202430_s_at Hs.130759 phospholipid scramblase 1 PLSCR1 9615 // response to virus // inferred from electronic annotation /// 17121 // phospholipid scrambling // traceable author statement /// 30168 // platelet activation // non-traceable author statement 5886 // plasma membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 5509 // calcium ion binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 17128 // phospholipid scramblase activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation --- 5359
218092_s_at Hs.591619 HIV-1 Rev binding protein HRB 6406 // mRNA export from nucleus // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 43087 // regulation of GTPase activity // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5643 // nuclear pore // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from

Figure 135

electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 3267 /// 649094
226448_at Hs.38516 family with sequence similarity 89, member A FAM89A --- --- --- --- 375061
223445_at Hs.571148 dystrobrevin binding protein 1 DTNBP1 6996 // organelle organization and biogenesis // inferred from sequence or structural similarity /// 7601 // visual perception // inferred from electronic annotation /// 50896 // response to stimulus // inferred from electronic annotation 5634 // nucleus // inferred from sequence or structural similarity /// 5737 // cytoplasm // inferred from electronic annotation /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 30424 // axon // inferred from sequence or structural similarity /// 42383 // sarcolemma // inferred from sequence or structural similarity 5515 // protein binding // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from sequence or structural similarity --- 84062
202716_at Hs.417549 protein tyrosine phosphatase, non-receptor type 1 PTPN1 6470 // protein amino acid dephosphorylation // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement 5625 // soluble fraction // not recorded /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5737 // cytoplasm // not recorded 4725 // protein tyrosine phosphatase activity // traceable author statement /// 16787 // hydrolase activity // inferred from electronic annotation /// 4721 // phosphoprotein phosphatase activity // inferred from electronic annotation /// 4725 // protein tyrosine phosphatase activity // inferred from electronic annotation Cell adhesion molecules (CAMs) // KEGG /// Adherens junction // KEGG /// Jak-STAT signaling pathway // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Leukocyte transendothelial migration // KEGG /// Insulin signaling pathway // KEGG /// Adipocytokine signaling pathway // KEGG /// Type I diabetes mellitus // KEGG /// Epithelial cell signaling in Helicobacter pylori // KEGG 5770
203665_at Hs.517581 heme oxygenase (decycling) 1 HMOX1 6788 // heme oxidation // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from mutant phenotype 5624 // membrane fraction // traceable author statement /// 5783 // endoplasmic reticulum // traceable author statement /// 5792 // microsome // inferred from electronic annotation /// 5783 // endoplasmic reticulum // inferred from electronic annotation 4392 // heme oxygenase (decyclizing) activity // traceable author statement /// 4871 // signal transducer activity // inferred from mutant phenotype /// 5506 // iron ion binding // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4392 // heme oxygenase (decyclizing) activity // inferred from electronic annotation Porphyrin and chlorophyll metabolism // KEGG 3162
225056_at Hs.268774 signal-induced proliferation-associated 1 like 2 SIPA1L2 --- --- 5096 // GTPase activator activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation --- 57568
225662_at Hs.444451 sterile alpha motif and leucine zipper containing kinase AZK ZAK 75 // cell cycle checkpoint // inferred from direct assay /// 77 // DNA damage checkpoint // inferred from

Figure 136

mutant phenotype /// 186 // activation of MAPKK activity // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from direct assay /// 6950 // response to stress // non-traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7050 // cell cycle arrest // inferred from mutant phenotype /// 7243 // protein kinase cascade // inferred from direct assay /// 7257 // activation of JNK activity // inferred from direct assay /// 8219 // cell death // non-traceable author statement /// 8283 // cell proliferation // non-traceable author statement /// 9314 // response to radiation // inferred from direct assay /// 30154 // cell differentiation // non-traceable author statement /// 43065 // positive regulation of apoptosis // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation 5737 // cytoplasm // inferred from sequence or structural similarity 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from direct assay /// 4674 // protein serine/threonine kinase activity // inferred from direct assay /// 4709 // MAP kinase kinase kinase activity // inferred from direct assay /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 287 // magnesium ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 51776

229937_x_at Hs.67846 Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 LILRB1 6955 // immune response // inferred from electronic annotation /// 9615 // response to virus // traceable author statement /// 6952 // defense response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6952 // defense response // not recorded 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 5886 // plasma membrane // non-traceable author statement 4872 // receptor activity // inferred from electronic annotation /// 8157 // protein phosphatase 1 binding // traceable author statement /// 3823 // antigen binding // traceable author statement /// 4888 // transmembrane receptor activity // traceable author statement /// 4872 // receptor activity // traceable author statement --- 10859

205471_s_at Hs.129452 dachshund homolog 1 (Drosophila) DACH1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7456 // eye development (sensu Endopterygota) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction --- 1602

Figure 137

1558279_a_at Hs.596777 CDNA FLJ36555 fis, clone TRACH2008716
--- --- --- --- --- ---
201761_at Hs.469030 methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase MTHFD2 6730 // one-carbon compound metabolism // inferred from electronic annotation /// 9396 // folic acid and derivative biosynthesis // inferred from electronic annotation /// 46653 // tetrahydrofolate metabolism // inferred from direct assay 5739 // mitochondrion // inferred from sequence or structural similarity /// 5739 // mitochondrion // inferred from electronic annotation 287 // magnesium ion binding // inferred from direct assay /// 4477 // methenyltetrahydrofolate cyclohydrolase activity // inferred from sequence or structural similarity /// 4487 // methylenetetrahydrofolate dehydrogenase (NAD+) activity // inferred from direct assay /// 4488 // methylenetetrahydrofolate dehydrogenase (NADP+) activity // inferred from direct assay /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 42301 // phosphate binding // inferred from direct assay /// 287 // magnesium ion binding // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 4477 // methenyltetrahydrofolate cyclohydrolase activity // inferred from electronic annotation /// 4487 // methylenetetrahydrofolate dehydrogenase (NAD+) activity // inferred from electronic annotation Nucleotide_Metabolism // GenMAPP /// Nucleotide_Metabolism // GenMAPP /// One carbon pool by folate // KEGG 10797
225962_at Hs.427284 zinc and ring finger 1 ZNRF1 6512 // ubiquitin cycle // inferred from electronic annotation --- 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 84937
211336_x_at Hs.67846 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 LILRB1 6955 // immune response // inferred from electronic annotation /// 9615 // response to virus // traceable author statement /// 6952 // defense response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6952 // defense response // not recorded 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 5886 // plasma membrane // non-traceable author statement 4872 // receptor activity // inferred from electronic annotation /// 8157 // protein phosphatase 1 binding // traceable author statement /// 3823 // antigen binding // traceable author statement /// 4888 // transmembrane receptor activity // traceable author statement /// 4872 // receptor activity // traceable author statement --- 10859
230031_at Hs.605502 heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) HSPA5 6916 // anti-apoptosis // inferred from mutant phenotype /// 6916 // anti-apoptosis // traceable author statement /// 43154 // negative regulation of caspase activity // inferred from direct assay /// 43066 // negative regulation of apoptosis // inferred from mutant phenotype 5634 // nucleus // inferred from direct assay /// 5788 // endoplasmic reticulum lumen // traceable author statement /// 5793 // ER-Golgi intermediate compartment // inferred from direct assay /// 8303 // caspase complex // inferred from direct assay ///

Figure 138

9986 // cell surface // inferred from expression pattern /// 30176 // integral to endoplasmic reticulum membrane // inferred from direct assay /// 48471 // perinuclear region // inferred from direct assay /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5783 // endoplasmic reticulum // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 5509 // calcium ion binding // traceable author statement /// 5524 // ATP binding // non-traceable author statement /// 30674 // protein binding, bridging // non-traceable author statement /// 43027 // caspase inhibitor activity // inferred from direct assay /// 51082 // unfolded protein binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation --- 3309
211936_at Hs.605502 heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) HSPA5 6916 // anti-apoptosis // inferred from mutant phenotype /// 6916 // anti-apoptosis // traceable author statement /// 43154 // negative regulation of caspase activity // inferred from direct assay /// 43066 // negative regulation of apoptosis // inferred from mutant phenotype 5634 // nucleus // inferred from direct assay /// 5788 // endoplasmic reticulum lumen // traceable author statement /// 5793 // ER-Golgi intermediate compartment // inferred from direct assay /// 8303 // caspase complex // inferred from direct assay /// 9986 // cell surface // inferred from expression pattern /// 30176 // integral to endoplasmic reticulum membrane // inferred from direct assay /// 48471 // perinuclear region // inferred from direct assay /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5783 // endoplasmic reticulum // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 5509 // calcium ion binding // traceable author statement /// 5524 // ATP binding // non-traceable author statement /// 30674 // protein binding, bridging // non-traceable author statement /// 43027 // caspase inhibitor activity // inferred from direct assay /// 51082 // unfolded protein binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation --- 3309
211192_s_at Hs.398093 CD84 molecule CD84 6952 // defense response // traceable author statement /// 7156 // homophilic cell adhesion // traceable author statement 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement --- --- 8832
239205_s_at Hs.334019 complement component (3b/4b) receptor 1 (Knops blood group) /// complement component (3b/4b) receptor 1-like /// similar to complement component (3b/4b) receptor 1 isoform F precursor CR1 /// CR1L /// LOC653907 6958 // complement activation, classical pathway // inferred from electronic annotation /// 45087 // innate immune response // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation /// 6956 // complement activation // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4877 // complement component C3b receptor activity // not recorded /// 4875 // complement receptor activity // traceable author statement --- 1378 /// 1379 /// 653907
226561_at Hs.352962 hypothetical protein LOC285086 LOC285086 --- --- --- --- 649094

Figure 139

203234_at Hs.488240 uridine phosphorylase 1 UPP1 9116 // nucleoside metabolism // inferred from electronic annotation /// 9166 // nucleotide catabolism // inferred from electronic annotation /// 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // traceable author statement 5737 // cytoplasm // inferred from electronic annotation 4850 // uridine phosphorylase activity // traceable author statement /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 4850 // uridine phosphorylase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation Pyrimidine metabolism // KEGG 7378
242733_at Hs.77348 Hydroxyprostaglandin dehydrogenase 15-(NAD) HPGD 6629 // lipid metabolism // inferred from electronic annotation /// 6631 // fatty acid metabolism // inferred from electronic annotation /// 6693 // prostaglandin metabolism // traceable author statement /// 7179 // transforming growth factor beta receptor signaling pathway // inferred from direct assay /// 7565 // pregnancy // inferred from direct assay /// 7567 // parturition // inferred from direct assay /// 8152 // metabolism // inferred from electronic annotation /// 19372 // lipoxygenase pathway // traceable author statement /// 45786 // negative regulation of progression through cell cycle // inferred from direct assay /// 6693 // prostaglandin metabolism // inferred from electronic annotation 5829 // cytosol // traceable author statement 4667 // prostaglandin-D synthase activity // not recorded /// 4957 // prostaglandin E receptor activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // non-traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 42803 // protein homodimerization activity // traceable author statement /// 51287 // NAD binding // inferred from direct assay /// 3824 // catalytic activity // inferred from direct assay /// 16404 // 15-hydroxyprostaglandin dehydrogenase (NAD+) activity // inferred from electronic annotation Prostaglandin_synthesis_regulation // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP /// Prostaglandin_synthesis_regulation // GenMAPP 3248
223234_at Hs.19400 MAD2 mitotic arrest deficient-like 2 (yeast) MAD2L2 7049 // cell cycle // inferred from electronic annotation /// 7067 // mitosis // non-traceable author statement /// 7094 // mitotic spindle checkpoint // traceable author statement /// 51301 // cell division // inferred from electronic annotation /// 7067 // mitosis // inferred from electronic annotation --- 5515 // protein binding // inferred from physical interaction Cell_cycle_KEGG // GenMAPP 10459
235458_at Hs.616365 hepatitis A virus cellular receptor 2 HAVCR2 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 84868
218091_at Hs.591619 HIV-1 Rev binding protein HRB 6406 // mRNA export from nucleus // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 43087 // regulation of GTPase activity // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5643 // nuclear pore // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding //

Figure 140

traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 3267 /// 649094
218854_at --- squamous cell carcinoma antigen recognized by T cells 2 SART2 --- 5783 // endoplasmic reticulum // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 29940
235204_at Hs.591916 COX15 homolog, cytochrome c oxidase assembly protein (yeast) COX15 6461 // protein complex assembly // inferred from electronic annotation /// 7585 // respiratory gaseous exchange // traceable author statement 5739 // mitochondrion // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5739 // mitochondrion // inferred from electronic annotation 4129 // cytochrome-c oxidase activity // traceable author statement --- 1355
202437_s_at Hs.154654 cytochrome P450, family 1, subfamily B, polypeptide 1 CYP1B1 1747 // eye development (sensu Mammalia) // traceable author statement /// 6118 // electron transport // inferred from electronic annotation /// 7601 // visual perception // traceable author statement 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5792 // microsome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 4497 // monooxygenase activity // inferred from electronic annotation /// 5506 // iron ion binding // inferred from electronic annotation /// 19825 // oxygen binding // traceable author statement /// 20037 // heme binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 50381 // unspecific monooxygenase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation --- 1545
1553402_a_at Hs.233325 hemochromatosis HFE 6461 // protein complex assembly // traceable author statement /// 6811 // ion transport // inferred from electronic annotation /// 6826 // iron ion transport // traceable author statement /// 6879 // iron ion homeostasis // traceable author statement /// 6898 // receptor mediated endocytosis // traceable author statement /// 19882 // antigen presentation // inferred from electronic annotation /// 19883 // antigen presentation, endogenous antigen // inferred from electronic annotation /// 19885 // antigen processing, endogenous antigen via MHC class I // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6826 // iron ion transport // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation 5737 // cytoplasm // traceable author statement /// 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 42612 // MHC class I protein complex // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5506 // iron ion binding // inferred from electronic annotation /// 30106 // MHC class I receptor activity // inferred from electronic annotation --- 3077
212136_at Hs.343522 ATPase, Ca++ transporting, plasma membrane 4 ATP2B4 6812 // cation transport // inferred from electronic annotation /// 6816 // calcium ion transport // inferred from

Figure 141

electronic annotation /// 8152 // metabolism // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6811 // ion transport // inferred from electronic annotation /// 6810 // transport // traceable author statement 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 5388 // calcium-transporting ATPase activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5516 // calmodulin binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 16820 // hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances // inferred from electronic annotation /// 3824 // catalytic activity // inferred from electronic annotation /// 5388 // calcium-transporting ATPase activity // inferred from electronic annotation /// 15085 // calcium ion transporter activity // inferred from electronic annotation /// 15662 // ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation Calcium signaling pathway // KEGG 493 201195_s_at Hs.513797 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 SLC7A5 6520 // amino acid metabolism // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 6810 // transport // traceable author statement /// 6865 // amino acid transport // inferred from electronic annotation 5886 // plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 15175 // neutral amino acid transporter activity // traceable author statement /// 15359 // amino acid permease activity // inferred from electronic annotation /// 5279 // amino acid-polyamine transporter activity // inferred from electronic annotation /// 15171 // amino acid transporter activity // inferred from electronic annotation --- 8140
204860_s_at Hs.191356 NLR family, apoptosis inhibitory protein /// similar to Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis inhibitory protein) NAIP /// LOC728519 6915 // apoptosis // inferred from electronic annotation /// 6916 // anti-apoptosis // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 7399 // nervous system development // traceable author statement 5622 // intracellular // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 17111 // nucleoside-triphosphatase activity // inferred from electronic annotation --- 4671 /// 648984 /// 653371
215977_x_at Hs.1466 glycerol kinase GK 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide

Figure 142

binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
Glycerolipid metabolism // KEGG 2710
1556583_a_at Hs.31961 CDNA FLJ37694 fis, clone BRHIP2015224
--- --- --- --- --- ---
213274_s_at Hs.520898 cathepsin B CTSB 6508 // proteolysis // traceable author statement /// 42981 // regulation of apoptosis // traceable author statement /// 50790 // regulation of enzyme activity // inferred from electronic annotation /// 6508 // proteolysis // inferred from electronic annotation 5622 // intracellular // traceable author statement /// 5764 // lysosome // inferred from electronic annotation /// 5764 // lysosome // not recorded 4213 // cathepsin B activity // traceable author statement /// 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4213 // cathepsin B activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Antigen processing and presentation // KEGG 1508
233177_s_at Hs.98475 paroxysmal nonkinesiogenic dyskinesia PNKD
--- --- --- --- 25953
217809_at Hs.487635 basic leucine zipper and W2 domains 2 BZW2
6446 // regulation of translational initiation // inferred from electronic annotation --- 3743 // translation initiation factor activity // inferred from electronic annotation --- 28969
236317_at Hs.435458 SET binding protein 1 SETBP1 --- 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation --- 26040
205098_at Hs.301921 chemokine (C-C motif) receptor 1 CCR1 6935 // chemotaxis // non-traceable author statement /// 6954 // inflammatory response // traceable author statement /// 7155 // cell adhesion // traceable author statement /// 7187 // G-protein signaling, coupled to cyclic nucleotide second messenger // traceable author statement /// 7204 // elevation of cytosolic calcium ion concentration // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // non-traceable author statement /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 6935 // chemotaxis // traceable author statement /// 6955 // immune response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 9611 // response to wounding // traceable author statement 5886 // plasma membrane // inferred from direct assay /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5886 // plasma membrane // traceable author statement 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 16493 // C-C chemokine receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic

Figure 143

annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4950 // chemokine receptor activity // traceable author statement GPCRDB_Class_A_Rhodopsin-like // GenMAPP /// Peptide_GPCRs // GenMAPP 1230
232331_at Hs.162646 Peroxisome proliferator-activated receptor gamma PPARG 6091 // generation of precursor metabolites and energy // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6629 // lipid metabolism // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7584 // response to nutrient // traceable author statement /// 50872 // white fat cell differentiation // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // not recorded 3700 // transcription factor activity // traceable author statement /// 3707 // steroid hormone receptor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4879 // ligand-dependent nuclear receptor activity // inferred from electronic annotation /// 4872 // receptor activity // traceable author statement /// 4879 // ligand-dependent nuclear receptor activity // traceable author statement Nuclear_Receptors // GenMAPP /// Nuclear_Receptors // GenMAPP 5468
208470_s_at Hs.134406 haptoglobin /// haptoglobin-related protein HP /// HPR 6508 // proteolysis // inferred from electronic annotation /// 6879 // iron ion homeostasis // non-traceable author statement /// 6952 // defense response // traceable author statement /// 398 // nuclear mRNA splicing, via spliceosome // inferred from electronic annotation /// 6118 // electron transport // inferred from electronic annotation /// 6397 // mRNA processing // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7067 // mitosis // inferred from electronic annotation /// 51301 // cell division // inferred from electronic annotation 5576 // extracellular region // inferred from electronic annotation /// 5576 // extracellular region // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation /// 5681 // spliceosome complex // inferred from electronic annotation 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 30492 // hemoglobin binding // inferred from electronic annotation /// 30492 // hemoglobin binding // non-traceable author statement --- 3240 /// 3250
225665_at Hs.444451 sterile alpha motif and leucine zipper containing kinase AZK ZAK 75 // cell cycle checkpoint // inferred from direct assay /// 77 // DNA damage checkpoint // inferred from mutant phenotype /// 186 // activation of MAPKK activity // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from direct assay /// 6950 // response to stress // non-traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7050 // cell cycle arrest // inferred from mutant phenotype /// 7243 // protein kinase cascade // inferred from

Figure 144

direct assay /// 7257 // activation of JNK activity // inferred from direct assay /// 8219 // cell death // non-traceable author statement /// 8283 // cell proliferation // non-traceable author statement /// 9314 // response to radiation // inferred from direct assay /// 30154 // cell differentiation // non-traceable author statement /// 43065 // positive regulation of apoptosis // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation 5737 // cytoplasm // inferred from sequence or structural similarity 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from direct assay /// 4674 // protein serine/threonine kinase activity // inferred from direct assay /// 4709 // MAP kinase kinase kinase activity // inferred from direct assay /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 42802 // identical protein binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 287 // magnesium ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 51776
203058_s_at Hs.524491 3'-phosphoadenosine 5'-phosphosulfate synthase 2 PAPSS2 103 // sulfate assimilation // inferred from electronic annotation /// 1501 // skeletal development // inferred from sequence or structural similarity /// 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // not recorded /// 1501 // skeletal development // traceable author statement 5622 // intracellular // inferred from sequence or structural similarity 166 // nucleotide binding // inferred from electronic annotation /// 4020 // adenylylsulfate kinase activity // inferred from electronic annotation /// 4781 // sulfate adenylyltransferase (ATP) activity // inferred from sequence or structural similarity /// 5524 // ATP binding // inferred from sequence or structural similarity /// 16779 // nucleotidyltransferase activity // inferred from sequence or structural similarity /// 16740 // transferase activity // inferred from sequence or structural similarity /// 3824 // catalytic activity // inferred from electronic annotation /// 4781 // sulfate adenylyltransferase (ATP) activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16772 // transferase activity, transferring phosphorus-containing groups // inferred from electronic annotation /// 16779 // nucleotidyltransferase activity // inferred from electronic annotation Purine metabolism // KEGG /// Selenoamino acid metabolism // KEGG /// Sulfur metabolism // KEGG /// Purine metabolism // KEGG /// Selenoamino acid metabolism // KEGG /// Sulfur metabolism // KEGG 9060
202446_s_at Hs.130759 phospholipid scramblase 1 PLSCR1 9615 // response to virus // inferred from electronic annotation /// 17121 // phospholipid scrambling // traceable author statement /// 30168 // platelet activation // non-traceable author statement 5886 // plasma membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane

Figure 145

// inferred from electronic annotation 5509 // calcium ion binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 17128 // phospholipid scramblase activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation --- 5359
227961_at Hs.520898 cathepsin B CTSB 6508 // proteolysis // traceable author statement /// 42981 // regulation of apoptosis // traceable author statement /// 50790 // regulation of enzyme activity // inferred from electronic annotation /// 6508 // proteolysis // inferred from electronic annotation 5622 // intracellular // traceable author statement /// 5764 // lysosome // inferred from electronic annotation /// 5764 // lysosome // not recorded 4213 // cathepsin B activity // traceable author statement /// 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4213 // cathepsin B activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Antigen processing and presentation // KEGG 1508
217167_x_at Hs.1466 glycerol kinase GK 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
Glycerolipid metabolism // KEGG 2710
215760_s_at Hs.408708 strawberry notch homolog 2 (Drosophila) SBNO2
--- --- --- --- 22904
229850_at Hs.595800 Full length insert cDNA clone YX81F03 ---
--- --- --- --- ---
200839_s_at Hs.520898 cathepsin B CTSB 6508 // proteolysis // traceable author statement /// 42981 // regulation of apoptosis // traceable author statement /// 50790 // regulation of enzyme activity // inferred from electronic annotation /// 6508 // proteolysis // inferred from electronic annotation 5622 // intracellular // traceable author statement /// 5764 // lysosome // inferred from electronic annotation /// 5764 // lysosome // not recorded 4213 // cathepsin B activity // traceable author statement /// 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4213 // cathepsin B activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Antigen processing and presentation // KEGG 1508
229373_at Hs.457403 Transcribed locus --- --- --- --- ---

201060_x_at Hs.253903 stomatin STOM --- 5856 // cytoskeleton // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from

Figure 146

electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 2040
1558173_a_at Hs.257900 leucine zipper protein 1 LUZP1 --- --- --- 7798
227037_at Hs.31652 similar to CG12314 gene product LOC201164 8152 // metabolism // inferred from electronic annotation --- 3824 // catalytic activity // inferred from electronic annotation --- 201164
203971_at Hs.532315 solute carrier family 31 (copper transporters), member 1 SLC31A1 6811 // ion transport // inferred from electronic annotation /// 6825 // copper ion transport // inferred from electronic annotation /// 6825 // copper ion transport // traceable author statement /// 6810 // transport // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5375 // copper ion transporter activity // inferred from electronic annotation /// 5375 // copper ion transporter activity // traceable author statement /// 5507 // copper ion binding // inferred from electronic annotation --- 1317
204999_s_at Hs.9754 activating transcription factor 5 ATF5 74 // regulation of progression through cell cycle // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3702 // RNA polymerase II transcription factor activity // traceable author statement /// 3714 // transcription corepressor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation Smooth_muscle_contraction // GenMAPP 22809
204068_at Hs.492333 serine/threonine kinase 3 (STE20 homolog, yeast) STK3 6468 // protein amino acid phosphorylation // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7243 // protein kinase cascade // inferred from direct assay /// 43065 // positive regulation of apoptosis // inferred from sequence or structural similarity /// 7165 // signal transduction // inferred from electronic annotation /// 6915 // apoptosis // not recorded 5634 // nucleus // inferred from electronic annotation /// 5737 // cytoplasm // not recorded 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from direct assay /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from direct assay /// 5524 // ATP binding // inferred from direct assay /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from sequence or structural similarity /// 287 // magnesium ion binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation /// 16301 // kinase activity //

Figure 147

inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // traceable author statement --- 6788
217388_s_at Hs.470126 kynureninase (L-kynurenine hydrolase) KYNU 6569 // tryptophan catabolism // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation /// 9435 // NAD biosynthesis // inferred from electronic annotation /// 19363 // pyridine nucleotide biosynthesis // inferred from electronic annotation /// 6569 // tryptophan catabolism // not recorded 5737 // cytoplasm // inferred from electronic annotation 8233 // peptidase activity // traceable author statement /// 8483 // transaminase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 30170 // pyridoxal phosphate binding // inferred from electronic annotation /// 30429 // kynureninase activity // inferred from electronic annotation Tryptophan metabolism // KEGG 8942
223939_at Hs.279575 succinate receptor 1 SUCNR1 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 16526 // G-protein coupled receptor activity, unknown ligand // non-traceable author statement /// 45028 // purinergic nucleotide receptor activity, G-protein coupled // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation GPCRDB_Class_A_Rhodopsin-like // GenMAPP 56670
204385_at Hs.470126 kynureninase (L-kynurenine hydrolase) KYNU 6569 // tryptophan catabolism // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation /// 9435 // NAD biosynthesis // inferred from electronic annotation /// 19363 // pyridine nucleotide biosynthesis // inferred from electronic annotation /// 6569 // tryptophan catabolism // not recorded 5737 // cytoplasm // inferred from electronic annotation 8233 // peptidase activity // traceable author statement /// 8483 // transaminase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 30170 // pyridoxal phosphate binding // inferred from electronic annotation /// 30429 // kynureninase activity // inferred from electronic annotation Tryptophan metabolism // KEGG 8942
220532_s_at Hs.647090 transmembrane protein 176B TMEM176B 9887 // organ morphogenesis // traceable author statement --- --- --- 28959
222670_s_at Hs.651210 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian) MAFB 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7423 // sensory organ development // traceable author statement 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 9935

Figure 148

231907_at Hs.159472 CDNA FLJ31718 fis, clone NT2RI2006647 ---
--- --- --- --- ---
207891_s_at Hs.170835 UCHL5 interacting protein UCHL5IP 6281
// DNA repair // traceable author statement /// 42177 // negative
regulation of protein catabolism // non-traceable author statement ///
43161 // proteasomal ubiquitin-dependent protein catabolism // non-
traceable author statement /// 42177 // negative regulation of protein
catabolism // inferred from sequence or structural similarity /// 43161
// proteasomal ubiquitin-dependent protein catabolism // inferred from
sequence or structural similarity /// 6281 // DNA repair // inferred
from electronic annotation /// 6974 // response to DNA damage stimulus
// inferred from electronic annotation 5634 // nucleus // inferred
from electronic annotation /// 5622 // intracellular // inferred from
electronic annotation 287 // magnesium ion binding // inferred from
electronic annotation /// 4527 // exonuclease activity // inferred from
electronic annotation /// 8296 // 3'-5'-exodeoxyribonuclease activity
// traceable author statement /// 8853 // exodeoxyribonuclease III
activity // inferred from electronic annotation /// 16787 // hydrolase
activity // inferred from electronic annotation /// 31996 //
thioesterase binding // inferred from physical interaction /// 31996 //
thioesterase binding // inferred from sequence or structural similarity
/// 4518 // nuclease activity // inferred from electronic annotation
--- 11219 /// 55559
210663_s_at Hs.470126 kynureninase (L-kynurenine hydrolase) KYNU
6569 // tryptophan catabolism // inferred from electronic
annotation /// 8152 // metabolism // inferred from electronic
annotation /// 9435 // NAD biosynthesis // inferred from electronic
annotation /// 19363 // pyridine nucleotide biosynthesis // inferred
from electronic annotation /// 6569 // tryptophan catabolism // not
recorded 5737 // cytoplasm // inferred from electronic annotation
8233 // peptidase activity // traceable author statement /// 8483
// transaminase activity // inferred from electronic annotation ///
16787 // hydrolase activity // inferred from electronic annotation ///
30170 // pyridoxal phosphate binding // inferred from electronic
annotation /// 30429 // kynureninase activity // inferred from
electronic annotation Tryptophan metabolism // KEGG 8942
217507_at Hs.591607 solute carrier family 11 (proton-coupled
divalent metal ion transporters), member 1 SLC11A1 6810 //
transport // inferred from electronic annotation /// 6811 // ion
transport // inferred from electronic annotation /// 6826 // iron ion
transport // inferred from electronic annotation /// 9613 // response
to pest, pathogen or parasite // traceable author statement /// 9617 //
response to bacteria // traceable author statement /// 6810 //
transport // traceable author statement 5624 // membrane fraction //
traceable author statement /// 5887 // integral to plasma membrane //
traceable author statement /// 16020 // membrane // inferred from
electronic annotation /// 16021 // integral to membrane // inferred
from electronic annotation 5215 // transporter activity // inferred
from electronic annotation /// 5215 // transporter activity //
traceable author statement /// 5506 // iron ion binding // inferred
from electronic annotation --- 6556
211327_x_at Hs.233325 hemochromatosis HFE 6461 // protein complex
assembly // traceable author statement /// 6811 // ion transport //
inferred from electronic annotation /// 6826 // iron ion transport //
traceable author statement /// 6879 // iron ion homeostasis //
traceable author statement /// 6898 // receptor mediated endocytosis //
traceable author statement /// 19882 // antigen presentation //

Figure 149

inferred from electronic annotation /// 19883 // antigen presentation, endogenous antigen // inferred from electronic annotation /// 19885 // antigen processing, endogenous antigen via MHC class I // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6826 // iron ion transport // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation 5737 // cytoplasm // traceable author statement /// 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 42612 // MHC class I protein complex // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5506 // iron ion binding // inferred from electronic annotation /// 30106 // MHC class I receptor activity // inferred from electronic annotation --- 3077
225831_at Hs.257900 leucine zipper protein 1 LUZP1 --- ---
--- --- 7798
207104_x_at Hs.67846 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 LILRB1 6955 // immune response // inferred from electronic annotation /// 9615 // response to virus // traceable author statement /// 6952 // defense response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6952 // defense response // not recorded 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 5886 // plasma membrane // non-traceable author statement 4872 // receptor activity // inferred from electronic annotation /// 8157 // protein phosphatase 1 binding // traceable author statement /// 3823 // antigen binding // traceable author statement /// 4888 // transmembrane receptor activity // traceable author statement /// 4872 // receptor activity // traceable author statement --- 10859
222687_s_at Hs.23862 phytoceramidase, alkaline PHCA 6412 // protein biosynthesis // inferred from electronic annotation /// 6672 // ceramide metabolism // inferred from electronic annotation 139 // Golgi membrane // inferred from electronic annotation /// 5622 // intracellular // inferred from electronic annotation /// 5789 // endoplasmic reticulum membrane // inferred from electronic annotation /// 5795 // Golgi stack // inferred from electronic annotation /// 5840 // ribosome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5783 // endoplasmic reticulum // inferred from electronic annotation 3735 // structural constituent of ribosome // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 16811 // hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides // inferred from electronic annotation --- 55331
201536_at Hs.651126 dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) DUSP3 6470 // protein amino acid dephosphorylation // traceable author statement /// 6470 // protein amino acid dephosphorylation // inferred from electronic annotation --- 4725 // protein tyrosine phosphatase activity // traceable author statement /// 8138 // protein tyrosine/serine/threonine phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 4721

Figure 150

// phosphoprotein phosphatase activity // inferred from electronic annotation Cell adhesion molecules (CAMs) // KEGG /// Adherens junction // KEGG /// Jak-STAT signaling pathway // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Leukocyte transendothelial migration // KEGG /// Insulin signaling pathway // KEGG /// Adipocytokine signaling pathway // KEGG /// Type I diabetes mellitus // KEGG /// Epithelial cell signaling in Helicobacter pylori // KEGG /// Calcium signaling pathway // KEGG /// Apoptosis // KEGG /// Wnt signaling pathway // KEGG /// TGF-beta signaling pathway // KEGG /// Axon guidance // KEGG /// VEGF signaling pathway // KEGG /// Focal adhesion // KEGG /// Tight junction // KEGG /// T cell receptor signaling pathway // KEGG /// B cell receptor signaling pathway // KEGG /// Long-term potentiation // KEGG /// Long-term depression // KEGG /// Insulin signaling pathway // KEGG 1845
209193_at Hs.81170 pim-1 oncogene /// pim-1 oncogene PIM1 6468 // protein amino acid phosphorylation // inferred from direct assay /// 7275 // development // traceable author statement /// 8283 // cell proliferation // inferred from direct assay /// 43066 // negative regulation of apoptosis // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5737 // cytoplasm // inferred from direct assay 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from direct assay /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 30145 // manganese ion binding // inferred from direct assay /// 46872 // metal ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 30145 // manganese ion binding // inferred from electronic annotation --- 5292
226931_at Hs.401954 transmembrane and tetratricopeptide repeat containing 1 TMTC1 --- --- 5488 // binding // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation --- 653626 /// 83857
201809_s_at Hs.76753 endoglin (Osler-Rendu-Weber syndrome 1) ENG 6810 // transport // inferred from electronic annotation /// 7155 // cell adhesion // inferred from electronic annotation /// 8015 // circulation // traceable author statement /// 9887 // organ morphogenesis // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5515 // protein binding // traceable author statement /// 5515 // protein binding // inferred from electronic annotation TGF_Beta_Signaling_Pathway // GenMAPP /// TGF_Beta_Signaling_Pathway // GenMAPP 2022
218451_at Hs.476093 CUB domain containing protein 1 CDCP1 --- --- --- --- 64866
207500_at Hs.213327 caspase 5, apoptosis-related cysteine peptidase CASP5 6508 // proteolysis // traceable author statement /// 42981

Figure 151

// regulation of apoptosis // inferred from electronic annotation /// 6508 // proteolysis // inferred from electronic annotation /// 6915 // apoptosis // inferred from electronic annotation /// 6915 // apoptosis // traceable author statement 5622 // intracellular // inferred from electronic annotation 5515 // protein binding // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // traceable author statement /// 30693 // caspase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 838
204252_at Hs.19192 cyclin-dependent kinase 2 /// beta-carotene dioxygenase 2 CDK2 /// BCDO2 86 // G2/M transition of mitotic cell cycle // traceable author statement /// 6275 // regulation of DNA replication // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7067 // mitosis // inferred from electronic annotation /// 7089 // traversing start control point of mitotic cell cycle // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 51301 // cell division // inferred from electronic annotation 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4693 // cyclin-dependent protein kinase activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 4672 // protein kinase activity // traceable author statement Cell_cycle_KEGG // GenMAPP /// DNA_replication_Reactome // GenMAPP /// G1_to_S_cell_cycle_Reactome // GenMAPP /// Cell_cycle_KEGG // GenMAPP /// DNA_replication_Reactome // GenMAPP /// G1_to_S_cell_cycle_Reactome // GenMAPP 1017
201061_s_at Hs.253903 stomatin STOM --- 5856 // cytoskeleton // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 2040
1554462_a_at Hs.6790 DnaJ (Hsp40) homolog, subfamily B, member 9 DNAJB9 6457 // protein folding // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5730 // nucleolus // inferred from sequence or structural similarity /// 5737 // cytoplasm // inferred from sequence or structural similarity 30188 // chaperone regulator activity // inferred from sequence or structural similarity /// 31072 // heat shock protein binding // inferred from electronic annotation /// 51082 // unfolded protein binding // inferred from electronic annotation --- 4189
218189_s_at Hs.522310 N-acetylneuraminic acid synthase (sialic acid synthase) NANS 9103 // lipopolysaccharide biosynthesis // non-traceable author statement /// 16051 // carbohydrate biosynthesis // inferred from electronic annotation 5737 // cytoplasm // non-traceable author statement 8781 // N-acylneuraminate cytidylyltransferase activity // non-traceable author statement /// 16740 // transferase activity // inferred from electronic annotation /// 47444 // N-

Figure 152

acylneuraminate-9-phosphate synthase activity // inferred from electronic annotation /// 50462 // N-acetylneuraminate synthase activity // inferred from electronic annotation --- 54187
208071_s_at Hs.572535 leukocyte-associated immunoglobulin-like receptor 1 LAIR1 --- --- 4872 // receptor activity // inferred from electronic annotation --- 3903
218345_at Hs.647116 transmembrane protein 176A TMEM176A --- --- --- --- 55365
218559_s_at Hs.651210 v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian) MAFB 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7423 // sensory organ development // traceable author statement 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 9935
216316_x_at Hs.1466 glycerol kinase /// glycerol kinase 3 pseudogene GK /// GK3P 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation Glycerolipid metabolism // KEGG 2710 /// 2713
215087_at Hs.17936 chromosome 15 open reading frame 39 C15orf39 --- --- --- --- 56905
227677_at Hs.515247 Janus kinase 3 (a protein tyrosine kinase, leukocyte) JAK3 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6468 // protein amino acid phosphorylation // traceable author statement /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7498 // mesoderm development // not recorded 5856 // cytoskeleton // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // traceable author statement /// 4718 // Janus kinase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation --- 3718
204269_at Hs.496096 pim-2 oncogene PIM2 6468 // protein amino acid phosphorylation // traceable author statement /// 7140 // male meiosis // traceable author statement /// 8283 // cell proliferation // traceable author statement /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation --- 166

Figure 153

// nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation --- 11040
211189_x_at Hs.398093 CD84 molecule CD84 6952 // defense response // traceable author statement /// 7156 // homophilic cell adhesion // traceable author statement 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement --- --- 8832
215966_x_at --- glycerol kinase 3 pseudogene GK3P 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6072 // glycerol-3-phosphate metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // inferred from electronic annotation /// 6071 // glycerol metabolism // non-traceable author statement 5737 // cytoplasm // non-traceable author statement /// 5741 // mitochondrial outer membrane // non-traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 4370 // glycerol kinase activity // inferred from electronic annotation /// 4370 // glycerol kinase activity // non-traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation --- 2713
225235_at Hs.532129 tetraspanin 17 TSPAN17 16567 // protein ubiquitination // non-traceable author statement 151 // ubiquitin ligase complex // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4842 // ubiquitin-protein ligase activity // non-traceable author statement --- 26262
201945_at Hs.513153 furin (paired basic amino acid cleaving enzyme) FURIN 6508 // proteolysis // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 6508 // proteolysis // inferred from electronic annotation 5794 // Golgi apparatus // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 30140 // trans-Golgi network transport vesicle // inferred from direct assay 4276 // furin activity // inferred from direct assay /// 4289 // subtilase activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 4276 // furin activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4276 // furin activity // traceable author statement --- 5045
234081_at Hs.435458 SET binding protein 1 SETBP1 --- 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation --- 26040
205349_at --- guanine nucleotide binding protein (G protein), alpha 15 (Gq class) GNA15 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled

Figure 154

receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7204 // elevation of cytosolic calcium ion concentration // inferred from genetic interaction /// 7207 // muscarinic acetylcholine receptor, phospholipase C activating pathway // traceable author statement 5834 // heterotrimeric G-protein complex // non-traceable author statement /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from genetic interaction /// 5525 // GTP binding // non-traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP 2769 202067_s_at Hs.213289 low density lipoprotein receptor (familial hypercholesterolemia) LDLR 6493 // protein amino acid O-linked glycosylation // traceable author statement /// 6629 // lipid metabolism // traceable author statement /// 6869 // lipid transport // inferred from electronic annotation /// 6897 // endocytosis // traceable author statement /// 8202 // steroid metabolism // inferred from electronic annotation /// 8203 // cholesterol metabolism // inferred from electronic annotation /// 6629 // lipid metabolism // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6897 // endocytosis // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 5905 // coated pit // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5886 // plasma membrane // traceable author statement 4872 // receptor activity // inferred from electronic annotation /// 4888 // transmembrane receptor activity // traceable author statement /// 5041 // low-density lipoprotein receptor activity // traceable author statement /// 5319 // lipid transporter activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 8034 // lipoprotein binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction Wnt_signaling // GenMAPP /// Statin_Pathway_PharmGKB // GenMAPP /// Wnt_signaling // GenMAPP /// Statin_Pathway_PharmGKB // GenMAPP 3949

228648_at Hs.131034 leucine-rich alpha-2-glycoprotein 1 LRG1 --- 5576 // extracellular region // non-traceable author statement /// 16020 // membrane // non-traceable author statement --- --- 116844

226777_at Hs.594351 CDNA FLJ31066 fis, clone HSYRA2001153 --- --- --- --- ---

204166_at Hs.408708 strawberry notch homolog 2 (Drosophila) SBNO2 --- --- --- --- 22904

226433_at Hs.500643 ring finger protein 157 RNF157 6512 // ubiquitin cycle // inferred from electronic annotation --- 5515 // protein binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 114804

210889_s_at Hs.352642 Fc fragment of IgG, low affinity IIb, receptor (CD32) FCGR2B 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement

Figure 155

/// 6457 // protein folding // inferred from electronic annotation /// 6986 // response to unfolded protein // inferred from electronic annotation /// 6986 // response to unfolded protein // traceable author statement /// 6955 // immune response // non-traceable author statement /// 6955 // immune response // not recorded 5886 // plasma membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement 4872 // receptor activity // inferred from electronic annotation /// 19864 // IgG binding // inferred from electronic annotation /// 166 // nucleotide binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 4888 // transmembrane receptor activity // non-traceable author statement /// 5057 // receptor signaling protein activity // not recorded --- 2213
205099_s_at Hs.301921 chemokine (C-C motif) receptor 1 CCR1 6935 // chemotaxis // non-traceable author statement /// 6954 // inflammatory response // traceable author statement /// 7155 // cell adhesion // traceable author statement /// 7187 // G-protein signaling, coupled to cyclic nucleotide second messenger // traceable author statement /// 7204 // elevation of cytosolic calcium ion concentration // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // non-traceable author statement /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 6935 // chemotaxis // traceable author statement /// 6955 // immune response // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 9611 // response to wounding // traceable author statement 5886 // plasma membrane // inferred from direct assay /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5886 // plasma membrane // traceable author statement 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 16493 // C-C chemokine receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4950 // chemokine receptor activity // traceable author statement GPCRDB_Class_A_Rhodopsin-like // GenMAPP /// Peptide_GPCRs // GenMAPP 1230
229865_at Hs.159430 fibronectin type III domain containing 3B FNDC3B --- --- --- --- 64778
215646_s_at Hs.643801 chondroitin sulfate proteoglycan 2 (versican) /// chondroitin sulfate proteoglycan 2 (versican) CSPG2 7155 // cell adhesion // traceable author statement /// 7275 // development // traceable author statement /// 8037 // cell recognition // traceable author statement /// 7155 // cell adhesion // inferred from electronic annotation 5578 // extracellular matrix (sensu Metazoa) // traceable author statement /// 5578 // extracellular matrix (sensu Metazoa) // inferred from electronic annotation 5509 // calcium ion binding // inferred from electronic annotation /// 5529 // sugar binding // inferred from electronic annotation /// 5540 // hyaluronic acid binding // traceable author statement /// 5540 // hyaluronic acid binding //

Figure 156

inferred from electronic annotation /// 5539 // glycosaminoglycan binding // traceable author statement --- 1462
222688_at Hs.23862 phytoceramidase, alkaline PHCA 6412 // protein biosynthesis // inferred from electronic annotation /// 6672 // ceramide metabolism // inferred from electronic annotation 139 // Golgi membrane // inferred from electronic annotation /// 5622 // intracellular // inferred from electronic annotation /// 5789 // endoplasmic reticulum membrane // inferred from electronic annotation /// 5795 // Golgi stack // inferred from electronic annotation /// 5840 // ribosome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5783 // endoplasmic reticulum // inferred from electronic annotation 3735 // structural constituent of ribosome // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 16811 // hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides // inferred from electronic annotation --- 55331
203857_s_at Hs.477352 protein disulfide isomerase family A, member 5 PDIA5 6118 // electron transport // inferred from electronic annotation /// 6457 // protein folding // traceable author statement /// 6950 // response to stress // traceable author statement 5783 // endoplasmic reticulum // traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation 3756 // protein disulfide isomerase activity // traceable author statement /// 16853 // isomerase activity // inferred from electronic annotation /// 3756 // protein disulfide isomerase activity // inferred from electronic annotation Antigen processing and presentation // KEGG 10954
202284_s_at Hs.370771 cyclin-dependent kinase inhibitor 1A (p21, Cip1) CDKN1A 79 // regulation of cyclin dependent protein kinase activity // traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7050 // cell cycle arrest // inferred from electronic annotation /// 7050 // cell cycle arrest // traceable author statement /// 8285 // negative regulation of cell proliferation // traceable author statement /// 8629 // induction of apoptosis by intracellular signals // traceable author statement /// 74 // regulation of progression through cell cycle // traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // traceable author statement 4672 // protein kinase activity // not recorded /// 4861 // cyclin-dependent protein kinase inhibitor activity // inferred from electronic annotation /// 4861 // cyclin-dependent protein kinase inhibitor activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4860 // protein kinase inhibitor activity // inferred from electronic annotation Cell_cycle_KEGG // GenMAPP /// Cell_cycle_KEGG // GenMAPP /// G1_to_S_cell_cycle_Reactome // GenMAPP /// G1_to_S_cell_cycle_Reactome // GenMAPP 1026
221831_at Hs.257900 leucine zipper protein 1 LUZP1 --- --- --- --- 7798
213577_at Hs.71465 squalene epoxidase SQLE 6118 // electron transport // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation /// 16126 // sterol biosynthesis // non-traceable author statement 5792 // microsome // non-traceable

Figure 157

author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4506 // squalene monooxygenase activity // non-traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 4506 // squalene monooxygenase activity // inferred from electronic annotation /// 4497 // monooxygenase activity // inferred from electronic annotation
Cholesterol_Biosynthesis // GenMAPP /// Cholesterol_Biosynthesis // GenMAPP /// Biosynthesis of steroids // KEGG /// Terpenoid biosynthesis // KEGG 6713
209218_at Hs.71465 squalene epoxidase SQLE 6118 // electron transport // inferred from electronic annotation /// 8152 // metabolism // inferred from electronic annotation /// 16126 // sterol biosynthesis // non-traceable author statement 5792 // microsome // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4506 // squalene monooxygenase activity // non-traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 4506 // squalene monooxygenase activity // inferred from electronic annotation /// 4497 // monooxygenase activity // inferred from electronic annotation
Cholesterol_Biosynthesis // GenMAPP /// Cholesterol_Biosynthesis // GenMAPP /// Biosynthesis of steroids // KEGG /// Terpenoid biosynthesis // KEGG 6713
241916_at Hs.130759 Phospholipid scramblase 1 PLSCR1 9615 // response to virus // inferred from electronic annotation /// 17121 // phospholipid scrambling // traceable author statement /// 30168 // platelet activation // non-traceable author statement 5886 // plasma membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 5509 // calcium ion binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 17128 // phospholipid scramblase activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation --- 5359
204907_s_at Hs.31210 B-cell CLL/lymphoma 3 BCL3 74 // regulation of progression through cell cycle // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7253 // cytoplasmic sequestering of NF-kappaB // traceable author statement 5634 // nucleus // inferred from electronic annotation --- --- 602
220150_s_at Hs.443789 chromosome 6 open reading frame 60 C6orf60 --- --- --- --- 79632
218648_at Hs.567572 CREB regulated transcription coactivator 3 CRTC3 --- --- --- --- 64784

Figure 158

probe UniGene.ID Gene.Title Gene.Symbol
Gene.Ontology.Biological.Process
Gene.Ontology.Cellular.Component
Gene.Ontology.Molecular.Function Pathway Entrez.Gene

223710_at Hs.131342 chemokine (C-C motif) ligand 26 CCL26 6935
// chemotaxis // traceable author statement /// 6954 // inflammatory
response // traceable author statement /// 7165 // signal transduction
// non-traceable author statement /// 7267 // cell-cell signaling //
traceable author statement /// 50896 // response to stimulus //
inferred from electronic annotation /// 6935 // chemotaxis // inferred
from electronic annotation /// 6954 // inflammatory response //
inferred from electronic annotation /// 6955 // immune response //
inferred from electronic annotation /// 6955 // immune response //
traceable author statement 5615 // extracellular space // inferred
from electronic annotation /// 5576 // extracellular region // inferred
from electronic annotation /// 5615 // extracellular space // not
recorded 8009 // chemokine activity // traceable author statement
/// 5125 // cytokine activity // inferred from electronic annotation
/// 8009 // chemokine activity // inferred from electronic annotation
--- 10344
221029_s_at Hs.306051 wingless-type MMTV integration site family,
member 5B /// wingless-type MMTV integration site family, member 5B
WNT5B 7223 // frizzled-2 signaling pathway // inferred from
electronic annotation /// 7275 // development // inferred from
electronic annotation /// 16055 // Wnt receptor signaling pathway //
inferred from electronic annotation 5576 // extracellular region //
inferred from electronic annotation 4871 // signal transducer activity
// inferred from electronic annotation Wnt_signaling // GenMAPP
81029
202468_s_at Hs.58488 catenin (cadherin-associated protein), alpha-
like 1 CTNNAL1 6915 // apoptosis // not recorded /// 7155 //
cell adhesion // inferred from electronic annotation 15629 // actin
cytoskeleton // inferred from electronic annotation /// 5856 //
cytoskeleton // inferred from electronic annotation 5198 //
structural molecule activity // inferred from electronic annotation ///
45296 // cadherin binding // inferred from electronic annotation ---
8727
223939_at Hs.279575 succinate receptor 1 SUCNR1 7165 //
signal transduction // inferred from electronic annotation /// 7186 //
G-protein coupled receptor protein signaling pathway // inferred from
electronic annotation 16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // non-traceable author
statement /// 16021 // integral to membrane // inferred from electronic
annotation 1584 // rhodopsin-like receptor activity // inferred from
electronic annotation /// 4872 // receptor activity // inferred from
electronic annotation /// 16526 // G-protein coupled receptor activity,
unknown ligand // non-traceable author statement /// 45028 //
purinergic nucleotide receptor activity, G-protein coupled // inferred
from electronic annotation /// 4871 // signal transducer activity //
inferred from electronic annotation /// 4930 // G-protein coupled
receptor activity // inferred from electronic annotation
GPCRDB_Class_A_Rhodopsin-like // GenMAPP 56670
213638_at Hs.436996 phosphatase and actin regulator 1 PHACTR1
--- --- 3779 // actin binding // inferred from electronic
annotation /// 4864 // protein phosphatase inhibitor activity //
inferred from electronic annotation --- 221692

Figure 159

223377_x_at Hs.8257 cytokine inducible SH2-containing protein CISH 1558 // regulation of cell growth // non-traceable author statement /// 7242 // intracellular signaling cascade // non-traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- --- --- 1154
205249_at Hs.1395 early growth response 2 (Krox-20 homolog, Drosophila) EGR2 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7420 // brain development // traceable author statement /// 7422 // peripheral nervous system development // traceable author statement /// 7638 // mechanosensory behavior // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from direct assay /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 1959
204438_at Hs.75182 mannose receptor, C type 1 /// mannose receptor, C type 1-like 1 MRC1 /// MRC1L1 6898 // receptor mediated endocytosis // traceable author statement /// 6907 // pinocytosis // not recorded /// 6897 // endocytosis // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5529 // sugar binding // inferred from electronic annotation /// 5537 // mannose binding // traceable author statement /// 4872 // receptor activity // inferred from electronic annotation --- 414308 /// 4360
217771_at Hs.494337 golgi phosphoprotein 2 GOLPH2 --- 5795 // Golgi stack // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5794 // Golgi apparatus // traceable author statement --- --- 51280
205698_s_at Hs.463978 mitogen-activated protein kinase kinase 6 MAP2K6 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6975 // DNA damage induced protein phosphorylation // traceable author statement /// 7050 // cell cycle arrest // traceable author statement /// 7165 // signal transduction // traceable author statement --- 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4708 // MAP kinase kinase activity // traceable author statement /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation Integrin-

Figure 160

mediated_cell_adhesion_KEGG // GenMAPP /// MAPK_Cascade // GenMAPP
5608
201042_at Hs.517033 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) TGM2 7186 // G-protein coupled receptor protein signaling pathway // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred from sequence or structural similarity /// 45785 // positive regulation of cell adhesion // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred from electronic annotation
5578 // extracellular matrix (sensu Metazoa) // inferred from sequence or structural similarity /// 5829 // cytosol // inferred from sequence or structural similarity /// 16020 // membrane // inferred from sequence or structural similarity 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from sequence or structural similarity /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5525 // GTP binding // inferred from sequence or structural similarity /// 8415 // acyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation Complement and coagulation cascades // KEGG /// Huntington's disease // KEGG 7052
205699_at --- --- --- --- --- --- --- ---
229569_at Hs.49329 CDNA clone IMAGE:5263455 --- --- ---
--- --- ---
205990_s_at Hs.643085 wingless-type MMTV integration site family, member 5A WNT5A 7165 // signal transduction // traceable author statement /// 7223 // frizzled-2 signaling pathway // inferred from electronic annotation /// 7267 // cell-cell signaling // traceable author statement /// 9653 // morphogenesis // traceable author statement /// 7275 // development // inferred from electronic annotation /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation 5615 // extracellular space // traceable author statement /// 5625 // soluble fraction // traceable author statement /// 5576 // extracellular region // inferred from electronic annotation
5102 // receptor binding // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4871 // signal transducer activity // traceable author statement
Wnt_signaling // GenMAPP 7474
232045_at Hs.436996 phosphatase and actin regulator 1 PHACTR1
--- --- 3779 // actin binding // inferred from electronic annotation /// 4864 // protein phosphatase inhibitor activity // inferred from electronic annotation --- 221692
221223_x_at Hs.8257 cytokine inducible SH2-containing protein CISH
1558 // regulation of cell growth // non-traceable author statement /// 7242 // intracellular signaling cascade // non-traceable author statement /// 9968 // negative regulation of signal transduction // inferred from electronic annotation /// 1558 // regulation of cell growth // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- ---
--- 1154
223961_s_at Hs.8257 cytokine inducible SH2-containing protein CISH
1558 // regulation of cell growth // non-traceable author statement /// 7242 // intracellular signaling cascade // non-traceable author statement /// 9968 // negative regulation of signal transduction

Figure 161

// inferred from electronic annotation /// 1558 // regulation of cell growth // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- --- --- 1154
221170_at Hs.287388 histamine receptor H4 HRH4 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4969 // histamine receptor activity // non-traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation GPCRDB_Other // GenMAPP /// GPCRDB_Other // GenMAPP 59340
223537_s_at Hs.306051 wingless-type MMTV integration site family, member 5B WNT5B 7223 // frizzled-2 signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation 5576 // extracellular region // inferred from electronic annotation 4871 // signal transducer activity // inferred from electronic annotation Wnt_signaling // GenMAPP 81029
216268_s_at Hs.224012 jagged 1 (Alagille syndrome) JAG1 1525 // angiogenesis // non-traceable author statement /// 1709 // cell fate determination // non-traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 7219 // Notch signaling pathway // non-traceable author statement /// 7275 // development // non-traceable author statement /// 7399 // nervous system development // non-traceable author statement /// 30097 // hemopoiesis // non-traceable author statement /// 30216 // keratinocyte differentiation // non-traceable author statement /// 30334 // regulation of cell migration // non-traceable author statement /// 42127 // regulation of cell proliferation // non-traceable author statement /// 45445 // myoblast differentiation // non-traceable author statement /// 45446 // endothelial cell differentiation // non-traceable author statement /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5112 // Notch binding // non-traceable author statement /// 5198 // structural molecule activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 8083 // growth factor activity // non-traceable author statement --- 182
210001_s_at Hs.50640 suppressor of cytokine signaling 1 SOCS1 1558 // regulation of cell growth // inferred from electronic annotation /// 1932 // regulation of protein amino acid phosphorylation // inferred from sequence or structural similarity /// 6512 // ubiquitin cycle // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT

Figure 162

cascade // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // inferred from sequence or structural similarity /// 42518 // negative regulation of tyrosine phosphorylation of Stat3 protein // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // non-traceable author statement /// 46627 // negative regulation of insulin receptor signaling pathway // inferred from sequence or structural similarity /// 9968 // negative regulation of signal transduction // inferred from electronic annotation 5737 // cytoplasm // traceable author statement 4860 // protein kinase inhibitor activity // traceable author statement /// 5159 // insulin-like growth factor receptor binding // inferred from physical interaction /// 19901 // protein kinase binding // inferred from physical interaction /// 19210 // kinase inhibitor activity // inferred from sequence or structural similarity --- 8651
223625_at Hs.85603 family with sequence similarity 126, member A FAM126A --- --- 4871 // signal transducer activity // non-traceable author statement --- 84668
228915_at Hs.129452 dachshund homolog 1 (Drosophila) DACH1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7456 // eye development (sensu Endopterygota) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction ---
1602
221724_s_at Hs.504657 C-type lectin domain family 4, member A CLEC4A 6955 // immune response // inferred from electronic annotation /// 7155 // cell adhesion // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 19735 // antimicrobial humoral response (sensu Vertebrata) // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation /// 9653 // morphogenesis // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4888 // transmembrane receptor activity // traceable author statement /// 5529 // sugar binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // traceable author statement --- 50856
219298_at Hs.22242 enoyl Coenzyme A hydratase domain containing 3 ECHDC3 8152 // metabolism // inferred from electronic annotation --- 3824 // catalytic activity // inferred from electronic annotation --- 79746
212094_at Hs.147492 paternally expressed 10 PEG10 --- --- 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation --- 23089

Figure 163

219947_at Hs.504657 C-type lectin domain family 4, member A CLEC4A 6955 // immune response // inferred from electronic annotation /// 7155 // cell adhesion // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 19735 // antimicrobial humoral response (sensu Vertebrata) // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation /// 9653 // morphogenesis // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4888 // transmembrane receptor activity // traceable author statement /// 5529 // sugar binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction /// 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // traceable author statement --- 50856
212741_at Hs.183109 monoamine oxidase A MAOA 6118 // electron transport // inferred from electronic annotation /// 6584 // catecholamine metabolism // inferred from electronic annotation /// 7610 // behavior // traceable author statement /// 42135 // neurotransmitter catabolism // inferred from electronic annotation /// 6576 // biogenic amine metabolism // traceable author statement 5739 // mitochondrion // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // not recorded 8131 // amine oxidase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 8131 // amine oxidase activity // not recorded Biogenic_Amine_Synthesis // GenMAPP /// Glycine, serine and threonine metabolism // KEGG /// Arginine and proline metabolism // KEGG /// Histidine metabolism // KEGG /// Tyrosine metabolism // KEGG /// Phenylalanine metabolism // KEGG /// Tryptophan metabolism // KEGG 4128
243606_at Hs.595933 Transcribed locus --- --- --- --- --- ---
229506_at Hs.592572 CDNA clone IMAGE:5263177 --- --- --- --- --- ---
1556314_a_at Hs.224794 (clone 1NIB-4) normalized cDNA library sequence --- --- --- --- --- ---
204388_s_at Hs.183109 monoamine oxidase A MAOA 6118 // electron transport // inferred from electronic annotation /// 6584 // catecholamine metabolism // inferred from electronic annotation /// 7610 // behavior // traceable author statement /// 42135 // neurotransmitter catabolism // inferred from electronic annotation /// 6576 // biogenic amine metabolism // traceable author statement 5739 // mitochondrion // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // not recorded 8131 // amine oxidase activity // inferred from electronic annotation /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 8131 // amine

Figure 164

oxidase activity // not recorded Biogenic_Amine_Synthesis // GenMAPP /// Glycine, serine and threonine metabolism // KEGG /// Arginine and proline metabolism // KEGG /// Histidine metabolism // KEGG /// Tyrosine metabolism // KEGG /// Phenylalanine metabolism // KEGG /// Tryptophan metabolism // KEGG 4128
226397_s_at Hs.484678 TBC1 domain family, member 7 TBC1D7 --- --- 5096 // GTPase activator activity // inferred from electronic annotation --- 51256
1556097_at Hs.459142 MRNA; cDNA DKFZp686A11113 (from clone DKFZp686A11113) --- --- --- --- --- ---
231183_s_at Hs.224012 Jagged 1 (Alagille syndrome) JAG1 1525 // angiogenesis // non-traceable author statement /// 1709 // cell fate determination // non-traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 7219 // Notch signaling pathway // non-traceable author statement /// 7275 // development // non-traceable author statement /// 7399 // nervous system development // non-traceable author statement /// 30097 // hemopoiesis // non-traceable author statement /// 30216 // keratinocyte differentiation // non-traceable author statement /// 30334 // regulation of cell migration // non-traceable author statement /// 42127 // regulation of cell proliferation // non-traceable author statement /// 45445 // myoblast differentiation // non-traceable author statement /// 45446 // endothelial cell differentiation // non-traceable author statement /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5112 // Notch binding // non-traceable author statement /// 5198 // structural molecule activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 8083 // growth factor activity // non-traceable author statement --- 182
1555326_a_at Hs.591852 ADAM metallopeptidase domain 9 (meltrin gamma) ADAM9 6508 // proteolysis // inferred from electronic annotation /// 7243 // protein kinase cascade // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement 4222 // metalloendopeptidase activity // inferred from electronic annotation /// 5178 // integrin binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 17124 // SH3 domain binding // inferred from physical interaction /// 19901 // protein kinase binding // traceable author statement /// 46872 // metal ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // traceable author statement /// 8237 // metallopeptidase activity // non-traceable author statement --- 8754

Figure 165

209099_x_at Hs.224012 jagged 1 (Alagille syndrome) JAG1 1525 // angiogenesis // non-traceable author statement /// 1709 // cell fate determination // non-traceable author statement /// 7154 // cell communication // inferred from electronic annotation /// 7219 // Notch signaling pathway // non-traceable author statement /// 7275 // development // non-traceable author statement /// 7399 // nervous system development // non-traceable author statement /// 30097 // hemopoiesis // non-traceable author statement /// 30216 // keratinocyte differentiation // non-traceable author statement /// 30334 // regulation of cell migration // non-traceable author statement /// 42127 // regulation of cell proliferation // non-traceable author statement /// 45445 // myoblast differentiation // non-traceable author statement /// 45446 // endothelial cell differentiation // non-traceable author statement /// 7219 // Notch signaling pathway // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5576 // extracellular region // non-traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5112 // Notch binding // non-traceable author statement /// 5198 // structural molecule activity // non-traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 8083 // growth factor activity // non-traceable author statement --- 182

228457_at Hs.592572 CDNA clone IMAGE:5263177 --- --- --- --- ---

225776_at Hs.505729 CDNA FLJ39093 fis, clone NT2RP7020112 --- 5975 // carbohydrate metabolism // traceable author statement /// 6486 // protein amino acid glycosylation // traceable author statement /// 42355 // L-fucose catabolism // non-traceable author statement /// 6396 // RNA processing // traceable author statement /// 6445 // regulation of translation // traceable author statement 5624 // membrane fraction // traceable author statement /// 5795 // Golgi stack // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation 8107 // galactoside 2-alpha-L-fucosyltransferase activity // traceable author statement /// 8417 // fucosyltransferase activity // traceable author statement /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement Blood group glycolipid biosynthesis - lactoseries // KEGG /// Blood group glycolipid biosynthesis - // KEGG /// Globoside metabolism // KEGG /// Glycan structures - biosynthesis 2 // KEGG 2523

235030_at Hs.130195 family with sequence similarity 55, member C FAM55C --- --- --- --- 91775

203464_s_at Hs.515176 epsin 2 EPN2 6897 // endocytosis // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- 8289 // lipid binding // inferred from electronic annotation --- 22905

1552875_a_at Hs.309158 CD200 receptor 1 CD200R1 --- 16020 // membrane // inferred from electronic annotation /// 16021 //

Figure 166

integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 131450
1553222_at Hs.168439 oxoeicosanoid (OXE) receptor 1 OXER1 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // non-traceable author statement /// 30817 // regulation of cAMP biosynthesis // inferred from direct assay /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 50646 // 5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid binding // non-traceable author statement /// 50647 // 5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic acid binding // non-traceable author statement /// 50648 // 5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetraenoic acid binding // non-traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // non-traceable author statement --- 165140
221385_s_at Hs.533926 free fatty acid receptor 3 /// G protein-coupled receptor 42 /// similar to Free fatty acid receptor 3 (G-protein coupled receptor 41) FFAR3 /// GPR42 /// LOC731823 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // traceable author statement GPCRDB_Class_A_Rhodopsin-like2 // GenMAPP 2865 /// 2866 /// 654110
218718_at Hs.570855 platelet derived growth factor C PDGFC 7417 // central nervous system development // traceable author statement 16020 // membrane // inferred from electronic annotation /// 5576 // extracellular region // non-traceable author statement 8083 // growth factor activity // inferred from electronic annotation /// 8083 // growth factor activity // traceable author statement --- 56034
209544_at Hs.103755 receptor-interacting serine-threonine kinase 2 RIPK2 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6954 // inflammatory response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 42981 // regulation of apoptosis // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from expression pattern /// 6915 // apoptosis // inferred from electronic annotation /// 6915 // apoptosis // traceable author statement 5622 // intracellular // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // traceable author statement /// 4871

Figure 167

// signal transducer activity // inferred from expression pattern /// 5515 // protein binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 30274 // LIM domain binding // inferred from physical interaction /// 50700 // CARD domain binding // inferred from physical interaction /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // traceable author statement mTOR signaling pathway // KEGG /// Wnt signaling pathway // KEGG /// Dorso-ventral axis formation // KEGG /// Hedgehog signaling pathway // KEGG /// TGF-beta signaling pathway // KEGG /// Axon guidance // KEGG /// VEGF signaling pathway // KEGG /// Focal adhesion // KEGG /// Adherens junction // KEGG /// Tight junction // KEGG /// Gap junction // KEGG /// B cell receptor signaling pathway // KEGG /// Fc epsilon RI signaling pathway // KEGG /// Long-term potentiation // KEGG /// Long-term depression // KEGG /// Regulation of actin cytoskeleton // KEGG /// Insulin signaling pathway // KEGG /// Alzheimer's disease // KEGG 8767

1553395_a_at Hs.309158 CD200 receptor 1 CD200R1 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 131450

220049_s_at Hs.532279 programmed cell death 1 ligand 2 PDCD1LG2 6955 // immune response // non-traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 80380

213425_at Hs.643085 wingless-type MMTV integration site family, member 5A /// wingless-type MMTV integration site family, member 5A WNT5A 7165 // signal transduction // traceable author statement /// 7223 // frizzled-2 signaling pathway // inferred from electronic annotation /// 7267 // cell-cell signaling // traceable author statement /// 9653 // morphogenesis // traceable author statement /// 7275 // development // inferred from electronic annotation /// 16055 // Wnt receptor signaling pathway // inferred from electronic annotation 5615 // extracellular space // traceable author statement /// 5625 // soluble fraction // traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 5102 // receptor binding // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation --- 7474

231972_at Hs.484678 TBC1 domain family, member 7 TBC1D7 --- --- 5096 // GTPase activator activity // inferred from electronic annotation --- 51256

232530_at Hs.382865 phospholipase D1, phosphatidylcholine-specific PLD1 --- --- --- --- 652226

222891_s_at Hs.370549 B-cell CLL/lymphoma 11A (zinc finger protein) BCL11A 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 30097 // hemopoiesis // non-traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement 3676 // nucleic acid binding // inferred from electronic annotation /// 8270

Figure 168

```
// zinc ion binding // inferred from electronic annotation /// 46872 //
metal ion binding // inferred from electronic annotation    ---    53335
226416_at    Hs.20000    three prime histone mRNA exonuclease 1    THEX1
      ---    5622 // intracellular // inferred from electronic
annotation  287 // magnesium ion binding // inferred from electronic
annotation /// 3677 // DNA binding // inferred from electronic
annotation /// 3723 // RNA binding // inferred from electronic
annotation /// 8408 // 3'-5' exonuclease activity // inferred from
direct assay /// 16787 // hydrolase activity // inferred from
electronic annotation /// 4518 // nuclease activity // inferred from
electronic annotation /// 4527 // exonuclease activity // inferred from
electronic annotation /// 46872 // metal ion binding // inferred from
electronic annotation    ---    90459
217540_at    Hs.598134    Transcribed locus ---    ---    ---    ---    ---
      ---
221463_at    Hs.247838    chemokine (C-C motif) ligand 24      CCL24 6935
// chemotaxis // traceable author statement /// 6954 // inflammatory
response // traceable author statement /// 7165 // signal transduction
// traceable author statement /// 7267 // cell-cell signaling //
traceable author statement /// 50896 // response to stimulus //
inferred from electronic annotation /// 6935 // chemotaxis // inferred
from electronic annotation /// 6954 // inflammatory response //
inferred from electronic annotation /// 6955 // immune response //
inferred from electronic annotation /// 6955 // immune response //
traceable author statement    5615 // extracellular space // inferred
from electronic annotation /// 5576 // extracellular region // inferred
from electronic annotation    8009 // chemokine activity // traceable
author statement /// 5125 // cytokine activity // inferred from
electronic annotation /// 8009 // chemokine activity // inferred from
electronic annotation    ---    6369
220014_at    Hs.157461    proline rich 16    PRR16 ---    ---    ---    ---
      51334
225778_at    Hs.648783    fucosyltransferase 1 (galactoside 2-alpha-L-
fucosyltransferase, H blood group)  FUT1  5975 // carbohydrate
metabolism // traceable author statement /// 6486 // protein amino acid
glycosylation // traceable author statement /// 42355 // L-fucose
catabolism // non-traceable author statement /// 6396 // RNA processing
// traceable author statement /// 6445 // regulation of translation //
traceable author statement    5624 // membrane fraction // traceable
author statement /// 5795 // Golgi stack // inferred from electronic
annotation /// 5887 // integral to plasma membrane // traceable author
statement /// 16020 // membrane // inferred from electronic annotation
/// 5634 // nucleus // inferred from electronic annotation  8107 //
galactoside 2-alpha-L-fucosyltransferase activity // traceable author
statement /// 8417 // fucosyltransferase activity // traceable author
statement /// 16757 // transferase activity, transferring glycosyl
groups // inferred from electronic annotation /// 166 // nucleotide
binding // inferred from electronic annotation /// 3676 // nucleic acid
binding // inferred from electronic annotation /// 3723 // RNA binding
// inferred from electronic annotation /// 3723 // RNA binding //
traceable author statement    Blood group glycolipid biosynthesis -
lactoseries // KEGG /// Blood group glycolipid biosynthesis - // KEGG
/// Globoside metabolism // KEGG /// Glycan structures - biosynthesis 2
// KEGG     2523
231852_at    Hs.20000    Three prime histone mRNA exonuclease 1    THEX1
      ---    5622 // intracellular // inferred from electronic
annotation  287 // magnesium ion binding // inferred from electronic
```

Figure 169

annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 8408 // 3'-5' exonuclease activity // inferred from direct assay /// 16787 // hydrolase activity // inferred from electronic annotation /// 4518 // nuclease activity // inferred from electronic annotation /// 4527 // exonuclease activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 90459

238439_at Hs.217484 ankyrin repeat domain 22 ANKRD22 --- --- --- --- 118932

229810_at Hs.391527 Transcribed locus --- --- --- --- ---

225646_at Hs.128065 cathepsin C CTSC 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 6508 // proteolysis // not recorded 5764 // lysosome // traceable author statement /// 5764 // lysosome // inferred from electronic annotation 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4214 // dipeptidyl-peptidase I activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1075

243011_at Hs.130195 family with sequence similarity 55, member C FAM55C --- --- --- --- 91775

211003_x_at Hs.517033 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) TGM2 7186 // G-protein coupled receptor protein signaling pathway // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred from sequence or structural similarity /// 45785 // positive regulation of cell adhesion // inferred from sequence or structural similarity /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from mutant phenotype /// 18153 // isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine // inferred from direct assay /// 18149 // peptide cross-linking // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 12501 // programmed cell death // traceable author statement /// 19933 // cAMP-mediated signaling // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // non-traceable author statement 5578 // extracellular matrix (sensu Metazoa) // inferred from sequence or structural similarity /// 5829 // cytosol // inferred from sequence or structural similarity /// 16020 // membrane // inferred from sequence or structural similarity /// 5622 // intracellular // non-traceable author statement 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from sequence or structural similarity /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5525 // GTP binding // inferred from sequence or structural similarity /// 8415 // acyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // traceable author statement /// 3924 // GTPase activity // traceable author statement /// 5524 // ATP binding // traceable author statement /// 5525 // GTP binding //

Figure 170

```
traceable author statement    Complement and coagulation cascades //
KEGG /// Huntington's disease // KEGG     7052
228108_at   Hs.592572   CDNA clone IMAGE:5263177      ---   ---   ---
      ---   ---   ---
223304_at   Hs.446021   solute carrier family 37 (glycerol-3-phosphate
transporter), member 3  SLC37A3     6810 // transport // inferred from
electronic annotation   16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from
electronic annotation   5215 // transporter activity // inferred from
electronic annotation   ---   84255
228565_at   Hs.547779   mixed lineage kinase 4  KIAA1804    7257 //
activation of JNK activity // inferred from sequence or structural
similarity /// 46777 // protein amino acid autophosphorylation //
inferred from sequence or structural similarity /// 6468 // protein
amino acid phosphorylation // inferred from sequence or structural
similarity /// 6468 // protein amino acid phosphorylation // inferred
from electronic annotation    ---   166 // nucleotide binding //
inferred from electronic annotation /// 4674 // protein
serine/threonine kinase activity // inferred from sequence or
structural similarity /// 4713 // protein-tyrosine kinase activity //
inferred from electronic annotation /// 5524 // ATP binding // inferred
from electronic annotation /// 16740 // transferase activity //
inferred from electronic annotation /// 42803 // protein
homodimerization activity // inferred from sequence or structural
similarity /// 4672 // protein kinase activity // inferred from
electronic annotation /// 4674 // protein serine/threonine kinase
activity // inferred from electronic annotation /// 16301 // kinase
activity // inferred from electronic annotation ---   84451
219497_s_at Hs.370549   B-cell CLL/lymphoma 11A (zinc finger protein)
      BCL11A      6350 // transcription // inferred from electronic
annotation /// 6355 // regulation of transcription, DNA-dependent //
inferred from electronic annotation /// 30097 // hemopoiesis // non-
traceable author statement    5634 // nucleus // inferred from
electronic annotation /// 5634 // nucleus // non-traceable author
statement /// 5737 // cytoplasm // non-traceable author statement 3676
// nucleic acid binding // inferred from electronic annotation /// 8270
// zinc ion binding // inferred from electronic annotation /// 46872 //
metal ion binding // inferred from electronic annotation    ---   53335
202948_at   Hs.557403   interleukin 1 receptor, type I      IL1R1 6954
// inflammatory response // not recorded /// 7166 // cell surface
receptor linked signal transduction // traceable author statement ///
6955 // immune response // traceable author statement 5887 // integral
to plasma membrane // traceable author statement /// 16020 // membrane
// inferred from electronic annotation /// 16021 // integral to
membrane // inferred from electronic annotation 4888 // transmembrane
receptor activity // traceable author statement /// 4909 //
interleukin-1, Type I, activating receptor activity // traceable author
statement /// 5515 // protein binding // inferred from physical
interaction /// 4872 // receptor activity // inferred from electronic
annotation /// 4888 // transmembrane receptor activity // inferred from
electronic annotation /// 4908 // interleukin-1 receptor activity //
inferred from electronic annotation /// 4909 // interleukin-1, Type I,
activating receptor activity // inferred from electronic annotation ///
4871 // signal transducer activity // traceable author statement ///
4908 // interleukin-1 receptor activity // traceable author statement
      Hypertrophy_model // GenMAPP  3554
```

Figure 171

219886_at Hs.444135 leucine-rich repeats and IQ motif containing 2 LRRIQ2 --- --- --- --- 79598
225567_at Hs.530791 MRNA; cDNA DKFZp762E1314 (from clone DKFZp762E1314) --- --- --- --- --- 388114
212658_at Hs.79299 lipoma HMGIC fusion partner-like 2 LHFPL2 --- --- --- --- 10184
203463_s_at Hs.515176 epsin 2 EPN2 6897 // endocytosis // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation --- 8289 // lipid binding // inferred from electronic annotation --- 22905
219525_at Hs.232054 hypothetical protein FLJ10847 FLJ10847 6855 // multidrug transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 15238 // drug transporter activity // inferred from electronic annotation /// 15297 // antiporter activity // inferred from electronic annotation --- 55244
226844_at Hs.651275 MOB1, Mps One Binder kinase activator-like 2B (yeast) MOBKL2B --- --- 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 79817
205471_s_at Hs.129452 dachshund homolog 1 (Drosophila) DACH1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7456 // eye development (sensu Endopterygota) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction --- 1602
202381_at Hs.591852 ADAM metallopeptidase domain 9 (meltrin gamma) ADAM9 6508 // proteolysis // inferred from electronic annotation /// 7243 // protein kinase cascade // traceable author statement 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement 4222 // metalloendopeptidase activity // inferred from electronic annotation /// 5178 // integrin binding // traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 8270 // zinc ion binding // inferred from electronic annotation /// 17124 // SH3 domain binding // inferred from physical interaction /// 19901 // protein kinase binding // traceable author statement /// 46872 // metal ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // traceable author statement /// 8237 // metallopeptidase activity // non-traceable author statement --- 8754
231431_s_at Hs.530791 MRNA; cDNA DKFZp762E1314 (from clone DKFZp762E1314) --- --- --- --- --- 388114 /// 649557
201482_at Hs.518374 quiescin Q6 QSCN6 74 // regulation of progression through cell cycle // traceable author statement /// 1558 // regulation of cell growth // non-traceable author statement /// 6118 // electron transport // inferred from electronic annotation /// 8285 // negative regulation of cell proliferation // traceable author statement --- --- --- 5768

Figure 172

222719_s_at Hs.570855 platelet derived growth factor C PDGFC 7417 // central nervous system development // traceable author statement 16020 // membrane // inferred from electronic annotation /// 5576 // extracellular region // non-traceable author statement 8083 // growth factor activity // inferred from electronic annotation /// 8083 // growth factor activity // traceable author statement --- 56034
210347_s_at Hs.370549 B-cell CLL/lymphoma 11A (zinc finger protein) BCL11A 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 30097 // hemopoiesis // non-traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 53335
235885_at Hs.591281 purinergic receptor P2Y, G-protein coupled, 12 P2RY12 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7599 // hemostasis // non-traceable author statement 16020 // membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 45028 // purinergic nucleotide receptor activity, G-protein coupled // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation GPCRDB_Class_A_Rhodopsin-like // GenMAPP 64805
212797_at Hs.485195 sortilin 1 SORT1 1503 // ossification // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6886 // intracellular protein transport // inferred from electronic annotation /// 6897 // endocytosis // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5764 // lysosome // inferred from electronic annotation /// 5768 // endosome // non-traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 8565 // protein transporter activity // inferred from electronic annotation /// 16492 // neurotensin receptor activity, G-protein coupled // non-traceable author statement --- 6272
219498_s_at Hs.370549 B-cell CLL/lymphoma 11A (zinc finger protein) BCL11A 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 30097 // hemopoiesis // non-traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement 3676 // nucleic acid binding // inferred from electronic annotation /// 8270

Figure 173

// zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 53335
222071_s_at Hs.127648 solute carrier organic anion transporter family, member 4C1 SLCO4C1 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 353189
211668_s_at Hs.77274 plasminogen activator, urokinase /// plasminogen activator, urokinase PLAU 6508 // proteolysis // inferred from electronic annotation /// 6508 // proteolysis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7596 // blood coagulation // inferred from electronic annotation /// 42730 // fibrinolysis // inferred from electronic annotation /// 7596 // blood coagulation // not recorded 5615 // extracellular space // not recorded 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8243 // plasminogen activator activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Wnt_signaling // GenMAPP /// Blood_Clotting_Cascade // GenMAPP /// Wnt_signaling // GenMAPP /// Blood_Clotting_Cascade // GenMAPP /// Complement and coagulation cascades // KEGG 5328
216243_s_at Hs.81134 interleukin 1 receptor antagonist IL1RN 6954 // inflammatory response // not recorded /// 6955 // immune response // inferred from electronic annotation /// 6955 // immune response // non-traceable author statement 5615 // extracellular space // traceable author statement /// 5622 // intracellular // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation /// 5622 // intracellular // not recorded 5152 // interleukin-1 receptor antagonist activity // traceable author statement /// 5149 // interleukin-1 receptor binding // inferred from electronic annotation /// 5152 // interleukin-1 receptor antagonist activity // inferred from electronic annotation --- 3557
209545_s_at Hs.103755 receptor-interacting serine-threonine kinase 2 RIPK2 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6954 // inflammatory response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 42981 // regulation of apoptosis // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from expression pattern /// 6915 // apoptosis // inferred from electronic annotation /// 6915 // apoptosis // traceable author statement 5622 // intracellular // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // traceable author statement /// 4871 // signal transducer activity // inferred from expression pattern /// 5515 // protein binding // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 30274 // LIM domain binding // inferred from physical interaction /// 50700 // CARD domain binding // inferred from physical interaction /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from

Figure 174

electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4871 // signal transducer activity // traceable author statement mTOR signaling pathway // KEGG /// Wnt signaling pathway // KEGG /// Dorso-ventral axis formation // KEGG /// Hedgehog signaling pathway // KEGG /// TGF-beta signaling pathway // KEGG /// Axon guidance // KEGG /// VEGF signaling pathway // KEGG /// Focal adhesion // KEGG /// Adherens junction // KEGG /// Tight junction // KEGG /// Gap junction // KEGG /// B cell receptor signaling pathway // KEGG /// Fc epsilon RI signaling pathway // KEGG /// Long-term potentiation // KEGG /// Long-term depression // KEGG /// Regulation of actin cytoskeleton // KEGG /// Insulin signaling pathway // KEGG /// Alzheimer's disease // KEGG 8767
212659_s_at Hs.81134 interleukin 1 receptor antagonist IL1RN 6954 // inflammatory response // not recorded /// 6955 // immune response // inferred from electronic annotation /// 6955 // immune response // non-traceable author statement 5615 // extracellular space // traceable author statement /// 5622 // intracellular // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation /// 5622 // intracellular // not recorded 5152 // interleukin-1 receptor antagonist activity // traceable author statement /// 5149 // interleukin-1 receptor binding // inferred from electronic annotation /// 5152 // interleukin-1 receptor antagonist activity // inferred from electronic annotation --- 3557
239196_at Hs.217484 ankyrin repeat domain 22 ANKRD22 --- --- --- 118932
242230_at Hs.434961 ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation --- 6310
227475_at Hs.591352 forkhead box Q1 FOXQ1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 94234
1559078_at Hs.370549 B-cell CLL/lymphoma 11A (zinc finger protein) BCL11A 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 30097 // hemopoiesis // non-traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // non-traceable author statement /// 5737 // cytoplasm // non-traceable author statement 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 53335
205220_at Hs.458425 G protein-coupled receptor 109B /// G protein-coupled receptor 109B GPR109B 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // traceable author statement /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity

Figure 175

```
// inferred from electronic annotation /// 4872 // receptor activity //
inferred from electronic annotation /// 45028 // purinergic nucleotide
receptor activity, G-protein coupled // inferred from electronic
annotation /// 4871 // signal transducer activity // inferred from
electronic annotation /// 4930 // G-protein coupled receptor activity
// inferred from electronic annotation /// 4930 // G-protein coupled
receptor activity // traceable author statement
      GPCRDB_Class_A_Rhodopsin-like2 // GenMAPP 8843
235236_at   Hs.586174   Dedicator of cytokinesis 2    DOCK2 30036 //
actin cytoskeleton organization and biogenesis // traceable author
statement /// 48247 // lymphocyte chemotaxis // inferred from sequence
or structural similarity      5856 // cytoskeleton // inferred from
electronic annotation /// 16020 // membrane // inferred from electronic
annotation  5515 // protein binding // inferred from physical
interaction /// 5525 // GTP binding // inferred from electronic
annotation /// 30676 // Rac guanyl-nucleotide exchange factor activity
// inferred from direct assay /// 42608 // T cell receptor binding //
inferred from direct assay /// 51020 // GTPase binding // inferred from
electronic annotation /// 5085 // guanyl-nucleotide exchange factor
activity // inferred from electronic annotation /// 5488 // binding //
inferred from electronic annotation ---   1794
224009_x_at Hs.179608   dehydrogenase/reductase (SDR family) member 9
      DHRS9 8152 // metabolism // inferred from electronic annotation
/// 8209 // androgen metabolism // inferred from direct assay /// 30855
// epithelial cell differentiation // non-traceable author statement
/// 42448 // progesterone metabolism // inferred from direct assay ///
42572 // retinol metabolism // non-traceable author statement /// 42904
// 9-cis-retinoic acid biosynthesis // inferred from direct assay ///
8209 // androgen metabolism // inferred from sequence or structural
similarity /// 30855 // epithelial cell differentiation // inferred
from sequence or structural similarity /// 42572 // retinol metabolism
// inferred from sequence or structural similarity /// 42904 // 9-cis-
retinoic acid biosynthesis // inferred from sequence or structural
similarity  5792 // microsome // inferred from direct assay /// 16020
// membrane // inferred from electronic annotation /// 30176 //
integral to endoplasmic reticulum membrane // inferred from direct
assay /// 5792 // microsome // inferred from sequence or structural
similarity /// 30176 // integral to endoplasmic reticulum membrane //
inferred from sequence or structural similarity 4022 // alcohol
dehydrogenase activity // inferred from direct assay /// 4745 //
retinol dehydrogenase activity // inferred from direct assay /// 16491
// oxidoreductase activity // inferred from electronic annotation ///
16854 // racemase and epimerase activity // non-traceable author
statement /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase
(NAD+) activity // inferred from direct assay /// 4022 // alcohol
dehydrogenase activity // inferred from sequence or structural
similarity /// 4745 // retinol dehydrogenase activity // inferred from
sequence or structural similarity /// 47035 // 3-alpha(17-beta)-
hydroxysteroid dehydrogenase (NAD+) activity // inferred from sequence
or structural similarity      ---   10170
227792_at   Hs.530899   Hypothetical protein LOC162073      LOC162073
      ---   ---   ---   ---   162073
227140_at   Hs.28792    CDNA FLJ11041 fis, clone PLACE1004405     ---
      ---   ---   ---   ---   ---
234657_at   Hs.545095   CDNA: FLJ23521 fis, clone LNG04928  ---   ---
      ---   ---   ---   ---
```

Figure 176

206760_s_at Hs.465778 Fc fragment of IgE, low affinity II, receptor for (CD23) FCER2 --- 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5057 // receptor signaling protein activity // not recorded /// 5178 // integrin binding // traceable author statement /// 5529 // sugar binding // inferred from electronic annotation /// 19863 // IgE binding // inferred from electronic annotation --- 2208
205479_s_at Hs.77274 plasminogen activator, urokinase PLAU 6508 // proteolysis // inferred from electronic annotation /// 6508 // proteolysis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7596 // blood coagulation // inferred from electronic annotation /// 42730 // fibrinolysis // inferred from electronic annotation /// 7596 // blood coagulation // not recorded 5615 // extracellular space // not recorded 4252 // serine-type endopeptidase activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8243 // plasminogen activator activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Wnt_signaling // GenMAPP /// Blood_Clotting_Cascade // GenMAPP /// Wnt_signaling // GenMAPP /// Blood_Clotting_Cascade // GenMAPP /// Complement and coagulation cascades // KEGG 5328
201554_x_at Hs.477892 glycogenin 1 GYG1 5978 // glycogen biosynthesis // inferred from electronic annotation /// 16051 // carbohydrate biosynthesis // inferred from electronic annotation --- 8466 // glycogenin glucosyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16758 // transferase activity, transferring hexosyl groups // inferred from electronic annotation /// 8466 // glycogenin glucosyltransferase activity // not recorded Glycogen_Metabolism // GenMAPP /// Glycogen_Metabolism // GenMAPP 2992
228785_at Hs.59757 Zinc finger protein 281 ZNF281 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5665 // DNA-directed RNA polymerase II, core complex // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3704 // specific RNA polymerase II transcription factor activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 23528
226175_at Hs.31704 tetratricopeptide repeat domain 9C TTC9C --- --- 5488 // binding // inferred from electronic annotation --- 283237
1555250_a_at Hs.131683 cytoplasmic polyadenylation element binding protein 3 CPEB3 --- --- 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 22849

Figure 177

231412_at Hs.651324 hypothetical gene supported by BX538329 DKFZp686L14188 --- --- --- --- 441366
211275_s_at Hs.477892 glycogenin 1 GYG1 5978 // glycogen biosynthesis // inferred from electronic annotation /// 16051 // carbohydrate biosynthesis // inferred from electronic annotation --- 8466 // glycogenin glucosyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16758 // transferase activity, transferring hexosyl groups // inferred from electronic annotation /// 8466 // glycogenin glucosyltransferase activity // not recorded Glycogen_Metabolism // GenMAPP /// Glycogen_Metabolism // GenMAPP 2992
201718_s_at Hs.486470 erythrocyte membrane protein band 4.1-like 2 EPB41L2 30866 // cortical actin cytoskeleton organization and biogenesis // inferred from electronic annotation 5737 // cytoplasm // inferred from electronic annotation /// 5856 // cytoskeleton // inferred from electronic annotation /// 5886 // plasma membrane // traceable author statement /// 8091 // spectrin // traceable author statement /// 16020 // membrane // inferred from electronic annotation 3779 // actin binding // inferred from electronic annotation /// 5198 // structural molecule activity // inferred from electronic annotation /// 5200 // structural constituent of cytoskeleton // not recorded /// 5488 // binding // inferred from electronic annotation /// 8092 // cytoskeletal protein binding // inferred from electronic annotation --- 2037
1569666_s_at Hs.446021 Solute carrier family 37 (glycerol-3-phosphate transporter), member 3 SLC37A3 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5215 // transporter activity // inferred from electronic annotation --- 84255
212657_s_at Hs.81134 interleukin 1 receptor antagonist IL1RN 6954 // inflammatory response // not recorded /// 6955 // immune response // inferred from electronic annotation /// 6955 // immune response // non-traceable author statement 5615 // extracellular space // traceable author statement /// 5622 // intracellular // non-traceable author statement /// 5576 // extracellular region // inferred from electronic annotation /// 5622 // intracellular // not recorded 5152 // interleukin-1 receptor antagonist activity // traceable author statement /// 5149 // interleukin-1 receptor binding // inferred from electronic annotation /// 5152 // interleukin-1 receptor antagonist activity // inferred from electronic annotation --- 3557
230354_at Hs.135108 Transcribed locus --- --- --- --- --- ---
229568_at Hs.651275 MOB1, Mps One Binder kinase activator-like 2B (yeast) MOBKL2B --- --- 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 79817
209298_s_at Hs.160324 intersectin 1 (SH3 domain protein) ITSN1 35023 // regulation of Rho protein signal transduction // inferred from electronic annotation /// 48488 // synaptic vesicle endocytosis // traceable author statement /// 6897 // endocytosis // inferred from electronic annotation 5622 // intracellular // inferred from electronic annotation 5089 // Rho guanyl-nucleotide exchange factor activity // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5509 // calcium ion binding

Figure 178

// inferred from electronic annotation /// 5085 // guanyl-nucleotide exchange factor activity // non-traceable author statement --- 6453
1559065_a_at Hs.220649 C-type lectin superfamily 4, member G CLEC4G --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5529 // sugar binding // inferred from electronic annotation --- 339390
221169_s_at Hs.287388 histamine receptor H4 HRH4 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 1584 // rhodopsin-like receptor activity // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 4969 // histamine receptor activity // non-traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 4930 // G-protein coupled receptor activity // inferred from electronic annotation GPCRDB_Other // GenMAPP /// GPCRDB_Other // GenMAPP 59340
224836_at Hs.516994 tumor protein p53 inducible nuclear protein 2 TP53INP2 --- 5634 // nucleus // inferred from electronic annotation --- --- 58476
244570_at --- --- --- --- --- --- --- ---
223952_x_at Hs.179608 dehydrogenase/reductase (SDR family) member 9 DHRS9 8152 // metabolism // inferred from electronic annotation /// 8209 // androgen metabolism // inferred from direct assay /// 30855 // epithelial cell differentiation // non-traceable author statement /// 42448 // progesterone metabolism // inferred from direct assay /// 42572 // retinol metabolism // non-traceable author statement /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from direct assay /// 8209 // androgen metabolism // inferred from sequence or structural similarity /// 30855 // epithelial cell differentiation // inferred from sequence or structural similarity /// 42572 // retinol metabolism // inferred from sequence or structural similarity /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from sequence or structural similarity 5792 // microsome // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 30176 // integral to endoplasmic reticulum membrane // inferred from direct assay /// 5792 // microsome // inferred from sequence or structural similarity /// 30176 // integral to endoplasmic reticulum membrane // inferred from sequence or structural similarity 4022 // alcohol dehydrogenase activity // inferred from direct assay /// 4745 // retinol dehydrogenase activity // inferred from direct assay /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 16854 // racemase and epimerase activity // non-traceable author statement /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from direct assay /// 4022 // alcohol dehydrogenase activity // inferred from sequence or structural similarity /// 4745 // retinol dehydrogenase activity // inferred from sequence or structural similarity /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from sequence or structural similarity --- 10170
211573_x_at Hs.517033 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) TGM2 7186 // G-protein coupled receptor protein signaling pathway // inferred from sequence or structural similarity /// 18149 // peptide cross-linking // inferred

Figure 179

from sequence or structural similarity /// 45785 // positive regulation of cell adhesion // inferred from sequence or structural similarity /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from mutant phenotype /// 18153 // isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine // inferred from direct assay /// 18149 // peptide cross-linking // inferred from electronic annotation /// 6916 // anti-apoptosis // traceable author statement /// 12501 // programmed cell death // traceable author statement /// 19933 // cAMP-mediated signaling // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // non-traceable author statement 5578 // extracellular matrix (sensu Metazoa) // inferred from sequence or structural similarity /// 5829 // cytosol // inferred from sequence or structural similarity /// 16020 // membrane // inferred from sequence or structural similarity /// 5622 // intracellular // non-traceable author statement 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from sequence or structural similarity /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5525 // GTP binding // inferred from sequence or structural similarity /// 8415 // acyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // traceable author statement /// 3924 // GTPase activity // traceable author statement /// 5524 // ATP binding // traceable author statement /// 5525 // GTP binding // traceable author statement Complement and coagulation cascades // KEGG /// Huntington's disease // KEGG 7052
204067_at Hs.558403 sulfite oxidase SUOX 6118 // electron transport // inferred from electronic annotation /// 9087 // methionine catabolism // not recorded 5739 // mitochondrion // inferred from electronic annotation 5506 // iron ion binding // inferred from electronic annotation /// 8482 // sulfite oxidase activity // traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 30151 // molybdenum ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 8482 // sulfite oxidase activity // inferred from electronic annotation Sulfur metabolism // KEGG 6821
243179_at Hs.408455 CDNA FLJ33993 fis, clone DFNES2007757 --- --- --- --- ---
205228_at Hs.645521 RNA binding motif, single stranded interacting protein 2 RBMS2 6396 // RNA processing // traceable author statement /// 6445 // regulation of translation // traceable author statement 5634 // nucleus // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation --- 5939
206759_at Hs.465778 Fc fragment of IgE, low affinity II, receptor for (CD23) FCER2 --- 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5057 // receptor signaling protein activity // not recorded /// 5178 // integrin binding // traceable

Figure 180

author statement /// 5529 // sugar binding // inferred from electronic annotation /// 19863 // IgE binding // inferred from electronic annotation --- 2208
215968_at Hs.130195 Family with sequence similarity 55, member C FAM55C --- --- --- --- 91775
210612_s_at Hs.434494 synaptojanin 2 SYNJ2 --- --- 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 4439 // phosphoinositide 5-phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 4437 // inositol or phosphatidylinositol phosphatase activity // inferred from electronic annotation --- 8871
206756_at Hs.129955 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7 CHST7 5976 // polysaccharide metabolism // traceable author statement /// 6044 // N-acetylglucosamine metabolism // inferred from direct assay /// 6790 // sulfur metabolism // inferred from direct assay /// 30206 // chondroitin sulfate biosynthesis // inferred from direct assay /// 5975 // carbohydrate metabolism // inferred from electronic annotation 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // traceable author statement /// 31228 // intrinsic to Golgi membrane // inferred from sequence or structural similarity /// 16021 // integral to membrane // inferred from electronic annotation 1517 // N-acetylglucosamine 6-O-sulfotransferase activity // inferred from direct assay /// 8459 // chondroitin 6-sulfotransferase activity // inferred from direct assay /// 16740 // transferase activity // inferred from electronic annotation /// 8146 // sulfotransferase activity // inferred from electronic annotation --- 56548
212173_at Hs.470907 adenylate kinase 2 AK2 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // inferred from electronic annotation 5739 // mitochondrion // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4017 // adenylate kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4017 // adenylate kinase activity // inferred from electronic annotation /// 16776 // phosphotransferase activity, phosphate group as acceptor // inferred from electronic annotation /// 19201 // nucleotide kinase activity // inferred from electronic annotation Purine metabolism // KEGG 204
222343_at Hs.469658 BCL2-like 11 (apoptosis facilitator) BCL2L11 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 43065 // positive regulation of apoptosis // inferred from electronic annotation 5624 // membrane fraction // traceable author statement /// 16020 // membrane // inferred from electronic annotation 5515 // protein binding // inferred from physical interaction Apoptosis // GenMAPP /// Apoptosis // GenMAPP 10018
235558_at Hs.648783 Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group) FUT1 5975 // carbohydrate metabolism // traceable author statement /// 6486 // protein amino acid glycosylation // traceable author statement /// 42355 // L-fucose catabolism // non-traceable author statement /// 6396 // RNA processing

Figure 181

// traceable author statement /// 6445 // regulation of translation // traceable author statement 5624 // membrane fraction // traceable author statement /// 5795 // Golgi stack // inferred from electronic annotation /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 5634 // nucleus // inferred from electronic annotation 8107 // galactoside 2-alpha-L-fucosyltransferase activity // traceable author statement /// 8417 // fucosyltransferase activity // traceable author statement /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement Blood group glycolipid biosynthesis - lactoseries // KEGG /// Blood group glycolipid biosynthesis - // KEGG /// Globoside metabolism // KEGG /// Glycan structures - biosynthesis 2 // KEGG 2523

231234_at Hs.128065 cathepsin C CTSC 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 6508 // proteolysis // not recorded 5764 // lysosome // traceable author statement /// 5764 // lysosome // inferred from electronic annotation 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4214 // dipeptidyl-peptidase I activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1075

206336_at Hs.164021 chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) CXCL6 6278 // RNA-dependent DNA replication // non-traceable author statement /// 6935 // chemotaxis // traceable author statement /// 6954 // inflammatory response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 50896 // response to stimulus // inferred from electronic annotation /// 6935 // chemotaxis // inferred from electronic annotation /// 6955 // immune response // inferred from electronic annotation 5615 // extracellular space // inferred from electronic annotation /// 5576 // extracellular region // inferred from electronic annotation 3964 // RNA-directed DNA polymerase activity // non-traceable author statement /// 8009 // chemokine activity // traceable author statement /// 8201 // heparin binding // inferred from electronic annotation /// 5125 // cytokine activity // inferred from electronic annotation /// 8009 // chemokine activity // inferred from electronic annotation --- 6372

225647_s_at Hs.128065 cathepsin C CTSC 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 6508 // proteolysis // not recorded 5764 // lysosome // traceable author statement /// 5764 // lysosome // inferred from electronic annotation 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4214 // dipeptidyl-peptidase I activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1075

216950_s_at Hs.77424 Fc fragment of IgG, high affinity Ia, receptor (CD64) FCGR1A 6911 // phagocytosis, engulfment // traceable

Figure 182

author statement /// 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6955 // immune response // non-traceable author statement 5887 // integral to plasma membrane // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5886 // plasma membrane // non-traceable author statement 4872 // receptor activity // inferred from electronic annotation /// 5057 // receptor signaling protein activity // traceable author statement /// 19864 // IgG binding // inferred from electronic annotation /// 19763 // immunoglobulin receptor activity // non-traceable author statement --- 2209
228486_at Hs.573495 solute carrier family 44, member 1 SLC44A1 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 23446
205773_at Hs.131683 cytoplasmic polyadenylation element binding protein 3 CPEB3 --- --- 166 // nucleotide binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 22849
235898_at Hs.446292 Transcribed locus, strongly similar to XP_515434.1 hypothetical protein XP_515434 [Pan troglodytes] --- --- --- --- ---
227954_at Hs.530899 hypothetical protein LOC162073 LOC162073 --- --- --- --- 162073
214511_x_at Hs.534956 Fc fragment of IgG, high affinity Ib, receptor (CD64) FCGR1B 6911 // phagocytosis, engulfment // traceable author statement /// 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6955 // immune response // non-traceable author statement 5887 // integral to plasma membrane // not recorded /// 16020 // membrane // inferred from electronic annotation /// 5886 // plasma membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 5057 // receptor signaling protein activity // traceable author statement /// 19864 // IgG binding // inferred from electronic annotation /// 19763 // immunoglobulin receptor activity // non-traceable author statement --- 2209 /// 440607 /// 652758
205258_at Hs.1735 inhibin, beta B (activin AB beta polypeptide) INHBB 1541 // ovarian follicle development // non-traceable author statement /// 6952 // defense response // traceable author statement /// 9605 // response to external stimulus // inferred from direct assay /// 30154 // cell differentiation // non-traceable author statement /// 40007 // growth // inferred from electronic annotation /// 46881 // positive regulation of follicle-stimulating hormone secretion // inferred from physical interaction /// 46882 // negative regulation of follicle-stimulating hormone secretion // inferred from physical interaction /// 48178 // negative regulation of hepatocyte growth factor biosynthesis // inferred from direct assay 5576 // extracellular region // traceable author statement /// 5576 // extracellular region // inferred from electronic annotation 5125 // cytokine activity // traceable author statement /// 5179 // hormone activity // traceable author statement /// 8083 // growth factor activity // inferred from electronic annotation /// 42803 // protein homodimerization activity // inferred from physical interaction /// 46789 // host cell surface receptor binding // traceable author

Figure 183

statement /// 5515 // protein binding // inferred from physical interaction /// 5179 // hormone activity // inferred from electronic annotation /// 5102 // receptor binding // non-traceable author statement --- 3625
1568593_a_at Hs.380350 nudix (nucleoside diphosphate linked moiety X)-type motif 16 pseudogene NUDT16P --- --- --- --- 152195
206513_at Hs.281898 absent in melanoma 2 AIM2 6955 // immune response // traceable author statement /// 6955 // immune response // inferred from electronic annotation --- --- --- 9447
218854_at --- squamous cell carcinoma antigen recognized by T cells 2 SART2 --- 5783 // endoplasmic reticulum // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 29940
206576_s_at Hs.512682 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) CEACAM1 1525 // angiogenesis // non-traceable author statement /// 7156 // homophilic cell adhesion // non-traceable author statement /// 7229 // integrin-mediated signaling pathway // non-traceable author statement /// 7565 // pregnancy // traceable author statement /// 16477 // cell migration // non-traceable author statement 5624 // membrane fraction // traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 634
239108_at Hs.298851 Male sterility domain containing 1 MLSTD1 --- --- --- --- 55711
226706_at --- hypothetical protein FLJ23867 FLJ23867 --- --- --- --- 200058
226456_at Hs.347524 chromosome 16 open reading frame 75 C16orf75 --- --- 3676 // nucleic acid binding // inferred from electronic annotation --- 116028
223241_at Hs.584900 sorting nexin 8 SNX8 7242 // intracellular signaling cascade // inferred from electronic annotation /// 15031 // protein transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation --- 5515 // protein binding // inferred from electronic annotation /// 35091 // phosphoinositide binding // inferred from electronic annotation --- 29886
243969_at Hs.510281 solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 SLC24A4 6811 // ion transport // inferred from electronic annotation /// 6813 // potassium ion transport // inferred from electronic annotation /// 6814 // sodium ion transport // inferred from electronic annotation /// 6816 // calcium ion transport // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 5509 // calcium ion binding // inferred from electronic annotation /// 15293 // symporter activity // inferred from electronic annotation /// 15297 // antiporter activity // inferred from electronic annotation /// 30955 // potassium ion binding // inferred from electronic annotation /// 31402 // sodium ion binding // inferred from electronic annotation --- 123041
218979_at Hs.284137 RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae) RMI1 --- --- 3676 // nucleic acid binding // inferred from electronic annotation --- 80010

Figure 184

235918_x_at --- --- --- --- --- --- --- ---
232232_s_at Hs.520319 solute carrier family 22 (organic cation transporter), member 16 SLC22A16 7338 // fertilization (sensu Metazoa) // inferred from mutant phenotype /// 30317 // sperm motility // inferred from mutant phenotype /// 7286 // spermatid development // inferred from sequence or structural similarity /// 15695 // organic cation transport // inferred from sequence or structural similarity /// 15879 // carnitine transport // inferred from sequence or structural similarity /// 15695 // organic cation transport // inferred from direct assay /// 15879 // carnitine transport // inferred from direct assay /// 46717 // acid secretion // inferred from direct assay /// 6810 // transport // inferred from electronic annotation /// 7286 // spermatid development // non-traceable author statement 16021 // integral to membrane // inferred from sequence or structural similarity /// 5886 // plasma membrane // inferred from direct assay /// 16021 // integral to membrane // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 15226 // carnitine transporter activity // inferred from sequence or structural similarity /// 15226 // carnitine transporter activity // inferred from direct assay /// 5215 // transporter activity // inferred from electronic annotation /// 15075 // ion transporter activity // non-traceable author statement --- 85413
219799_s_at Hs.179608 dehydrogenase/reductase (SDR family) member 9 DHRS9 8152 // metabolism // inferred from electronic annotation /// 8209 // androgen metabolism // inferred from direct assay /// 30855 // epithelial cell differentiation // non-traceable author statement /// 42448 // progesterone metabolism // inferred from direct assay /// 42572 // retinol metabolism // non-traceable author statement /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from direct assay /// 8209 // androgen metabolism // inferred from sequence or structural similarity /// 30855 // epithelial cell differentiation // inferred from sequence or structural similarity /// 42572 // retinol metabolism // inferred from sequence or structural similarity /// 42904 // 9-cis-retinoic acid biosynthesis // inferred from sequence or structural similarity 5792 // microsome // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation /// 30176 // integral to endoplasmic reticulum membrane // inferred from direct assay /// 5792 // microsome // inferred from sequence or structural similarity /// 30176 // integral to endoplasmic reticulum membrane // inferred from sequence or structural similarity 4022 // alcohol dehydrogenase activity // inferred from direct assay /// 4745 // retinol dehydrogenase activity // inferred from direct assay /// 16491 // oxidoreductase activity // inferred from electronic annotation /// 16854 // racemase and epimerase activity // non-traceable author statement /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from direct assay /// 4022 // alcohol dehydrogenase activity // inferred from sequence or structural similarity /// 4745 // retinol dehydrogenase activity // inferred from sequence or structural similarity /// 47035 // 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity // inferred from sequence or structural similarity --- 10170
227514_at Hs.648523 CDNA clone IMAGE:4402981 --- --- --- --- --- 162073
242388_x_at --- --- --- --- --- --- --- ---
1554835_a_at Hs.208267 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 B3GNT5 7417 // central nervous

Figure 185

system development // inferred from direct assay /// 6486 // protein amino acid glycosylation // inferred from electronic annotation /// 6486 // protein amino acid glycosylation // traceable author statement /// 9247 // glycolipid biosynthesis // traceable author statement 5622 // intracellular // inferred from direct assay /// 16020 // membrane // inferred from electronic annotation 8457 // beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,3-acetylglucosaminyltransferase activity // inferred from direct assay /// 8378 // galactosyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation --- 84002
231771_at Hs.511757 gap junction protein, beta 6 (connexin 30) GJB6 7154 // cell communication // inferred from electronic annotation /// 7605 // sensory perception of sound // traceable author statement /// 7605 // sensory perception of sound // inferred from electronic annotation 5922 // connexon complex // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation /// 5921 // gap junction // inferred from electronic annotation 15285 // connexon channel activity // inferred from electronic annotation Calcium_regulation_in_cardiac_cells // GenMAPP 10804
224863_at Hs.269782 Guanine nucleotide binding protein (G protein), q polypeptide GNAQ 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7596 // blood coagulation // traceable author statement 5737 // cytoplasm // traceable author statement /// 5834 // heterotrimeric G-protein complex // not recorded /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 2776
227239_at Hs.85603 family with sequence similarity 126, member A FAM126A --- --- 4871 // signal transducer activity // non-traceable author statement --- 84668
235889_at Hs.618649 Transcribed locus --- --- --- --- --- ---
220162_s_at Hs.647176 caspase recruitment domain family, member 9 CARD9 42981 // regulation of apoptosis // inferred from electronic annotation 5622 // intracellular // inferred from electronic annotation 5515 // protein binding // inferred from electronic annotation --- 64170
225622_at Hs.266175 phosphoprotein associated with glycosphingolipid microdomains 1 PAG1 6955 // immune response // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 55824
209297_at Hs.160324 intersectin 1 (SH3 domain protein) ITSN1 35023 // regulation of Rho protein signal transduction // inferred from

Figure 186

electronic annotation /// 48488 // synaptic vesicle endocytosis // traceable author statement /// 6897 // endocytosis // inferred from electronic annotation 5622 // intracellular // inferred from electronic annotation 5089 // Rho guanyl-nucleotide exchange factor activity // inferred from electronic annotation /// 5509 // calcium ion binding // non-traceable author statement /// 5515 // protein binding // inferred from physical interaction /// 5509 // calcium ion binding // inferred from electronic annotation /// 5085 // guanyl-nucleotide exchange factor activity // non-traceable author statement --- 6453
222619_at Hs.59757 zinc finger protein 281 ZNF281 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5665 // DNA-directed RNA polymerase II, core complex // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3704 // specific RNA polymerase II transcription factor activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 23528
216015_s_at Hs.159483 NLR family, pyrin domain containing 3 NLRP3 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // non-traceable author statement /// 6952 // defense response // traceable author statement /// 6954 // inflammatory response // inferred from mutant phenotype /// 7165 // signal transduction // non-traceable author statement /// 7605 // sensory perception of sound // inferred from electronic annotation /// 9595 // detection of biotic stimulus // traceable author statement /// 51259 // protein oligomerization // traceable author statement 5737 // cytoplasm // traceable author statement 42834 // peptidoglycan binding // traceable author statement --- 114548
1552542_s_at Hs.529984 T-cell activation GTPase activating protein TAGAP --- --- 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation --- 117289
223713_at Hs.154628 radial spokehead-like 2 RSHL2 --- --- --- --- 83861
209921_at Hs.390594 solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 SLC7A11 6461 // protein complex assembly // not recorded /// 6810 // transport // inferred from electronic annotation /// 6865 // amino acid transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 15327 // cystine:glutamate antiporter activity // traceable author statement /// 15359 // amino acid permease activity // inferred from electronic annotation /// 5279 // amino acid-polyamine transporter activity // inferred from electronic annotation /// 15171 // amino acid transporter activity // inferred from electronic annotation --- 23657
215573_at Hs.502302 Catalase CAT 6118 // electron transport // inferred from electronic annotation /// 6979 // response to oxidative stress // inferred from electronic annotation /// 42744 // hydrogen peroxide catabolism // inferred from electronic annotation 5777 // peroxisome // inferred from electronic annotation 4096 // catalase activity // traceable author statement /// 5506 // iron ion binding // inferred from electronic annotation /// 16491 // oxidoreductase

Figure 187

activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 4096 // catalase activity // inferred from electronic annotation /// 4601 // peroxidase activity // inferred from electronic annotation Tryptophan metabolism // KEGG /// Methane metabolism // KEGG /// Amyotrophic lateral sclerosis (ALS) // KEGG 847
224861_at Hs.269782 Guanine nucleotide binding protein (G protein), q polypeptide GNAQ 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7596 // blood coagulation // traceable author statement 5737 // cytoplasm // traceable author statement /// 5834 // heterotrimeric G-protein complex // not recorded /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 2776
220615_s_at Hs.298851 male sterility domain containing 1 MLSTD1 --- --- --- --- 55711
34187_at Hs.645521 RNA binding motif, single stranded interacting protein 2 RBMS2 6396 // RNA processing // traceable author statement /// 6445 // regulation of translation // traceable author statement 5634 // nucleus // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // traceable author statement /// 3676 // nucleic acid binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation --- 5939
222154_s_at Hs.120323 DNA polymerase-transactivated protein 6 DNAPTP6 --- --- --- --- 26010
204925_at Hs.187667 cystinosis, nephropathic CTNS 6520 // amino acid metabolism // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 15811 // L-cystine transport // traceable author statement 5765 // lysosomal membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 5764 // lysosome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // not recorded 15184 // L-cystine transporter activity // traceable author statement --- 1497
1569624_at Hs.382630 Homo sapiens, clone IMAGE:4248008, mRNA --- --- --- --- --- --- --- ---
207596_at --- --- --- --- --- --- --- ---
218880_at Hs.220971 FOS-like antigen 2 FOSL2 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 8219 // cell death // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity //

Figure 188

inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 2355
203627_at Hs.592020 Insulin-like growth factor 1 receptor IGF1R 74 // regulation of progression through cell cycle // traceable author statement /// 6916 // anti-apoptosis // traceable author statement /// 7165 // signal transduction // traceable author statement /// 8284 // positive regulation of cell proliferation // traceable author statement /// 8286 // insulin receptor signaling pathway // traceable author statement /// 46777 // protein amino acid autophosphorylation // inferred from direct assay /// 48009 // insulin-like growth factor receptor signaling pathway // inferred from direct assay /// 51262 // protein tetramerization // inferred from direct assay /// 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from electronic annotation 5887 // integral to plasma membrane // Unknown /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4872 // receptor activity // inferred from electronic annotation /// 5006 // epidermal growth factor receptor activity // inferred from electronic annotation /// 5010 // insulin-like growth factor receptor activity // inferred from direct assay /// 5520 // insulin-like growth factor binding // inferred from direct assay /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 43548 // phosphoinositide 3-kinase binding // inferred from physical interaction /// 43560 // insulin receptor substrate binding // inferred from physical interaction /// 5515 // protein binding // inferred from physical interaction /// 4713 // protein-tyrosine kinase activity // inferred from direct assay /// 4672 // protein kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4714 // transmembrane receptor protein tyrosine kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 5010 // insulin-like growth factor receptor activity // traceable author statement --- 3480
211810_s_at Hs.513439 galactosylceramidase GALC 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6683 // galactosylceramide catabolism // inferred from electronic annotation 5764 // lysosome // traceable author statement 4336 // galactosylceramidase activity // inferred from electronic annotation /// 16798 // hydrolase activity, acting on glycosyl bonds // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 2581
232251_at Hs.380350 nudix (nucleoside diphosphate linked moiety X)-type motif 16 pseudogene NUDT16P --- --- --- --- 152195
1560679_at Hs.516245 hypothetical protein LOC151438 LOC151438 --- --- --- --- 151438
232744_x_at Hs.434961 Ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310
229373_at Hs.457403 Transcribed locus --- --- --- --- --- ---

Figure 189

219607_s_at Hs.325960 membrane-spanning 4-domains, subfamily A, member 4 MS4A4A 7165 // signal transduction // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 51338
236404_at Hs.434961 Ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation
3723 // RNA binding // inferred from electronic annotation --- 6310
1569189_at Hs.31704 tetratricopeptide repeat domain 9C TTC9C ---
--- 5488 // binding // inferred from electronic annotation
--- 283237
211372_s_at Hs.25333 interleukin 1 receptor, type II IL1R2 6955 // immune response // traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4910 // interleukin-1, Type II, blocking receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // traceable author statement --- 7850
223158_s_at Hs.197071 NIMA (never in mitosis gene a)-related kinase 6 NEK6 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 43123 // positive regulation of I-kappaB kinase/NF-kappaB cascade // inferred from mutant phenotype 5634 // nucleus // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4713 // protein-tyrosine kinase activity // inferred from electronic annotation /// 4871 // signal transducer activity // inferred from mutant phenotype /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 10783
228790_at Hs.154652 chromosome 8 open reading frame 72 C8orf72 --- --- --- --- 90362
209999_x_at Hs.50640 suppressor of cytokine signaling 1 SOCS1 1558 // regulation of cell growth // inferred from electronic annotation /// 1932 // regulation of protein amino acid phosphorylation // inferred from sequence or structural similarity /// 6512 // ubiquitin cycle // inferred from electronic annotation /// 7242 // intracellular signaling cascade // inferred from electronic annotation /// 7259 // JAK-STAT cascade // traceable author statement /// 19221 // cytokine and chemokine mediated signaling pathway // inferred from sequence or structural similarity /// 42518 // negative regulation of tyrosine phosphorylation of Stat3 protein // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // inferred from sequence or structural similarity /// 46426 // negative regulation of JAK-STAT cascade // non-traceable author statement /// 46627 // negative regulation of insulin receptor signaling pathway // inferred from sequence or structural similarity /// 9968 // negative regulation of signal transduction // inferred from

Figure 190

electronic annotation 5737 // cytoplasm // traceable author statement 4860 // protein kinase inhibitor activity // traceable author statement /// 5159 // insulin-like growth factor receptor binding // inferred from physical interaction /// 19901 // protein kinase binding // inferred from physical interaction /// 19210 // kinase inhibitor activity // inferred from sequence or structural similarity --- 8651
229723_at Hs.529984 T-cell activation GTPase activating protein TAGAP --- --- 5085 // guanyl-nucleotide exchange factor activity // inferred from electronic annotation --- 117289
205403_at Hs.25333 interleukin 1 receptor, type II IL1R2 6955 // immune response // traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4910 // interleukin-1, Type II, blocking receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // inferred from electronic annotation /// 4908 // interleukin-1 receptor activity // traceable author statement --- 7850
225612_s_at Hs.208267 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 B3GNT5 6486 // protein amino acid glycosylation // inferred from electronic annotation /// 7417 // central nervous system development // inferred from direct assay /// 6486 // protein amino acid glycosylation // traceable author statement /// 9247 // glycolipid biosynthesis // traceable author statement 16020 // membrane // inferred from electronic annotation /// 5622 // intracellular // inferred from direct assay 8378 // galactosyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 8457 // beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,3-acetylglucosaminyltransferase activity // inferred from direct assay --- 84002
203305_at Hs.335513 coagulation factor XIII, A1 polypeptide F13A1 7596 // blood coagulation // traceable author statement /// 18149 // peptide cross-linking // inferred from electronic annotation /// 7596 // blood coagulation // inferred from electronic annotation 5576 // extracellular region // traceable author statement 3810 // protein-glutamine gamma-glutamyltransferase activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 8415 // acyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 3810 // protein-glutamine gamma-glutamyltransferase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation Complement and coagulation cascades // KEGG /// Huntington's disease // KEGG 2162
218401_s_at Hs.59757 zinc finger protein 281 ZNF281 122 // negative regulation of transcription from RNA polymerase II promoter // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation /// 5665 // DNA-directed RNA polymerase II, core complex // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3704 // specific RNA polymerase II transcription factor activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic

Figure 191

annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation --- 23528
213030_s_at Hs.497626 plexin A2 PLXNA2 7275 // development // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 5362
214738_s_at Hs.7200 NIMA (never in mitosis gene a)- related kinase 9 NEK9 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 7049 // cell cycle // inferred from electronic annotation /// 7067 // mitosis // inferred from electronic annotation /// 51301 // cell division // inferred from electronic annotation --- 166 // nucleotide binding // inferred from electronic annotation /// 287 // magnesium ion binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation --- 91754
201487_at Hs.128065 cathepsin C CTSC 6508 // proteolysis // inferred from electronic annotation /// 6955 // immune response // traceable author statement /// 6508 // proteolysis // not recorded 5764 // lysosome // traceable author statement /// 5764 // lysosome // inferred from electronic annotation 4197 // cysteine-type endopeptidase activity // inferred from electronic annotation /// 4214 // dipeptidyl-peptidase I activity // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8234 // cysteine-type peptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 1075
224862_at Hs.269782 Guanine nucleotide binding protein (G protein), q polypeptide GNAQ 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7596 // blood coagulation // traceable author statement 5737 // cytoplasm // traceable author statement /// 5834 // heterotrimeric G-protein complex // not recorded /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 2776
203060_s_at Hs.524491 3'-phosphoadenosine 5'-phosphosulfate synthase 2 PAPSS2 103 // sulfate assimilation // inferred from electronic annotation /// 1501 // skeletal development // inferred from sequence or structural similarity /// 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // not recorded /// 1501 // skeletal development // traceable author statement 5622 // intracellular // inferred from sequence or structural similarity 166 // nucleotide binding // inferred from electronic annotation /// 4020

Figure 192

// adenylylsulfate kinase activity // inferred from electronic annotation /// 4781 // sulfate adenylyltransferase (ATP) activity // inferred from sequence or structural similarity /// 5524 // ATP binding // inferred from sequence or structural similarity /// 16779 // nucleotidyltransferase activity // inferred from sequence or structural similarity /// 16740 // transferase activity // inferred from sequence or structural similarity /// 3824 // catalytic activity // inferred from electronic annotation /// 4781 // sulfate adenylyltransferase (ATP) activity // inferred from electronic annotation /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 16772 // transferase activity, transferring phosphorus-containing groups // inferred from electronic annotation /// 16779 // nucleotidyltransferase activity // inferred from electronic annotation Purine metabolism // KEGG /// Selenoamino acid metabolism // KEGG /// Sulfur metabolism // KEGG /// Purine metabolism // KEGG /// Selenoamino acid metabolism // KEGG /// Sulfur metabolism // KEGG 9060
36566_at Hs.187667 cystinosis, nephropathic CTNS 6520 // amino acid metabolism // traceable author statement /// 6810 // transport // inferred from electronic annotation /// 15811 // L-cystine transport // traceable author statement 5765 // lysosomal membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation /// 5764 // lysosome // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // not recorded 15184 // L-cystine transporter activity // traceable author statement --- 1497
205016_at Hs.170009 transforming growth factor, alpha TGFA 74 // regulation of progression through cell cycle // inferred from electronic annotation /// 7267 // cell-cell signaling // not recorded /// 8283 // cell proliferation // traceable author statement /// 8283 // cell proliferation // inferred from electronic annotation 5615 // extracellular space // not recorded /// 5625 // soluble fraction // not recorded /// 5886 // plasma membrane // non-traceable author statement /// 5887 // integral to plasma membrane // not recorded /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4713 // protein-tyrosine kinase activity // traceable author statement /// 4871 // signal transducer activity // traceable author statement /// 5155 // epidermal growth factor receptor activating ligand activity // not recorded /// 5515 // protein binding // traceable author statement /// 8083 // growth factor activity // inferred from electronic annotation --- 7039
1567101_at Hs.129452 Dachshund homolog 1 (Drosophila) DACH1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7456 // eye development (sensu Endopterygota) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction --- 1602
209498_at Hs.512682 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) CEACAM1 1525 // angiogenesis // non-traceable author statement /// 7156 // homophilic cell adhesion // non-traceable author statement /// 7229 // integrin-mediated signaling

Figure 193

pathway // non-traceable author statement /// 7565 // pregnancy // traceable author statement /// 16477 // cell migration // non-traceable author statement 5624 // membrane fraction // traceable author statement /// 5887 // integral to plasma membrane // non-traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation --- --- 634
230179_at Hs.593631 hypothetical protein LOC285812 LOC285812 --- --- --- --- 285812
202615_at Hs.269782 Guanine nucleotide binding protein (G protein), q polypeptide GNAQ 6471 // protein amino acid ADP-ribosylation // inferred from electronic annotation /// 7165 // signal transduction // inferred from electronic annotation /// 7186 // G-protein coupled receptor protein signaling pathway // inferred from electronic annotation /// 7202 // phospholipase C activation // traceable author statement /// 7596 // blood coagulation // traceable author statement 5737 // cytoplasm // traceable author statement /// 5834 // heterotrimeric G-protein complex // not recorded /// 5886 // plasma membrane // traceable author statement 166 // nucleotide binding // inferred from electronic annotation /// 3924 // GTPase activity // traceable author statement /// 4871 // signal transducer activity // inferred from electronic annotation /// 5525 // GTP binding // inferred from electronic annotation /// 19001 // guanyl nucleotide binding // inferred from electronic annotation G_Protein_Signaling // GenMAPP /// Calcium_regulation_in_cardiac_cells // GenMAPP /// Smooth_muscle_contraction // GenMAPP 2776
210715_s_at Hs.31439 serine peptidase inhibitor, Kunitz type, 2 SPINT2 6928 // cell motility // traceable author statement 5576 // extracellular region // traceable author statement /// 5625 // soluble fraction // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4867 // serine-type endopeptidase inhibitor activity // traceable author statement /// 4866 // endopeptidase inhibitor activity // inferred from electronic annotation /// 4867 // serine-type endopeptidase inhibitor activity // inferred from electronic annotation /// 4866 // endopeptidase inhibitor activity // traceable author statement --- 10653
223461_at Hs.484678 TBC1 domain family, member 7 TBC1D7 --- --- 5096 // GTPase activator activity // inferred from electronic annotation --- 51256
223834_at Hs.521989 CD274 molecule CD274 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 7166 // cell surface receptor linked signal transduction // traceable author statement /// 8283 // cell proliferation // traceable author statement 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation --- 29126
1552263_at Hs.431850 mitogen-activated protein kinase 1 MAPK1 6468 // protein amino acid phosphorylation // inferred from electronic annotation /// 6917 // induction of apoptosis // traceable author statement /// 6935 // chemotaxis // traceable author statement /// 6950 // response to stress // traceable author statement /// 7049 // cell cycle // inferred from electronic annotation /// 7165 // signal transduction // traceable author statement /// 7268 // synaptic transmission // traceable author statement --- 166 // nucleotide

Figure 194

binding // inferred from electronic annotation /// 4674 // protein serine/threonine kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4672 // protein kinase activity // inferred from electronic annotation /// 4707 // MAP kinase activity // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation
MAPK_Cascade // GenMAPP /// S1P_Signaling // GenMAPP 5594
212807_s_at Hs.485195 sortilin 1 SORT1 1503 // ossification // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6886 // intracellular protein transport // inferred from electronic annotation /// 6897 // endocytosis // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5764 // lysosome // inferred from electronic annotation /// 5768 // endosome // non-traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation
4872 // receptor activity // inferred from electronic annotation /// 8565 // protein transporter activity // inferred from electronic annotation /// 16492 // neurotensin receptor activity, G-protein coupled // non-traceable author statement --- 6272
205472_s_at Hs.129452 dachshund homolog 1 (Drosophila) DACH1 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation /// 7456 // eye development (sensu Endopterygota) // traceable author statement 5634 // nucleus // inferred from electronic annotation 3677 // DNA binding // inferred from electronic annotation /// 5515 // protein binding // inferred from physical interaction --- 1602
220358_at Hs.62919 Jun dimerization protein p21SNFT SNFT 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // traceable author statement /// 9613 // response to pest, pathogen or parasite // traceable author statement 5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus // traceable author statement 3677 // DNA binding // inferred from electronic annotation /// 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3700 // transcription factor activity // traceable author statement /// 3714 // transcription corepressor activity // traceable author statement ---
55509
228231_at Hs.594383 MRNA; cDNA DKFZp761E1721 (from clone DKFZp761E1721) --- --- --- --- --- ---
1560224_at Hs.300887 AT hook containing transcription factor 1
AHCTF1 --- --- --- --- 25909
219821_s_at Hs.484686 glucose-fructose oxidoreductase domain containing 1 GFOD1 6118 // electron transport // inferred from electronic annotation /// 8152 // metabolism // inferred from

Figure 195

electronic annotation --- 16491 // oxidoreductase activity // inferred from electronic annotation --- 54438
215268_at --- hypothetical LOC643314 KIAA0754 --- --- --- --- 643314
204417_at Hs.513439 galactosylceramidase GALC 5975 // carbohydrate metabolism // inferred from electronic annotation /// 6683 // galactosylceramide catabolism // inferred from electronic annotation 5764 // lysosome // traceable author statement 4336 // galactosylceramidase activity // inferred from electronic annotation /// 16798 // hydrolase activity, acting on glycosyl bonds // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation --- 2581
205409_at Hs.220971 FOS-like antigen 2 FOSL2 6357 // regulation of transcription from RNA polymerase II promoter // traceable author statement /// 8219 // cell death // traceable author statement /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation 5634 // nucleus // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // traceable author statement /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 46983 // protein dimerization activity // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation --- 2355
207075_at Hs.159483 NLR family, pyrin domain containing 3 NLRP3 6915 // apoptosis // inferred from electronic annotation /// 6917 // induction of apoptosis // non-traceable author statement /// 6952 // defense response // traceable author statement /// 6954 // inflammatory response // inferred from mutant phenotype /// 7165 // signal transduction // non-traceable author statement /// 7605 // sensory perception of sound // inferred from electronic annotation /// 9595 // detection of biotic stimulus // traceable author statement /// 51259 // protein oligomerization // traceable author statement 5737 // cytoplasm // traceable author statement 42834 // peptidoglycan binding // traceable author statement --- 114548
214438_at Hs.74870 H2.0-like homeobox 1 (Drosophila) HLX1 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 6366 // transcription from RNA polymerase II promoter // not recorded /// 7275 // development // traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // inferred from electronic annotation /// 43565 // sequence-specific DNA binding // inferred from electronic annotation /// 3677 // DNA binding // inferred from electronic annotation /// 3677 // DNA binding // not recorded --- 3142
238452_at Hs.517422 Fc receptor-like B FCRLB --- --- 4872 // receptor activity // inferred from electronic annotation --- 127943
225707_at Hs.516468 ADP-ribosylation-like factor 6 interacting protein 6 ARL6IP6 --- --- --- --- 151188
229298_at --- --- --- --- --- --- --- ---
212172_at Hs.470907 adenylate kinase 2 AK2 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // inferred from electronic annotation 5739 // mitochondrion // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4017 // adenylate kinase activity //

Figure 196

traceable author statement /// 5524 // ATP binding // inferred from electronic annotation /// 16301 // kinase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation /// 4017 // adenylate kinase activity // inferred from electronic annotation /// 16776 // phosphotransferase activity, phosphate group as acceptor // inferred from electronic annotation /// 19201 // nucleotide kinase activity // inferred from electronic annotation Purine metabolism // KEGG 204
224818_at Hs.485195 sortilin 1 SORT1 1503 // ossification // inferred from electronic annotation /// 6810 // transport // inferred from electronic annotation /// 6886 // intracellular protein transport // inferred from electronic annotation /// 6897 // endocytosis // inferred from electronic annotation /// 30154 // cell differentiation // inferred from electronic annotation /// 7275 // development // inferred from electronic annotation 5764 // lysosome // inferred from electronic annotation /// 5768 // endosome // non-traceable author statement /// 5783 // endoplasmic reticulum // inferred from electronic annotation /// 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // non-traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 8565 // protein transporter activity // inferred from electronic annotation /// 16492 // neurotensin receptor activity, G-protein coupled // non-traceable author statement --- 6272
1568619_s_at Hs.648523 CDNA clone IMAGE:4402981 --- --- --- --- --- 162073
203233_at Hs.513457 interleukin 4 receptor IL4R 6955 // immune response // traceable author statement /// 7165 // signal transduction // traceable author statement /// 6955 // immune response // inferred from electronic annotation 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4872 // receptor activity // inferred from electronic annotation /// 4896 // hematopoietin/interferon-class (D200-domain) cytokine receptor activity // inferred from electronic annotation /// 4913 // interleukin-4 receptor activity // traceable author statement /// 5057 // receptor signaling protein activity // traceable author statement /// 5515 // protein binding // inferred from physical interaction Inflammatory_Response_Pathway // GenMAPP 3566
203434_s_at Hs.307734 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase) MME 6508 // proteolysis // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 6508 // proteolysis // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4245 // neprilysin activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Hematopoietic cell lineage // KEGG /// Alzheimer's disease // KEGG 4311

Figure 197

239488_at Hs.634885 CDNA FLJ30948 fis, clone FEBRA2007900 --- --- --- --- ---
227458_at --- --- --- --- --- --- --- ---
203397_s_at Hs.170986 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3) GALNT3 5975 // carbohydrate metabolism // non-traceable author statement 5624 // membrane fraction // traceable author statement /// 5795 // Golgi stack // inferred from electronic annotation /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 4653 // polypeptide N-acetylgalactosaminyltransferase activity // traceable author statement /// 5509 // calcium ion binding // inferred from electronic annotation /// 5529 // sugar binding // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation /// 30145 // manganese ion binding // inferred from electronic annotation /// 4653 // polypeptide N-acetylgalactosaminyltransferase activity // inferred from electronic annotation /// 16740 // transferase activity // inferred from electronic annotation O-Glycan biosynthesis // KEGG /// Glycan structures - biosynthesis 1 // KEGG 2591
217678_at Hs.390594 solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 SLC7A11 6461 // protein complex assembly // not recorded /// 6810 // transport // inferred from electronic annotation /// 6865 // amino acid transport // inferred from electronic annotation 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // traceable author statement /// 16021 // integral to membrane // inferred from electronic annotation 15327 // cystine:glutamate antiporter activity // traceable author statement /// 15359 // amino acid permease activity // inferred from electronic annotation /// 5279 // amino acid-polyamine transporter activity // inferred from electronic annotation /// 15171 // amino acid transporter activity // inferred from electronic annotation --- 23657
212828_at Hs.434494 synaptojanin 2 SYNJ2 --- --- 166 // nucleotide binding // inferred from electronic annotation /// 3723 // RNA binding // inferred from electronic annotation /// 4439 // phosphoinositide 5-phosphatase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation /// 3676 // nucleic acid binding // inferred from electronic annotation /// 4437 // inositol or phosphatidylinositol phosphatase activity // inferred from electronic annotation --- 8871
36564_at Hs.591504 IBR domain containing 3 IBRDC3 --- 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 5515 // protein binding // inferred from electronic annotation --- 127544
243578_at Hs.44780 Glycosyltransferase-like domain containing 1 GTDC1 9058 // biosynthesis // inferred from electronic annotation --- 16740 // transferase activity // inferred from electronic annotation /// 16757 // transferase activity, transferring glycosyl groups // inferred from electronic annotation --- 79712
212092_at Hs.147492 paternally expressed 10 PEG10 --- --- 3676 // nucleic acid binding // inferred from electronic annotation /// 8270 // zinc ion binding // inferred from electronic annotation --- 23089

Figure 198

203435_s_at Hs.307734 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase) MME 6508 // proteolysis // traceable author statement /// 7267 // cell-cell signaling // traceable author statement /// 6508 // proteolysis // inferred from electronic annotation 5886 // plasma membrane // traceable author statement /// 5887 // integral to plasma membrane // traceable author statement /// 16020 // membrane // inferred from electronic annotation /// 16021 // integral to membrane // inferred from electronic annotation 4245 // neprilysin activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // traceable author statement /// 8270 // zinc ion binding // inferred from electronic annotation /// 46872 // metal ion binding // inferred from electronic annotation /// 8233 // peptidase activity // inferred from electronic annotation /// 8237 // metallopeptidase activity // inferred from electronic annotation /// 16787 // hydrolase activity // inferred from electronic annotation Hematopoietic cell lineage // KEGG /// Alzheimer's disease // KEGG 4311

201169_s_at Hs.171825 basic helix-loop-helix domain containing, class B, 2 BHLHB2 6355 // regulation of transcription, DNA-dependent // non-traceable author statement /// 6350 // transcription // inferred from electronic annotation /// 6355 // regulation of transcription, DNA-dependent // inferred from electronic annotation /// 45449 // regulation of transcription // inferred from electronic annotation 5634 // nucleus // non-traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3700 // transcription factor activity // non-traceable author statement /// 3677 // DNA binding // inferred from electronic annotation /// 30528 // transcription regulator activity // inferred from electronic annotation --- 8553

207358_x_at Hs.580782 microtubule-actin crosslinking factor 1 MACF1 7050 // cell cycle arrest // inferred from electronic annotation /// 5975 // carbohydrate metabolism // inferred from electronic annotation 5737 // cytoplasm // inferred from direct assay /// 5737 // cytoplasm // inferred from sequence or structural similarity /// 5856 // cytoskeleton // inferred from sequence or structural similarity /// 5856 // cytoskeleton // non-traceable author statement /// 5856 // cytoskeleton // inferred from electronic annotation 3779 // actin binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from electronic annotation /// 5509 // calcium ion binding // inferred from sequence or structural similarity /// 5509 // calcium ion binding // non-traceable author statement /// 8017 // microtubule binding // inferred from sequence or structural similarity /// 8017 // microtubule binding // non-traceable author statement /// 51015 // actin filament binding // non-traceable author statement /// 3779 // actin binding // inferred from direct assay /// 4553 // hydrolase activity, hydrolyzing O-glycosyl compounds // inferred from electronic annotation --- 23499

1565804_at Hs.434961 Ataxin 1 ATXN1 --- 5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement /// 5634 // nucleus // inferred from electronic annotation 3723 // RNA binding // inferred from electronic annotation --- 6310

212175_s_at Hs.470907 adenylate kinase 2 AK2 6139 // nucleobase, nucleoside, nucleotide and nucleic acid metabolism // inferred from electronic annotation 5739 // mitochondrion // inferred from electronic annotation 166 // nucleotide binding // inferred from electronic annotation /// 4017 // adenylate kinase activity //

Figure 199

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

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