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(54) **BIOMARKERS FOR NEUROLOGICAL CONDITIONS**

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(57) **ABSTRACT**

Low molecular weight (LMW) peptides have been discovered that are indicative of neurological conditions, such as Alzheimer's Disease (AD), cognitive impairment and brain microhemmorhages. Evaluating patient samples for the presence of such LMW peptides is an effective means of detecting neurological conditions and monitoring the progression of the disease. The LMW peptides are particularly useful in detecting neurological conditions during the early stages without invasive procedures.

BIOMARKERS FOR NEUROLOGICAL CONDITIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 60/855,749, filed Nov. 1, 2006, which is hereby incorporated by reference.

BACKGROUND

[0002] Alzheimer's disease (AD) is a progressive degenerative disease of the brain primarily associated with aging. AD is one of several disorders that cause the gradual loss of brain cells and is one of and possibly the leading cause of dementia. Clinical presentation of AD is characterized by loss of memory, cognition, reasoning, judgment, and orientation. Mild cognitive impairment (MCI) is often the first identified stage of AD. As the disease progresses, motor, sensory, and linguistic abilities also are affected until there is global impairment of multiple cognitive functions. These cognitive losses occur gradually, but typically lead to severe impairment and eventual death in the range of three to twenty years.

[0003] An early diagnosis of AD has many advantages including additional time to make choices that maximize quality of life, less anxiety about unknown problems, a better chance of benefiting from treatment and more time to plan for the future. However, reliable noninvasive methods for diagnosing AD are not available.

[0004] Alzheimer's disease is characterized by two major pathologic observations in the brain: neurofibrillary tangles (NFT) and beta-amyloid plaques, comprised predominantly of an aggregate of fragments known as Aβ peptides. Individuals with AD exhibit characteristic beta-amyloid deposits in the brain (beta-amyloid plaques) and in cerebral blood vessels (beta-amyloid angiopathy) as well as neurofibrillary tangles. Neurofibrillary tangles occur not only in Alzheimer's disease but also in other dementia-inducing disorders. On autopsy, presently the only definitive method of diagnosing AD, large numbers of these lesions are generally found in areas of the human brain important for memory and cognition.

[0005] There is an urgent clinical need to develop diagnostic markers that can detect early stage AD, particularly at the stage of MCI. While advances have been made in imaging beta-amyloid, (Lopresti et al. J. Nucl. Med. (2005) 46:1959-1972), no serum biomarkers for AD are clinically available. To date there are no validated biomarkers for confirming the diagnosis of a major neurodegenerative disorder or to monitor progression (Castano et al. Neurol. Res. (2006) 28:1155-163).

[0006] Despite the enthusiasm for the use of proteomic technology to discover blood markers of AD, and decades of effort, progress towards identifying useful markers has been slow, possibly because putative high specificity AD markers are assumed to be in very low abundance because they are shed from small volumes of diseased tissue and are expected to be rapidly cleared and metabolized. In addition, researchers have avoided studying blood because the blood proteome is dominated by, and complicated by, resident proteins such as albumin that can exist at a concentration many millions of times greater than the target low abundance biomarker. For this reason, researchers have focused on cerebrospinal fluid (CSF) as the target fluid for AD biomarkers (see Zhang et al., J. Alzheimer's Disease (2005) 8:377-3386). The CSF approach, however, has limited clinical application to routine screening. Moreover, the blood brain vascular circulation perfuses AD lesions with a higher efficiency, particularly in the case for amyloid angiopathy.

SUMMARY

[0007] In one aspect, methods are provided for diagnosing a neurological condition in a patient comprising obtaining a biological sample from the patient and evaluating the sample for the abundance of at least one biomarker selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NOs:1-440, wherein the abundance of said at least one biomarker is indicative of a neurological condition. In one embodiment, the abundance of the biomarker is greater than that of a control sample. In another embodiment, the abundance of the biomarker is less than that of a control sample.

[0008] The method also can comprise, prior to the evaluation step, harvesting low molecular weight peptides from said sample to generate at least one fraction comprising said peptides. The biomarker can be a low molecular weight protein complexed with a carrier protein. In a further embodiment, the low molecular weight protein is further purified from said carrier protein. In another embodiment, the low molecular weight protein is digested and optionally sequenced. In one embodiment, the biological sample is blood, serum or plasma. In another embodiment, the evaluation step comprises an assay selected from the group consisting of mass spectrometry, such as tandem mass spectrotrometry (MS MS), immunoassay, such as enzyme-linked immunosorbent assay (ELISA), immuno-mass spectrometry and suspension bead array. The method also can comprise obtaining a neuroimage of the brain microvasculopathy, which can be optionally obtained using susceptibility weighted imaging, perfusion weighted imaging and magnetic resonance spectroscopy.

[0009] The neurological condition can be Alzheimer's disease (AD), mild cognitive impairment (MCI), stable mild cognitive impairment (stable MCI), progressive mild cognitive impairment (PMCI), vascular dementia (VD), angiopathy black holes, cerebral amyloid angiopathy (CAA) and brain microhemorrages. In one embodiment, methods are provided for diagnosing Alzheimer's disease in a patient comprising obtaining a biological sample from said patient, and evaluating said sample for the abundance of at least one biomarker selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NOs:1, 3-13, 15, 16, 21, 22, 24-28, 31-33, 37-44, 56-59, 66-68, 93-101, 111-128, 143-153, 156-1170, 172-183, 263-279, 310-335, 348, 355-359, 362, 363, 365, 372, 373, 376-402, 406-426 and 436-44, wherein the abundance of said at least one biomarker is indicative of Alzheimer's disease. In another aspect, the biomarker is a peptide associated with a metabolic pathway or cellular process. In others aspects, the biomarker is a peptide associated with inflammation, estrogen activity, pigment epithelium-derived factor (PEDF), vitamin D metabolism and bone mineralization, coagulation and platelet activity, the complement cascade, acyl-peptide hydrolase (APH) activity, vitamin A and thyroxine, phospholipase activity, globin activity, glycosylation or is glycosylated, protease inhibition, keratins and related proteins, heme degradation, pyruvate metabolism, calcium related proteins, defensin, gelsolin, vitronectin, profilin, thrombospondin, peroxiredoxin, alcohol

dehydrogenase, apolipoproteins, iron and copper metabolism, or NMDA receptor-related proteins.

[0010] In another aspect, methods are provided for diagnosing mild cognitive impairment in a patient comprising obtaining a biological sample from the patient and evaluating the sample for the abundance of at least one biomarker selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NOs: 2, 4, 14, 17, 23, 29, 34, 45-55, 60-65, 69-92, 102-110, 129-142, 154, 155, 171, 184-191, 193-226, 248-279, 281-320, 333, 336-347, 349-354, 360, 361, 364, 366-371, 374, 375, 403-405 and 427-435, wherein the abundance of said at least one biomarker is indicative of mild cognitive impairment.

[0011] In yet another aspect, methods are provided for diagnosing brain microhemorrhages in a patient comprising obtaining a biological sample from the patient and evaluating the sample for the abundance of at least one biomarker selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NOs:441-452, wherein the abundance of said at least one biomarker is indicative of brain microhemorrhages.

[0012] In some embodiments, the inventive methods comprise, prior to the evaluation step, harvesting low molecular weight peptides from the biological sample to generate at least one fraction comprising the peptides. The size of the low molecular weight peptides can be, for example, less than 50 KDa, less than 25 KDa, or less than 15 KDa. The methods also can comprise digesting the low molecular weight peptides. Such digestion can be accomplished using enzymatic or chemical means. In one example, trypsin can be used to digest the peptides.

[0013] In other aspects, antibodies are provided that are specific for biomarkers for a neurological condition, as well as kits for detecting a neurological condition in a patient, comprising at least one such antibody. The antibody can be, for example, a monoclonal or polyclonal antibody, and also be a chimeric, humanized or human antibody.

[0014] Other objects, features and advantages will become apparent from the following detailed description. The detailed description and specific examples are given for illustration only since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description. Further, the examples demonstrate the principle of the invention and cannot be expected to specifically illustrate the application of this invention to all the examples where it will be obviously useful to those skilled in the prior art.

DETAILED DESCRIPTION

[0015] Low molecular weight (LMW) peptides have been discovered from the repertoire of proteins bound to carrier proteins such as albumin that are indicative of a neurological condition. Evaluating patient samples for the presence of such LMW peptides is an effective means of detecting a neurological condition and monitoring the progression of the disease, for example during treatment. The LMW peptides are particularly useful in detecting a neurological condition during its early stages. The LMW peptides are particularly useful for detecting AD, MCI and brain microhemorrhages.

[0016] The LMW peptides, which are biomarkers, can be detected using a variety of methods known in the art. For example, antibodies can be utilized in immunoassays to detect the presence of a biomarker. Exemplary immunoassays include, e.g., ELISA, radioimmunoassay, immunofluorescent assay, "sandwich" immunoassay, western blot, immunoprecipitation assay and immunoelectrophoresis assays. In other aspects, microbeads, arrays, microarrays, etc. can be used in detecting the LMW peptides. Exemplary assays include, but are not limited to, a suspension bead assay (Schwenk et al., "Determination of binding specificities in highly multiplexed bead-based assays for antibody proteomics," *Mol. Cell Proteomics,* 6(1): 125-132 (2007)), an antibody microarray (Borrebaeck et al., "High-throughput proteomics using antibody microarrays: an update," *Expert Rev. Mol. Diagn.* 7(5): 673-686 (2007)), an aptamer array (Walter et al., "High-throughput protein arrays: prospects for molecular diagnostics," *Trends Mol. Med.* 8(6): 250-253 (2002)), an affybody array (Renberg et al., "Affibody molecules in protein capture microarrays: evaluation of multidomain ligands and different detection formats," *J. Proteome Res.* 6(1): 171-179 (2007)), and a reverse phase array (VanMeter et al., "Reverse-phase protein microarrays: application to biomarker discovery and translational medicine," *Expert Rev. Mol. Diagn.* 7(5): 625-633 (2007)). All of these publications are incorporated herein by reference.

[0017] In another example, the inventive biomarkers can be detected using mass spectrometry (MS). One example of this approach is tandem mass spectrometry (MS/MS), which involves multiple steps of mass selection or analysis, usually separated by some form of fragmentation. Most such assays use electrospray ionization followed by two stages of mass selection: a first stage (MS1) selecting the mass of the intact analyte (parent ion) and, after fragmentation of the parent by collision with gas atoms, a second stage (MS2) selecting a specific fragment of the parent, collectively generating a selected reaction monitoring assay. In one embodiment, collision-induced dissociation is used to generate a set of fragments from a specific peptide ion. The fragmentation process primarily gives rise to cleavage products that break along peptide bonds. Because of the simplicity in fragmentation, the observed fragment masses can be compared to a database of predicted masses for known peptide sequences. A number of different algorithmic approaches have been described to identify peptides and proteins from tandem mass spectrometry (MS/MS) data, including peptide fragment fingerprinting (SEQUEST, MASCOT, OMSSA and X!Tandem), peptide de novo sequencing (PEAKS, LuteFisk and Sherenga) and sequence tag based searching (SPIDER, GutenTAG).

[0018] Likewise, multiple reaction monitoring (MRM) can be used to identify the inventive biomarkers in patient samples. This technique applies the MS/MS approach to, for example, tryptic digests of the input sample, followed by selected ion partitioning and sampling using MS to make the analyte selection more objective and discrete by following the exact m/z ion of the tryptic fragment that represents the analyte. Such an approach can be performed in multiplex so that multiple ions can be measured at once, providing an antibody-free method for analyte measurement. See, e.g. Andersen et al., *Molecular & Cellular Proteomics,* 5.4: 573-588 (2006); Whiteaker et al., *J. Proteome Res.* 6(10): 3962-75 (2007). Both publications are incorporated herein by reference.

[0019] In another example, the inventive biomarkers can be detected using nanoflow reverse-phase liquid chromatography-tandem mass spectrometry. See, e.g., Domon B, Aebersold R. *Science,* 312(5771):212-7(2006), which is incorporated herein by reference. Using this approach, practitioners obtain peptide fragments, usually by trypsin digest, and gen-

erate mass spectrograms of the fragments, which are then compared to a database, such as SEQUEST, for protein identification.

[0020] In another aspect, the inventive biomarkers can be detected using immuno-mass spectrometry. See, e.g., Liotta L et al. *J Clin Invest.,* 116(1):26-30 (2006), Nedelkov, Expert Rev. Proteomics, 3(6): 631-640 (2006), which are incorporated herein by reference. Immuno-mass spectrometry provides a means for rapidly determining the exact size and identity of a peptide biomarker isoform present within a patient sample. When developed as a high throughput diagnostic assay, a drop of patient's blood, serum or plasma can be applied to a high density matrix of microcolumns or microwells filled with a composite substratum containing immobilized polyclonal antibodies, directed against the peptide marker. All isoforms of the peptide that contain the epitope are captured. The captured population of analytes including the analyte fragments are eluted and analyzed directly by a mass spectrometer such as MALDI-TOF MS. The presence of the specific peptide biomarker at its exact mass/charge (m/z) location can be used as a diagnostic test result. The analysis can be performed rapidly by simple software that determines if a series of ion peaks are present at defined m/z locations.

[0021] In yet another example, the inventive biomarkers can be detected using standard immunoassay-based approaches whereby fragment specific antibodies are used to measure and record the presence of the diagnostic fragments. See, e.g., Naya et al. "Evaluation of precursor prostate-specific antigen isoform ratios in the detection of prostate cancer." *Urol Oncol.* 23(1):16-21 (2005). Moreover, additional immunoassays are well known to one skilled in the field, such as ELISA (Maeda et al., "Blood tests for asbestos-related mesothelioma," *Oncology* 71: 26-31 (2006)), microfluidic ELISA (Lee et al., "Microfluidic enzyme-linked immunosorbent assay technology," *Adv. Clin. Chem.* 42: 255-259 (2006)), nanocantilever immunoassay (Kurosawa et al., "Quartz crystal microbalance immunosensors for environmental monitoring," *Biosens Bioelectron,* 22(4): 473-481 (2006)), and plasmon resonance immunoassay (Nedelkov, "Development of surface Plasmon resonance mass spectrometry array platform," *Anal. Chem.* 79(15): 5987-5990 (2007)). All publications are incorporated herein by reference.

[0022] In a further example, the inventive biomarkers can be detected using electrochemical approaches. See, e.g., Lin et al., Anal. Sci. 23(9): 1059-1063 (2007)).

[0023] In one embodiment, the LMW peptides are harvested from a biological sample prior to the evaluation step. For example, 100 μl of serum can be mixed with 2×SDS-PAGE Laemmli Buffer (containing 200 mM DTT), boiled for 10 minutes, and loaded on Prep Cell (Model 491 Prep Cell, Bio-Rad Laboratories, Calif.) comprising a 5 cm length 10% acrylamide gel. Electrophoresis is performed under a constant voltage of 250V. Immediately after the bromophenol blue indicator dye is eluted from the system, LMW peptides and proteins migrate out of the gel and are trapped in a dialysis membrane in the elution chamber. These molecules can be eluted at a flow rate of 400 ml/min by a buffer with the same composition of the Tris-Glycine running buffer and collected for 10 minutes in one fraction.

[0024] Alternatively, LMW peptides can be harvested from a sample using a capture-particle that comprises a molecular sieve portion and an analyte binding portion as described in U.S. patent application Ser. No. 11/527,727, filed Sep. 27, 2006, which is incorporated herein by reference. Briefly, either the molecular sieve portion or the analyte binding portion or both comprise a cross-linked region having modified porosity, or pore dimensions sufficient to exclude high molecular weight molecules.

[0025] In another embodiment, the LMW peptides are digested prior to detection, so as to reduce the size of the peptides. Such digestion can be carried out using standard methods well known in the field. Exemplary treatments, include but are not limited to, enzymatic and chemical treatments. Such treatments can yield partial as well as complete digestions. One example of an enzymatic treatment is a trypsin digestion.

[0026] The inventive biomarkers are particularly useful in detecting a neurological condition during its early stages, such as while the condition is still associated with MCI or PMCI or for detecting brain vasculopathy, such as brain microhemorrhages. For clarification, mild cognitive impairment (MCI) cases fulfill the Mayo Clinic criteria for classification as MCI-multiple domain impairment (MCI-MCDI) with the following characteristics: i) A memory complaint confirmed by either corrected Logical Memory testing or reports of the informant and a CDR=0.5. ii) Normal activities of daily living. iii) Normal general cognitive function. iv) Abnormal memory for age as measured by standard scores and education. v) A global CDR of 0.5 and no dementia. vi) No history of significant vascular problems, insulin-requiring diabetes, or uncontrolled hypertension. Meanwhile, stable mild cognitive impairment (stable MCI) is based on a Sum of boxes=0.5-3.5 on several evaluations, CDR logical memory impairment with logical memory impairment on at least one evaluation, neuropsychological testing in MCI range inconsistently and clinical judgment. Progressive mild cognitive impairment (PMCI) denotes patients with a Sum of Boxes≧3.5 on two occasions, neuropsychological tests congruent with CDR, a Logical Memory raw score low to zero and clinical judgment.

[0027] The abundance of the biomarker can be measured by detecting the biomarker as described above and comparing the amount of the biomarker to a control. The abundance of the biomarker is an indicator of the neurological condition. If the biomarker is "less abundant" in the control, then the biomarker is present in the tested sample in a significantly less amount than in the control sample. If the biomarker is "more abundant" than the control, then the biomarker is present in the tested sample in a significantly greater amount than in the control sample. For instance, the difference may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 110%, 125%, 150%, 175%, 200%, 250%, 300%, 350%, 400%, 450%, 500%, 550%, 600%, 650%, 700%, 750%, 800%, 850%, 900%, 950%, 1000%, or greater. The control can be a sample or its equivalent from a normal patient or from a patient in a known disease state. For instance, the control can be from a patient with AD, MCI or brain microhemorrhages. The control can also be a standard or known amount of a reference peptide.

[0028] The neurological condition being detected can be, for example, Alzheimer's disease (AD), mild cognitive impairment (MCI), stable mild cognitive impairment (stable MCI), progressive mild cognitive impairment (PMCI), vascular dementia (VD), angiopathy black holes, cerebral amyloid angiopathy (CAA) and brain microhemorrhages. Unless otherwise indicated, the conditions and activities noted herein

refer to the commonly accepted definitions thereof. For instance, as described in more detail in the Examples, cognitive impairment is defined according to the Mayo Clinic criteria.

[0029] In another embodiment, the biomarker is a peptide associated with a metabolic pathway or cellular process. In further embodiments, the biomarker is a peptide associated with inflammation, estrogen activity, pigment epithelium-derived factor (PEDF)vitamin D metabolism and bone mineralization, coagulation and platelet activity, the complement cascade, acyl-peptide hydrolase (APH) activity, vitamin A and thyroxine, phospholipase activity, globin activity, glycosylation or is glycosylated, protease inhibition, keratins and related proteins, heme degradation, pyruvate metabolism, calcium related proteins, defensin, gelsolin, vitronectin, profilin, thrombospondin, peroxiredoxin, alcohol dehydrogenase, apolipoproteins, iron and copper metabolism, or NMDA receptor-related proteins.

[0030] In one aspect, more than one biomarker can be evaluated simultaneously. For example, at least two, at least five, at least 10, at least 20, at least 30, at least 50, at least 75, at least 100 biomarkers are evaluated in the methods. Analyzing more than one biomarker can increase accuracy of the diagnosis.

[0031] The present methods can be combined with neuroimaging techniques for the detection of neuropathy and brain microvasculopathy associated with a neurological condition. For example, neuroimaging can be used to detect brain microhemorrages associated with cognitive impairment. Using magnetic resonance imaging, focal signal intensity losses secondary to iron-containing hemosiderin residuals can be detected. These spots on the MR image have been termed "signal voids," "susceptibility artifacts," "black holes," "dots," "microbleeds," "old microbleeds" (OMBs), "multifocal signal loss lesions" or "microhemorrhages" (MH). Generically, these spots are called small hypointensities (SH) and are associated with AD and MCI (Cordonnier et al. Neurology (2006) 66:1356-1360; Werring et al. Brain (2004) 127:2265-2275). Suitable MR imaging techniques include gradient refocused echo T_2* (GRE-T_2) and susceptibility weighted imaging (SWI).

[0032] Neuroimaging methods that detect metabolic changes in the brain also can be used in conjunction with the present biomarkers. MR spectroscopy that detects, for instance, differences in neurotransmitters, such as glutamine, glutamate and gamma-aminobutryic acid (GABA), can be used to analyze changes in these systems associated with a neurological condition. These metabolic changes can be correlated with cognitive decline and biomarker abundance.

[0033] Antibodies specific for the inventive biomarkers can be produced readily using well known methods in the art. (See, J. Sambrook, E. F. Fritsch and T. Maniatis, *Molecular Cloning, a Laboratory Manual,* second edition, Cold Spring Harbor Laboratory Press, pp. 18.7-18.18, 1989) For example, the inventive biomarkers can be prepared readily using an automated peptide synthesizer. Next, injection of an immunogen, such as $(\text{peptide})_n$-KLH (n=1-30) in complete Freund's adjuvant, followed by two subsequent injections of the same immunogen suspended in incomplete Freund's adjuvant into immunocompetent animals, is followed three days after an i.v. boost of antigen, by spleen cell harvesting. Harvested spleen cells are then fused with Sp2/0-Ag14 myeloma cells and culture supernatants of the resulting clones analyzed for anti-peptide reactivity using a direct-binding ELISA. Fine specificity of generated antibodies can be detected by using peptide fragments of the original immunogen.

[0034] In certain embodiments, one or more antibodies directed to the inventive biomarkers is provided in a kit, for use in a diagnostic method. Such kits also can comprise reagents, instructions and other products for performing the diagnostic method.

[0035] In other aspects, the biomarkers and antibodies of the present invention are useful for discovering novel aspects of neurological conditions, such as those described herein.

[0036] The following examples are illustrative only, and should not be construed as limiting. Also, each reference disclosed herein, and throughout the specification, is incorporated by reference in its entirety.

Examples

Example 1

Background and Patient Summary

[0037] A community-based cohort of 103 participants (75 MCI and 28 cognitively normal subjects) was recruited for the study. Of the original 75 MCI subjects, 20 have been censored from the study for various reasons not related to dementia, leaving 55 which are currently being followed. Seventeen of these have become demented over a 0.5 to 4.1-year observation period (15% annual conversion rate) based upon on the Clinical Dementia Rating (CDR) Sum of Boxes score≧3.5 as documented by NINCDS-ADRDA criteria.(Schafer et al. Alzheimer Dis Assoc Disord.(2004) 18:219-222; McKhann et al. Neurology.(1984) 34:939-944) Four of 28 cognitively normal subjects have progressed to the MCI category with significant SH detected by SWI in two. Two MCI cases are on the verge of dementia at present, one with significant SH. SWI brain imaging has demonstrated increasing and "significant" numbers (n≧5) of SH in 7 of the 17 demented and progressively cognitively impaired subjects. This progressive increase in SH in a lobar, posteriorly situated cortical-subcortical pattern fits the diagnostic pattern for "probable CAA."(Knudsen et. al. Neurology. (2001) 56:537-539) This observation is the first prospective evidence for a subset of sporadic late-onset dementia correlating temporally with increasing SH in a pattern typical for CAA.

Subject Selection:

[0038] After screening 1348 community based individuals at publicized memory clinics, 28 elderly "controls" and 75 subjects with MCI qualified for the study using inclusion and exclusion criteria defined by the Mayo Clinic Group (Petersen R C, et al. Arch Neurol. March (1999) 56:303-308.) Subjects have been continuously evaluated with serial cognitive (bi-yearly) and radiologic (yearly) procedures over 4.1 years (range 0.5 to 4.10 years, average total follow-up time 2.3±1.2 years, total person years of follow-up 241.7 years). All subjects gave informed consent and all studies were approved by the Loma Linda University Institutional Review Board. Complete medication, medical and smoking histories were obtained on all subjects, and thyroid function, serum B12 levels, and ApoE genotype were defined in all subjects.

[0039] Normal Subjects: (n=28)

[0040] All "control subjects" were without objective or subjective memory deficits and within normal limits on neuropsychological testing (Global CDR of 0, CDR memory

component of 0 and a sum of CDR boxes of 1 or less at baseline). The sum of CDR boxes is used as a measure of cognitive performance.(107)

[0041] MCI Subjects: (n=75)

[0042] All MCI cases fulfilled the Mayo Clinic criteria for classification as MCI-multiple domain impairment (MCI-MCDI) with the following characteristics: i) a memory complaint confirmed by either corrected Logical Memory testing or reports of the informant and a CDR=0.5; ii) normal activities of daily living. iii) normal general cognitive function; iv) abnormal memory for age as measured by standard scores and education; v) a global CDR of 0.5 and no dementia; and vi) no history of significant vascular problems, insulin-requiring diabetes, or uncontrolled hypertension. Twenty MCI subjects have now been censored for varying reasons: cancer 2, co-morbidity 1, claustrophobia 2, loss of care support/moved 9, lost interest 5 and pacemaker 1.

Cognitive Testing:

[0043] All cognitive assessments were conducted within 4 weeks of the MR evaluation by the same team of neuropsychologists with re-evaluations at approximately 6 month intervals. A total of 476 cognitive tests have been performed with some subjects having as many as 9 evaluations. The battery of cognitive tests included a videotaped CDR plus the following: Logical Memory I, II, North American Adult Reading Test, Word Fluency: Phonetic and Semantic, Wisconsin Card Sorting Test, Trail Making Test A&B, Boston Naming Test, Draw-A-Clock, Depression Features Battery Version II, and Geriatric Depression Scale.

[0044] Results of radiologic and cognitive assessments were reviewed bimonthly. On the rare occasion if cognitive testing and neurologic examination indicates development of a disorder other than AD, e.g. frontotemporal dementia, progressive supranuclear palsy, primary progressive aphasia, the subject was removed from the study. Results of the neuropsychological testing were noted as abnormal if below>1.5 standard deviation (SD) on normative data based on age and education. The diagnosis of dementia is based on a clinical judgment (consensus conference), NINCDS-ADRDA criteria, and a Sum of Boxes (SOB) on the CDR≧3.5.(107)

The Cognitive Course of Cohorts and Current Neuropsychological (NP) Classification:

[0045] The cognitive course of the cohorts has been carefully monitored over the past 4.1 years and a five stage classification has emerged (Table 5). This classification is the matrix on which the MR and proteomic findings are co-analyzed. Special attention has been given to the MCI and control cases that under observation have proceeded to cognitive loss (MCI), "dementia," or "progressed MCI."

TABLE 5

Five Stage Cognitive NP Classification
NORMAL: Sum of Boxes = 0 to 0.5. CDR Memory = 0, with deference to clinical judgment. Some occasional abnormalities in neuropsychological tests. Logical memory consistently normal
UNSTABLE NORMAL (U-normal): Sum of Boxes ≦1 but variable. Some indication of CDR memory impairment. Trend upward or downward based on clinical judgment. Neuropsychological testing shows moderate abnormalities with improvement or decline. Clinical judgment.
MCI: Sum of boxes = 0.5-3.5 on several evaluations. CDR logical memory impairment with logical memory impairment on at least one evaluation. Neuropsychological testing is in MCI range inconsistently. Clinical judgment.
UNSTABLE MCI (U-MCI): Sum of Boxes varies from 0.5 to 3.5. Neuropsychological tests are congruent with Sum of Boxes. Considerable logical memory impairment. A downward trend indicated. Clinical judgment.
PROGRESSED MCI (PMCI) or mild AD [please confirm]: Sum of Boxes ≧3.5 on two occasions. Neuropsychological tests congruent with CDR. Logical Memory raw score low to zero. Clinical judgment.

[0046] The above scoring was derived after examination of results of multiple NP evaluations. Subjects with only one evaluation at baseline are classed as Normal or MCI.

TABLE 6

Table of 476 NP Evaluations

	Number of Evaluations:								
	1	2	3	4	5	6	7	8	9
Number of Participants:	9	7	12	17	26	12	15	3	2

[0047] Clear fluctuations in cognitive performance were found in both the Unstable Normal and Unstable MCI cohorts. The unstable MCI cohort has a cognitive status on occasion of dementia (CDR=3.5) but can improve to 3.0 with medication. A complete medication history has been obtained on all cohorts.

TABLE 7

Baseline NP (original two categories) and Current NP status per Table 5

		Current NP					
Baseline NP		Normal	U-Normal	MCI	U-MCI	PMCI	Total
n = 28	Normal	17	7	4	0	0	28
n = 75	MCI	1	9	40	8	17	75
Total		18	16	44	8	17	103

[0048] Table 7 gives the current NP status of the cohorts using the five stage classification as derived from entrance

classification (normal or MCI). Note progressive movement of normal to MCI and 10 MCI cases moving to U-Normal and Normal, 25 of the MCI cases have moved to U-MCI (8) and PMCI (17). The human experiment was designed to determine MR and proteomic changes during dementia development.

Materials and Methods

[0049] Low molecular weight protein harvesting by PrepCell

[0050] 100 μl of serum was mixed with SDS-PAGE loading buffer, boiled for 10 minutes, and loaded to PrepCell (Bio-Rad, CA). After 2 hours of electrophoresis, low molecular weight proteins migrated out of the gel and were eluted to collection tubes.

[0051] Nanoflow reversed-phase liquid chromatography-tandem MS (nanoRPLC-MS/MS)

[0052] Eluted proteins from PrepCell were further passed through detergent clean-up micro kit ProteoSpin (Norgen, Canada) to remove the SDS in the elution buffer that could interfere with mass spectrometry analysis. The cleaned proteins were reduced by 10 mM DTT, alkylated by 50 mM iodoacetamide, and digested by trypsin (from Promega) at 37° C. overnight. Tryptic peptides were further purified by Sep-Pak cartridges (Waters, Mass.) and analyzed by reversed-phase liquid chromatography nanospray tandem mass spectrometry using a linear ion-trap mass spectrometer (LTQ, ThermoElectron, San Jose, Calif.). Separation column was slurry-packed in-house with 5 μm, 200 Å pore size C18 resin (Michrom BioResources, CA) in 100 μm i.d.×10 cm long fused silica capillary (Polymicro Technologies, Phoenix, Ariz.) with a laser-pulled tip. After sample injection, the column was washed for 5 minutes with mobile phase A (0.4% acetic acid) and peptides were eluted using a linear gradient of 0% mobile phase B (0.4% acetic acid, 80% acetonitrile) to 50% mobile phase B in 30 minutes at 250 nanoliter/min, then to 100% B in an additional 5 minutes. The LTQ mass spectrometer was operated in a data-dependent mode in which each full MS scan was followed by five MS/MS scans where the five most abundant molecular ions were dynamically selected for collision-induced dissociation (CID) using a normalized collision energy of 35%.

[0053] The ETD method with Thermo LTQ instrument also can be used. The ETD method (Syka et al. Proc. Natl. Acad. Sci. U.S.A. (2004) 101:9528-9533) accomplishes peptide fragmentation in the MS-MS analysis by electron transfer, in contrast to the traditional collision-induced dissociation (CID). ETD has been demonstrated to be more powerful than CID in providing more easily interpretable MS-MS sequence data from larger, higher-charge state peptides (including intact small proteins), as well as those with post-translational modifications (PTMs). (Coon et al. Proc. Natl. Acad. Sci. U.S.A. (2005) 102:9463-9468). The novel combination of CID and ETD analysis can enhance peptide identification productivity.

Example 2

Serum Proteomic Analysis

[0054] Fractionating LMW Proteins

[0055] In the first serum proteomic study, A, 100-μL aliquots of whole serum samples were prepared for high performance liquid chromatography/mass spectrometry (LC-MS) analysis by reduction and alkylation (DTT, iodoacetamide) followed by digestion of the proteins followed by LTQ mass spectroscopy. For subsequent studies, B and C a proteome subset consisting of low molecular weight (LMW) proteins was prepared from each serum sample to reduce the complexity of the protein mixture. The resulting LMW proteins were fractionated by SDS-PAGE and proteins were visualized by Coomassie staining.

[0056] For study B, the samples consisted of pooled serum samples from 14-15 subjects (control, MCI and PMCI). With improved LMW isolation, serum proteins with molecular weights 25 kDa were collected and fractionated by SDS-PAGE.

[0057] For study C serum samples from 5 individuals who had progressed from control to MCI (1 sample) and from MCI to PMCI were prepared to yield LMW proteins and the LC-MS analyses performed using a Thermo hybrid LTQ-Orbitrap mass spectrometer. This represents the state of the art in the MS technology and provides several advantages compared with the LTQ, such as superior high mass resolution and mass accuracy in the spectra acquired of the precursor peptide molecular ions.

Data Analysis and Results

[0058] MS-MS spectra were searched against a public human protein database (NCBI) using the SEQUEST search algorithm to obtain matches. Results in study A only identified abundant serum proteins. The results led to a focus on low molecular weight (LMW) serum proteins (study B). The threshold of 50 kDa was insufficient to reduce the complexity of proteins, and TCA protein precipitation resulted in unacceptable protein loss. As a result, a high-quality analysis of study B was conducted using pooled samples of a relatively large number (14) of individual subject serum samples per group. This study compared LMW proteins identified in control vs. MCI vs. PMCI sample/subject groups. This qualitative analysis identified candidate biomarkers (differentially abundant proteins). The objective of study C was to identify LMW serum proteins with differential abundances that correlated with progression from MCI to PMCI (4 individuals; 4 sample pairs) and control to MCI (1 individual; 1 pair of samples) diagnoses. These 10 sample analyses yielded identification of more than 500 proteins. No major differences in apoE genotype between subjects are found in the subject cohorts.

[0059] Determination of candidate biomarker proteins was achieved by comparing the number of tandem mass spectra (MS2 scans) that were matched to peptide sequences corresponding to the source proteins in the database against which the data were searched. A higher abundance protein relative to a lower abundance one will yield a greater number of, and more abundant, peptides from the enzyme digest, and these peptides often will result in more matched MS2 spectra. In this way, the number of MS2 spectra, termed "spectral count", is an approximate measure of the relative abundance of proteins in a mixture (Analytical Chemistry, 76(14), 4193-4201 (2004)). The evaluation of candidate differentially abundant proteins focuses on proteins that yielded a 50% or greater spectral count difference in one sample set versus the other.

[0060] The results of the studies are shown in Tables 8-10.

Example 3

Detection of Brain Microhemorrhages

[0061] SH are counted independently at two sites (Detroit MRI Institute for Biomedical Research (DMRI) and Loma

Linda University (LLU)) but currently primarily at LLU by raters who are integral to the project using an identical protocol blinded to clinical status. SWI filtered phase images were reviewed for the presence of SH one 2 mm slice at a time. All magnitude images, high pass (HP) filtered phase images and contrast enhanced SWI magnitude images were used in the data review process. Images were placed side by side for identifying SH and HP filtered phase images are used to mark them with review above and below to check for vascular connections. One slice may contain more than one SH as in FIG. **2**., then every SH was highlighted with a different colored boundary. Any slice that showed a SH appearing in a previous slice was not recounted. SH are assigned a slice and serial number, size (1-3, 3-5, >5 mm O.D.) and anatomical location. Differentiating microaneurysms with blood in and/or around vessel walls was uncertain since blood collecting in a microaneurysm produces a significant signal void. Subarachnoid and sulcal vascular voids, symmetrical focal basal ganglia signal losses were not counted.

[0062] The biomarkers identified as associated with brain microhemorrages are presented in Table 11.

Example 4

Further Evaluation of Biomarkers

[0063] The inventive biomarkers can be evaluated further using a variety of methods. In addition to traditional biological validation assays, mass spectrometric methods can be used. One method of validation is Western assays of serum samples using commercially available antibodies specific for the candidate proteins. If antibodies are not available commercially, they can be produced readily using methods well know in the art and disclosed herein.

[0064] In addition, triple quadruple mass spectrometry (TQMS) technology can be used to further evaluate the biomarkers. The technique employs multiple reaction monitoring (MRM), which consists of (1) detection and selection of molecular ions with the first quadruple, (2) fragmentation of these ions in the second quadruple, and (3) detection of a small number of known fragment ions in the third quadruple. The analysis yields an analyte's molecular weight and the relative abundances of fragment ions that are characteristic of analyte structure and chromatographic elution time (LC/MS). Modern TQMS instruments provide advanced MRM performance with higher resolution and accuracy mass measurement, fast electronics for switching between a large number of selected analyte and fragmentation masses monitored, and ease of use. Inherent advantages of LC/TQMS include high detection sensitivity, large dynamic range of detection response, and the ability to incorporate stable isotope labeled synthetic analogs of the targeted analytes, which allows superior quantitative analytical performance.(Anderson, Mol. Cell. Proteomics (2006) 5:573-588; Frewen et al. Anal. Chem. (2006) 78:5678-5684)

[0065] Such studies can be augmented with spiked internal standards, as in the discovery phase, and with isotopically-labeled synthetic analogs of the biomarkers. In addition, an autosampler and other methods can be used to enhance throughput (e.g., plate-based sample peptide enrichment and cleanup prior to LC/MS).

TABLE 1

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
(O60602) Toll-like receptor 5 precursor (Toll/interleukin-1 receptor-like protein 3)	TLR5_HUMAN	97713	1	LYFCGLSDAVLKD GYFRNLK	2379.22	126	145
(O60687) Sushi-repeat-containing protein, X-linked 2	O60687	52954	2	DSADGTITRVTLR	1404.74	212	224
(O95793) Double-stranded RNA-binding protein Staufen homolog	STAU_HUMAN	63250	3	ALRILQNEPLPERL EVNGR	2217.25	156	174
(P01764) Ig heavy chain V-III region VH26 precursor	HV3C_HUMAN	12565	4	AEDTAVYYCAK	1290.57	107	117
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	5	AADDTWEPFASGK	1394.62	56	68
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	6	ALGISPFHEHAEVV FTANDSGPRR	2607.31	101	124
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	7	GSPAINVAVHVFR	1366.76	42	54

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	8	GSPAINVAVHVFR K	1494.85	42	55
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	9	KAADDTWEPFASG K	1522.72	55	68
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	10	RYTIAALLSPYSYS TTAVVTNPKE	2645.38	124	147
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	11	TSESGELHGLTTEE EFVEGIYKVEIDTK	3140.52	69	96
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	12	VLDAVRGSPAINV AVHVFR	2020.15	36	54
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	13	YTIAALLSPYSYST TAVVTNPKE	2489.28	125	147
(P09758) Tumor-associated calcium signal transducer 2 precursor (Pancreatic carcinoma marker protein GA733-1) (Cell surface glycoprotein Trop-2)	TACD2_HUMAN	35692	14	HRPTAGAFNHSDL DAELRR	2163.08	160	178
(P09874) Poly [ADP-ribose] polymerase 1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase 1) (Poly [ADP-ribose]synthetase 1)	PARP1_HUMAN	112939	15	EDAIEHFMKLYEE K	1781.84	607	620
(P09874) Poly [ADP-ribose] polymerase 1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase 1) (Poly [ADP-ribose]synthetase 1	PARP1_HUMAN	112939	16	MKLTLKGGAAVD PDSGLEHSAHVLE K	2703.41	522	547
(P10643) Complement component C7 precursor	CO7_HUMAN	93499	17	AASGTQNNVLR	1130.59	362	372
(P10643) Complement component C7 precursor	CO7_HUMAN	93499	18	FSSHGCK	822.36	348	354
(P10643) Complement component C7 precursor	CO7_HUMAN	93499	19	MHVLHCQGR	1137.54	745	753
(P10643) Complement component C7 precursor	CO7_HUMAN	93499	20	SYTSHTNEIHK	1316.62	234	244
(P13667) Protein disulfide-isomerase A4 precursor (EC 5.3.4.1) (Protein ERp-72) (ERp72)	PDIA4_HUMAN	72916	21	LAPEYEKAAKELS K	1576.86	212	225
(P16591) Proto-oncogene tyrosine-protein kinase FER (EC 2.7.1.112) (p94-FER) (c-FER)	FER_HUMAN	94609	22	FLQEAKILKQYDH PNIVK	2184.22	605	622

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
(P20701) Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha chain) (CD11a)	ITAL_HUMAN	128804	23	EGVNITICFQIKS LYPQFQGR	2498.29	646	666
(P22792) Carboxypeptidase N subunit 2 precursor (Carboxy-peptidase N polypeptide 2) (Carboxypeptidase N 83 kDa chain) (Carboxypeptidase N regulatory subunit) (Carboxy-peptidase N large subunit)	CPN2_HUMAN	60599	24	TLNLAQNLLAQLP EELFHPLTSLQTLK	3045.70	173	199
(P35542) Serum amyloid A-4 protein precursor (Consti-tutively expressed serum amy-loid A protein) (C-SAA)	SAA4_HUMAN	14789	25	FRPDGLPK	929.52	121	128
(Q05513) Protein kinase C, zeta type (EC 2.7.1.37) (nPKC-zeta)	KPCZ_HUMAN	67644	26	EGLGPGDTTSTFCG TPNYIAPEILR	2666.28	400	424
(Q15166) Serum paraoxonase/ lactonase 3 (EC 3.1.1.-)	PON3_HUMAN	39590	27	ILIGTVFHK	1027.63	340	348
(Q4V312) Colony stimulating factor 2 receptor, alpha, low-affinity (Granulocyte-macrophage)	Q4V312	46884	28	DKLNDNHEVEDE MGPQR	2025.89	364	380
(Q6N092) Hypothetical pro-tein DKFZp686K18196 (Fragment)	Q6N092	56405	29	SAVQGPPDR	926.47	335	343
(Q6N092) Hypothetical pro-tein DKFZp686K18196 (Fragment)	Q6N092	56405	30	SAVQGPPDR	926.47	335	343
(Q7Z3Z2) Protein C1orf36	CA036_HUMAN	22686	31	PRGSLATFK	976.56	146	154
(Q8N7W7) Hypothetical protein FLJ40259	Q8N7W7	66111	32	ILIDGTLIIFR	1273.79	124	134
(Q96MA6) Hypothetical protein FLJ32704 (Chromosome 9 open reading frame 98) (OTTHUMP00000022737)	Q96MA6	54909	33	KTVPSALLVQLIQE RLAEEDCIK	2653.46	111	133
(Q96S24) Hypothetical pro-tein gs30	Q96S24	3503	34	GMGSDRTALSLQG AWGIFLSTFYK	2606.31	3	26
(Q99996) A-kinase anchor pro-tein 9 (Protein kinase A anchoring protein 9) (PRKA9) (A-kinase anchor protein 450 kDa) (AKAP 450) (A-kinase anchor protein 350 kDa) (AKAP 350) (hgAKAP 350) (AKAP 120-like protein) (Hyperion pro-tein) (Yotiao protein) (Centrosome- and Golgi-localized PKN-associated protein) (CG-NAP)	AKAP9_HUMAN	453646	35	CEVNAEDKENSGD YISENEDPELQDYR	3218.33	1232	1258

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
(Q99996) A-kinase anchor protein 9 (Protein kinase A anchoring protein 9) (PRKA9) (A-kinase anchor protein 450 kDa) (AKAP 450) (A-kinase anchor protein 350 kDa) (AKAP 350) (hgAKAP 350) (AKAP 120-like protein) (Hyperion protein) (Yotiao protein) (Centrosome- and Golgi-localized PKN-associated protein) (CG-NAP)	AKAP9_HUMAN	453646	36	KAYINTISSLKDLITK	1808.05	2989	3004
(Q9BXB9) LIM mineralization protein 2	Q9BXB9	46492	37	HSQPATPTPLQSR	1419.73	212	224
(Q9H2I2) HNRBF-2	Q9H2I2	31791	38	NCYSLLNLAEVRSKYLGK	2128.12	236	253
(Q9H2I2) HNRBF-2	Q9H2I2	31791	39	NCYSLLNLAEVRSKYLGK	2128.12	236	253
(Q9NPP6) Immunoglobulin heavy chain variant (Fragment)	Q9NPP6	44767	40	VEDTAVYYCAR	1346.61	48	58
(Q9NYQ6) Cadherin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo homolog 2) (hFmi2)	CELR1_HUMAN	329464	41	ENLEVGYEVLTIRASDRDSPINANLR	2944.51	364	389
(Q9NYQ6) Cadherin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo homolog 2) (hFmi2)	CELR1_HUMAN	329464	42	ETKETHVLR	1112.61	314	322
(Q9NYQ6) Cadherin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo homolog 2) (hFmi2)	CELR1_HUMAN	329464	43	QFVGCMRNLSVDGK	1610.78	1616	1629
(Q9NYQ6) Cadherin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo homolog 2) (hFmi2)	CELR1_HUMAN	329464	44	VPGGTRAFALRPGCTYAVGAACTPR	2606.31	35	59
adenylosuccinate synthase [*Homo sapiens*]	gi|34577063| ref| NP_001117.2|	50080	45	DGVYFLYEALHGPPKK	1833.95	233	248
alpha 1B-glycoprotein [*Homo sapiens*]	gi|21071030| ref| NP_570602.2|	54235	46	ATWSGAVLAGR	1088.59	407	417
alpha 1B-glycoprotein [*Homo sapiens*]	gi|21071030| ref| NP_570602.2|	54235	47	SLPAPWLSMAPVSWITPGLK	2151.17	115	134
alpha 1B-glycoprotein [*Homo sapiens*]	gi|21071030| ref| NP_570602.2|	54235	48	SWVPHTFESELSDPVELLVAES	2471.20	474	495
alpha 1B-glycoprotein [*Homo sapiens*]	gi|21071030| ref| NP_570602.2|	54235	49	TPGAAANLELIFVGPQHAGNYR	2296.18	448	469

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	50	ADLSGITGAR	960.51	341	350
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	51	AVLDVFEEGTEAS AATAVK	1907.96	361	379
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	52	DYNLNDILLQLGIE EAFTSK	2296.17	321	340
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	53	ITLLSALVETR	1215.73	380	390
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	54	NLAVSQVVHK	1094.63	351	360
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	55	YNLNDILLQLGIEE AFTSK	2181.14	322	340
Apolipoprotein C-I precursor (Apo-CI) (ApoC-I)	APOC1_HUMAN	9314	56	EWFSETFQK	1201.55	66	74
Apolipoprotein C-I precursor (Apo-CI) (ApoC-I)	APOC1_HUMAN	9314	57	IKQSELSAK	1003.58	55	63
Apolipoprotein C-I precursor (Apo-CI) (ApoC-I)	APOC1_HUMAN	9314	58	LKEFGNTLEDK	1293.67	37	47
Apolipoprotein C-I precursor (Apo-CI) (ApoC-I)	APOC1_HUMAN	9314	59	TPDVSSALDK	1032.52	27	36
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518| ref| NP_000474.2|	11266	60	ESLSSYWESAK	1286.59	42	52
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518| ref| NP_000474.2|	11266	61	LRDLYSK	894.50	71	77
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518| ref| NP_000474.2|	11266	62	STAAMSTYTGIFTD QVLSVLK	2233.14	78	98
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518| ref| NP_000474.2|	11266	63	STAAMSTYTGIFTD QVLSVLKGEE	2548.25	78	101
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518| ref| NP_000474.2|	11266	64	TAAQNLYEK	1037.53	53	61
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518| ref| NP_000474.2|	11266	65	TYLPAVDEK	1035.54	62	70
Apolipoprotein C-IV precursor (Apo-CIV) (ApoC-IV)	APOC4_HUMAN	14536	66	AWFLESK	880.46	99	105

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Apolipoprotein C-IV precursor (Apo-CIV) (ApoC-IV)	APOC4_HUMAN	14536	67	DGWQWFWSPSTFR	1699.77	67	79
Apolipoprotein C-IV precursor (Apo-CIV) (ApoC-IV)	APOC4_HUMAN	14536	68	ELLETVVNR	1072.60	56	64
apolipoprotein L1 isoform a precursor [*Homo sapiens*]	gi|21735614| ref| NP_003652.2|, gi|217353616| ref| NP_663318.1|	43957	69	ILQADQEL	929.49	391	398
apolipoprotein L1 isoform a precursor [*Homo sapiens*]	gi|21735614| ref| NP_003652.2|, gi|21735616| ref| NP_663318.1|	43957	70	LNILNNNYK	1105.60	382	390
apolipoprotein M [*Homo sapiens*]	gi|22091452| ref| NP_061974.2|	21236	71	EELATFDPVDNIVF NMAAGSAPMQLH LR	3086.51	58	85
apolipoprotein M [*Homo sapiens*]	gi|22091452| ref| NP_061974.2|	21236	72	EFPEVHLGQWYFI AGAAPTK	2261.14	38	57
apolipoprotein M [*Homo sapiens*]	gi|22091452| ref| NP_061974.2|	21236	73	KWIYHLTEGSTDL R	1718.89	99	112
apolipoprotein M [*Homo sapiens*]	gi|22091452| ref| NP_061974.2|	21236	74	MKDGLCVPR	1091.53	90	98
apolipoprotein M [*Homo sapiens*]	gi|22091452| ref| NP_061974.2|	21236	75	SLTSCLDSK	1010.48	163	171
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	76	EFTPPVQAAYQK	1378.70	122	133
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	77	FFESFGDLSTPDAV MGNPK	2058.95	42	60
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	78	FFESFGDLSTPDAV MGNPKVK	2286.11	42	62
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	79	GTFATLSELHCDK	1478.70	84	96
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1	15980	80	GTFATLSELHCDKL HVDPENFR	2586.24	84	105
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	81	KVLGAFSDGLAHL DNLK	1797.99	67	83
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	82	LHVDPENFR	1126.56	97	105

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	83	LLGNVLVCVLAHH FGK	1776.99	106	121
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	84	LLVVYPWTQR	1274.73	32	41
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	85	LLVVYPWTQRFFE SFGDLSTPDAVMG NPK	3314.66	32	60
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	86	SAVTALWGK	932.52	10	18
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	87	SAVTALWGKVNV DEVGGEALGR	2228.17	10	31
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	88	SAVTALWGKVNV DEVGGEALGRLLV VYPWTQR	3483.87	10	41
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	89	VLGAFSDGLAHLD NLK	1669.89	68	83
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	90	VNVDEVGGEALGR	1314.67	19	31
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	91	VVAGVANALAHK	1149.67	134	145
beta globin [*Homo sapiens*]	gi|4504349| ref| NP_000509.1|	15980	92	VVAGVANALAHK YH	1449.80	134	147
biliverdin reductase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419| ref| NP_000704.1|	22101	93	LPSEGPRPAHVVV GDVLQAADVDK	2469.31	40	63
biliverdin reductase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419| ref| NP_000704.1|	22101	94	NIVAAMK	746.42	93	99
biliverdin reductase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419| ref| NP_000704.1|	22101	95	PAHVVVGDVLQA ADVDK	1732.92	47	63
biliverdin reductase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419| ref| NP_000704.1|	22101	96	TVAGQDAVIVLLG TR	1512.88	64	78
biliverdin reductase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419| ref| NP_000704.1|	22101	97	VVACTSAFLLWDP TK	1707.88	106	120
biliverdin reductase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419| ref| NP_000704.1|	22101	98	YVAVMPPHIGDQP LTGAYTVTLDGR	2671.36	146	170
chromosome 1 open reading frame 48 [*Homo sapiens*]	gi|21361470| ref| NP_056286.2|	32112	99	EISEAMK	823.39	183	189

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
chromosome 9 open reading frame 19 [*Homo sapiens*]	gi|11641247| ref| NP_071738.1|	17200	100	EAQQYSEALASTR	1453.69	38	50
citron [*Homo sapiens*]	gi|32698688| ref| NP_009105.1|	231418	101	QQKFYLETQAGK	1440.75	814	825
coagulation factor II precursor [*Homo sapiens*]	gi|4503635| ref| NP_000497.1|	70019	102	ELLESYIDGR	1194.60	354	363
coagulation factor II precursor [*Homo sapiens*]	gi|4503636| ref| NP_000497.1|	70019	103	HQDFNSAVQLVENFCR	1963.91	248	263
coagulation factor II precursor [*Homo sapiens*]	gi|4503635| ref| NP_000497.1|	70019	104	IVEGSDAEIGMSPWQVMLFR	2265.11	364	383
coagulation factor II precursor [*Homo sapiens*]	gi|4503635| ref| NP_000497.1|	70019	105	LAVTTHGLPCLAWASAQAK	1995.05	225	243
coagulation factor II precursor [*Homo sapiens*]	gi|4503635| ref| NP_000497.1|	70019	106	SEGSSVNLSPPLEQCVPDR	2070.98	199	217
coagulation factor II precursor [*Homo sapiens*]	gi|4503635| ref| NP_000497.1|	70019	107	SLEDKTERELLESYIDGR	2153.07	346	363
coagulation factor II precursor [*Homo sapiens*]	gi|4503635| ref| NP_000497.1|	70019	108	TATSEYQTFFNPR	1561.73	315	327
coagulation factor II precursor [*Homo sapiens*]	gi|4503635| ref| NP_000497.1|	70019	109	TFGSGEADCGLRPLFEK	1883.90	328	344
coagulation factor II precursor [*Homo sapiens*]	gi|4503635| ref| NP_000497.1|	70019	110	YGFYTHVFR	1189.58	600	608
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|	192735	111	DFALLSLQVPLK	1343.79	81	92
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|, gi|67190748| ref| NP_009224.2|	192735	112	DFALLSLQVPLKDAK	1657.95	81	95
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|	192735	113	DHAVDLIQK	1038.56	1043	1051
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|, gi|67190748| ref| NP_009224.2|	192735	114	EPFLSCCQFAESLR	1743.78	730	743

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|, gi|67190748| ref| NP_009224.2|	192735	115	GLEEELQFSLGSK	1436.73	1353	1365
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|	192735	116	GPEVQLVAHSPWLK	1560.85	105	118
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|	192735	117	KADGSYAAWLSR	1324.66	1061	1072
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|	192735	118	LHLETDSLALVAL GALDTALYAAGSK	2613.41	589	614
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|, gi|67190748| ref| NP_009224.2|	192735	119	SCGLHQLLR	1083.57	96	104
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|, gi|67190748| ref| NP_009224.2|	192735	120	TYNVLDMK	983.49	1383	1390
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|	192735	121	VDFTLSSER	1053.52	72	80
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|	192735	122	VGLSGMAIADVTL LSGFHALR	2128.16	1478	1498
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|	192735	123	VLSLAQEQVGGSP EK	1541.82	1085	1099
complement component 4B pre-proprotein [*Homo sapiens*]	gi|50345296| ref|NP_001002029.1|	192735	124	YVSHFETEGPHVL LYFDSVPTSR	2680.30	1511	1533
complement component 5 [*Homo sapiens*]	gi|38016947| ref| NP_001726.2|	188291	125	FQNSAILTIQPK	1359.76	79	90
complement component 5 [*Homo sapiens*]	gi|38016947| ref| NP_001726.2|	188291	126	MVETTAYALLTSL NLK	1783.95	1247	1262
complement component 5 [*Homo sapiens*]	gi|38016947| ref| NP_001726.2|	188291	127	VFQFLEK	910.50	623	629
complement component 5 [*Homo sapiens*]	gi|38016947| ref| NP_001726.2|	188291	128	YIYPLDSLTWIEYW PR	2115.06	1635	1650
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	129	AEATTLHVAPQGT AMAVSTFR	2159.09	70	90

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	130	ANFDAQQFAGTW LLVAVGSACR	2382.17	40	61
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	131	GAVHVVVAETDY QSFAVLYLER	2466.27	121	142
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	132	KLDGICWQVR	1274.67	91	100
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	133	LDGICWQVR	1146.57	92	100
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	134	QLYGDTGVLGR	1178.62	101	111
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	135	RPASPISTIQPK	1294.75	28	39
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	136	SLPVSDSVLSGFEQ R	1620.82	154	168
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	137	VQEAHLTEDQIFYF PK	1964.98	169	184
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393| ref| NP_000597.1|	22201	138	YGFCEAADQFHVL DEVR	2055.92	185	201
complement factor H isoform a precursor [*Homo sapiens*]	gi|62739186| ref| NP_000177.2|	139052	139	EIMENYNIALR	1365.68	1172	1182
complement factor H isoform a precursor [*Homo sapiens*]	gi|62739186| ref| NP_000177.2|	139052	140	KGEWVALNPLR	1282.73	68	78
complement factor H isoform a precursor [*Homo sapiens*]	gi|62739186| ref| NP_000177.2|, gi|62739188| ref|NP_ 001014975.1|	139052	141	NTEILTGSWSDQT YPEGTQAIYK	2602.23	29	51
complement factor H isoform a precursor [*Homo sapiens*]	gi|62739186| ref| NP_000177.2|	139052	142	SLGNVIMVCR	1148.59	58	67
core-binding factor, runt domain, alpha subunit 2; translocated to, 2 isoform MTGR1b [*Homo sapiens*]	gi|4826663| ref| NP_005084.1|	67115	143	MAKESGISLKEIQV LAR	1873.06	1	17
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	144	EFTPQMQAAYQK	1441.68	122	133
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	145	GTFSQLSELHCDK	1521.70	84	96

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	146	GTFSQLSELHCDKL HVDPENFR	2629.25	84	105
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	147	LLGNVLVCVLAR	1326.79	106	117
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	148	LLVVYPWTQR	1274.73	32	41
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	149	TAVNALWGK	959.53	10	18
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	150	VLGAFSDGLAHLD NLK	1669.89	68	83
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	151	VNVDAVGGEALGR	1256.66	19	31
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	152	VVAGVANALAHK	1149.67	134	145
delta globin [*Homo sapiens*]	gi|4504351| ref| NP_000510.1|	16037	153	VVAGVANALAHK YH	1449.80	134	147
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)	DESP_HUMAN	331765	154	ANSSATETINK	1135.56	1517	1527
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)	DESP_HUMAN	331765	155	GFFDPNTEENLTYL QLK	2028.99	2414	2430
diacylglycerol kinase, theta [*Homo sapiens*]	gi|40806175| ref| NP_001338.2|	101135	156	PGSPACSPVLGSGG RAR	1625.82	20	36
Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A]	FIBA_HUMAN	94955	157	TFPGFFSPMLGEFV SETESR	2265.05	528	547
Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A]	FIBA_HUMAN	94955	158	VTSGSTTTTR	1010.51	449	458
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629| ref| NP_068657.1|, gi|4503689| ref| NP_000499.1|	69739	159	ESSSHHPGIAEFPS R	1637.77	559	573
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629| ref| NP_068657.1|, gi|4503689| ref| NP_000499.1|	69739	160	EVDLKDYEDQQK	1509.71	191	202

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629| ref| NP_068657.1|, gi|4503689| ref| NP_000499.1|	69739	161	GLIDEVNQDFTNR	1520.73	72	84
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629| ref| NP_068657.1|, gi|4503689| ref| NP_000499.1|	69739	162	GSESGIFTNTK	1140.55	548	558
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629| ref| NP_068657.1|, gi|4503689| ref| NP_000499.1|	69739	163	HPDEAAFFDTASTGK	1593.72	513	527
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629| ref| NP_068657.1|, gi|4503689| ref| NP_000499.1|	69379	164	HRHPDEAAFFDTASTGK	1886.88	511	527
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629| ref| NP_068357.1|, gi|4503689| ref| NP_000499.1|	69739	165	TFPGFFSPMLGEFVSETESR	2265.05	528	547
gelsolin isoform a precursor [*Homo sapiens*]	gi|4504165| ref| NP_000168.1|	85680	166	DSQEEEKTEALTSAK	1665.78	714	728
gelsolin isoform a precursor [*Homo sapiens*]	gi|4504165| ref| NP_000168.1|	85680	167	EVQGFESATFLGYFK	1722.84	148	162
gelsolin isoform a precursor [*Homo sapiens*]	gi|4504165| ref| NP_000168.1|	85680	168	FDLVPVPTNLYGDFFTGDAYVILK	2704.39	76	99
gelsolin isoform a precursor [*Homo sapiens*]	gi|4504165| ref| NP_000168.1|	85680	169	HVVPNEVVVQR	1275.72	178	188
gelsolin isoform a precursor [*Homo sapiens*]	gi|4504165| ref| NP_000168.1|	85680	170	PNSMVVEHPEFLK	1526.77	49	61
hect domain and RLD 5 [*Homo sapiens*]	gi|7705931| ref| NP_057407.1|	116834	171	RTTEMMPVYLDLNK	1726.85	434	447
Hepatitis B virus receptor binding protein (Fragment)	Q6PYx1	38143	172	GQGTTVTVSSASTK	1323.68	9	22
Hepatitis B virus receptor binding protein (Fragment)	Q6PYX1	38143	173	GTTVTVSSASTK	1138.60	11	22
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	174	ALDLINKR	942.57	34	41

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	175	DGYLFQLLR	1124.61	44	52
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	176	DSPVLIDFFEDTER	1682.79	140	153
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	177	GEVLPLPEANFPSF PLPHHK	2226.17	467	486
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	178	HPLKPDNQPFPQSV SESCPGK	2349.13	487	507
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	179	KGEVLPLPEANFPS FPLPHHK	2354.27	466	486
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	180	LPPLR	595.39	461	465
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	181	RDGYLFQLLR	1280.71	43	52
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	182	RPSEIVIGQCK	1286.69	96	106
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489| ref| NP_000403.1|	59559	183	SGFPQVSMFFTHTF PK	1857.90	510	525
Hypothetical protein DKFZp686J11235 (Fragment)	Q6MZW0	54441	184	GTTTFAVTSILR	1266.71	441	452
Hypothetical protein DKFZp686J11235 (Fragment)	Q6MZW0	54441	185	TPLTATLSK	931.55	366	374
Hypothetical protein DKFZp686J11235 (Fragment)	Q6MZW0	54441	186	VTVSSASPTSPK	1160.62	149	160
Hypothetical protein DKFZp781M0386	Q5CZ94	24984	187	AGVETTKPSK	1017.56	179	188
Hypothetical protein DKFZp781M0386	Q5CZ94	24984	188	ANPTVTLFPPSSEE LQANK	2043.04	133	151
Hypothetical protein DKFZp781M0386	Q5CZ94	24984	189	VTVLGQPK	841.51	125	132
Ig heavy chain V-II region WAH	HV2F_HUMAN	14099	190	TGYYWGWIR	1201.58	32	40
Ig heavy chain V-III region GAL	HV3T_HUMAN	12708	191	GLEWVANIK	1029.57	44	52
Ig kappa chain V-II region Cum	KV2A_HUMAN	12659	192	FSGSGSGTDFTLK	1303.62	69	81
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984| ref| NP_002209.2|	103340	193	AEAQAQYSAAVAK	1307.66	99	111

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984| ref| NP_002209.2|	103340	194	AGFSWIEVTFK	1284.66	778	788
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984| ref| NP_002209.2|	103340	195	ANTVQEATFQMELPK	1706.84	61	75
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984| ref| NP_002209.2|	103340	196	FSSHVGGTLGQFYQEVLWGSPAASDDGR	2968.39	867	894
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984| ref| NP_002209.2|	103340	197	GPDVLTATVSGK	1144.62	501	512
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984| ref| NP_002209.2|	103340	198	LWAYLTIQQLLEQTVSASDADQQALR	2961.53	547	572
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984| ref| NP_002209.2|	103340	199	MNFRPGVLSSR	1263.66	658	668
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984| ref| NP_002209.2|	103340	200	NVHSGSTFFK	1123.55	617	626
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984| ref| NP_002209.2|	103340	201	VTIGLLFWDGR	1276.71	843	853
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	202	AEAESLYQSK	1125.54	367	376
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	203	AQYEDIAQK	1065.52	356	364
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	204	DYQELMNTK	1141.52	464	472
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	205	EQIKSLNNQFASFIDK	1881.97	182	197
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	206	FLEQQNQVLQTK	1475.79	200	211
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	207	FSSCGGGGGSFGAGGGFGSR	1765.74	46	65
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	208	GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR	2383.95	519	549
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	209	IEISELNR	973.53	396	403
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	210	LALDLEIATYR	1277.71	473	483

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	211	LNDLEDALQQAK	1357.70	444	455
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	212	MSGECAPNVSVSV STSHTTISGGGSR	2565.17	493	518
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	213	NKLNDLEDALQQAK	1599.83	442	455
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	214	NKYEDEINKR	1308.65	268	277
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	215	NMQDMVEDYR	1300.53	258	267
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	216	NMQDMVEDYR	1300.53	258	267
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	217	QISNLQQSISDAEQ R	1716.85	418	432
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	218	SKAEAESLYQSK	1340.67	365	376
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	219	SLDLDSIIAEVK	1302.72	344	355
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	220	THNLEPYFESFINN LR	1993.98	224	239
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	221	TLLEGEESR	1033.52	484	492
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	223	TNAENEFVTIK	1265.64	278	288
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	224	WELLQQVDTSTR	1475.75	212	223
keratin 1 [*Homo sapiens*]	gi|17318569| ref| NP_006112.2|	66050	225	YEELQITAGR	1179.60	377	386
Keratin 10	Q14664	57231	226	GSSGGGCFGGSSG GYGGLGGFGGGSF R	2342.99	53	79
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	227	ADLEMQIESLTEEL AYLK	2112.04	267	284
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	228	AETECQNTEYQQL LDIK	2082.97	423	439

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	229	ALEESNYELEGK	1381.65	166	177
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	230	DAEAWFNEK	1109.49	335	343
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	231	ELTTEIDNNIEQIS SYK	1996.97	346	362
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	232	GSLGGGFSSGGFSG GSFSR	1707.77	41	59
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	233	GSSGGGCFGGSSG GYGGLGGFGGGSF R	2342.99	60	86
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	234	IKEWYEK	995.52	178	184
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	235	LASYLDK	809.44	157	163
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	236	LENEIQTYR	1165.59	442	450
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	237	LKYENEVALR	1234.68	236	245
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	238	NVSTGDVNVEMN AAPGVDLTQLLNN MR	2872.39	296	322
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	239	SKELTTEIDNNIEQ ISSYK	2212.10	344	362
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	240	SLLEGEGSSGGGGR	1262.60	451	464
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	241	SQYEQLAEQNR	1365.64	323	333
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	242	SQYEQLAEQNRK	1493.73	323	334
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	243	TIDDLKNQILNLTT DNANILLQIDNAR	3052.63	202	228
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	244	VLDELTLTK	1031.60	258	266
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	245	VTMQNLNDR	1090.53	148	156

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	246	YCVQLSQIQAQISA LEEQLQQIR	2746.42	400	422
keratin 10 [*Homo sapiens*]	gi|40354192| ref| NP_000412.2|	58811	247	YENEVALR	993.50	238	245
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	248	DIENQYETQITQIE HEVSSSGQEVQSS AK	3264.51	340	368
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	249	EIETYHNLLEGGQE DFESSGAGK	2510.13	450	472
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	250	FSSSSGYGGGSSR	1235.53	47	59
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	251	GGGGSFGYSYGGG SGGGFSASSLGGGF GGGSR	2705.16	64	95
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	252	HGVQELEIELQSQL SK	1837.97	375	390
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	253	IKFEMEQNLR	1307.68	241	250
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	254	IQDWYDKK	1095.55	185	192
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	255	LASYLDK	809.44	164	170
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	256	NYSPYYNTIDDLK DQIVDLTVGNNK	2902.41	200	224
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	257	SDLEMQYETLQEE LMALK	2171.03	272	289
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	258	SGGGGGGGLGSGG SIR	1232.60	14	29
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	259	STMQELNSR	1065.50	155	163
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	260	TLLDIDNTR	1060.56	225	233
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	261	VQALEEANNDLEN K	1586.77	171	184
keratin 9 [*Homo sapiens*]	gi|55956899| ref| NP_000217.2|	62048	262	YCGQLQMIQEQIS NLEAQITDVR	2753.32	405	427

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	263	AETECQNTEYQQL LDIKIR	2352.15	423	441
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	264	GSLGGGFSSGGFSG GSF	1464.64	41	57
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	265	ILLQIDNAR	1055.62	220	228
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	266	IRLENEIQTYR	1434.77	440	450
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	267	ISALEEQLQQIR	1427.79	411	422
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	268	LAADDFR	807.40	229	235
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	269	LASYLDK	809.44	157	163
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	270	LENEIQTYR	1165.59	442	450
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	271	LKYENEVALR	1234.68	236	245
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10 Keratin-10) (K10)	K1C10_HUMAN	59502	272	NQILNLTTDNAN	1330.66	208	219
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	273	NQILNLTTDNANIL LQIDNAR	2367.26	208	228
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	274	NVQALEIELQSQLA LK	1797.01	371	386
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	275	RVLDELTLTK	1187.70	257	266
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	276	SGGGGGGGGCGG GGGVSSLR	1549.68	16	35
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	277	SKELTTEIDNNIEQ ISSYK	2212.10	344	362
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	278	SLLEGEGSSGGGG R	1262.60	451	464
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK 10) (Keratin-10) (K10)	K1C10_HUMAN	59502	279	VQALEIELQSQLAL K	1682.97	372	386

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type I cytoskeletal 13 (Cytokeratin-13) (CK 13) (Keratin-13) (K13)	K1C13_HUMAN	49569	280	LEQEIATYR	1122.58	398	406
Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK 14) (Keratin-14) (K14)	K1C14_HUMAN	51473	281	EVATNSELVQSGK	1361.69	315	327
Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK 14) (Keratin-14) (K14)	K1C14_HUMAN	51473	282	GSCGIGGGIGGGSSR	1278.59	15	29
Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK 14) (Keratin-14) (K14)	K1C14_HUMAN	51473	283	ISSVLAGGSCR	1106.56	30	40
Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK 14) (Keratin-14) (K14)	K1C14_HUMAN	51473	284	VLDELTLAR	1029.59	223	231
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	285	AEAESLYQSK	1125.54	366	375
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	286	ELLQQVDTSTR	1289.67	212	222
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	287	GGSGGGGGGSSGGRGSGGGSSGGSIGGR	2079.92	588	615
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	288	GSGGGSSGGSIGGR	1092.50	602	615
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	289	KQISNLQQSISDAEQR	1844.95	416	431
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	290	LALDLEIATYR	1277.71	472	482
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	291	NKLNDLEDALQQAK	1599.83	441	454
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	292	NVEIDPEIQK	1184.62	165	174

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	293	SEIDNVKK	932.51	409	416
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	294	SGGGFSSGSAGIINYQR	1657.79	12	28
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	295	SISDAEQR	905.43	424	431
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	296	SISISVARGGGR	1159.65	74	85
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	297	SKAEAESLYQSK	1340.67	364	375
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	658780	298	SLDLDSIIAEVK	1302.72	343	354
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	299	SLNNQFASFIDK	1383.69	185	196
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	300	SLNNQFASFIDKVR	1638.86	185	198
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	301	SLVNLGGSK	874.50	65	73
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	302	THNLEPYFESF	1383.62	223	233
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	303	THNLEPYFESFINNLR	1993.98	223	238

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	304	TLLEGEESR	1033.52	483	491
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	305	TNAENEFVTIK	1265.64	277	287
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	306	VDQLKSDQSR	1175.60	241	250
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	307	VEIDPEIQK	1070.57	166	174
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	308	WELLQQVDTSTR	1475.75	211	222
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	309	YEELQITAGR	1179.60	376	385
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	310	GFSSGSAVVSGGSR	1254.61	21	34
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	311	IEISELNR	973.53	400	407
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	312	LALDVEIATYR	1263.69	477	487
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	313	LNDLEEALQQAK	1371.71	448	459
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	314	NLDLDSIIAEVK	1329.73	348	359
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	315	NVQDAIADAEQR	1329.64	425	436
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	316	VDLLNQEIEFLK	1460.80	309	320
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	317	YEDEINKR	1066.52	274	281

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	318	YEELQVTVGR	1193.62	381	390
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	319	YLDGLTAER	1037.53	245	253
KIAA1199 [*Homo sapiens*]	gi|38638698| ref| NP_061159.1|	152983	320	PFLSIISARYSPHQ DADPLK	2255.18	755	774
lipocalin 2 (oncogene 24p3) [*Homo sapiens*]	gi|38455402| ref| NP_005555.2|	22571	321	TFVPGCQPGEFTLG NIK	1864.93	102	118
lipocalin 2 (oncogene 24p3) [*Homo sapiens*]	gi|38455402| ref| NP_005555.2|	22571	322	VPLQQNFQDNQFQ GK	1790.88	36	50
lysozyme precursor [*Homo sapiens*]	gi|4557894| ref| NP_000230.1|	16519	323	GISLANWMCLAK	1363.69	40	51
lysozyme precursor [*Homo sapiens*]	gi|4557894| ref| NP_000230.1|	16519	324	LGMDGYR	811.38	33	39
lysozyme precursor [*Homo sapiens*]	gi|4557894| ref| NP_000230.1|	16519	325	QYVQGCGV	910.41	141	148
lysozyme precursor [*Homo sapiens*]	gi|4557894| ref| NP_000230.1|	16519	326	RLGMDGYR	967.48	32	39
lysozyme precursor [*Homo sapiens*]	gi|4557894| ref| NP_000230.1|	16519	327	STDYGIFQINSR	1400.68	69	80
lysozyme precursor [*Homo sapiens*]	gi|4557894| ref| NP_000230.1|	16519	328	TPGAVNACHLSCS ALLQDNIADAVAC AK	2927.38	88	115
lysozyme precursor [*Homo sapiens*]	gi|4557894| ref| NP_000230.1|	16519	329	WESGYNTR	1012.45	52	59
mannan-binding lectin serine protease 2 isoform 1 precursor [*Homo sapiens*]	gi|21264363| ref| NP_006601.2|	75685	330	VLATLCGQESTDT ER	1679.79	85	99
matrix Gla protein [*Homo sapiens*]	gi|49574514| ref| NP_000891.2|	12336	331	NANTFISPQQR	1275.64	39	49
membrane associated guanylate kinase, WW and PDZ domain containing 1 isoform b [*Homo sapiens*]	gi|66346708| ref| NP_004733.2|, gi|74272282| ref| NP_056335.1|, gi|74272284| ref|NP_ 001028229.1|	140360	332	NPSELKGKFIHTK	1498.84	462	474
Mov10, Moloney leukemia virus 10, homolog [*Homo sapiens*]	gi|14211540| ref| NP_066014.1|	133658	333	ISFGTPAPGFSSML YGMK	1906.91	45	62

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
myosin IIIA [*Homo sapiens*]	gi|24586657| ref| NP_059129.2|	186070	334	DKVNGDK	775.40	89	95
myotubularin-related protein 9 [*Homo sapiens*]	gi|19923424| ref| NP_056273.2|	63446	335	AGKRGYIIDTR	1249.70	227	237
Novel protein (Keratinocyte proline-rich protein)	Q5T749	64115	336	GRPAVCQPQGR	1225.62	167	177
Novel protein (Keratinocyte proline-rich protein)	Q5T749	64115	337	IEISSPCCPR	1218.56	327	336
Novel protein (Keratinocyte proline-rich protein)	Q5T749	64115	338	RPISSCSQR	1090.54	312	320
pericentriolar material 1 [*Homo sapiens*]	gi|34878902| ref| NP_006188.2|	228284	339	LPEMEPLVPRVKE VK	1780.00	1906	1920
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392| ref| NP_005800.3|, gi|33188452| ref| NP_859427.1|	21874	340	ATAVVDGAFK	978.53	17	26
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392| ref| NP_005800.3|, gi|33188452| ref| NP_859427.1|	21874	341	EGGLGPLNIPLLAD VTR	1734.98	93	109
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392| ref| NP_005800.3|, gi|33188452| ref| NP_859427.1|	21874	342	EGGLGPLNIPLLAD VTR	1734.98	93	109
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392| ref| NP_005800.3|, gi|33188452| ref| NP_859427.1|	21874	343	GLFIIDGK	862.50	128	135
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392| ref| NP_005800.3|, gi|33188452| ref| NP_859427.1|	21874	344	KEGGLGPLNIPLLA DVTR	1863.07	92	109
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392| ref| NP_005800.3|, gi|33188452| ref| NP_859427.1|	21874	345	LSEDYGVLK	1023.54	111	119

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392| ref| NP_005800.3|, gi|33188452| ref| NP_859427.1|	21874	346	RLSEDYGVLK	1179.64	110	119
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392| ref| NP_005800.3|, gi|33188452| ref| NP_859427.1|	21874	347	TDEGIAYR	924.44	120	127
phospholipase D1, phophatidylcholine-specific [*Homo sapiens*]	gi|4505873| ref| NP_002653.1|	124170	348	IAADMSNIIENLDTR	1691.83	17	31
plasma carboxypeptidase B2 isoform a preproprotein [*Homo sapiens*]	gi|4503005| ref| NP_001863.1|	48425	349	DTGTYGFLLPER	1368.68	388	399
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]	gi|4505733| ref| NP_002610.1|	10828	350	AGPHCPTAQLIATLK	1577.85	63	77
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]	gi|4505733| ref| NP_002610.1|	10828	351	HITSLEVIK	1039.62	54	62
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]	gi|4505733| ref| NP_002610.1|	10828	352	ICLDLQAPLYK	1333.72	82	92
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]	gi|4505733| ref| NP_002610.1|	10828	353	ICLDLQAPLYKK	1461.81	82	93
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]	gi|4505733| ref| NP_002610.1|	10828	354	KICLDLQAPLYK	1461.81	81	92
PREDICTED: similar to Neutrophil defensin 1 precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1) [*Homo sapiens*]	gi|113419903| ref|XP_ 001127929.1|, gi|4758146| ref| NP_004075.1|, gi|4885179| ref| NP_005208.1|	10183	355	ADEVAAAPEQIAA DIPEVVVSLAWDE SLAPK	3204.63	26	56
PREDICTED: similar to Neutrophil defensin 1 precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1) [*Homo sapiens*]	gi|113419903| ref|XP_ 001127929.1|, gi|4758146| ref| NP_004075.1|, gi|4885179| ref| NP_005208.1|	10183	356	IPACIAGER	986.51	70	78

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
PREDICTED: similar to Neutrophil defensin 1 precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1) [*Homo sapiens*]	gi|113419903| ref|XP_001127929.1|, gi|4758146| ref|NP_004075.1|, gi|4885179| ref|NP_005208.1|	10183	357	RYGTCIYQGR	1273.61	79	88
PREDICTED: similar to Neutrophil defensin 1 precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1) [*Homo sapiens*]	gi|113419903| ref|XP_001127929.1|, gi|4758146| ref|NP_004075.1|, gi|4885179| ref|NP_005208.1|	10183	358	YGTYCIYQGR	1117.51	80	88
PREDICTED: similar to ribosomal protein S2 [*Homo sapiens*]	gi|113426784| ref|XP_001134158.1|, gi|113427383| ref|XP_001126232.1|	27009	359	HMKIKSLEEMYVFSLPMK	2259.12	12	29
profilin family, member 4 [*Homo sapiens*]	gi|40786418| ref|NP_955378.1|	14302	360	CVRADEYSLYAKNENTGVVVVK	2514.27	73	94
propionyl-Coenzyme A carboxylase, alpha polypeptide precursor [*Homo sapiens*]	gi|65506442| ref|NP_000273.2|	80041	361	YSSAGTVEFLVDSK	1502.74	329	342
prosaposin [*Homo sapiens*]	gi|11386147| ref|NP_002769.1|	58094	362	LGPGMADICK	1061.51	233	242
pyruvate kinase 3 isoform 1 [*Homo sapiens*]	gi|33286418| ref|NP_002645.3|, gi|33286420| ref|NP_872270.1|, gi|33286422| ref|NP_872271.1|	57920	363	IYVDDGLISLQVK	1462.82	174	186
regulatory solute carrier protein, family 1, member 1 [*Homo sapiens*]	gi|5730021| ref|NP_006502.1|	66771	364	DLGQGIQNSVTDRPETR	1885.94	523	539
ribosomal protein S6 kinase, 90 kDa, polypeptide 3 [*Homo sapiens*]	gi|4759050| ref|NP_004577.1|	83721	365	LGMPQFLSPEAQSLLRMLFK	2306.24	285	304
roundabout, axon guidance receptor, homolog 2 [*Homo sapiens*]	gi|61888896| ref|NP_002933.1|	151182	366	QTSGLQATSSWQNLDAK	1834.89	674	690
Rsb-66 protein [*Homo sapiens*]	gi|33285006| ref|NP_061829.3|	19271	367	PISSIGQVQSYMEHYCNSSTDRR	2731.22	42	64
S100 calcium-binding protein A7 (Psoriasin)	S10A7_HUMAN	11309	368	ENFPNFLSACDK	1441.64	37	48

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
S100 calcium-binding protein A7 (Psoriasin)	S10A7_HUMAN	11309	369	GTNYLADVFEK	1256.62	50	60
S100 calcium-binding protein A7 (Psoriasin)	S10A7_HUMAN	11309	370	IDFSEFLSLLGDIATDYHK	2184.09	69	87
S100 calcium-binding protein A7 (Psoriasin)	S10A7_HUMAN	11309	371	KIDFSEFLSLLGDIATDYHK	2312.18	68	87
S100 calcium-binding protein A7 [*Homo sapiens*]	gi|4506769| ref| NP_002954.1|	11440	372	IDFSEFLSLLGDIATDYHK	2184.09	70	88
S100 calcium-binding protein A7 [*Homo sapiens*]	gi|4506769| ref| NP_002954.1|	11440	373	KIDFSEFLSLLGDIATDYHK	2312.18	69	88
secretoglobin, family 3A, member 1 [*Homo sapiens*]	gi|50363226| ref| NP_443095.2|	10082	374	LLLSSLGIPVNHLIEGSQK	2018.17	59	77
secretoglobin, family 3A, member 1 [*Homo sapiens*]	gi|50363226| ref| NP_443095.2|	10082	375	PVAQPVAALESAAEAGAGTLANPLGTLNPLK	2941.60	28	58
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_001002236.1|, gi|50363221| ref|NP_001002235.1|	46720	376	AVLTIDEK	888.50	360	367
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_001002236.1|, gi|50363221| ref|NP_001002235.1|	46720	377	FLENEDR	922.43	299	305
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_001002236.1|, gi|50363221| ref|NP_001002235.1|	46720	378	FNKPFVFLMIEQNTK	1855.98	390	404
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_001002236.1|, gi|50363221| ref|NP_001002235.1|	46720	379	GTEAAGAMFLEAIPMSIPPEVK	2259.14	368	389

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_ 001002236.1|, gi|50363221| ref|NP_ 001002235.1|	46720	380	ITPNLAEFAFSLYR	1641.86	50	63
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_ 001002236.1|, gi|50363221| ref|NP_ 001002235.1|	46720	381	KLSSWVLLMK	1204.71	258	267
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_ 001002236.1|, gi|50363221| ref|NP_ 001002235.1|	46720	382	LQHLENELTHDIIT K	1803.96	284	298
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_ 001002236.1|, gi|50363221| ref|NP_ 001002235.1|	46720	383	LSITGTYDLK	1110.61	315	324
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_ 001002236.1|, gi|50363221| ref|NP_ 001002235.1|	46720	384	LSSWVLLMK	1076.62	259	267
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_ 001002236.1|, gi|50363221| ref|NP_ 001002235.1|	46720	385	SASLHLPK	852.49	307	314

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_ 001002236.1|, gi|50363221| ref|NP_ 001002235.1|	46720	386	SPLFMGK	779.41	405	411
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_ 001002236.1|, gi|50363221| ref|NP_ 001002235.1|	46720	387	SVLGQLGITK	1015.62	325	334
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217| ref| NP_000286.3|, gi|50363219| ref|NP_ 001002236.1|, gi|50363221| ref|NP_ 001002235.1|	46720	388	VFSNGADLSGVTE EAPLK	1833.92	335	352
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 [*Homo sapiens*]	gi|28076869| ref| NP_002965.1|, gi|5902072| ref| NP_008850.1|	44837	389	FMFDLFQQFR	1378.66	11	20
serum amyloid A2 [*Homo sapiens*]	gi|13540475| ref| NP_110381.1|	13491	390	DPNHFRPAGLPEK Y	1640.82	109	122
serum amyloid A2 [*Homo sapiens*]	gi|13540475| ref| NP_110381.1|	13491	391	EANYIGSDKYFHA R	1670.79	44	57
serum amyloid A2 [*Homo sapiens*]	gi|13540475| ref| NP_110381.1|	13491	392	LTGHGAEDSLADQ AANK	1697.81	86	102
serum amyloid A2 [*Homo sapiens*]	gi|13540475| ref| NP_110381.1|	13491	393	RGPGGAWAAEVIS NAR	1611.84	65	80
serum amyloid A2 [*Homo sapiens*]	gi|13540475| ref| NP_110381.1|	13491	394	SFFSFLGEAFDGAR	1550.73	20	33
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095| ref| NP_006503.1|	14789	395	AYWDIMISNHQNS NR	1848.84	38	52
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095| ref| NP_006503.1|	14789	396	EALQGVGDMGR	1132.54	27	37
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095| ref| NP_006503.1|	14789	397	FRPDGLPK	929.52	121	128

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095| ref| NP_006503.1|	14789	398	GPGGVWAAK	842.45	66	74
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095| ref| NP_006503.1|	14789	399	SFFKEALQGVGDMGR	1641.81	23	37
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095| ref| NP_006503.1|	14789	400	SNEKAEEWGR	1205.56	104	113
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095| ref| NP_006503.1|	14789	401	VYLQGLIDYYLFGNSSTVLEDSK	2624.31	81	103
stanniocalcin 2 precursor [*Homo sapiens*]	gi|4507267| ref| NP_003705.1|	33230	402	EMVSQLQRECYLK	1699.81	130	142
Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein)	TETN_HUMAN	22549	403	GGTLSTPQTGSENDALYEYLR	2272.07	102	122
Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein)	TETN_HUMAN	22549	404	LDTLAQEVALLK	1313.77	51	62
thrombospondin 4 precursor [*Homo sapiens*]	gi|31543806| ref| NP_003239.2|	105851	405	LNPGALLPVLTDPALNDLYVISTFK	2684.49	41	65
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	406	AIAANEADAVTLDAGLVYDAYLAPNNLKPVVAEFYGSK	3954.02	70	107
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	407	ASYLDCIR	997.48	62	69
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	408	CSTSSLLEAGTFR	1531.69	684	696
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	409	DDTVCLAK	921.44	652	659
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	410	DGAGDVAFVK	978.49	216	225
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	411	DLLFRDDTVCLAK	1565.80	647	659
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	412	DSGFQMNQLR	1195.55	123	132
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	413	DYELLCLDGTR	1354.63	577	587
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	414	EDPQTFYYAVAVVK	1629.82	108	121

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	415	HSTIFENLANK	1273.65	226	236
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	416	KASYLDCIR	1125.57	61	69
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	417	KCSTSSLLEACTFR	1659.78	683	696
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	418	KDSGFQMNQLR	1323.65	122	132
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	419	KPVEEYANCHLAR	1586.77	588	600
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	420	NLNEKDYELLCLD GTR	1952.94	572	587
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	421	NPDPWAK	827.41	565	571
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	422	SAGWNIPIGLLYCD LPEPR	2171.10	144	162
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	423	SVIPSDGPSVACVK	1415.72	47	60
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	424	WCAVSEHEATK	1317.59	27	37
transferrin [*Homo sapiens*]	gi|4557871| ref| NP_001054.1|	77032	425	YLGEEYVK	1000.50	669	676
triggering receptor expressed on myeloid cells-like 1 [*Homo sapiens*]	gi|30794266| ref| NP_835468.1|	32661	426	FLPEGCQPLVSSAV DR	1774.88	54	69
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410| ref| NP_000574.2|	52900	427	EDFTSLSLVLYSR	1529.79	38	50
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410| ref| NP_000574.2|	52900	428	EFSHLGKEDFTSLS LVLYSR	2328.19	31	50
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410| ref| NP_000574.2|	52900	429	ELSSFIDK	938.48	395	402
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410| ref| NP_000574.2|	52900	430	FPSGTFEQVSQLVK	1566.82	52	65
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410| ref| NP_000574.2|	52900	431	KFPSGTFEQVSQLV K	1694.91	51	65

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410| ref| NP_000574.2|	52900	432	LPDATPTELAK	1155.63	430	440
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410| ref| NP_000574.2|	52900	433	RTHLPEVFLSK	1326.75	353	363
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410| ref| NP_000574.2|	52900	434	VPTADLEDVLPLA EDITNILSK	2366.27	243	264
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410| ref| NP_000574.2|	52900	435	YTFELSR	915.46	346	352
vitronectin precursor [*Homo sapiens*]	gi|88853069| ref| NP_000629.3|	54288	436	IYISGMAPR	1007.53	354	362
vitronectin precursor [*Homo sapiens*]	gi|88853069| ref| NP_000629.3|	54288	437	MDWLVPATCEPIQ SVFFFSGDK	2574.21	422	443
vitronectin precursor [*Homo sapiens*]	gi|88853069| ref| NP_000629.3|	54288	438	RVDTVDPPYPR	1314.68	453	463
vitronectin precursor [*Homo sapiens*]	gi|88853069| ref| NP_000629.3|	54288	439	SIAQYWLGCPAPG HL	1669.82	464	478
vitronectin precursor [*Homo sapiens*]	gi|88853069| ref| NP_000629.3|	54288	440	VDTVDPPYPR	1158.58	454	463
(P21817) Ryanodine receptor 1 (Skeletal muscle-type ryanodine receptor) (RyR1) (RYR-1) (Skeletal muscle calcium release channel)	RYR1_HUMAN	565156	441	EEQNFVVQNEINN MSFLTADNK	2584.20	3454	3475
(Q9NVE5) Ubiquitin carboxyl-terminal hydrolase 40 (EC 3.1.2.15) (U	Q9NVE5	140130	442	IGISWNKK	945.55	372	379
(Q5NV79) V5-4 protein (Fragment)	QSNV79	10661	443	FSGSSSGADR	970.42	66	75
(P51843) Nuclear receptor 0B1 (Nuclear receptor DAX-1) (DSS-AHC critical region on the X chromosome protein 1)	DAX1_HUMAN	51700	444	YLPCFQVLPLDQQ LVLVR	2201.22	271	288
(Q96SU4) Oxysterol binding protein-related protein 9 (OSBP-related	Q96SU4	83185	445	HCIVLLQIAKDQSN AEK	1967.04	172	188
(P17706) Tyrosine-protein phosphatase, non-receptor type 2 (EC 3.1.3.48) (T-cell protein-tyrosine phospha-tase) (TCPTP)	PTN2_HUMAN	48511	446	VKLQNAENDYINA SLVDIEEAQR	2632.32	59	81
(O15013) Rho guanine nucleo-tide exchange factor 10	ARHGA_HUMAN	127102	447	YILGSVVDSEKNY VDALKR	2169.16	194	212

TABLE 1-continued

Biomarkers associated with neurological conditions.

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
(O75129) KIAA0634 protein (Fragment)	O75129	145410	448	EAFKSALMSSYWCSGK	1851.84	1006	1021
(Q8N543) Hypothetical protein FLJ10826	Q8N543	63230	449	EPHISTLRKILFEDFR	2001.09	109	124
(Q96AE7) Tetratricopeptide repeat protein 17 (TPR repeat protein 17)	TTC17_HUMAN	129543	450	IHIEENEDRDTGLEQRHNK	2333.12	91	109
(Q96AE7) Tetratricopeptide repeat protein 17 (TPR repeat protein 17)	TTC17_HUMAN	129543	451	GLRIHELSSDDYSTEEEAQTPDCSITDFR	3371.50	530	558
(Q96AE7) Tetratricopeptide repeat protein 17 (TPR repeat protein 17)	TTC17_HUMAN	129543	452	IQQQVDSPMNLK	1400.72	50	61

TABLE 2

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
(O60602) Toll-like receptor 5 precursor (Toll/interleukin-1 receptor-like protein 3)	TLR5_HUMAN	97713	1	LYFCGLSDAVLKDGYF RNLK	2379.22	126	145
(O95793) Double-stranded RNA-binding protein Staufen homolog	STAU_HUMAN	63250	3	ALRILQNEPLPER-LEVN GR	2217.25	156	174
(P01764) Ig heavy chain V-III region VH26 precursor	HV3C_HUMAN	12565	4	AEDTAVYYCAK	1290.57	107	117
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	5	AADDTWEPFASGK	1394.62	56	68
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	6	ALGISPFHEHAEVVFT ANDSGPRR	2607.31	101	124
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	7	GSPAINVAVHVFR	1366.76	42	54
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	8	GSPAINVAVHVFRK	1494.85	42	55
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	9	KAADDTWEPFASGK	1522.72	55	68
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	10	RYTIAALLSPY-SYSTTA	2645.38	124	147
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	11	TSESGELHGLT-TEEEFV EGIYKVEIDTK	3140.52	69	96
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	TTHY_HUMAN	15869	12	VLDAVRGSPAINVAV HVFR	2020.15	36	54
(P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	ITHY_HUMAN	15869	13	YTIAALLSPYSYST-TAV VTNPKE	2489.28	125	147

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
(P09874) Poly [ADP-ribose] polymerase 1 (EC 2.4.2.30) (PARP 1) (ADPRT) (NAD(+) ADP-ribosyltransferase 1) (Poly[ADP ribose]synthetase 1)	PARP1_HUMAN	112939	15	EDAIEHFMKIYEEK	1781.84	607	620
(P09874) Poly [ADP-ribose] polymerase 1 (EC 2.4.2.30) (PARP 1) (ADPRT) (NAD(+) ADP-ribosyltransferase 1) (Poly[ADP-ribose]synthetase 1)	PARP1_HUMAN	112939	16	MKLTLKGGAAVDPDS GLEHSAHVLEK	2703.41	522	547
(P13667) Protein disulfide-isomerase A4precursor(EC5.3.4.1)(Protein ERp-72) (ERp72)	PDIA4_HUMAN	72916	21	LAPEYEKAAKELSK	1576.86	212	225
(P16591) Proto-oncogene tyrosine-protein kinase FER (EC 2.7.1.112) (p94-FER) (c-FER)	FER_HUMAN	94609	22	FLQEAKILKQYDHPNI VK	2184.22	605	622
(P22792) Carboxypeptidase N subunit 2 precursor (Carboxypeptidase N polypeptide 2) (Carboxypeptidase N 83 kDa chain) (Carboxypeptidase N regulatory subunit) (Carboxypeptidase N large subunit)	CPN2_HUMAN	60599	24	TLNLAQNLLAQLPEEL FHPLTSLQTLK	3045.70	173	199
(P35542) Serum amyloid A-4 protein precursor (Constitutively expressed serum amyloid A protein) (C-SAA)	SAA4_HUMAN	14789	25	FRPDGLPK	929.52121	128	
(Q05513) Protein kinase C, zeta type EC 2.7.137) (nPKC-zeta)	KPCZ_HUMAN	67644	26	EGLGPGDTTSTFCGTP NYIAPEILR	2666.28	400	424
(Q15166) Serum paraoxonase/Iactonase 3 (EC 3.1.1.-)	PON3_HUMAN	39590	27	ILIGTVFHK	1027.63	340	348
(Q4V312) Colony stimulating factor 2 receptor, alpha, low-affinity (Granulocyte-macrophage)	Q4V312 QR	46884	28	DKLNDNHEVEDEMGP	2025.89	364	380

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
(Q7Z3Z2) Protein Clorf36	CA036_HUMAN	22686	31	PRGSLATFK	976.56	146	154
(Q8N7W7) Hypothetical protein FLJ40259	Q8N7W7	66111	32	ILIDGTLIIFR	1273.79	124	134
(Q96MA6) Hypothetical protein FLJ32704 (Chromosome 9 open reading frame 98) (OTTHUMP00000022737)	Q96MA6	54909	33	KTVPSALLVQLIQERL AEEDCIK	2653.46	111	133
(Q9BXB9) LIM mineralization protein 2	Q9BXB9	46492	37	HSQPATPTPLQSR	1419.73	212224	
(Q9H212) HNRBF-2	Q9H212	31791	38	NCYSLLNLAEVRSKYL GK	2128.12	236	253
(Q9H212) HNRBF-2	Q9H212	31791	39	NCYSLLNLAEVRSKYL GK	2128.12	236	253
(Q9NPP6) Immunoglobulin heavy chain variant (Fragment)	Q9NPP6	44767	40	VEDTAVYYCAR	1346.61	48	58
(Q9NYQ6) Cadherin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo homolog 2) (hFmi2)	CELR1_HUMAN	329464	41	ENLEVGYEVLTIRASD RDSPINANLR	2944.51	364389	
(Q9NYQ6) Cadherin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo homolog 2) (hFmi2)	CELR1_HUMAN	329464	42	ETKETHVLR	1112.61314	322	
(Q9NYQ6) Cadherin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo homolog 2) (hFmi2)	CELR1_HUMAN	329464	43	QFVGCMRNLSVDGK	1610.78	1616	1629
(Q9NYQ6) Cadherin EGF LAG seven-pass G-precursor (Flamingo homolog 2) (hFmi2)	CELR1_HUMAN	329464	44	VPGGTRAFALRPGCTY AVGAACTPR	2606.31	35	59
Apolipoprotein C-I precursor (Apo-CI) (ApoC-I)	APOC1_HUMAN	9314	56	EWFSETFQK	1201.55	66	74

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Apolipoprotein C-I precursor (Apo-CI) (ApoC-I)	APOC1_HUMAN	9314	57	IKQSELSAK	1003.58	55	63
Apolipoprotein C-I precursor (Apo-CI) (ApoC-I)	APOC1_HUMAN	9314	58	LKEFGNTLEDK	1293.67	37	47
Apolipoprotein C-I precursor (Apo-CI) (ApoC-I)	APOC1_HUMAN	9314	59	TPDVSSALDK	1032.52	27	36
Apolipoprotein C-IV precursor (Apo-CIV) (ApoC-IV)	APOC4_HUMAN	14536	66	AWFLESK	880.46	99	105
Apolipoprotein C-IV precursor (Apo-CIV) (ApoC-IV)	APOC4_HUMAN	14536	67	DGWQWFWSPSTFR	1699.77	67	79
Apolipoprotein C-IV precursor (Apo-CIV) (ApoC-IV)	APOC4_HUMAN	14536	68	ELLETVVNR	1072.60	56	64
biliverdin reductase B (flavin reductase (NADPH)) [*Homosapiens*]	gi|4502419|ref|NP_000704.1|	22101	93	LPSEGPRPAHVVVGDV	2469.31	40	63 LQAADVDK
biliverdin reducrase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419|ref|NP_000704.1|	22101	94	NIVAAMK	746.42	93	99
biliverdinreductase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419|ref|NP_000704.1|	22101	95	PAHVVVGDVLQAADV DK	1732.92	47	63
biliverdin reductase B (flavin reductase (NADPH)) [*Homo sapiens*]	giF4502419|ref|NP_000704.1|	22101	96	TVAGQDAVIVLLGTR	1512.88	64	78
biliverdin reductase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419fref|NP_000704.1|	22101	97	VVACTSAFLLWDPTK	1707.88	106	120
biliverdin reductase B (flavin reductase (NADPH)) [*Homo sapiens*]	gi|4502419|ref|NP_000704.1|	22101	98	YVAVMPPHIGDQPLTG AYTVTLDGR	2671.36	146	170
chromosome 1 open reading frame 48 [*Homo sapiens*]	gi|21361470|ref|NP_056286.21	32112	99	EISEAMK	823.39	183	189
chromosome 9 open reading frame 19 [*Homo sapiens*]	gi|11641247|ref|NP_071738.11	17200	100	EAQQYSEALASTR	1453.69	38	50
citron [*Homo sapiens*]	gi|32698688|ref|NP_009105.1|	231418	101	QQKFYLETQAGK	1440.75	814	825

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_00100202 9.1|	192735	111	DFALLSLQVPLK	1343.79	81	92
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_00100202 9.1|,gi167190748|ref|NP_00922 4.2|	192735	112	DFALLSLQVPLKDAK	1657.95	81	95
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_00100202 9.1|	192735	113	DHAVDLIQK	1038.56	1043 1051	
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_00100202 9.1|,gi167190748|ref|NP_00922 4.21	192735	114	EPFLSCCQFAESLR	1743.78	730	743
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_00100202 9.1|,gi|67190748|ref|NP_00922 4.21	192735	115	GLEEELQFSLGSK	1436.73	1353 1365	
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296fref|NP_00100202 9.1|	192735	116	GPEVQLVAHSPWLK	1560.85	105	118
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_00100202 9.1|	192735	117	KADGSYAAWLSR	1324.66	1061	1072
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_00100202 9.1|	192735	118	LHLETDSLALVALGAL DTALYAAGSK	2613.41	589	614
complement component 4B preproprotein [*Homo sapiens*]	gi1503452961ref|NP_00100202 9.1|,gi|67190748|ref|NP_00922 4.2|	192735	119	SCGLHQLLR	1083.57	96	104
complement component 4B preproprotein [*Homo sapiens*] 4.2|	gi|50345296|ref|NP00100202 9.1|,gi|67190748|ref|NP_00922	192735	120	TYNVLDMK	983.49	1383 1390	
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_00100202 9.1|	192735	121	VDFTLSSER	1053.52	72	80
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_00100202 9.1|	192735	122	VGLSGMAIADVTLLSG FHALR	2128.16	1478 1498	

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_001002029.1|	192735	123	VLSLAQEQVGGSPEK	1541.82	1085	1099
complement component 4B preproprotein [*Homo sapiens*]	gi|50345296|ref|NP_001002029.1|	192735	124	YVSHFETEGPHVLLYFDSVPTSR	2680.30	1511	1533
complement component 5 [Homo sapiens]	gi|38016947|ref|NP_001726.2|	188291	125	FQNSAILTIQPK	1359.76	79	90
complement component 5 [Homo sapiens]	gi|38016947|ref|NP_001726.2|	188291	126	MVETTAYALLTSLNLK	1783.95	1247	1262
complement component 5 [Homo sapiens]	gi|38016947|ref|NP_001726.2|	188291	127	VFQFLEK	910.50	623	629
complement components [Homo sapiens]	gi|38016947|ref|NP_001726.2|	188291	128	YIYPLDSLTWIEYWPR	2115.06	1635	1650
core-binding factor, runt domain, alpha subunit 2; translocated to, 2 isoform MTGR1b [*Homo sapiens*]	gi|4826663|ref|NP_005084.11	67115	143	MAKESGISLKEIQVLAR	1873.06	1	17
delta globin [*Homo sapiens*]	gi|4504351|ref1NP_000510.1|	16037	144	EFTPQMQAAYQK	1441.68	122	133
delta globin [*Homo sapiens*]	gi|4504351|ref|NP_000510.1|	16037	145	GTFSQLSELHCDK	1521.70	84	96
delta globin [*Homo sapiens*]	gi|4504351|ref|NP_000510.1|	16037	146	GTFSQLSELHCDKLHVDPENFR	2629.25	84	105
delta globin [*Homo sapiens*]	gi|4504351|ref|NP_000510.1|	16037	147	LLGNVLVCVLAR	1326.79	106	117
delta globin [*Homo sapiens*]	gi|4504351|ref|NP_000510.1|	16037	148	LLVVYPWTQR	1274.73	32	41
delta globin [*Homo sapiens*]	gi|4504351|ref|NP_000510.1|	16037	149	TAVNALWGK	959.53	10	18
delta globin [*Homo sapiens*]	gi|4504351|ref|NP_000510.1|	16037	150	VLGAFSDGLAHLDNLK	1669.89	68	83
delta globin [*Homo sapiens*]	gi|4504351|ref|NP_000510.1|	16037	151	VNVDAVGGEALGR	1256.66	19	31
delta globin [*Homo sapiens*]	gi|4504351|ref|NP_000510.1|	16037	152	VVAGVANALAHK	1149.67	134	145
delta globin [*Homo sapiens*]	gi|4504351|ref|NP_000510.1|	16037	153	VVAGVANALAHKYH	1449.80	134	147

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
diacyiglycerol kinase, theta [Homo sapiens]	gi|40806175|ref1NP_001338.21	101135	156	PGSPACSPVLGSGGRA R	1625.82	20	36
Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A]	FIBA_HUMAN	94955	157	TFPGFFSPM-LGEFVSET ESR	2265.0	5528	547
Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A]	FIBA_HUMAN	94955	158	VTSGSTTTTR	1010.51	449	458
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629|ref1NP_068657.1|, gi|4503689|ref|NP_000499.1|	69739	159	ESSSHHPGIAEFPSR	1637.77	559	573
fibrinogen, alpha polypeptide isoform alpba preproprotein [*Homo sapiens*]	gi|11761629|ref|NP_068657.1|, gi|45O3689|ref|NP_000499.1|	69739	160	EVDLKDYEDQQK	1509.71	191	202
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629|ref|NP_068657.1|, gi|4SO3689|ref|NP_000499.1|	69739	161	GLIDEVNQDFTNR	1520.73	72	84
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629|ref|NP_068657.1|, gi|4503689|ref|NP_000499.1|	69739	162	GSESGIFTNTK	1140.55	548	558
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629|ref|NP_068657.1|, gi|4SO3689|ref|NP_000499.1|	69739	163	HPDEAAFFDTASTGK	1593.72	513	527
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629|ref|NP_068657.1|, gi|4503689|ref|NP_000499.1|	69739	164	HRHIPDEAAFFD-TASTG K	1886.88	511	527
fibrinogen, alpha polypeptide isoform alpha preproprotein [*Homo sapiens*]	gi|11761629|ref|NP_068657.1|, gi|4503689|ref|NP_000499.1|	69739	165	TFPGFFSPM-LGEFVSET ESR	2265.05	528	547
gelsolin isoform a precursor [Homo *sapiens*]	gi|4504165|ref|NP_000168.1|	85680	166	DSQEEEKTEALTSAK	1665.78	714	728
gelsolin isoform a precursor [Homo *sapiens*]	gi|4504165|refaNP_000168.1|	85680	167	EVQGFESATFLGYFK	1722.84	148	162
gelsolin isoform a precursor [Homo *sapiens*]	gi|4504165|ref|NP_000168.1|	85680	168	FDLVPVPTNLYGDFFT GDAYVILK	2704.39	76	99
gelsolin isoform a precursor [Homo *sapiens*]	gi|4504165|ref|NP_000168.1|	85680	169	HVVPNEVVVQR	1275.72	178	188

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
gelsolin isoform a precursor [Homo *sapiens*]	gi|4504165|ref|NP_000168.1|	85680	170	PNSMVVEHPEFLK	1526.77	49	61
Hepatitis B virus receptor binding protein (Fragment)	Q6PYX1	38143	172	GQGTTVTVSSASTK	1323.68	9	22
Hepatitis B virus receptor binding protein (Fragment)	Q6PYX1	38143	173	GTTVTVSSASTK	1138.60	11	22
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489|ref|NP_000403.1|	59559	174	ALDLINKR	942.57	34	41
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489|refINP_000403.1|	59559	175	DGYLFQLLR	1124.61	44	52
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489|ref|NP_000403.1|	59559	176	DSPVLIDFFEDTER	1682.79	140	153
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489|ref|NP_000403.11	59559	177	GEVLPLPEANFPSF-PLP HHK	2226.17	467	486
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489|refINP_000403.1|	159559	178	HPLKPDNQPFPQSVSE SCPGK	2349.13	487	507
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489|ref|NP_000403.1|	59559	179	KGEVLPLPEANFPS-FPL PHHK	2354.27	466	486
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489|ref|NP_000403.1|	59559	180	LPPLR	595.39	461	465
histidine-rinch glycoprotein precursor [*Homo sapiens*]	gi|4504489|ref|NP_000403.11	59559	181	RDGYLFQLLR	1280.71	43	52
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489|ref|NP_000403.1|	59559	182	RPSEIVIGQCK	1286.69	96	106
histidine-rich glycoprotein precursor [*Homo sapiens*]	gi|4504489|ref|NP_000403.1|	59559	183	SGFPQVSMFFTHTFPK	1857.90	510	525
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	263	AETECQNTEYQQLLDI KIR	2352.15	423	441

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	264	GSLGGGFSSGGFSGGSF	1464.6	441	57
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	265	ILLQIDNAR	1055.62	220	228
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	266	IRLENEIQTYR	1434.77	440	450
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	267	ISALEEQLQQIR	1427.79	411	422
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	268	LAADDFR	807.40	229	235
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	269	LASYLDK	809.44	157	163
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	270	LENEIQTYR	1165.59	442	450
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	271	LKYENEVALR	1234.68	236	245
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	272	NQILNLTTDNAN	1330.66	208	219
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	273	NQILNLTTDNA-NILLQI DNAR	2367.26	208	228
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	274	NVQALEIELQSQLALK	1797.01	371	386

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type I cytoskeletal 10 (Cytokeratin-10)(CK-10)(Keratin-10) (K10)	KIC10_HUMAN	59502	275	RVLDELTLTK	1187.70	257	266
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	276	SGGGGGGGGCGGGGG VSSLR	1549.68	16	35
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	277	SKELTTEIDNNIE-QISSY K	2212.10	334	362
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	278	SLLEGEGSSGGGGR	1262.60	451	464
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KIC10_HUMAN	59502	279	VQALEIELQSQLALK	1682.97	372	386
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	310	GFSSGSAVVSGGSR	1254.61	21	34
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	311	IEISELNR	973.53	400	407
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	312	LALDVEIATYR	1263.69	477	487
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	313	LNDLEEALQQAK	1371.71	448	459
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	314	NLDLDSIIAEVK	1329.73	348	359
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	315	NVQDAIADAEQR	1329.64	425	436

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	316	VDLLNQEIEFLK	1460.80	309	320
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK2e)	K22E_HUMAN	65848	317	YEDEINKR	1066.52	274	281
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	318	YEELQVTVGR	1193.62	381	390
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK2e)	K22E_HUMAN	65848	319	YLDGLTAER	1037.53	245	253
KIAA1199 [*Homo sapiens*]	gi|38638698|ref|NP_061159.1|	152983	320	PFLSI-ISARYSPHQDAD PLK	2255.18	755	774
lipocalin 2 (oncogene 24p3) [Homo *sapiens*]	gi|38455402|ref|NP_005555.21	22571	321	TFVPGCQPGEFTLGNI K	1864.93	102	118
lipocalin 2 (oncogene 24p3) [Homo *sapiens*]	gi|38455402|ref|NP_005555.21	22571	322	VPLQQNFQDNQFQGK	1790.88	36	50
lysozyme precursor [*Homo sapiens*]	gi|45S7894|ref|NP_000230.1|	16519	323	GISLANWMCLAK	1363.69	40	51
lysozyme precursor [*Homo sapiens*]	gi|4S57894|ref|NP_000230.1|	16519	324	LGMDGYR	811.38	33	39
lysozyme precursor [*Homo sapiens*]	gi|4557894|ref|NP_000230.1|	16519	325	QYVQGCGV	910.41	141	148
lysozyme precursor [*Homo sapiens*]	gi|4557894|ref|NP_000230.1|	16519	326	RLGMDGYR	967.48	32	39
lysozyme precursor [*Homo sapiens*]	gi|45S7894|ref|NP_000230.1|	16519	327	STDYGIFQINSR	1400.68	69	80
lysozyme precursor [*Homo sapiens*]	gi|4557894|ref|NP_000230.1|	16519	328	TPGAVNACHLSCSALL QDNIADAVACAK	2927.38	88	115
lysozyme precursor [*Homo sapiens*]	gi|4557894fref|NP_000230.11|	16519	329	WESGYNTR	1012.45	52	59
mannan-binding lectin serine protease 2 isoform 1 precursor [*Homo sapiens*]	gi|21264363|ref|NP_006601.2|	75685	330	VLATLCGQESTDTER	1679.79	85	99

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
matrix Gla protein [*Homo sapiens*]	gi|49574514|ref|NP_000891.2|	12336	331	NANTFISPQQR	1275.64	39	49
membrane associated guanylate kinase, WW and PDZ domain containing 1 isoform b [Homo *sapiens*]	gi|66346708|ref|NP_004733.2|, gi|74272282|ref|NP_056335.1|, gi|74272284|ref|NP_00102822 9.1|	140360	332	NPSELKGKFIHTK	1498.84	462	474
myosin IIIA [*Homo sapiens*]	gi|24586657|ref|NP_059129.21	186070	334	DKVNGDK	775.40	89	95
myotubularin-related protein 9 [*Homo sapiens*]	gi|19923424|ref|NP_056273.21	63446	335	AGKRGYIIDTR	1249.70	227	237
phospholipase D1, phophatidylcholine-specific [Homo *sapiens*]	gi|4505873|ref|NP_002653.1|	124170	348	IAADMSNIIENLDTR	1691.83	17	31
PREDICTED: similar to Neutrophil defensin I precursor (KNP-I) (HP-1) (HP1) (Defensin, alpha 1) [Homo *sapiens*]	gi|13419903|ref|XP_0011279 29.1|,gi|4758146|ref|NP_00407 5.1|,gi|4885179|ref|NP_00520 8.1|	10183	349	ADEVAAAPEQIAADIP EVVVSLAWDESLAPK	3204.63	26	56
PREDICTED: similar to Neutrophil defensin 1 precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1) [Homo *sapiens*]	gi||13419903|ref|XP_0011279 29.1|,gi|4758146|ref|NP_00407 5.1|,gi|4885179|ref|NP_00520 8.1|	10183	356	IPACIAGER	986.51	70	78
PREDICTED: similar to Neutrophil defensin I precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1) [Homo *sapiens*]	gi|113419903|ref1XP_0011279 29.11,gi|47581461ref|NP_00407 5.11,gi|48851791ref|NP_00520 8.1|	10183	357	RYGTCIYQGR	1273.61	79	88
PREDICTED: similar to Neutrophil defensin I precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1) [Homo *sapiens*]	gi|113419903|ref1XP_0011279 29,1|,gi|4758146|ref|NP_00407 5.1|,gi|4885179|ref|NP_00520 8.1|	10183	358	YGTCIYQGR	1117.51	80	88
PREDICTED: similar to ribosomal protein S2 [*Homo sapiens*]	gi|113426784|ref|XP_0011341 58.1|,gi|113427383|ref|XP_001 126232.1|	27009	359	HMKIKSLEEMYVFSLP MK	2259.12	12	29
prosaposin [*Homo sapiens*]	gi|11386147|ref|NP_002769.1|	58094	362	LGPGMADICK	1061.51	233	242
pyruvate kinase 3 isoform I [Homo sapiens]	gi|33286418|ref|NP_002645.31, gi|33286420|ref|NP_872270.1|, gi|33286422|ref|NP_872271.1|	57920	363	IYVDDGLISLQVK	1462.82	174	186

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
ribosomal protein S6 kinase, 90kDa, polypeptide 3 [*Homo sapiens*]	gi|4759050|ref|NP_004577.1|	83721	365	LGMPQFLSPEAQSLLR MLFK	2306.24285	304	
S100 calcium-binding protein A7 [*Homo sapiens*]	gi|506769|ref|NP_002954.1|	11440	372	IDFSEFLSLLGDI-ATDY HK	2184.09	70	88
S100 calcium-binding protein A7 [*Homo sapiens*]	gi|4506769|ref|NP_002954.1|	11440	373	KIDFSEFLSLLGDI-ATD YHK	2312.18	69	88
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	376	AVLTIDEK	888.50	360	367
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref1NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	377	FLENEDR	922.43	299	305
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	378	FNKPFVFLMIEQNTK	1855.98	390	404
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	379	GTEAAGAMFLEAIPMS IPPEVK	2259.14	368	389
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	380	ITPNLAEFAFSLYR	1641.86	50	63
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	381	KLSSWVLLMK	1204.71	258	267
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	382	LQHLENELTHDIITK	1803.96	284	298

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitlypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	383	LSITGTYDLK	1110.61	315	324
serine (or cysteine) proteinase inhibitor; clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	384	LSSWVLLMK	1076.62	259	267
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	385	SASLHLPK	852.49	307	314
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	386	SPLFMGK	779.41	405	411
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219|ref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	387	SVLGQLGITK	1015.62	325	334
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [*Homo sapiens*]	gi|50363217|ref|NP_000286.3|, gi|50363219fref|NP_00100223 6.1|,gi|50363221|ref|NP_00100 2235.1|	46720	388	VFSNGADLSGVTEEAP LK	1833.92	335	352
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 [*Homo sapiens*]	gi|28076869|ref|NP_002965.1|, gi|5902072|ref|NP_008850.1|	44837	389	FMFDLFQQFR	1378.66	11	20
serum amyloid A2 [*Homo sapiens*]	gi|13540475|ref|NP_110381.1|	13491	390	DPNHFRPAGLPEKY	1640.82	109	122
serum amyloid A2 [*Homo sapiens*]	gi|13540475|ref|NP_110381.1|	13491	391	EANYIGSDKYFHAR	1670.79	44	57
serum amyloid A2 [*Homo sapiens*]	gi|13540475|ref|NP_110381.1|	13491	392	LTGHGAEDSLADQAA NK	1697.81	86	102
serum amyloid A2 [*Homo sapiens*]	gi|13540475|ref|NP_110381.1|	13491	393	RGPGGAWAAEVISNA R	1611.84	65	80

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
serum amyloid A2 [*Homo sapiens*]	gi|13540475|ref|NP_110381.1|	13491	394	SFFSFLGEAFDGAR	1550.73	20	33
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095|ref|NP_006503.1|	14789	395	AYWDIMISNHQNSNR	1848.84	38	52
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095|ref|NP_006503.1|	14789	396	EALQGVGDMGR	1132.54	27	37
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095|ref|NP_006503.1|	14789	397	FRPDGLPK	929.52	121	128
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095|ref|NP_006503.1|	14789	398	GPGGVWAAK	842.4566	74	
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095|ref|NP_006503.1|	14789	399	SFFKEALQGVGDMGR	1641.81	23	37
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095|ref|NP_006503.1|	14789	400	SNEKAEEWGR	1205.56	104	113
serum amyloid A4, constitutive [*Homo sapiens*]	gi|10835095|ref|NP_006503.1|	14789	401	VYLQGLIDYYLFGNSS TVLEDSK	2624.31	81	103
stanniocalcin 2 precursor [Homo sapiens]	gi|4507267|ref|NP_003705.1|	33230	402	EMVSQLQRECYLK	1699.81	130	142
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.11	77032	406	AIAANEADAVTLDAG LVYDAYLAPNNLKPV VAEFYGSK	3954.02	70	107
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	407	ASYLDCIR	997.48	62	69
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	408	CSTSSLLEACTFR	1531.69	684	696
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	409	DDTVCLAK	921.44	652	659
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	410	DGAGDVAFVK	978.49	216	225
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	411	DLLFRDDTVCLAK	1565.80	647	659
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	412	DSGFQMNQLR	1195.55	123	132
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	413	DYELLCLDGTR	1354.63	577	587
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	414	EDPQTFYYAVAVVK	1629.82	108	121

TABLE 2-continued

Biomarkers associated with Alzheimer's Disease

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	415	HSTIFENLANK	1273.65	226	236
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	416	KASYLDCIR	1125.57	61	69
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	417	KCSTSSLLEACTFR	1659.78	683	696
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	418	KDSGFQMNQLR	1323.65	122	132
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	419	KPVEEYANCHLAR	1586.77	588	600
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	420	NLNEKDYELLCLDGTR	1952.94	572	587
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	421	NPDPWAK	827.41	565	571
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	422	SAGWNIPIGLLY-CDLPE PR	2171.10	144	162
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	423	SVIPSDGPSVACVK	1415.72	47	60
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	424	WCAVSEHEATK	1317.59	27	37
transferrin [*Homo sapiens*]	gi|4557871|ref|NP_001054.1|	77032	425	YLGEEYVK	1000.50	669	676
triggering receptor expressed on myeloid cells-like 1 [*Homo sapiens*]	gi|30794266|ref|NP_835468.11	32661	426	FLPEGCQPLVSSAVDR	1774.88	54	69
vitronectin precursor [*Homo sapiens*]	gi|88853069|ref|NP_000629.3|	54288	436	IYISGMAPR	1007.53	354	362
vitronectin precursor [*Homo sapiens*]	gi|88853069|ref|NP_000629.3|	54288	437	MDWLVPATCEPIQSVF FFSGDK	2574.21	422	443
vitronectin precursor [*Homo sapiens*]	gi|88853069|ref|NP_000629.3|	54288	438	RVDTVDPPYPR	1314.68	453	463
vitronectin precursor [*Homo sapiens*]	gi|88853069|ref|NP_000629.3|	54288	439	SIAQYWLGCPAPGHL	1669.82	464	478
vitronectin precursor [*Homo sapiens*]	gi|88853069|ref|NP_000629.3|	54288	440	VDTVDPPYPR	1158.58	454	463

TABLE 3

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
(O60687) Sushi-repeat-containing protein, X-linked 2	O60687	52954	2	DSADGTITRVTLR	1404.74	212	224
(P01764) Ig heavy chain VIII region VH26 precursor	HV3C_HUMAN	12565	4	AEDTAVYYCAK	1290.57	107	117
(P09758) Tumor-associated calcium signal transducer 2 precursor (Pancreatic carcinoma marker protein GA733-1) (Cell surface glycoprotein Trop-2)	TACD2_HUMAN	35692	14	HRPTAGAFNHSDLDAELRR	2163.08	160	178
(P10643) Complement component C7 precursor	CO7_HUMAN	93499	17	AASGTQNNVLR	1130.59	362	372
(P20701) Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha chain CD11a)	ITAL_HUMAN	128804	23	EGVNITICFQIKSLYPQFQGR	2498.29	646	666
(Q6N092) Hypothetical protein DKFZp686K18196 (Fragment)	Q6N092	56405	29	SAVQGPPDR	926.47	335	343
(Q96S24) Hypothetical protein gs30	Q96S24	3503	34	GMGSDRTALSLQGAWGIFLSTFYK	2606.31	3	26
adenylosuccinate synthase [*Homo sapiens*]	gi|34577063|ref|NP_001117.2|	50080	45	DGVYFLYEALHGPPKK	1833.95	233	248
alpha 1B-glycoprotein [*Homo sapiens*]	gi|21071030|ref|NP_570602.2|	54235	46	ATWSGAVLAGR	1088.59	407	417
alpha 1B-glycoprotein [*Homo sapiens*]	gi|21071030|ref|NP_570602.2|	54235	47	SLPAPWLSMAPVSWITPGLK	2151.17	115	134
alpha 1B-glycoprotein [*Homo sapiens*]	gi|21071030|ref|NP_570602.21	54235	48	SWVPHTFESELSDPVELL-VAES	2471.20	474	495
alpha 1B-glycoprotein [*Homo sapiens*]	gi|21071030|ref|NP_570602.21	54235	49	TPGAAANLELIFVGPQHAGNYR	2296.18	448	469

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	50	ADLSGITGAR	960.51	341	350
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	51	AVLDVFEEGTEASAATAVK	1907.96	361	379
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	52	DYNLNDILLQLGIEEAFTSK	2296.17	321	340
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	53	ITLLSALVETR	1215.73	380	390
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	54	NLAVSQVVHK	1094.63	351	360
Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	AACT_HUMAN	47635	55	YNLNDILLQLGIEEAFTSK	2181.14	322	340
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518|ref|NP_000474.21	11266	60	ESLSSYWESAK	1286.59	42	52
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130348|ref1NP_000474.21	11266	61	LRDLYSK	894.50	71	77
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518|ref|NP_000474.21	11266	62	STAAMSTYTGIFTDQVLSVLK	2233.14	78	98
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518|ref|NP_000474.21	11266	63	STAAMSTYTGIFTDQVLSVLK GEE	2548.25	78	101
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518|ref|NP_000474.21	11266	64	TAAQNLYEK	1037.53	53	61
apolipoprotein C-II precursor [*Homo sapiens*]	gi|32130518|ref|NP_000474.21	11266	65	TYLPAVDEK	1035.54	62	70

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
apolipoprotein L1 isoform a precursor [*Homo sapiens*]	gi|21735614|ref|NP_003652.2|,gi|21735616|ref|NP_663318.1|	43957	69	ILQADQEL	929.49	391	398
apolipoprotein L1 isoform a precursor [*Homo sapiens*]	gi|21735614|ref|NP_003652.2|,gi|21735616|ref|NP_663318.1|	43957	70	LNILNNNYK	1105.60	382	390
apolipoprotein M [*Homo sapiens*]	gi|22091452|ref|NP_061974.2|	21236	71	EELATFDPVDNIVFNMAAGSAPMQLHLR	3086.51	58	85
apolipoprotein M [*Homo sapiens*]	gi|22091452|ref|NP_061974.2|	21236	72	EFPEVHLGQWYFIAGAAPTK	2261.14	38	57
apolipoprotein M [*Homo sapiens*]	gi|22091452|ref|NP_061974.2|	21236	73	KWIYHLTEGSTDLR	1718.89	99	112
apolipoprotein M [*Homo sapiens*]	gi|22091452|ref|NP_061974.2|	21236	74	MKDGLCVPR	1091.53	90	98
apolipoprotein M [*Homo sapiens*]	gi|22091452|ref|NP_061974.2|	21236	75	SLTSCLDSK	1010.48	163	171
beta globin [*Homo sapiens*]	gi|450349|ref|NP_000509.1|	15980	76	EFTPPVQAAYQK	1378.70	122	133
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	77	FFESFGDLSTPDAVMGNPK	2058.95	42	60
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	78	FFESFGDLSTPDAVMGNPKVK	2286.11	42	62
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	79	GTFATLSELHCDK	1478.70	84	96
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	80	GTFATLSELHCDKLHVD-PENFR	2586.24	84	105
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	81	KVLGAFSDGLAHLDNLK	1797.99	67	83
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	82	LHVDPENFR	1126.5697	105	

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	83	LLGNVLVCVLAHHFGK	1776.99	106	121
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	84	LLVVYPWTQR	1274.73	32	41
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	85	LLVVYPWTQRFFESFGDLSTPDAVMGNPK	3314.66	32	60
beta globin [*Homo sapiens*]	gi|4504349ref|NP_000509.1|	15980	86	SAVTALWGK	932.52	10	18
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	87	SAVTALWGKVNVDEVGGEALGR	2228.17	10	31
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	88	SAVTALWGKVNVDEVGGEALGRLLVVYPWTQR	3483.87	10	41
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	89	VLGAFSDGLAHLDNLK	1669.89	68	83
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	90	VNVDEVGGEALGR	1314.67	19	31
beta globin [*Homo sapiens*]	gi|4504349|ref|NP_000509.1|	15980	91	VVAGVANALAHK	1149.67	134	145
beta globin [*Homo sapiens*] 509.1|	gi|4504349|ref|NP_000	15980	92	VVAGVANALAHKYH	1449.80	134	147
coagulation factor II precursor [*Homo* sapiens]	gi|4503635|ref|NP_000497.1|	70019	102	ELLESYIDGR	1194.60	354	363
coagulation factor II precursor [*Homo* sapiens]	gi|4503635|ref|NP_000497.1|	70019	103	HQDFNSAVQLVENFCR	1963.91	248	263
coagulation factor II precursor [*Homo* sapiens]	gi|4503635|ref|NP_000497.11	70019	104	IVEGSDAEIGMSPWQVMLFR	2265.11	364	383
coagulation factor II precursor [*Homo* sapiens]	gi|4503635ref|NP_000497.1|	70019	105	LAVITHGLPGLAWASAQAK	1995.05	225	243
coagulation factor II precursor [*Homo* sapiens]	gi|4503635|ref|NP_000497.1|	70019	106	SEGSSVNLSPPLEQCVPDR	2070.98	199	217

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
coagulation factor II precursor [*Homo sapiens*]	gi|4503635|ref|NP_000497.1|	70019	107	SLEDKTERELLESYIDGR	2153.07	346	363
coagulation factor II precursor [*Homo sapiens*]	gi|4503635|ref|NP_000497.1|	70019	108	TATSEYQTFFNPR	1561.73	315	327
coagulation factor II precursor [*Homo sapiens*]	gi|4503635|ref|NP_000497.1|	70019	109	TFGSGEADCGLRPLFEK	1883.90	328	344
coagulation factor II precursor [*Homo sapiens*]	gi|4503635|ref|NP_000497.1|	70019	110	YGFYTHVFR	1189.58	600	608
complement component 8, gamma polypeptide [*Homo sapiens*]	gi14557393|ref|NP_000597.1|	22201	129	AEATTLHVAPQGTAMAVSTFR	2159.09	70	90
complement componeni 8, gamma polypeptide [*Homo sapiens*]	gi|4557393|ref|NP_000597.1|	22201	130	ANFDAQQFAGTWLLVAVGSACR	2382.17	40	61
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393|ref|NP_000597.1|	22201	131	GAVHVVVAETDYQSFAVLYLER	2466.27	121	142
complement component 8, gamma nolypeptide [*Homo sapiens*]	gi|4557393|ref|NP_000597.1|	22201	132	KLDGICWQVR	1274.67	91	100
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393|ref|NP_000597.1|	22201	133	LDGICWQVR	1146.57	92	100
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393|ref|NP_000597.1|	22201	134	QLYGDTGVLGR	1178.62	101	111
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393|ref|NP_|000597.1|	22201	135	RPASPISTIQPK	1294.75	28	39
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393|ref|NP_000597.1|	22201	136	SLPVSDSVLSGFEQR	1620.82	154	168
complement component 8, gamma polypeptide [*Homo sapiens*]	gi|4557393|ref|NP_000597.1|	22201	137	VQEAHLTEDQIFYFPK	1964.98	169	184
complement component 8, gamma nolypeptide [*Homo sapiens*]	gi|4557393~refjNP_000597.1|	22201	138	YGFCEAADQFHVLDEVR	2055.92	185	201
complement factor H isoform a recursor [*Homo sapiens*]	gi|62739186|ref|NP_000177.2|	139052	139	EIMENYNIALR	1365.68	1172	1182

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
complement factor H isoform a precursor [*Homo sapiens*]	gi|62739186|ref|NP_000177.2|	139052	140	KGEWVALNPLR	1282.73	68	78
complement factor H isoform a precursor [*Homo sapiens*]	gi|62739186|ref|NP_000177.2|,gi|62739188|ref|NP_001014975.|	139052	141	NTEILTGSWSDQTYPEGTQAIYK	2602.23	29	51
complement factor H isoform a recursor [*Homo sapiens*]	gi|62739186|ref|NP_000177.2|	139052	142	SLGNVIMVCR	1148.59	58	67
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)	DESP_HUMAN	331765	154	ANSSATETINK	1135.56	1517	1527
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)	DESP_HUMAN	331765	155	GFFDPNTEENLTYLQLK	2028.99	2414	2430
hect domain and RLDS [*Homo sapiens*]	gi|7705931|ref|NP_057407.1|	116834	171	RTTEMMPVYLDLNK	1726.85	434	447
Hypothetical protein DKFZp686J11235	Q6MZW0	54441	184	GTTTFAVTSILR	1266.71	441	452
Hypothetical protein DKFZp686J11235	Q6MZW0	54441	185	TPLTATLSK	931.55	366	374
Hypothetical protein DKFZp686J11235	Q6MZW0	54441	186	VTVSSASPTSPK	1160.62	149	160
Hypothetical protein DKFZp781M0386	Q5CZ94	24984	187	AGVETTKPSK	1017.56	179	188
Hypothetical protein DKFZp781M0386	QSCZ94	24984	188	ANPTVTLFPPSSEELQANK	2043.04	133	151
Hypothetical protein DKFZp781M0386	QSCZ94	24984	189	VTVLGQPK	841.51	125	132
Ig heavy chain V-III region GAL	HV3T_HUMAN	12708	191	GLEWVANIK	1029.57	44	52
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984|ref|NP_002209.2|	103340	193	AEAQAQYSAAVAK	1307.66	99	111
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|315429841ref|NP_002209.2|	103340	194	AGFSWIEVTFK	1284.66	778	788
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984|ref|NP_002209.2|	103340	195	ANTVQEATFQMELPK	1706.84	61	75
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984|ref|NP_002209.2|	103340	196	FSSHVGGTLGQFYQEVLWGSPAASDDGR	2968.39	867	894

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984|ref|NP_002209.2|	103340	197	GPDVLTATVSGK	1144.62	501	512
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984|ref|NP_002209.2|	103340	198	LWAYLTIQQLLEQTVSASDADQQALR	2961.53	547	572
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984|ref|NP_002209.2|	103340	199	MNFRPGVLSSR	1263.66	658	668
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984|ref|NP_002209.2|	103340	200	NVHSGSTFFK	1123.55	617	626
inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	gi|31542984|ref|NP_002209.2|	103340	201	VTIGLLFWDGR	1276.71	843	853
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	202	AEAESLYQSK	1125.54	367	376
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	203	AQYEDIAQK	1065.52	356	364
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	204	DYQELMNTK	1141.52	464	472
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	205	EQIKSLNNQFASFIDK	1881.97	182	197
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	206	FLEQQNQVLQTK	1475.79	200	211
keratin 1 [*Homo sapiens*] 6112.2|	gi|17318569|ref|NP_00	66050	207	FSSCGGGGGSFGAGGGFGSR	1765.74	46	65
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	208	GGGGGGYGSGGSSYGSGGGSYGSGGGGGGR	2383.95	519549	
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	209	IEISELNR	973.53	396	403
keratin 1 [*Homo sapiens*]	gi|17318569ref|NP_|006112.2|	66050	210	LALDLEIATYR	1277.71	473	483
keratin 1 [*Homo sapiens*]	gi|17318569|re|NP_006112.2|	66050	211	LNDLEDALQQAK	1357.70	444	455

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050 GGGSR	212	MSGECAPNVSVSVSTSHTTIS	2565.17	493	518
keratan 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	213	NKLNDLEDALQQAK	1599.83	442	455
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	214	NKYEDEINKR	1308.65	268	277
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	215	NMQDMVEDYR	1300.53	258	267
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	216	NMQDMVEDYR	1300.53	258	267
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	217	QISNLQQSISDAEQR	1716.85	418	432
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	218	SKAEAESLYQSK	1340.67	365	376
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	219	SLDLDSIIAEVK	1302.72	344	355
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	220	THNLEPYFESFINNLR	1993.98	224	239
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	221	TLLEGEESR	1033.52	484	492
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	223	TNAENEFVTIK	1265.64	278	288
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	224	WELLQQVDTSTR	1475.75	212	223
keratin 1 [*Homo sapiens*]	gi|17318569|ref|NP_006112.2|	66050	225	YEELQITAGR	1179.60	377	386
Keratin 10	Q14664	57231	226	GSSGGGGFGGSSGGYGGLGGF GGGSFR	2342.99	53	79
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	248	DIENQYETQITQIEHEVSSSG QEVQSSAK	3264.51	340	368

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	249	EIETYHNLLEGGQEDFESSGAGK	2510.13	450	472
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	250	FSSSSGYGGGSSR	1235.53	47	59
keratin 9 [*Homo sapiens*]	gi|559568991ref]NP_000217.2|	62048	251	GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR	2705.16	64	95
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	252	HGVQELEIELQSQLSK	1837.97	375	390
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	253	IKFEMEQNLR	1307.68	241	250
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	254	IQDWYDKK	1095.55	185	192
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	255	LASYLDK	809.44	164	170
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	256	NYSPYYNTIDDLKDQIVDLTVGNNK	2902.41	200	224
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	257	SDLEMQYETLQEELMALK	2171.03	272	289
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	258	SGGGGGGGLGSGGSIR	1232.60	14	29
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	259	STMQELNSR	1065.50	155	163
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	260	TLLDIDNTR	1060.56	225	233
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	261	VQALEEANNDLENK	1586.77	171	184
keratin 9 [*Homo sapiens*]	gi|55956899|ref|NP_000217.2|	62048	262	YCGQLQMIQEQISNLEAQITDVR	2753.32	405	427
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1CIO_HUMAN	59502	263	AETECQNTEYQQLLDIKIR	2352.15	423	441

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	264	GSLGGGFSSGGFSGGSF	1464.64	41	57
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	265	ILLQIDNAR	1055.62	220	228
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1CIO_HUMAN	59502	266	IRLENEIQTYR	1434.77	440	450
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	267	ISALEEQLQQIR	1427.79	411	422
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	268	LAADDFR	807.40	229	235
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	269	LASYLDK	809.44	157	163
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	270	LENEIQTYR	1165.59	442	450
Keratin, type I cytoskeletal 10 (Gytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C1O_HUMAN	59502	271	LKYENEVALR	1234.68	236	245
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	272	NQILNLTTDNAN	1330.66	208	219
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C1O_HUMAN	59502	273	NQILNLTTDNANILLQIDNAR	2367.26	208	228
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C1O_HUMAN	59502	274	NVQALEIELQSQLALK	1797.01	371	386

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	275	RVLDELTLTK	1187.70	257	266
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	276	SGGGGGGGGCGGGGGVSSLR	1549.68	16	35
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) K10)	K1C10_HUMAN	59502	277	SKELTTEIDNNIEQISSYK	2212.10	344	362
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	278	SLLEGEGSSGGGGR	1262.60	451	464
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	K1C10_HUMAN	59502	279	VQALEIELQSQLALK	1682.97	372	386
Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK-14) (Keratin-14) (K14)	K1C14_HUMAN	51473	281	EVATNSELVQSGK	1361.69	315	327
Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK-14) (Keratin-14) (K14)	K1C14_HUMAN	51473	282	GSCGIGGGIGGGSSR	1278.59	15	29
Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK-14) (Keratin-14) (K14)	K1C14_HUMAN	51473	283	ISSVLAGGSCR1106.56	30	40	
Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK-14) (Keratin-14) (K14)	K1C14_HUMAN	51473	284	VLDELTLAR	1029.59	223	231
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	285	AEAESLYQSK	1125.54	366	375
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	286	ELLQQVDTSTR	1289.67	212	222

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN GGSIGGR	65870	287	GGSGGGGGGSSGGRGSGGGSS	2079.92	588	615
Keratin, type II cytoskeletal 1 (Cytokeratin-I) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	288	GSGGGSSGGSIGGR	1092.50	602	615
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratini) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	289	KQISNLQQSISDAEQR	1844.95	416	431
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	290	LALDLEIATYR	1277.71	472	482
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	291	NKLNDLEDALQQAK	1599.83	441	454
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	292	NVEIDPEIQK	1184.62	165	174
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	293	SEIDNVKK	932.51	409	416
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	294	SGGGFSSGSAGIINYQR	1657.79	12	28
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	295	SISDAEQR	905.43	424	431
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	296	SISISVARGGGR	1159.65	74	85
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	297	SKAEAESLYQSK	1340.67	364	375

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-I) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	298	SLDLDSIIAEVK	1302.72	343	354
Keratin, type 11 cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	299	SLNNQFASFIDK	1383.69	185	196
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	300	SLNNQFASFIDKVR	1638.86	185	198
Keratin, type 11 cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	301	SLVNLGGSK	874.50	65	73
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	302	THNLEPYFESF	1383.62	223	233
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (GK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	303	THNLEPYFESFINNLR	1993.98	223	238
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	304	TLLEGEESR	1033.52	483	491
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	305	TNAENEFVTIK	1265.64	277	287
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	306	VDQLKSDQSR	1175.60	241	250
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	307	VEIDPEIQK	1070.57	166	174
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	308	WELLQQVDTSTR	1475.75	211	222

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	K2C1_HUMAN	65870	309	YEELQITAGR	1179.60	376	385
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	310	GFSSGSAVVSGGSR	1254.61	21	34
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	311	IEISELNR	973.53	400	407
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	312	LALDVEIATYR	1263.69	477	487
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	313	LNDLEEALQQAK	1371.71	448	459
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	314	NLDLDSHAEVK	1329.73	348	359
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	315	NVQDAIADAEQR	1329.64	425	436
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	316	VDLLNQEIEFLK	1460.80	309	320
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	317	YEDEINKR	1066.52	274	281
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	318	YEELQVTVGR	1193.62	381	390
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	K22E_HUMAN	65848	319	YLDGLTAER	1037.53	245	253
KIAA1199 [*Homo sapiens*]	gi|38638698|re|NP_061159.1|	152983	320	PFLSIISARYSPHQDADPLK	2255.18	755	774
Moy10, Moloney leukemia virus 10, homolog [*Homo sapiens*]	gi|14211540|ref|NP_066014.1|	113658	333	ISFGTPAPGFSSMLYGMK	1906.91	45	62
Novel protein (Keratinocyte proline-rich protein)	Q5T749	64115	336	GRPAVCQPQGR	1225.62	167	177
Novel protein (Keratinocyte proline-rich protein)	Q5T749	64115	337	IEISSPCCPR	1218.56	327	336

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Novel protein (Keratinocyte praline-rich protein)	Q5T749	64115	338	RPISSCSQR	1090.54	312	320
pericentriolar material 1 [*Homo sapiens*]	gi|34878902|ref|NP_006188.2|	228284	339	LPEMEPLVPRVKEVK	1780.00	1906	1920
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392|ref|NP_005800.31,gi|33188452|ref|NP_859427.1|	21874	340	ATAVVDGAFK	978.53	17	26
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392|ref|NP_005800.3|,gi|33188452|ref|NP_859427.11	21874	341	EGGLGPLNIPLLADVTR	1734.98	93	109
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392|ref|NP_005800.3|,gi|33188452|ref|NP_859427.1|	21874	342	EGGLGPLNIPLLADVTR	1734.98	93	109
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392|ref|NP_005800.3|,gi|33188452|ref|NP_859427.1|	21874	343	GLFIIDGK	862.50	128	135
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392|ref|NP_005800.3|,gi|33188452|ref|NP_859427.1|	21874	344	KEGGLGPLNIPLLADVTR	1863.07	92	109
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392|ref|NP_005800.3|,gi|331884521ref|NP_859427.1|	21874	345	LSEDYGVLK	1023.54	111	119
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392|ref|NP_005800.3|,gi|33188452|ref|NP_859427.1|	21874	346	RLSEDYGVLK	1179.64	110	119
peroxiredoxin 2 isoform a [*Homo sapiens*]	gi|32189392|ref|NP_005800.3|,gi|33188452|ref|NP_859427.1|	21874	347	TDEGIAYR	924.44	120	127
plasma carboxypeptidase B2 isoform a preproprotein [*Homo sapiens*]	gi|4503005|ref|NP_001863.1|	48425	349	DTGTYGFLLPER	1368.68	388	399
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]	gi|4505733|ref|NP_002610.1|	10828	350	AGPHCPTAQLIATLK	1577.85	63	77

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]	gi|4505733|ref|NP_002610.1|	10828	351	HTSLEVIK	1039.62	54	62
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]	gi|4505733|ref|NP_002610.1|	10828	352	ICLDLQAPLYK	1333.72	82	92
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]	gi|4505733|ref|NP_002610.1|	10828	353	ICLDLQAPLYKK	1461.81	82	93
platelet factor 4 (chemokine (C-X-C motif) ligand 4) [*Homo sapiens*]610.1|	gi|4505733|ref|NP_002	10828	354	KICLDLQAPLYK	1461.81	81	92
profilin family, member 4 [*Homo sapiens*]	gi|40786418|ref|NP_955378.1|	14302	360	CVRADEYSLYAKNENTGVVVVK	2514.27	73	94
propionyl-Coenzyme A carboxylase, alpha polypeptide precursor [*Homo sapiens*]	gi|65506442|ref|NP_000273.2|	80041	361	YSSAGTVEFLVDSK	1502.74	329	342
regulatory solute carrier protein, family 1, member 1 [*Homo sapiens*]	gi|5730021|ref|NP_006502.1|	66771	364	DLGQGIQNSVTDRPETR	1885.94	523	539
roundabout, axon guidance receptor, homolog 2 [*Homo sapiens*]	gi|61888896|ref|NP_002933.1|	151182	366	QTSGLQATSSWQNLDAK	1834.89	674	690
Rsb-66 protein [*Homo sapiens*]	gi|33285006|ref|NP_061829.3|	19271	367	PISSIGQVQSYMEHYCNSSTDRR	2731.22	42	64
S100 calcium-binding protein A7 (Psoriasin)	S10A7_HUMAN	11309	368	ENFPNFLSACDK	1441.64	37	48
S100 calcium-binding protein A7 (Psoriasin)	S10A7_HUMAN	11309	369	GTNYLADVFEK	1256.62	50	60
S100 calcium-binding protein A7 (Psoriasin)	S10A7_HUMAN	11309	370	IDFSEFLSLLGDIATDYHK	2184.09	69	87
S100 calcium-binding protein A7 (Psoriasin)	S10A7_HUMAN	11309	371	KIDFSEFLSLLGDIATDYHK	2312.18	68	87
secretoglobin, family 3A, member 1 [*Homo sapiens*]	gi|50363226|ref|NP_443095.2|	10082	374	LLLSSLGIPVNHLIEGSQK	2018.17	59	77
secretoglobin, family 3A, member 1 [*Homo sapiens*]	gi|50363226|ref|NP_443095.21	10082	375	PVAQPVAALESAAEAGAGTLANPLGTLNPLK	2941.60	28	58

TABLE 3-continued

Biomarkers associated with Mild Cognitive Impairment (MCI)

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index	Peptide stop index
Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein)	TETN_HUMAN	22549	403	GGTLSTPQTGSENDALYEYLR	2272.07	102	122
Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein)	TETN_HUMAN	22549	404	LDTLAQEVALLK	1313.77	51	62
thrombospondin 4 precursor [*Homo sapiens*]	gi|31543806|ref|NP_003239.2|	105851	405	LNPGALLPVLTDPALNDLYVISTFK	2684.49	41	65
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410|ref|NP_000574.2|	52900	427	EDFTSLSLVLYSR	1529.79	38	50
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410|ref|NP_000574.2|	52900	428	EFSHLGKEDFTSLSLVLYSR	2328.19	31	50
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410|ref|NP_000574.2|	52900	429	ELSSFIDK	938.48	395	402
vitamin D-binding protein precursor *Homo sapiens*]	gi|32483410|ref|NP_000574.2|	52900	430	FPSGTFEQVSQLVK	1566.82	52	65
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410|ref|NP_000574.2|	52900	431	KFPSGTFEQVSQLVK	1694.91	51	65
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410|ref|NP_000574.2|	52900	432	LPDATPTELAK	1155.63	430	440
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410|ref|NP_000574.2|	52900	433	RTHLPEVFLSK	1326.75	353	363
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410|ref|NP_000574.2|	52900	434	VPTADLEDVLPLAEDITNILSK	2366.27	243	264
vitamin D-binding protein precursor [*Homo sapiens*]	gi|32483410|ref|NP_000574.2|	52900	435	YTFELSR	915.46	346	352

TABLE 4

Biomarkers associated with brain microhemorrhages

Protein name	Protein accession numbers	Protein molecular weight (Da)	SEQ ID NO:	Peptide sequence	Calculated Peptide Mass (AMU)	Peptide start index
(P21817) Ryanodine receptor 1 (Skeletal muscle-type ryanodine receptor) (RyR1) (RYR-1) (Skeletal muscle calcium release channel)	RYR1_HUMAN	565156	441	EEQNFVVQNEINNM SFLTADNK	2584.20	3454
(Q9NVES) Ubi|uitin carboxyl-terminal hydrolase 40 (EC 3.1.2.15) (U	Q9NVE5	140130	442	IGISWNKK	945.55	372
(Q5NV79) V5-4 protein (Fragment)	Q5NV79	10661	443	FSGSSSGADR	970.42	66
(P51843) Nuclear receptor 0B1 (Nuclear receptor DAX-1) (DSS-AHC critical region on the X chromosome protein 1)	DAX1_HUMAN	51700	444	YLPCFQVLPLDQQL VLVR	2201.22	271
(Q96SU4) Oxysterol binding protein-related protein 9 (OSBP-related	Q96SU4	83185	445	HCIVLLQIAKDQSNA EK	1967.04	172
(P17706) Tyrosine-protein phosphatase, non-receptor type 2 (EC 3.1.3.48) (T-cell protein-tyrosine phosphatase) (TCPTP)	PTN2_HUMAN	48511	446	VKLQNAENDYINAS LVDIEEAQR	2632.32	59
(O15013) Rho guanine nucleotide exchange factor 10	ARHGA_HUMAN	127102	447	YILGSVVDSEKNYV DALKR	2169.16	194
(O75129) KJAA0634 protein (Fragment)	O75129	145410	448	EAFKSALMSSYWCS GK	1851.84	1006
(Q8N543) Hypothetical protein FLJ10826	Q8N543	63230	449	EPHISTLRKILFEDFR	2001.09	109
(Q96AE7) Tetratricopeptide repeat protein 17 (TPR repeat protein 17)	TTC17_HUMAN	129543	450	IHIEENEDRDTGLEQ RHNK	2333.12	91
(Q96AE7) Tetratricopeptide repeat protein 17 (TPR repeat protein 17)	TTC17_HUMAN	129543	451	GLRIHELSSDDYSTE EEAQTPDCSITDFR	3371.50	530
(Q96AE7) Tetratricopeptide repeat protein 17 (TPR repeat protein 17)	TTC17_HUMAN	129543	452	IQQQVDSPMNLK	1400.72	50

TABLE 8

Analysis of candidate biomarkers in normal and mild AD patients.

Accession	Protein name	MW	Normal	MCI	mild AD	Normal vs mild AD	Normal vs MCI	MCI vs mild AD
P13645	**(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)**	**59502.3**	**0**	**57**	**4**	**100%**	**100%**	**87%**
P35908	**(P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)**	**65848.4**	**0**	**16**	**4**	**100%**	**100%**	**60%**
P02671	**(P02671) Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A]**	**94955.4**	**1**	**5**	**7**	**75%**	**67%**	**17%**
Q6PYX1	**(Q6PYX1) Hepatitis B virus receptor binding protein (Fragment)**	**38143**	**1**	**8**	**5**	**67%**	**78%**	**23%**
O75179	**(O75179) KIAA0697 protein (Fragment)**	**263225.4**	**1**	**2**	**5**	**67%**	**33%**	**43%**
P55056	**(P55056) Apolipoprotein C-IV precursor (Apo-CIV) (ApoC-IV)**	**14535.5**	**2**	**2**	**7**	**56%**	**0%**	**56%**
Q6GTG1	(Q6GTG1) Vitamin D-binding protein,	52919.5	6	6	0	100%	0%	100%
O95978	(O95978) VH1 protein precursor (Fragment)	17285	6	1	0	100%	71%	100%
P01781	(P01781) Ig heavy chain V-III region GAL	12708.1	5	4	0	100%	11%	100%
P01614	(P01614) Ig kappa chain V-II region Cum	12658.6	4	2	0	100%	33%	100%
P13798	(P13798) Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Oxidized protein hydrolase) (OPH) (DNF15S2 protein)	81206.1	4	0	0	100%	100%	
P55073	(P55073) Type III iodothyronine deiodinase (EC 1.97.1.11) (Type-III 5'deiodinase) (DIOIII) (Type 3 DI) (5DIII)	31386.2	4	0	0	100%	100%	
Q6MZW0	(Q6MZW0) Hypothetical protein DKFZp686J11235 (Fragment)	54440.5	6	5	1	71%	9%	67%
Q5CZ94	(Q5CZ94) Hypothetical protein DKFZp781M0386	24983.5	8	6	2	60%	14%	50%
P01011	(P01011) Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	47635	12	13	4	50%	4%	53%

Biomarkers for: Normal versus mild AD
Experiment: LMW__b (pooled samples of Normal/MCI/mild AD)
Filters: SEQUEST => XC +1 > 1.9, +2 > 2.2, +3 > 3.5
at least 4 spectra per protein in one group
over 50% difference between normal and mild AD
Key: **more abundant in mild AD**
more abundant in Normals

Accession	Name	Probability	MW	Stable Normal [av samples] (n = 3)	Unstable Normal [av samples] (n = 4)	Normal (stable + unstable) [av samples] (n = 7)	Stable MCI [av samples] (n = 5)	mild AD [av samples] (n = 12)	mild AD vs Normal	Unstable Normal vs Stable Normal	Stable Normal vs Stable MCI	Unstable Normal vs Stable MCI	Stable MCI vs mild AD	Unstable Normal vs mild AD	Stable Normal vs mild AD
P16591	**FER_HUMAN (P16591) Proto-oncogene tyrosine-protein kinase FER (EC 2.7.1.112) (p94-FER) (c-FER)**	**1.25E−04**	**94563.8**	**0.00**	**0.00**	**0.00**	**0.40**	**0.67**	**100%**	**0%**	**100%**	**100%**	**25%**	**100%**	**100%**

TABLE 8-continued

P22792	CPN2_HUMAN (P22792) Carboxypeptidase N subunit 2 precursor (Carboxypeptidase N polypeptide 2) (Carb	2.00E−07	60576.3	0.00	0.00	0.00	0.60	0.58	100%	0%	100%	100%	1%	100%	100%
Q6ZVQ3	Q6ZVQ3 (Q6ZVQ3) Hypothetical protein FLJ42220	9.19E−04	17595.2	0.00	0.00	0.00	0.80	0.50	100%	0%	100%	100%	23%	100%	100%
Q9H2I2	Q9H2I2 (Q9H2I2) HNRBF-2	2.53E−04	31787.4	0.00	0.00	0.00	0.20	0.33	100%	0%	100%	100%	25%	100%	100%
P13667	PDIA4_HUMAN (P13667) Protein disulfide-isomerase A4 precursor (EC 5.3.4.1) (Protein ERp-72) (ERp72)	2.62E−04	72887.1	0.00	0.00	0.00	0.20	0.33	100%	0%	100%	100%	25%	100%	100%
O60602	TLR5_HUMAN (O60602) Toll-like receptor 5 precursor (Toll/interleukin-1 recepto	2.76E−04	97663.4	0.00	0.00	0.00	0.00	0.33	100%	0%	0%	0%	100%	100%	100%
O95793	STAU_HUMAN (O95793) Double-stranded RNA-binding protein Staufen homolog	2.83E−04	63227.9	0.00	0.00	0.00	0.40	0.33	100%	0%	100%	100%	9%	100%	100%
Q7Z3Z2	CA036_HUMAN (Q7Z3Z2) Protein C1orf36	8.02E−05	22689.6	0.00	0.00	0.00	0.20	0.33	100%	0%	100%	100%	25%	100%	100%
Q05513	KPCZ_HUMAN (Q05513) Protein kinase C, zeta type (EC 2.7.1.37) (nPKC-zeta)	1.14E−04	67616.8	0.00	0.00	0.00	0.40	0.33	100%	0%	100%	100%	9%	100%	100%

TABLE 8-continued

Q4V312	**Q4V312 (Q4V312) Colony stimulating factor 2 receptor, alpha, low-affinity (Granulocyte-macrophage)**	**5.36E−05**	**46871.6**	**0.00**	**0.00**	**0.00**	**0.60**	**0.33**	**100%**	**0%**	**100%**	**100%**	**29%**	**100%**	**100%**
Q93088	**BHMT_HUMAN (Q93088) Betaine--homocysteine S-methyltransferase (EC 2.1.1.5)**	**6.52E−04**	**44941.8**	**0.00**	**0.25**	**0.14**	**0.60**	**0.75**	**68%**	**100%**	**100%**	**41%**	**11%**	**50%**	**100%**
Q8N7W7	**Q8N7W7 (Q8N7W7) Hypothetical protein FLJ40259**	**5.41E−04**	**66086.9**	**0.00**	**0.25**	**0.14**	**0.40**	**0.58**	**61%**	**100%**	**100%**	**23%**	**19%**	**40%**	**100%**
P35542	**SAA4_HUMAN (P35542) Serum amyloid A-4 protein precursor (Constitutively expres**	**9.09E−04**	**14797.3**	**0.00**	**0.25**	**0.14**	**0.00**	**0.58**	**61%**	**100%**	**0%**	**100%**	**100%**	**40%**	**100%**
Q9BXB9	**Q9BXB9 (Q9BXB9) LIM mineralization protein 2**	**2.79E−04**	**46480**	**0.00**	**0.25**	**0.14**	**0.60**	**0.50**	**56%**	**100%**	**100%**	**41%**	**9%**	**33%**	**100%**
Q99996	AKAP9_HUMAN (Q99996) A-kinase anchor protein 9 (Protein kinase A anchoring pro	1.98E−04	453386.1	0.33	0.50	0.43	0.00	0.00	100%	20%	100%	100%	0%	100%	100%
P09758	TACD2_HUMAN (P09758) Tumor-associated calcium signal transducer 2 precursor (P	3.03E−04	35686.6	0.67	0.25	0.43	0.40	0.08	67%	45%	25%	23%	66%	50%	78%
Q5VVM6	Q5VVM6 (Q5VVM6) Novel protein	3.55E−04	91277.5	0.67	0.25	0.43	0.20	0.08	67%	45%	54%	11%	41%	50%	78%

TABLE 8-continued

P12814	ACTN1_HUMAN (P12814) Alpha-actinin 1 (Alpha-actinin cytoskeletal isoform) (Non	4.70E−04	102992.7	1.00	0.00	0.43	0.00	0.08	67%	100%	100%	0%	100%	100%	85%

Biomarkers for: Normal versus mild AD
Experiment: whole serum (individual samples of Normal/MCI/mild AD)
Filters: SEQUEST
found in more than 33% of either normals or mild AD patients
over 50% difference between normal and mild AD (in average samples with positive identification)
probability score of less than 1.00E−03
Key: **more abundant in mild AD**
more abundant in Normals

TABLE 9

Analysis of candidate biomarkers in MCI and mild AD patients

Accession	Protein name	MW	Normal	MCI	mild AD	Normal vs mild AD	Normal vs MCI	MCI vs mild AD
P02654	**(P02654) Apolipoprotein C-I precursor (Apo-CI) (ApoC-I)**	**9314.4**	**6**	**2**	**9**	**20%**	**50%**	**64%**
P55056	**(P55056) Apolipoprotein C-IV precursor (Apo-CIV) (ApoC-IV)**	**14535.5**	**2**	**2**	**7**	**56%**	**0%**	**56%**
Q6GTG1	(Q6GTG1) Vitamin D-binding protein,	52919.5	6	6	0	100%	0%	100%
P01824	(P01824) Ig heavy chain V-II region WAH	14099.1	0	5	0		100%	100%
P02533	(P02533) Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK-14) (Keratin-14) (K14)	51473.4	0	5	0		100%	100%
P15924	(P15924) Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)	331765.3	0	5	0		100%	100%
Q5KSL6	(Q5KSL6) Diacylglycerol kinase kappa	141814.6	0	5	0		100%	100%
P31151	(P31151) S100 calcium-binding protein A7 (Psoriasin)	11308.5	0	4	0		100%	100%
Q5T749	(Q5T749) Novel protein (Keratinocyte proline-rich protein)	64114.6	0	4	0		100%	100%
Q14664	(Q14664) Keratin 10	57231.3	1	4	0	100%	60%	100%
P01781	(P01781) Ig heavy chain V-III region GAL	12708.1	5	4	0	100%	11%	100%
P13645	(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	59502.3	0	57	4	100%	100%	87%
Q6MZW0	(Q6MZW0) Hypothetical protein DKFZp686J11235 (Fragment)	54440.5	6	5	1	71%	9%	67%
P04264	(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair alpha protein)	65870	6	78	17	48%	86%	64%
P35908	(P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e)	65848.4	0	16	4	100%	100%	60%
P05452	(P05452) Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein)	22549.1	0	4	1	100%	100%	60%
P23945	(P23945) Follicle-stimulating hormone receptor precursor (FSH-R) (Follitropin receptor)	78280.1	1	7	2	33%	75%	56%
P01011	(P01011) Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1-antichymotrypsin His-Pro-less]	47635	12	13	4	50%	4%	53%
Q5CZ94	(Q5CZ94) Hypothetical protein DKFZp781M0386	24983.5	8	6	2	60%	14%	50%

Biomarkers for: MCI versus mild AD
Experiment: LMW_b (pooled samples of Normal/MCI/mild AD)
Filters: SEQUEST => XC +1 > 1.9, +2 > 2.2, +3 > 3.5
at least 4 spectra per protein in one group
over 50% difference between MCI and mild AD
Key: **more abundant in mild AD**
more abundant in MCI

Accession			MCI			PMCI/unst. MCI						MCI –	%
(GI_Number)	Protein name	MW	397	531	667	397	531	667	MCI + PMCI	MCI	PMCI	PMCI	Diff.
gi|11386147	prosaposin *[Homo sapiens]*	**58094**	**0**	**0**	**0**	**1**	**2**	**1**	**4**	**0**	**4**	**−4**	**100%**
gi|4505873	**phospholipase D1, phophatidylcholine-specific** *[Homo sapiens]*	**124170**	**0**	**0**	**1**	**2**	**1**	**2**	**6**	**1**	**5**	**−4**	**67%**
gi|13540475	**serum amyloid A2** *[Homo sapiens]*	**13491**	**0**	**0**	**1**	**1**	**1**	**2**	**5**	**1**	**4**	**−3**	**60%**

TABLE 9-continued

gi|4504351	delta globin [Homo sapiens]	16037	22	9	12	50	14	13	120	43	77	−34	28%
gi|4759050	ribosomal protein S6 kinase, 90 kDa, polypeptide 3 [Homo sapiens]	83721	4	4	3	6	5	4	26	11	15	−4	15%
gi|4504489	histidine-rich glycoprotein precursor [Homo sapiens]	59559	5	10	13	8	11	19	66	28	38	−10	15%
gi|11761629	fibrinogen, alpha polypeptide isoform alpha preproprotein [Homo sapiens]	69739	25	44	18	46	54	19	206	87	119	−32	16%
gi|4557871	transferrin [Homo sapiens]	77032	61	78	81	68	104	101	493	220	273	−53	11%
gi|10835095	serum amyloid A4, constitutive [Homo sapiens]	14789	60	134	120	70	139	128	651	314	337	−23	4%
gi|49574514	matrix Gla protein [Homo sapiens]	12336	0	0	0	3	0	1	4	0	4	−4	100%
gi|4506769	S100 calcium-binding protein A7 [Homo sapiens]	11440	0	1	0	1	1	4	7	1	6	−5	71%
gi|4502419	biliverdin reductase B (fiavin reductase (NADPH)) [Homo sapiens]	22101	0	0	0	1	0	3	4	0	4	−4	100%
gi|30794266	triggering receptor expressed on myeloid cells-like 1 [Homo sapiens]	32661	1	0	0	1	1	1	4	1	3	−2	50%
gi|32698688	citron [Homo sapiens]	231418	0	0	0	2	2	0	4	0	4	−4	100%
gi|28076869	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 [Homo sapiens]	44837	0	0	0	1	0	3	4	0	4	−4	100%
gi|40806175	diacylglycerol kinase, theta [Homo sapiens]	101135	0	0	0	2	0	1	3	0	3	−3	100%
gi|38455402	lipocalin 2 (oncogene 24p3) [Homo sapiens]	22571	0	0	0	0	1	1	2	0	2	−2	100%
gi|113417691	PREDICTED: hypothetical protein [Homo sapiens]	24550	0	0	0	0	1	1	2	0	2	−2	100%
gi|21361470	chromosome 1 open reading frame 48 [Homo sapiens]	32112	0	0	0	1	1	0	2	0	2	−2	100%
gi|33286418	pyruvate kinase 3 isoform 1 [Homo sapiens]	57920	0	0	0	1	1	0	2	0	2	−2	100%
gi|66346708	membrane associated guanylate kinase, WW and PDZ domain containing 1 isoform b [Homo sapiens]	136902	0	0	0	0	1	1	2	0	2	−2	100%
gi|24586657	myosin IIIA [Homo sapiens]	186070	0	0	0	0	1	1	2	0	2	−2	100%
gi|11641247	chromosome 9 open reading frame 19 [Homo sapiens]	17200	0	0	0	1	1	0	2	0	2	−2	100%
gi|4507267	stanniocalcin 2 precursor [Homo sapiens]	33230	0	0	0	1	0	1	2	0	2	−2	100%
gi|113426784	PREDICTED: similar to ribosomal protein S2 [Homo sapiens]	27009	0	0	0	0	1	1	2	0	2	−2	100%
gi|19923424	myotubularin-related protein 9 [Homo sapiens]	63446	0	0	0	1	1	0	2	0	2	−2	100%

TABLE 9-continued

gi|4826663	**core-binding factor, runt domain, alpha subunit 2; translocated to, 2 isoform MTGR1b *[Homo sapiens]***	**67115**	**0**	**0**	**0**	**1**	**0**	**1**	**2**	**0**	**2**	**−2**	**100%**
gi|21264361	**mannan-binding lectin serine protease 2 isoform 1 precursor *[Homo sapiens]***	**75685**	**0**	**0**	**1**	**1**	**0**	**2**	**4**	**1**	**3**	**−2**	**50%**
gi|113419903	**PREDICTED: similar to Neutrophil defensin 1 precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1) *[Homo sapiens]***	**10183**	**0**	**2**	**1**	**0**	**4**	**18**	**25**	**3**	**22**	**−19**	**76%**
gi|4557894	**lysozyme precursor *[Homo sapiens]***	**16519**	**1**	**0**	**3**	**1**	**2**	**5**	**12**	**4**	**8**	**−4**	**33%**
gi|38016947	**complement component 5 *[Homo sapiens]***	**188291**	**4**	**3**	**2**	**4**	**5**	**4**	**22**	**9**	**13**	**−4**	**18%**
gi|38044288	**gelsolin isoform a precursor *[Homo sapiens]***	**85680**	**2**	**5**	**2**	**5**	**7**	**2**	**23**	**9**	**14**	**−5**	**22%**
gi|50363217	**serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 *[Homo sapiens]***	**46720**	**21**	**25**	**17**	**30**	**25**	**31**	**149**	**63**	**86**	**−23**	**15%**
gi|51339291	**sterile alpha motif domain containing 9-like *[Homo sapiens]***	**184523**	**3**	**2**	**4**	**4**	**3**	**4**	**20**	**9**	**11**	**−2**	**10%**
gi|88853069	**vitronectin precursor *[Homo sapiens]***	**54288**	**7**	**5**	**12**	**9**	**7**	**12**	**52**	**24**	**28**	**−4**	**8%**
gi|50345296	**complement component 4B preproprotein *[Homo sapiens]***	**192735**	**12**	**12**	**10**	**13**	**16**	**10**	**73**	**34**	**39**	**−5**	**7%**
gi|31542984	inter-alpha (globulin) inhibitor H4 [*Homo sapiens*]	103340	2	4	4	0	0	0	10	10	0	10	100%
gi|55956899	keratin 9 [*Homo sapiens*]	62048	6	1	7	0	0	0	14	14	0	14	100%
gi|62739186	complement factor H isoform a precursor [*Homo sapiens*]	139052	4	2	4	1	0	0	11	10	1	9	82%
gi|21735614	apolipoprotein L1 isoform a precursor [*Homo sapiens*]	43957	3	3	1	0	1	0	8	7	1	6	75%
gi|22091452	apolipoprotein M [*Homo sapiens*]	21236	4	4	2	2	1	0	13	10	3	7	54%
gi|24234699	keratin 10 [*Homo sapiens*]	58811	8	7	11	2	3	3	34	26	8	18	53%
gi|7705931	hect domain and RLD 5 [*Homo sapiens*]	116834	3	3	2	1	1	1	11	8	3	5	45%
gi|17318569	keratin 1 [*Homo sapiens*]	66050	36	5	7	3	4	3	58	48	10	38	66%
gi|21071030	alpha 1B-glycoprotein [*Homo sapiens*]	54235	3	5	5	1	3	2	19	13	6	7	37%
gi|4505733	platelet factor 4 (chemokine (C—X—C motif) ligand 4) [*Homo sapiens*]	10828	13	13	10	7	7	7	57	36	21	15	26%
gi|4557393	complement component 8, gamma polypeptide [*Homo sapiens*]	22201	25	36	64	23	24	16	188	125	63	62	33%
gi|4504349	beta globin [*Homo sapiens*]	15980	289	100	110	109	61	95	764	499	265	234	31%
gi|32130518	apolipoprotein C-II precursor [*Homo sapiens*]	11266	41	96	268	38	52	154	649	405	244	161	25%
gi|4503635	coagulation factor II precursor [*Homo sapiens*]	70019	13	9	14	11	5	11	63	36	27	9	14%
gi|32483410	vitamin D-binding protein precursor [*Homo sapiens*]	52900	9	10	12	7	7	10	55	31	24	7	13%

TABLE 9-continued

gi|34878902	pericentriolar material 1 [*Homo sapiens*]	228284	1	1	1	1	0	0	4	3	1	2	50%
gi|5730021	regulatory solute carrier protein, family 1, member 1 [*Homo sapiens*]	66771	0	2	1	0	0	0	3	3	0	3	100%
gi|38045901	leader-binding protein 32 isoform 1 [*Homo sapiens*]	70096	0	1	2	0	0	0	3	3	0	3	100%
gi|40786418	profilin family, member 4 [*Homo sapiens*]	14302	1	2	0	0	0	0	3	3	0	3	100%
gi|34577063	adenylosuccinate synthase [*Homo sapiens*]	50080	1	0	1	0	0	0	2	2	0	2	100%
gi|88973313	PREDICTED: similar to Zinc finger CCHC domain-containing protein 4 isoform 1 [*Homo sapiens*]	58993	1	1	0	0	0	0	2	2	0	2	100%
gi|4503005	plasma carboxypeptidase B2 isoform a preproprotein [*Homo sapiens*]	48425	1	1	0	0	0	0	2	2	0	2	100%
gi|50363226	secretoglobin, family 3A, member 1 [*Homo sapiens*]	10082	1	1	0	0	0	0	2	2	0	2	100%
gi|38638698	KIAA1199 [*Homo sapiens*]	152983	1	1	0	0	0	0	2	2	0	2	100%
gi|31742536	fidgetin-like 1 [*Homo sapiens*]	74061	1	1	0	0	0	0	2	2	0	2	100%
gi|65506442	propionyl-Coenzyme A carboxylase, alpha polypeptide precursor [*Homo sapiens*]	80041	10	7	5	3	0	5	30	22	8	14	47%
gi|61888896	roundabout, axon guidance receptor, homolog 2 [*Homo sapiens*]	151182	2	2	0	0	1	0	5	4	1	3	60%
gi|33285006	Rsb-66 protein [*Homo sapiens*]	19271	2	0	2	0	0	1	5	4	1	3	60%
gi|31543806	thrombospondin 4 precursor [*Homo sapiens*]	105851	2	1	1	1	1	0	6	4	2	2	33%
gi|32189392	peroxiredoxin 2 isoform a [*Homo sapiens*]	21874	3	2	3	3	0	2	13	8	5	3	23%
gi|14211540	Mov10, Moloney leukemia virus 10, homolog [*Homo sapiens*]	113658	3	2	3	2	2	2	14	8	6	2	14%

Biomarkers for: MCI versus mild AD
Experiment: LMW__c (same patients before and after cognitive decline)
Filters: SEQUEST
increases in at least two of three samples OR
decreases in at least two of three samples
third sample can not decrease OR third sample can not increase (can only be equal)
Key: **more abundant in mild AD**
more abundant in MCI

Accession	Name	Probability	MW	Stable Normal [av samples] (n = 3)	Unstable Normal [av samples] (n = 4)	Normal (stable + unstable) [av samples] (n = 7)	Stable MCI [av samples] (n = 5)	mild AD [av samples] (n = 12)	Stable MCI vs Normal	mild AD vs Normal	Unstable Normal vs Stable Normal	Stable Normal vs Stable MCI	Unstable Normal vs Stable MCI	Stable MCI vs mild AD	Unstable Normal vs mild AD	Stable Normal vs mild AD
P35542	**SAA4_HUMAN (P35542) Serum**	**9.09E−04**	**14797.3**	**0.00**	**0.25**	**0.14**	**0.00**	**0.58**	**100%**	**61%**	**100%**	**0%**	**100%**	**100%**	**40%**	**100%**

TABLE 9-continued

	amyloid A-4 protein precursor (Constitutively expres															
P02766	TTHY_HUMAN (P02766) Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR)	2.78E−13	15877.1	1.00	0.50	0.71	0.00	0.50	100%	18%	33%	100%	100%	100%	0%	33%
P09874	PARP1_HUMAN (P09874) Poly [ADP-ribose] polymerase 1 (EC 2.4.2.30) (PARP-1) (AD	4.55E−04	112881.4	0.00	0.50	0.29	0.00	0.42	100%	19%	100%	0%	100%	100%	9%	100%
P01764	HV3C_HUMAN (P01764) Ig heavy chain V-III region VH26 precursor	4.40E−05	12574.2	0.00	0.75	0.43	0.00	0.42	100%	1%	100%	0%	100%	100%	29%	100%
Q9NPP6	Q9NPP6 (Q9NPP6) Immunoglobulin heavy chain variant (Fragment)	7.65E−04	44758.1	0.33	0.50	0.43	0.00	0.33	100%	13%	20%	100%	100%	100%	20%	0%
Q96MA6	Q96MA6 (Q96MA6) Hypothetical protein FLJ32704 (Chromosome 9 open reading frame	5.15E−04	54890.7	0.33	0.25	0.29	0.00	0.33	100%	8%	14%	100%	100%	100%	14%	0%
Q9NYQ6	CELR1_HUMAN (Q9NYQ6) Cadherin EGF LAG seven-pass G-type receptor 1 precursor (	1.30E−04	329276.7	0.33	0.50	0.43	0.00	0.33	100%	13%	20%	100%	100%	100%	20%	0%

TABLE 9-continued

O60602	**TLR5_HUMAN (O60602) Toll-like receptor 5 precursor (Toll/interleukin-1 recepto**	**2.76E−04**	**97663.4**	**0.00**	**0.00**	**0.00**	**0.00**	**0.33**		**100%**	**0%**	**0%**	**0%**	**100%**	**100%**	**100%**
Q15166	**PON3_HUMAN (Q15166) Serum paraoxonase/ lactonase 3 (EC 3.1.1.—)**	**1.52E−05**	**39582.4**	**0.33**	**0.00**	**0.14**	**0.00**	**0.33**	**100%**	**40%**	**100%**	**100%**	**0%**	**100%**	**100%**	**0%**
O60687	O60687 (O60687) Sushi-repeat-containing protein, X-linked 2	2.32E−04	52937.8	0.00	0.00	0.00	0.40	0.00	100%		0%	100%	100%	100%	0%	0%
Q6N092	Q6N092 (Q6N092) Hypothetical protein DKFZp686K18196 (Fragment)	9.38E−04	56387.9	0.00	0.25	0.14	0.40	0.00	47%	100%	100%	100%	23%	100%	100%	0%
Q96S24	Q96S24 (Q96S24) Hypothetical protein gs30	9.13E−05	3518.7	0.00	0.00	0.00	0.40	0.00	100%			100%	100%	100%	0%	0%
P20701	ITAL_HUMAN (P20701) Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain)	2.34E−04	128738	0.00	0.00	0.00	0.60	0.08	100%	100%	0%	100%	100%	76%	100%	100%
Q8N549	Q8N549 (Q8N549) Hypothetical protein C8orf36	9.74E−05	27915	0.00	0.25	0.14	0.40	0.08	47%	26%	100%	100%	23%	66%	50%	100%

TABLE 9-continued

P09758	TACD2_HUMAN (P09758) Tumor-associated calcium signal transducer 2 precursor (P	3.03E−04	35686.6	0.67	0.25	0.43	0.40	0.08	3%	67%	45%	25%	23%	66%	50%	78%
P10643	CO7_HUMAN (P10643) Complemet component C7 precursor	1.10E−04	93457.3	0.00	0.50	0.29	0.80	0.25	47%	7%	100%	100%	23%	52%	33%	100%

Biomarkers for: MCI versus mild AD
Experiment: whole serum (individual samples of Normal/MCI/mild AD)
Filters: SEQUEST
found in more than 33% of either normals or mild AD patients
over 50% difference between normal and mild AD (in average samples with positive identification)
probability score of less than 1.00E−03
Key: **more abundant in mild AD**
more abundant in MCI

TABLE 10

Analysis of biomarkers in different patient populations.

whole serum:	Accession	Name	StudySet	Identified spectra/Number of samples				Samples with hits/Number of samples				
				0 (n = 3)	1 (n = 4)	2 (n = 5)	4 (n = 12)	0 (n = 3)	1 (n = 4)	0 + 1 (n = 7)	2 (n = 5)	4 (n = 12)
LMW__b:	Accession	Name	StudySet	Identified spectra								
				Norm (n = 14)	MCI (n = 14)	PMCI (n = 14)						
LMW__c:	GI__Number	Protein name	StudySet	Norm 50	Unst Norm 50	MCI 1305	MCI 1305	397	MCI 531	667	PMCI/unst MCI 397	531	667
homocysteine metabolism	Q13867	Bleomycin hydrolase	whole serum	0.67	0.25	0.00	0.00	0.67	0.25	0.43	0.00	0.00	
	Q13867	Bleomycin hydrolase	LMW__b	0	1	0							
	Q93088	Betaine-homocysteine S-methyltransferase	whole serum	0.00	1.25	2.80	2.33	0.00	0.25	0.14	0.60	0.75	
	P27169	Serum paraoxonase 1	LMW__b	3	2	1							
	Q6B0J6	Serum paraoxonase 1	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	P27169	Serum paraoxonase 1	whole serum	7.33	4.00	3.20	2.00	1.00	0.75	0.86	0.80	0.67	
	gi|19923106	Serum paraoxonase 1	LMW__c	3	0	2	0	4	2	2	3	2	4
	Q15166	Serum paraoxonase 3	whole serum	0.33	0.00	0.00	0.58	0.33	0.00	0.14	0.00	0.33	

Bleomycin hydrolase protects against homocysteine toxicity (Zimny2006)
Elevated serum homocysteine is a risk factor for Alzheimer's disease
Polymorphisms in bleomycin hydrolase have been found to be correlated with the incidence of AD - however replication of the finding shows mixed results
Bleomycin hydrolase regulates the secretion of soluble APP and Abeta (Lefterov2001)
Betaine--homocysteine S-methyltransferase is one of two key enzymes involved in the removal of homocysteine (Brosnan2004)
Betaine is considered as a therapeutic in AD to lower plasma homocysteine (Knopman2001)
Methionyl tRNA synthetase edits homocysteine out if it gets inserted into proteins instead of methionine - this results in homocysteine-thiolacetone (Zimny2006)
Homocysteine-thiolacetone gets cleared by bleomycin hydrolase inside cells (Zimny2006)
Homocysteine-thiolacetone gets cleared by serum paraoxonase 1 in the serum (Himbergen2006)
Homocysteine-thiolacetone can impair protein synthesis and lead to endothelial dysfunction and vascular damage (Himbergen2006)

inflammation	Q4V312	Colony stimulating factor 2 receptor (GM-CSF)	whole serum	0.00	0.00	2.40	1.50	0.00	0.00	0.00	0.60	0.33	
	gi|4506765	S100 calcium-binding protein A4	LMW__c	0	0	1	0	0	0	0	0	0	0
	gi|7657532	S100 calcium-binding protein A6	LMW__c	0	0	0	1	0	0	0	0	0	0
	P31151	S100 calcium-binding protein A7	LMW__b	0	4	0							
	gi|4506769	S100 calcium-binding protein A7	LMW__c	0	6	1	0	0	1	0	1	1	4
	P05109	S100 calcium-binding protein A8	LMW__b	2	6	3							
	gi|21614544	S100 calcium-binding protein A8	LMW__c	3	11	15	3	5	4	4	2	14	5
	P06702	S100 calcium-binding protein A9	LMW__b	0	1	0							
	gi|4506773	S100 calcium-binding protein A9	LMW__c	2	4	3	4	3	3	6	3	5	5
	P02735	Serum amyloid A protein precursor (SAA)	LMW__b	3	6	5							
	P02735	Serum amyloid A protein precursor (SAA)	whole serum	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.17	
	gi|40316910	Serum amyloid A1 isoform 2 (SAA1)	LMW__c	11	7	5	8	15	7	2	10	13	0
	gi|13540475	Serum amyloid A2 (SAA2)	LMW__c	0	0	4	1	0	0	1	1	1	2

TABLE 10-continued

	P22614	Putative serum amyloid A3 (SAA3)	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	P22614	Putative serum amyloid A3 (SAA3)	LMW_b	0	1	1							
	P35542	Serum amyloid A4 protein precursor (SAA4)	whole serum	0.00	0.25	0.00	1.25	0.00	0.25	0.14	0.00	0.58	
	P35542	Serum amyloid A4 protein precursor (SAA4)	LMW_b	41	53	28							
	gi|10835095	Serum amyloid A4 protein precursor (SAA4)	LMW_c	98	87	82	82	60	134	120	70	139	128
GM-CSF receptor alpha is upregulated in ischemic brain + increased GM-CSF helps to reduce neuronal injury (Schaebitz2007)													
GM-CSF levels are highly increased in AD and vascular dementia serum and CSF (Tarkowski2001)													
Abeta activated microglia upregulate S100A8 expression (Walker2006) - however, it is not associated with AD brain lesions (Shepherd2006)													
SAA2 is an acute phase protein that is induced by the inflammatory cytokines IL-1 and IL-6 (Longley1999)													
estrogen	P03372	Estrogen receptor alpha	whole serum	0.00	0.00	1.00	0.25	0.00	0.00	0.00	0.60	0.25	
	Q92731	Estrogen receptor beta	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00	
	O95718	Estrogen-related receptor (Steroid hormone receptor ERR2)	whole serum	0.33	0.00	0.00	0.17	0.33	0.00	0.14	0.00	0.17	
	Q5TF95	Estrogen nuclear receptor coactivator 1	whole serum	0.33	0.50	0.00	0.08	0.33	0.25	0.29	0.00	0.08	
	P49888	Estrogen sulfotransferase (EC 2.8.2.4)	whole serum	0.33	0.00	0.40	0.17	0.33	0.00	0.14	0.20	0.08	
	P50224	Placental estrogen sulfotransferase (EC 2.8.2.1)	LMW_b	1	0	0							
	P11511	Estrogen synthetase (Cytochrome P450 19A1)	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	gi|62244004	Modulator of estrogen induced transcription	LMW_c	0	0	0	0	1	0	0	0	0	0
	P23945	Follicle-stimulating hormone receptor precursor (Follitropin receptor)	LMW_b	78280.1	1	7	2						
Estrogen has a neuroprotective effect - possibly via mitochondria (Singh2006)													
Brain estrogen is reduced in AD women (Combarros2007)													
Estrogen receptor alpha and butylylcholinesterase genes seem to interact with regard to AD (Combarros2007)													
Estrogen receptor alpha gene variants are associated with AD (Luckhaus2007)													
FSH regulates estrogen production													
FSH-R knockout mice have reduced estrogen production and neurodegenerative symptoms (Danilovich2004)													
PEDF	P36955	Pigment epithelium-derived factor precursor	whole serum	0.00	0.25	1.20	0.33	0.00	0.25	0.14	0.80	0.33	
	gi|39725934	Pigment epithelium-derived factor precursor	LMW_c	0	0	0	0	0	0	0	0	0	1
	Q9HD28	Retinitis pigmentosa GTPase regulator	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00	
	Q8IWN7	Retinitis pigmentosa 1-like 1 protein	whole serum	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.17	
PEDF is upregulated in AD brain (Yamagishi2004)													
PEDF has been identified in CSF proteomics to be increased in AD (Castano2006)													
vitamin D	Q6GTG1	Vitamin D-binding protein	LMW_b	6	6	2							
metabolism	Q6GTG1	Vitamin D-binding protein	whole serum	33.00	40.25	46.00	40.50	1.00	1.00	1.00	1.00	1.00	
and bone		Vitamin D-binding protein precursor	LMW_c	8	4	11	4	9	10	12	7	7	10

TABLE 10-continued

mineralization	O95425	Supervillin	whole serum	1.00	0.00	2.00	1.17	0.33	0.00	0.14	0.80	0.67
	gi|49574514	Matrix Gla protein	LMW_c	2	0	1	1	0	0	0	3	0	1
Vitamin D-binding protein shows higher carbonylation in AD men (identified in CSF) (Korolainen2007)												
Vitamin D-binding protein is found in AD CSF (Finehout2007)												
Vitamin D receptor expression is downregulated in AD hippocampal CA1 cells (Sutherland1992)												
Vitamin D is neuroprotective (regulates neuronal calcium homeostasis) and vitamin D receptor polymorphisms are associated with AD (Gezen-Ak2007)												
Supervillin enhances the transactivation of vitamin D receptor (Ting2005)												
Elderly women with AD show reduced bone density, vitamin D deficiency and higher Gla concentration (Sato1998)												
Vitamin D is involved in bone mineralization (Demay2007)												
Gla is cleaved by HtrA1, which is implicated in AD (Canfield2007)												
HtrA1 degrades APP fragments, colocalizes with Abeta deposits in brain and causes accumulation of Abeta if inhibited (Grau2005)												
Gla is a potent matrix mineralization inhibitor (Demay2007)												
coagulation and platelets	P02671	Fibrinogen alpha chain precursor	LMW_b	0	4	4						
	gi|11761629	Fibrinogen, alpha polypeptide isoform alpha preproprotein	LMW_c	31	28	52	20	25	44	18	46	54	19
	P02671	Fibrinogen alpha chain precursor	whole serum	0.00	0.25	0.40	0.75	0.00	0.25	0.14	0.40	0.33
	gi|70906437	fibrinogen, gamma chain isoform gamma-A precursor	LMW_c	0	0	0	0	1	0	0	0	0	0
	gi|4503635	Coagulation factor II precursor (Prothrombin precursor)	LMW_c	11	8	10	4	13	9	14	11	5	11
	P00734	Coagulation factor II precursor (Prothrombin precursor)	LMW_b	2	0	0						
	P00734	Coagulation factor II precursor (Prothrombin precursor)	whole serum	9.67	8.75	10.40	10.25	1.00	1.00	1.00	1.00	1.00
	P12259	Coagulation factor V precursor	whole serum	3.00	0.00	0.40	0.83	1.00	0.00	0.43	0.20	0.42
	gi|4503643	Coagulation factor V precursor	LMW_c	2	0	0	0	0	0	0	0	1	0
	P00451	Coagulation factor VIII precursor	LMW_b	1	0	0						
	P00451	Coagulation factor VIII precursor	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00
	gi|4503649	Coagulation factor IX	LMW_c	0	1	0	0	0	0	0	0	0	0
	gi|4503625	Coagulation factor X preproprotein	LMW_c	0	0	4	0	0	1	0	0	1	1
	P00742	Coagulation factor X precursor	whole serum	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.20	0.00
	P03951	Coagulation factor XI precursor	whole serum	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.25
	P00748	Coagulation factor XII precursor	whole serum	0.67	0.75	0.60	0.50	0.33	0.50	0.43	0.40	0.42
	P00488	Coagulation factor XIII A chain precursor	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08
	P05160	Coagulation factor XIII B chain precursor	whole serum	0.33	0.00	0.00	0.00	0.33	0.00	0.14	0.00	0.00
	Q7KZ97	Antithrombin III variant	LMW_b	0	1	1						
	Q7KZ97	Antithrombin III variant	whole serum	2.00	1.75	1.20	2.00	1.00	0.75	0.86	0.80	0.83
	gi|4502261	Antithrombin (serine (or cysteine) proteinase inhibitor, clade C member 1)	LMW_c	14	8	12	4	5	11	12	7	7	8
	Q96P15	SERPINB11	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08
	Q8TCE1	SERPINC1	LMW_b	2	1	1						

TABLE 10-continued

Q8TCE1	SERPINC1	whole serum	1.00	1.25	3.20	2.50	0.33	0.75	0.57	0.80	0.83	
P05546	SERPIND1 percursor (Heparin cofactor II precursor)	LMW_b	2	1	0							
gi|50659080	Serpin peptidase inhibitor, clade A, member 3 precursor	LMW_c	9	4	5	6	5	4	3	7	10	1
gi|4507377	Serine (or cysteine) proteinase inhibitor, clade A, member 7	LMW_c	0	1	0	0	1	0	0	0	0	1
gi|39725934	Serine (or cysteine) proteinase inhibitor, clade F member 1 (PEDF)	LMW_c	0	0	0	0	0	0	0	0	0	1
gi|50363217	Alpha-1-antitrypsin (serine (or cysteine) proteinase inhibitor, clade A member 1)	LMW_c	27	21	24	19	21	25	17	30	25	31
gi|28076869	Ovalbumin (serine (or cysteine) proteinase inhibitor, clade B member 4)	LMW_c	0	3	0	0	0	0	0	1	0	3
gi|4505733	Platelet factor 4	LMW_c	13	8	10	7	13	13	10	7	7	7
gi|4505735	Platelet factor 4 variant 1	LMW_c	0	0	0	1	0	1	0	0	1	1
P10720	Platelet factor 4 variant precursor	whole serum	2.33	0.75	0.20	1.00	1.00	0.75	0.86	0.20	0.58	
P10720	Platelet factor 4 variant precursor	LMW_b	4	4	6							
P02776	Platelet factor 4 precursor	whole serum	1.67	1.00	0.40	0.67	0.67	0.75	0.71	0.20	0.33	
P02776	Platelet factor 4 precursor	LMW_b	4	3	5							
P02775	Platelet basic protein precursor	LMW_b	17	9	18							
P02775	Platelet basic protein precursor	whole serum	0.33	0.75	0.40	1.58	0.33	0.25	0.29	0.40	0.67	
gi|4505981	Pro-platelet basic protein precursor	LMW_c	33	20	23	16	20	14	12	19	11	15
gi|4503445	Endothelial cell growth factor 1 (platelet-derived)	LMW_c	0	0	0	0	0	0	0	0	0	1
gi|30794266	Triggering receptor expressed on myeloid cells-like 1	LMW_c	1	0	1	0	1	0	0	1	1	1
O76036	Natural cytotoxicity triggering receptor 1 precursor	whole serum	0.67	3.50	0.80	1.33	0.33	0.75	0.57	0.40	0.58	
gi|4503005	Plasma carboxypeptidase B2 isoform a preproprotein	LMW_c	1	1	0	0	1	1	0	0	0	0
Q96IY4	Carboxypeptidase B2 precursor	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
P14384	Carboxypeptidase M precursor	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
P22792	Carboxypeptidase N subunit 2 precursor	whole serum	0.00	0.00	2.00	1.50	0.00	0.00	0.00	0.60	0.58	
Q96SM3	Probable carboxypeptidase X precursor	LMW_b	0	0	1							
Q04609	Glutamate carboxypeptidase II	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
Q96KN2	Glutamate carboxypeptidase-like protein 2 precursor	whole serum	0.00	0.00	0.40	0.08	0.00	0.00	0.00	0.20	0.08	
O75636	Ficolin-3 precursor	whole serum	0.33	0.00	0.00	0.00	0.33	0.00	0.14	0.00	0.00	

Serum fibrinogen is elevated in AD (Oijen2005)
Platelets are one of the major sources for APP and Abeta outside of the brain
Platelets are activated in elderly and depressed individuals (Whyte2001)
Platelet factor 4 can be used as coagulant (Schulman2007)
Platelet factor 4 acts in immune response and affects every cell in the blood - with different results (depending on receptor) (Hundelshausen2007)

TABLE 10-continued

Triggering receptor TLT-1 is expressed in platelets and exists as platelet-membrane bound version and soluble version (in serum) (Gattis2006
The soluble version of TLT-1 is released from platelets in response to activation by thrombin (Gattis2006)
Triggering receptors (of other cell lines) are known to play a role in immune response and polymorphisms are studied in AD (with negative results so far) (Fenoglio2007)
Abeta fibrils cause aggregation of platelets (Kowalska1994)

complement cascade	gi|21264361	Mannan-binding lectin serine protease 2 isoform 1 precursor	LMW_c	1	2	0	0	0	0	1	1	0	2
	O00187	Mannan-binding lectin serine protease 2 precursor	LMW_b	0	1	1							
	Q96RS4	Complement factor MASP-3	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	P00751	Complement factor B precursor (C3/C5 convertase)	LMW_b	5	5	5							
	P00751	Complement factor B precursor	whole serum	21.33	19.75	24.20	16.92	1.00	1.00	1.00	1.00	1.00	
	gi|67782358	Complement factor B preproprotein	LMW_c	2	2	23	3	2	2	2	0	15	1
	P02747	Complement C1q subcomponent, C chain precursor	LMW_b	0	0	1							
	P02745	Complement C1q subcomponent, A chain precursor	whole serum	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.17	
	P02746	Complement C1q subcomponent, B chain precursor	whole serum	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.08	
	P02746	Complement C1q subcomponent, B chain precursor	LMW_b	0	0	1							
	P02746	Complement C1q subcomponent, B chain precursor	LMW_b	0	0	1							
	gi|87298828	Complement component 1, q subcomponent, B chain precursor	LMW_c	0	1	0	0	0	0	1	1	0	0
	P02747	Complement C1q subcomponent, C chain precursor	LMW_b	0	0	1							
	P02747	Complement C1q subcomponent, C chain precursor	whole serum	3.33	0.50	1.80	1.50	1.00	0.25	0.57	0.80	0.67	
	gi|56786155	Complement component 1, q subcomponent, gamma polypeptide	LMW_c	2	3	2	5	2	1	1	2	2	1
	P00736	Complement C1r subcomponent precursor	LMW_b	1	1	0							
	P00736	Complement C1r subcomponent precursor	whole serum	2.67	0.50	0.40	0.67	0.67	0.50	0.57	0.20	0.58	
	gi|66347875	Complement component 1, r subcomponent	LMW_c	0	0	0	0	0	1	0	0	1	0
	Q53GX9	Complement component 1, r subcomponent-like variant	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	P09871	Complement C1s subcomponent precursor	whole serum	0.33	0.25	0.20	0.08	0.33	0.25	0.29	0.20	0.08	
	P06681	Complement C2 precursor (C3/C5 convertase)	whole serum	0.33	0.25	0.00	0.08	0.33	0.25	0.29	0.00	0.08	
	P01024	Complement C3 precursor	LMW_b	32	21	19							
	P01024	Complement C3 precursor	whole serum	143.67	146.00	190.80	169.42	1.00	1.00	1.00	1.00	1.00	
	gi|4557385	Complement component 3 precursor	LMW_c	20	30	19	16	10	17	16	11	20	15
	P0C0L4	Complement C4-A precursor	LMW_b	14	17	8							
	P0C0L4	Complement C4-A precursor	whole serum	45.33	44.00	59.80	65.92	1.00	1.00	1.00	1.00	1.00	
	Q5JQM8	Complement component 4A	whole serum	0.67	0.25	0.80	0.83	0.33	0.25	0.29	0.40	0.33	

TABLE 10-continued

	P0C0L5	Complement C4-B precursor	whole serum	1.67	1.25	0.80	0.33	0.67	0.50	0.57	0.40	0.33	
	Q6U2E9	Complement component C4B	whole serum	0.00	0.00	0.20	0.33	0.00	0.00	0.00	0.20	0.08	
	gi|50345296	Complement component 4B preproprotein	LMW_c	24	15	17	18	12	12	10	13	16	10
	P01031	Complement C5 precursor	LMW_b	3	1	2							
	P01031	Complement C5 precursor	whole serum	0.67	4.25	5.60	4.17	0.67	1.00	0.86	1.00	0.83	
	gi|38016947	Complement component 5	LMW_c	3	2	2	1	4	3	2	4	5	4
	P13671	Complement component C6 precursor	whole serum	1.00	1.00	0.80	1.42	0.67	0.75	0.71	0.60	0.75	
	P10643	Complement component C7 precursor	whole serum	0.00	0.50	1.00	0.42	0.00	0.50	0.29	0.80	0.25	
	P07357	Complement component C8 alpha chain precursor	whole serum	0.33	0.25	0.00	0.00	0.33	0.25	0.29	0.00	0.00	
	P07358	Complement component C8 beta chain precursor	whole serum	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.20	0.00	
	P07360	Complement component C8 gamma chain precursor	whole serum	0.33	1.25	2.60	1.83	0.33	0.50	0.43	0.60	0.58	
	P07360	Complement component C8 gamma chain precursor	LMW_b	14	11	9							
	gi|4557393	Complement component 8, gamma polypeptide	LMW_c	18	14	33	50	25	36	64	23	24	16
	P02748	Complement component C9 precursor	LMW_b	1	1	0							
	P02748	Complement component C9 precursor	whole serum	3.33	2.25	1.40	1.50	1.00	0.75	0.86	0.60	0.75	
	gi|4502511	Complement component 9	LMW_c	2	1	1	0	0	3	0	1	2	0
	P00746	Complement factor D precursor	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	gi|42544239	Complement factor D preproprotein	LMW_c	0	0	0	3	0	0	0	0	0	0
	P08603	Complement factor H precursor	LMW_b	1	1	0							
	gi|62739186	Complement factor H isoform a precursor	LMW_c	2	1	4	0	4	2	4	1	0	0
	P08603	Complement factor H precursor	whole serum	18.33	14.75	16.60	20.42	1.00	1.00	1.00	1.00	1.00	
	Q03591	Complement factor H-related protein 1 precuror	whole serum	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.25	
	gi|11321587	Complement factor H isoform a precursor	LMW_c	0	0	0	0	0	0	0	0	0	3
	P05156	Complement factor I precursor	whole serum	0.67	0.75	2.20	1.67	0.33	0.50	0.43	0.80	0.75	
	P05156	Complement factor I precursor (C3B/C4B inactivator)	LMW_b	2	2	0							
	P10909	Clusterin precursor (Complement-associated protein SP-40,4)	whole serum	6.33	5.00	3.20	4.83	1.00	1.00	1.00	0.80	0.92	
	Q5VWT3	Complement component (3b/4b) receptor 1-like	whole serum	0.00	0.00	0.20	0.17	0.00	0.00	0.00	0.20	0.17	
	gi|4502503	Complement component 4 binding protein, alpha chain precursor	LMW_c	1	0	0	0	1	0	0	0	1	0
	gi|4502505	Complement component 4 binding protein, beta chain isoform 1 precursor	LMW_c	0	0	0	0	1	0	0	0	0	0
	gi|4504579	I factor (complement)	LMW_c	3	1	1	2	0	2	0	2	1	3
APH	P13798	Acylamino-acid-releasing enzyme (Acyl-peptide hydrolase) (APH)	LMW_b	81206.1	4	0	0						

TABLE 10-continued

	P49748	Acyl-CoA dehydrogenase	whole serum	0.33	0.25	0.20	0.50	0.33	0.25	0.29	0.20	0.17	
	P28330	Acyl-CoA dehydrogenase	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	Q5SQN7	Acyl-Coenzyme A dehydrogenase	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	Q6IEE5	Acyl CoA:monoacylglycerol acyltransferase 2	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00	
	gi|81295404	Acyl-Coenzyme A thioesterase 2, mitochondrial isoform b	LMW_c	0	0	0	1	0	0	0	0	0	0
	gi|4557233	Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain precursor	LMW_c	0	0	0	0	0	0	0	1	0	0
	Q59FX8	Hydroxyacylglutathione hydrolase-like isoform 1 variant	whole serum	0.00	0.00	0.00	0.17	0.00	0.00	000	0.00	0.17	
	P49753	Peroxisomal acyl-coenzyme A thioester hydrolase 2a	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	gi|23510451	N-acylaminoacyl-peptide hydrolase	LMW_c	0	0	0	0	1	0	0	0	0	0
APH is a serine protease that degrades Abeta (Yamin2007)													
APH expression in AD brain is reduced (Yamin2007)													
APH can be a blood marker for exposure to organophosphate toxicants (Quistad2005)													
APH may be the target for the cognitive-enhancing effects of certain organophosphorus compounds (Richards2000)													
APH clears preferentially oxidatively damaged proteins (Fujino2000)													
vitamin A/ thyroxine	P02753	Plasma retinol-binding protein precursor	LMW_b	22992.3	4	14	7						
	P02753	Plasma retinol-binding protein precursor	whole serum	1.67	3.00	6.40	4.58	0.67	1.00	0.86	1.00	1.00	
	gi|55743122	Retinol-binding protein 4, plasma precursor	LMW_c	298	409	435	349	351	435	454	410	336	446
	Q9HBH5	Retinol dehydrogenase 14	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00	
	P02766	Transthyretin precursor (Prealbumin)	whole serum	2.00	2.00	0.00	7.50	1.00	0.50	0.71	0.00	0.50	
	P02766	Transthyretin precursor	LMW_b	126	155	173							
	gi|4507725	Transthyretin	LMW_c	486	517	567	347	429	451	694	424	527	513
PRBP binds transthyretin in the plasma to transport vitamin A (retinol) and thyroxine (thyroid hormone T4) - this also keeps PRBP from being cleared from the plasma (Raghu2004)													
PRBP binding prohibits transthyretin misfolding (Raghu2004)													
Vitamin A is necessary for good cognitive function and vitamin A deficiency is seen in AD brain (Goodman2006)													
Proteins involved in vitamin A transport to the brain (including PRBP) are proposed as therapeutic targets in AD (Goodman2006)													
Transthyretin inhibits Abeta aggregation (Liu2006, Choi2007)													
Thyroxine inhibits the expression of APP (O'Barr2006)													
Free plasma thyroxine (fT4) negatively correlates with MMSE scores: the higher the levels, the more cognitive decline (Stuerenburg2006)													
phospholipases	O95712	Cytosolic phospholipase A2 beta	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	Q9Y263	Phospholipase A-2-activating protein	LMW_b	0	1	1							
	Q5VWL4	Phospholipase C, epsilon 1	LMW_b	0	0	1							
	Q4KWH8	Phospholipase C-eta1b	whole serum	0.00	1.00	1.80	1.42	0.00	0.50	0.29	0.60	0.58	
	gi|4505873	Phospholipase D1	LMW_c	3	2	0	1	0	0	1	2	1	2
	O14939	Phospholipase D2	LMW_b	0	0	2							
	O14939	Phospholipase D2	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00	

TABLE 10-continued

	P41247	Patatin-like phospholipase domain containing protein 4	whole serum	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.20	0.00		
PLD is upregulated in AD brain mitochondria + interacts with APP/Abeta (Jin2006)														
PLD is upregulated in AD reactive astroglia + induced by APP (Jin2007)														
PLD changes Abeta trafficking in cell an may be able to rescue cell function (Cai2005)														
globins	Q53F97	Alpha 2 globin variant	whole serum	4.00	6.50	5.40	2.92	1.00	0.75	0.86	0.80	0.67		
	Q53F97	Alpha 2 globin variant	LMW_b	74	90	52								
	gi|4504345	Alpha 2 globin	LMW_c	149	185	194	239	127	80	168	212	72	234	
	gi|4504349	Beta globin	LMW_c	102	112	213	128	289	100	110	109	61	95	
	Q14473	Beta globin	whole serum	7.33	10.25	8.80	6.67	1.00	1.00	1.00	1.00	0.83		
	Q14473	Beta globin	LMW_b	55	61	51								
	P69891	Gamma globin	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00		
	P69891	Gamma globin	LMW_b	1	1	0								
	gi|28302131	G-gamma globin	LMW_c	2	4	2	1	1	1	1	1	0	4	
	gi|4504351	Delta globin	LMW_c	14	15	25	15	22	9	12	50	14	13	
	P02042	Delta globin	whole serum	9.00	10.50	11.40	9.50	1.00	0.75	0.86	1.00	1.00		
	P02042	Delta globin	LMW_b	60	56	66								
	gi|4826762	Haptoglobin	LMW_c	303	155	256	238	352	205	105	201	285	126	
	P00738	Haptoglobin precursor	whole serum	34.00	42.50	45.40	46.92	1.00	1.00	1.00	1.00	1.00		
	P00738	Haptoglobin precursor	LMW_b	26	34	40								
	gi|45580723	Haptoglobin-related protein	LMW_c	3	2	3	3	1	0	0	0	2	3	
	P00739	Haptoglobin-related protein precursor	whole serum	43.33	60.50	60.80	74.00	1.00	1.00	1.00	1.00	1.00		
	P00739	Haptoglobin-related protein precursor	LMW_b	54	53	58								
	gi|4507809	Secretoglobin, family 1A, member 1	LMW_c	0	1	0	0	0	0	0	0	1	0	
	gi|50363226	Secretoglobin, family 3A, member 1	LMW_c	0	0	0	0	1	1	0	0	0	0	
An increased number of hemoglobin alpha and beta fragments are found in AD cerebellum (Slemmon1994)														
Hemoglobin alpha binds to Abeta (Oyama2000)														
Red blood cells take up Abeta fibrils in blood, which leads to increased oxidative damage and hemoglobin degradation (Jayakumar2003)														
Hemoglobin alpha (and beta?) fragments are more abundant in AD serum (Zhang2004)														
Hemorphins (opioid receptor-binding proteins that originate from hemoglobin beta chain) are increased in AD temporal cortex - indicative of vascular abnormalities resulting from CAA (Poljak2004)														
Hemoglobin alpha and beta induce oligomerization of Abeta and are found increasingly in AD brain (leakage from blood + increased expression in brain) (Wu2004)														
Female patients with severe cognitive impairment have lower hemoglobin (Riccio2007)														
Binding to Abeta is strongest for gamma-globin, followed by oxidized adult hemoglobin (alpha + beta chains) and then oxidized fetal hemoglobin (gamma chains) (Perry2006)														
glycoproteins	gi|4504489	Histidine-rich glycoprotein precursor	LMW_c	6	6	9	3	5	10	13	8	11	19	A
	P04196	Histidine-rich glycoprotein precursor	LMW_b	6	10	5								
	P04196	Histidine-rich glycoprotein precursor	whole serum	15.33	8.00	8.40	8.17	1.00	1.00	1.00	1.00	1.00		
	P02790	Hemopexin precursor (Beta-1B-glycoprotein)	LMW_b	3	5	5								
	P02790	Hemopexin precursor (Beta-1B-glycoprotein)	whole serum	46.33	53.75	73.40	66.33	1.00	1.00	1.00	1.00	1.00		
	gi|11321561	Hemopexin	LMW_c	10	8	9	6	6	11	15	7	10	7	
	P02763	Alpha-1-acid glycoprotein 1 precursor	whole serum	24.00	31.00	31.60	35.67	1.00	1.00	1.00	1.00	1.00		
	P02763	Alpha-1-acid glycoprotein 1 precursor	LMW_b	1	0	0								
	P04217	Alpha-1B-glycoprotein precursor	whole serum	24.33	15.75	28.80	24.42	1.00	1.00	1.00	1.00	1.00		

TABLE 10-continued

	gi|21071030	Alpha 1B-glycoprotein	LMW_c	3	2	3	2	3	5	5	1	3	2	B
	P19652	Alpha-1-acid glycoprotein 2 precursor	whole serum	4.33	9.25	12.00	11.50	1.00	1.00	1.00	0.80	1.00		
	P02765	Alpha-2-HS-glycoprotein precursor	LMW_b	7	7	5								
	gi|4502005	Alpha-2-HS-glycoprotein	LMW_c	22	11	6	4	7	31	16	9	11	51	
	P02765	Alpha-2-HS-glycoprotein precursor	whole serum	13.33	6.50	8.80	8.75	1.00	1.00	1.00	1.00	1.00		
	gi|4502337	Alpha-2-glycoprotein 1, zinc	LMW_c	1	1	1	0	1	0	2	5	1	0	
	P02749	Beta-2-glycoprotein I precursor (Apolipoprotein H)	whole serum	26.67	22.25	24.00	23.33	1.00	1.00	1.00	1.00	1.00		
	Q6X3Y4	Rhesus-associated C glycoprotein	whole serum	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.20	0.00		
	Q5SZW4	Rhesus blood group, B glycoprotein	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	P25311	Zinc-alpha-2-glycoprotein precursor	whole serum	0.00	1.00	1.00	2.00	0.00	0.50	0.29	0.40	0.50		
	P25311	Zinc-alpha-2-glycoprotein precursor	LMW_b	1	2	0								
	P00751	Complement factor B precursor (Glycine-rich beta glycoprotein)	LMW_b	5	5	5								
	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITIH4) (Plasma kallikrein sensitive glycoprotein 120)	LMW_b	3	5	3								
	P21439	Multidrug resistance protein 3 (P-glycoprotein 3)	LMW_b	0	1	0								
	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 precursor	whole serum	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.25		
	P20701	Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain)	whole serum	0.00	0.00	0.60	0.08	0.00	0.00	0.00	0.60	0.08		B
	Q5VU65	Nuclear pore membrane glycoprotein 210-like	whole serum	0.33	0.00	0.00	0.00	0.33	0.00	0.14	0.00	0.00		
	P02750	Leucine-rich alpha-2-glycoprotein precursor	whole serum	5.67	1.75	1.00	1.08	1.00	0.50	0.71	0.40	0.58		
	P02760	AMBP protein precursor [Contains: Alpha-1-microglobulin (Protein HC) (Complex-forming glycoprotein heterogeneous in charge) (Alpha-1 microglycoprotein); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)]	LMW_b	1	2	0								
	gi|4504489	Aistidine-rich glycoprotein precursor	LMW_c	6	6	9	3	5	10	13	8	11	19	B
	gi|10863987	Zona pellucida glycoprotein 4 preproprotein	LMW_c	2	0	0	1	1	0	1	0	1	0	
HRG is more abundant in AD serum (Zhang2004)														
HRG can inhibit coagulation (Jones2005)														
HRG binds heme (Jones2005)														
HRG binds metals (Jones2005)														
HRG inhibits plasminogen activation by fibrin (Mosesson2005)														
HRG binds to cells (platelets, lymphocytes, monocytes) much more strongly in the presence of zinc and copper (Horne2001)														
HRG is involved in the disposal of immune complexes and apoptotic cells (Gorgani2007)														
protease inhibitors	gi|50363217	Alpha-1-antitrypsin (serine (or cysteine) proteinase inhibitor, clade A member 1)	LMW_c	27	21	24	19	21	25	17	30	25	31	B
	P01009	Alpha-1-antitrypsin precursor	whole serum	98.33	115.00	124.60	115.50	1.00	1.00	1.00	1.00	1.00		
	P01009	Alpha-1-antitrypsin precursor	LMW_b	14	15	8								
	P20848	Alpha-1-antitrypsin-related protein precursor	LMW_b	1	2	0								

TABLE 10-continued

P01011	Alpha-1-antichymotrypsin precursor	LMW_b	12	13	4								A
P01011	Alpha-1-antichymotrypsin precursor	whole serum	11.33	12.00	12.40	16.17	1.00	1.00	1.00	1.00	1.00		
P08697	Alpha-2-antiplasmin precursor	whole serum	2.00	0.75	2.20	1.75	1.00	0.50	0.71	0.60	0.92		
gi|39725934	Alpha-2-antiplasmin (PEDF/serine (or cysteine) proteinase inhibitor, clade F, member 1	LMW_c	0	0	0	0	0	0	0	0	0	1	
P01042	Alpha-2-thiol proteinase inhbitor (Kininogen-1 precursor)	whole serum	15.00	13.00	24.20	17.50	1.00	1.00	1.00	1.00	1.00		
P01042	Alpha-2-thiol proteinase inhbitor (Kininogen-1 precursor)	LMW_b	6	3	3								B
gi|4502261	Antithrombin (serine (or cysteine) proteinase inhibitor, clade C member 1)	LMW_c	14	8	12	4	5	11	12	7	7	8	
gi|28076869	Ovalbumin (serine (or cysteine) proteinase inhibitor, clade B member 4)	LMW_c	0	3	0	0	0	0	0	1	0	3	
gi|4504781	Inter-alpha (globulin) inhibitor H1	LMW_c	1	1	2	0	0	2	0	2	1	3	
gi|70778918	Inter-alpha (globulin) inhibitor H2 polypeptide	LMW_c	0	0	1	0	0	2	2	1	2	1	
gi|31542984	Inter-alpha (Globulin) inhibitor H4	LMW_c	6	2	4	1	2	4	4	0	0	0	B
Q59FS1	Inter-alpha (Globulin) inhibitor H4	whole serum	0.33	0.00	0.60	1.08	0.33	0.00	0.14	0.40	0.42		
P19827	Inter-alpha-trypsin inhibitor heavy chain H1 precursor (ITIH1)	LMW_b	3	2	0								B
P19827	Inter-alpha-trypsin inhibitor heavy chain H1 precursor (ITIH1)	whole serum	4.33	3.50	4.60	5.92	1.00	1.00	1.00	1.00	0.92		
P19823	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITIH2)	whole serum	12.00	13.00	21.00	20.00	1.00	1.00	1.00	1.00	1.00		B
P19823	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITIH2)	LMW_b	1	0	0								
Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITIH4)	whole serum	7.00	8.00	11.80	11.00	1.00	1.00	1.00	1.00	1.00		
Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITIH4)	LMW_b	3	5	3								
P05546	Heparin cofactor II precursor (Protease inhibitor leuserpin 2)	LMW_b	2	1	0								
P05546	Heparin cofactor II precursor (Protease inhibitor leuserpin 2)	whole serum	0.67	2.25	0.80	1.00	0.67	1.00	0.86	0.40	0.58		
gi|4507377	Serine (or cysteine) proteinase inhibitor, clade A member 7	LMW_c	0	1	0	0	1	0	0	0	0	1	
gi|50659080	Serpin peptidase inhibitor, clade A member 3 precursor	LMW_c	9	4	5	6	5	4	3	7	10	1	
Q9NQ38	Serine protease inhibitor Kazal-type 5 precursor	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
P05155	Plasma protease C1 inhibitor precursor	whole serum	9.00	8.00	8.80	11.00	1.00	1.00	1.00	1.00	1.00		
P02760	AMBP protein precursor [Contains: Alpha-1-microglobulin (Protein HC) (Complex-forming glycoprotein heterogeneous in charge) (Alpha-1 microglycoprotein); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)]	LMW_b	1	2	0								

Alpha 1 antichymotrypsin (ACT) is found to be upregulated in AD brain and serum (Licastro1998 & Licastro2000, DeKosky2003)
ITI is the most similar inhibitor to the Kunitz-type serine protease inhibitor domain found in APP (Yoshida1991)
ITI has been investigated as serum marker for AD (together with ACT) (Furby1991)

TABLE 10-continued

Alpha 1 antitrypsin is the inhibitor of HO-1 activity in AD plasma (HO-1 activity and expression is reduced in AD) (Maes2006)													
Alpha 1 antitrypsin shows greater abundance and oxidation indices in AD blood (Yu2003)													
keratins	gi|17318569	Keratin 1	LMW_c	45	4	3	22	36	5	7	3	4	3	
and	P04264	Keratin 1	LMW_b	6	65	15								A
related	gi|47132620	Keratin 2	LMW_c	23	7	2	4	2	7	4	2	1	6	
proteins	Q4VAQ2	Keratin 2a	LMW_b	0	1	0								
	P35908	Keratin 2e	LMW_b	0	14	4								B
	P19013	Keratin 4	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	P13647	Keratin 5	LMW_b	1	3	0								
	gi|4557890	keratin 5 [*Homo sapiens*]	LMW_c	1	1	0	2	0	0	0	0	0	0	
	gi|5031839	keratin 6A [*Homo sapiens*]	LMW_c	2	0	0	1	0	0	0	0	0	0	
	gi|55956899	Keratin 9	LMW_c	29	4	0	17	6	1	7	0	0	0	
	P35527	Keratin 9	LMW_b	1	3	3								
	P13645	Keratin 10	LMW_b	0	48	2								B
	P13646	Keratin 13	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	P13646	Keratin 13	LMW_b	0	2	0								
	P02533	Keratin 14	LMW_b	0	5	0								B
	gi|15431310	Keratin 14	LMW_c	0	0	0	3	0	0	0	0	0	0	
	Q04695	Keratin 17	LMW_b	0	1	0								
	gi|24234699	Keratin 19	LMW_c	49	6	0	12	8	7	11	2	3	3	
	Q9C075	Keratin 23	LMW_b	0	0	1								
	Q7Z3Y9	Keratin 25	LMW_b	0	1	0								
	Q14664	Keratin ??	LMW_b	1	3	0								B
	Q92764	Hair keratin, type I Ha5	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	O76013	Hair keratin, type I Ha6	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	Q14533	Hair keratin, type II Hb1	whole serum	0.00	1.00	2.60	3.08	0.00	0.75	0.43	0.80	0.67		
	Q9NSB4	Hair keratin, type II Hb2	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	gi|10337581	Hair keratin, type IIIb	LMW_c	4	1	0	0	0	0	0	0	0	0	
	Q7Z794	Keratin, type II cytoskeletal 1b	LMW_b	0	2	0								
	Q01546	Keratin, type II cytoskeletal 2 oral	LMW_b	0	2	0								
	O95678	Cytokeratin type II	whole serum	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.20	0.00		
	Q9BYQ6	Keratin-associated protein 4-14	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	gi|38490587	Keratin associated protein 10-12	LMW_c	1	1	0	0	0	0	0	0	0	0	
	Q5T749	Novel protein (Keratinocyte proline-rich protein)	LMW_b	0	4	0								B
	P15924	Desmoplakin	LMW_b	0	4	0								B
Keratin antibodies have been found in serum of neurodegenerative disease patients - however, in AD alone this was not significant (Schott1996)													
Presinilin-1 (responsible for early onset AD) is involved in development of skin barrier formation - however, keratin 1 did not change with PS1−/− (Nakajima2006)													
Cytokeratin 1 is involved in bradykinin generation - which has been implicated in AD													
Chronic oxidative stress can lead to mallory bodies in the liver - which consist of among other ubiquinated keratins (Janig2005)													

TABLE 10-continued

heme degradation	gi|4502419	Biliverdin reductase B	LMW_c	0	4	3	1	0	0	0	1	0	3	A
	P53004	Biliverdin reductase A precursor	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
Biliverdin reductase and heme oxygenase degrade heme to bilirubin														
heme oxygenase activity is upregulated in AD - and so are CSF bilirubin derivatives (Kimpara2000)														
pyruvate metabolism	gi|33286418	Pyruvate kinase 3 isoform 1	LMW_c	0	0	0	0	0	0	0	1	1	0	B
	P08559	Pyruvate dehydrogenase E1 component alpha subunit	whole serum	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.20	0.00		
	Q5JPU1	Pyruvate dehydrogenase alpha 1	whole serum	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.17		
	O00330	Pyruvate dehydrogenase protein X component	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
PK activity is upregulated in frontal and temporal cortex in AD brain (BigI1999) - however, different PK isoform (?)														
PK is one of the glycolytic enzymes														
PK is upregulated in mitochondria of neurons stimulated with Abeta (LoveII2005) - however, different PK isoform														
PK is oxidatively modified in MCI hippocampus (Butterfield2006) - however, different PK isoform														
calcium related proteins	gi|4507267	Stanniocalcin 2 precursor	LMW_c	0	0	0	0	0	0	0	1	0	1	A
	Q9Y6J0	Calcineurin-binding protein (Cabin 1)	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00		
	Q9Y6J0	Calcineurin-binding protein (Cabin 1)	LMW_b	1	0	1								
	Q16602	Calcitonin gene-related peptide type 1 receptor precursor	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00		
	Q9NZU7	Calcium-binding protein 1 (Calbrain)	whole serum	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.17		
	P09758	Tumor-associated calcium signal transducer 2 precursor	whole serum	1.00	0.50	0.40	0.08	0.67	0.25	0.43	0.40	0.08		B
	gi|32129214	Neuronal calcium-binding protein 2	LMW_c	0	0	1	0	0	0	0	0	0	0	
	P84074	Neuron-specific calcium-binding protein (Hippocalcin)	whole serum	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.17		
	P37235	Hippocalcin-like protein 1	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	P02458	Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin]	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	Q9H4F8	SPARC related modular calcium-binding protein 1 precursor	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	Q16566	Calcium/calmodulin-dependent protein kinase type IV	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	Q9HAR2	Latrophilin-3 precursor (Calcium-independent alpha-latrotoxin receptor 3)	whole serum	0.00	0.00	0.60	0.08	0.00	0.00	0.00	0.40	0.08		B
	Q9H9S4	Calcium-binding protein 39-like	LMW_b	0	1	0								
	P20020	Plasma membrane calcium-transporting ATPase 1	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00		
	Q01814	Plasma membrane calcium-transporting ATPase 2	LMW_b	1	0	1								
	gi|48255953	Plasma membrane calcium ATPase 3 isoform 3a	LMW_c	0	0	0	0	0	1	0	0	0	0	
	P98194	Calcium-transporting ATPase type 2C member 1	whole serum	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.20	0.00		
	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	Q9UHB1	Voltage-gated L-type calcium channel alpha-1 subunit	whole serum	0.33	0.00	0.00	0.00	0.33	0.00	0.14	0.00	0.00		

TABLE 10-continued

	O60721	Sodium/potassium/calcium exchanger 1	whole serum	0.00	0.25	0.00	0.08	0.00	0.25	0.14	0.00	0.08	
	Q12791	Calcium-activated potassium channel alpha subunit 1	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	O95151	Calcium-dependent chloride channel-1	LMW_b	1	0	0							
	gi|4506765	S100 calcium-binding protein A4	LMW_c	0	0	1	0	0	0	0	0	0	0
	gi|7657532	S100 calcium-binding protein A6	LMW_c	0	0	0	1	0	0	0	0	0	0
	gi|4506769	S100 calcium-binding protein A7	LMW_c	0	6	1	0	0	1	0	1	1	4
	P31151	S100 calcium-binding protein A7	LMW_b	0	4	0							
	gi|21614544	S100 calcium-binding protein A8	LMW_c	3	11	15	3	5	4	4	2	14	5
	P05109	S100 calcium-binding protein A8	LMW_b	2	6	3							
	gi|4506773	S100 calcium-binding protein A9	LMW_c	2	4	3	4	3	3	6	3	5	5
	P06702	S100 calcium-binding protein A9	LMW_b	0	1	0							
STC 2 is upregulated in neurons stimulated with Abeta (Kim2003)													
STC's are involved in calcium and phosphate regulation													
defensin	gi|113419903	PREDICTED: similar to Neutrophil defensin 1 precursor	LMW_c	11	3	2	3	0	2	1	0	4	18	A
	P59665	Neutrophil defensin 1 precursor	LMW_b	1	1	1							
Defensin expression is changed in peripheral lymphocytes in Ad (Kalman2005)													
gelsolin	gi|38044288	Gelsolin isoform a precursor	LMW_c	3	4	5	3	2	5	2	5	7	2	B
	P06396	Gelsolin precursor	whole serum	3.67	4.75	3.60	4.00	0.67	0.75	0.71	1.00	0.92	
	P06396	Gelsolin precursor	LMW_b	0	2	0							A
Peripheral injection of plasmid DNA encoding for gelsolin reduces brain Abeta in mice (Hirko2007)													
Low intake of n-3 polyunsaturated fatty acids is a risk factor for AD - they cause NMDA receptor subunit loss and increased levels of gelsolin fragments in APP transgenic mice (Calon2005)													
Mutations in gelsolin can lead to CAA (Tian2004)													
Gelsolin inhibits Abeta induced cell death (Qiao2005)													
Gelsolin binds Abeta very well and peripheral application of Gelsolin reduces brain Abeta (Matsuoka2003)													
vitronectin	gi|88853069	Vitronectin precursor	LMW_c	5	6	7	6	7	5	12	9	7	12	B
	P04004	Vitronectin precursor	whole serum	5.33	5.25	11.20	7.33	1.00	1.00	1.00	1.00	1.00	
	P04004	Vitronectin precursor	LMW_b	3	1	3							
Vitronectin precursor is found upregulated in AD serum (proteomics study) (Zhang2004)													
Vitronectin receptor is found in glial cells associated with plaques and vitronectin is found in plaques (Eikelenboom 1994)													
Microglial expression of vitronectin receptor is upregulated in AD (McGeer1993)													
Vitronectin protects against bystander lysis by the membrane attack complex (complement) (McGeer1993)													
Microglia in gray and white matter of AD brain stain for vitronectin receptor - as do control and AD platelets (Akiyama1991)													
profilin	gi|40786418	Profilin 4	LMW_c	0	0	0	0	1	2	0	0	0	0	B
	gi|4826898	Profilin 1	LMW_c	1	1	0	0	4	1	0	0	2	1
	P07737	Profilin 1	LMW_b	0	1	1							
Profilin shows specific binding to Abeta (like Gelsolin) (Chauhan1999)													
Profilin-2 is less oxidized after reduction of mouse brain Abeta burden (Poon2005)													
thrombospondin	gi|40317626	Thrombospondin 1 precursor	LMW_c	0	0	0	1	0	0	0	0	0	0
	P07996	Thrombospondin 1 precursor	whole serum	0.00	0.00	0.20	0.25	0.00	0.00	0.00	0.20	0.17	
	P35442	Thrombospondin 2 precursor	whole serum	0.00	0.50	0.20	0.17	0.00	0.25	0.14	0.20	0.17	
	gi|31543806	Thrombospondin 4 precursor	LMW_c	1	0	2	1	2	1	1	1	1	0	B
	P35443	Thrombospondin 4 precursor	LMW_b	2	1	2							
Thrombospondin immunostaining is increased in a subset of pyramidal neurons that may be affected early in AD (Buee1992)													
Thrombospondin immunostaining is found in plaques (Buee1992)													

TABLE 10-continued

peroxiredoxin	gi|32189392	Peroxiredoxin 2 isoform a	LMW_c	4	7	9	4	3	2	3	3	0	2	B
and	P32119	Peroxiredoxin 2	LMW_b	0	1	0								
alcohol	gi|32483377	Peroxiredoxin 3 isoform b	LMW_c	0	0	0	0	0	1	0	0	0	1	
dehydrogenase	P11766	Alcohol dehydrogenase class III chi chain	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
	P07327	Alcohol dehydrogenase alpha chain	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08		
Peroxiredoxin 2 is more abundant in AD hippocampus (proteomics study) (Sultana2007)														
Peroxiredoxin 2 is upregulated in AD peripheral leukocytes after stimulation with divalproex sodium (proteomics study) (Mhyre2007)														
Peroxiredoxin 2 is upregulated in the brains of mice having high levels of Abeta42 and alcohol dehydrogenase - Peroxiredoxin 2 levels go down if the interaction between Abeta and alcohol dehydrogenase is disturbed (Yao2007)														
Peroxiredoxins are antioxidant enzymes (Krapfenbauer2003)														
apolipoproteins	P08519	Apolipoprotein(a) precursor	whole serum	0.67	0.25	0.00	0.67	0.33	0.25	0.29	0.00	0.17		
	P02647	Apolipoprotein A-I precursor	LMW_b	47	57	52								
	gi|4557321	Apolipoprotein A-I preproprotein	LMW_c	388	253	274	285	426	327	430	333	374	325	
	P02647	Apolipoprotein A-I precursor	whole serum	129.67	135.75	154.80	150.00	1.00	1.00	1.00	1.00	1.00		
	P02652	Apolipoprotein A-II precursor	LMW_b	109	85	114								
	P02652	Apolipoprotein A-II precursor	whole serum	26.00	31.75	56.80	44.83	1.00	1.00	1.00	1.00	1.00		
	gi|4502149	Apolipoprotein A-II preproprotein	LMW_c	88	86	245	163	65	185	110	89	95	78	
	P06727	Apolipoprotein A-IV precursor	LMW_b	0	0	1								
	P06727	Apolipoprotein A-IV precursor	whole serum	16.33	18.75	18.20	24.33	1.00	1.00	1.00	1.00	1.00		
	gi|71773110	Apolipoprotein A-IV precursor	LMW_c	5	7	3	2	4	7	4	4	4	5	
	gi|4502153	Apolipoprotein B precursor	LMW_c	3	3	10	5	2	6	6	5	8	5	
	P04114	Apolipoprotein B-100 precursor	LMW_b	5	6	3								
	P04114	Apolipoprotein B-100 precursor	whole serum	41.67	25.00	35.80	41.25	1.00	1.00	1.00	1.00	1.00		
	P02654	Apolipoprotein C-I precursor	LMW_b	6	2	9								
	P02654	Apolipoprotein C-I precursor	whole serum	5.00	1.50	0.40	0.83	1.00	0.75	0.86	0.40	0.42		
	gi|4502157	Apolipoprotein C-I precursor	LMW_c	15	14	11	20	13	20	17	19	19	24	
	P02655	Apolipoprotein C-II precursor	LMW_b	25	26	26								
	P02655	Apolipoprotein C-II precursor	whole serum	0.67	0.50	0.60	0.67	0.33	0.25	0.29	0.20	0.33		
	gi|32130518	Apolipoprotein C-II precursor	LMW_c	43	33	193	64	41	96	268	38	52	154	
	P02656	Apolipoprotein C-III precursor	LMW_b	32	29	36								
	P02656	Apolipoprotein C-III precursor			10.00	12.40	12.42	1.00	1.00	1.00	1.00	1.00		
	gi|4557323	Apolipoprotein C-III precursor			35	49	33	43	39	65	38	48	55	
	P55056	Apolipoprotein C-IV precursor			2	7								
	gi|4502161	whole serum	15.00		5	7	3	9	3	11	8	9	12	
	P05090	LMW_c	54		0.25	0.40	0.50	0.67	0.25	0.43	0.40	0.42		
	gi|4502163	LMW_b	2		1	0	0	0	0	0	0	0	0	
	P02649	LMW_c	5		9	4								
	P02649	whole serum	0.67		1.75	2.20	3.00	1.00	0.75	0.86	1.00	0.92		
	gi|4557325	LMW_c	0		4	23	14	6	17	17	17	12	15	
	gi|4502165	LMW_b	6	1	1	0	0	0	0	0	0	1	0	
	P02749	whole serum	6.33	26.67	22.25	24.00	23.33	1.00	1.00	1.00	1.00	1.00		
	gi|4557327	LMW_c	12	2	0	0	1	2	1	0	1	1	1	

TABLE 10-continued

	O14791	Apolipoprotein-L1 precursor	whole serum	0.67	0.50	1.60	0.67	0.67	0.50	0.57	0.60	0.42	
	O14791	Apolipoprotein-L1 precursor	LMW_b	0	0	0							
	gi|21735614	Apolipoprotein L1 isoform a precursor	LMW_c	2	3	1	2	3	3	1	0	1	0
	Q9BQE5	Apolipoprotein-L2	whole serum	0.00	0.00	0.20	0.08	0.00	0.00	0.00	0.20	0.08	
	Q9BWW8	Apolipoprotein-L6	whole serum	0.00	0.25	0.00	0.00	0.00	0.25	0.14	0.00	0.00	
	O95445	Apolipoprotein M	whole serum	0.33	0.25	0.00	0.25	0.33	0.25	0.29	0.00	0.08	
	gi|22091452	Apolipoprotein M	LMW_c	4	1	6	5	4	4	2	2	1	0
iron and copper metabolism	gi|4557871	Transferrin	LMW_c	61	61	70	34	61	78	81	68	104	101
	P02787	Transferrin	LMW_b	26	21	22							
	P02787	Transferrin	whole serum	179.67	207.00	249.80	222.58	1.00	1.00	1.00	1.00	1.00	
	P00450	Ceruloplasmin precursor	LMW_b	7	6	6							
	P00450	Ceruloplasmin precursor	whole serum	51.33	31.50	48.60	41.67	1.00	1.00	1.00	1.00	1.00	
	gi|4557485	Ceruloplasmin precursor	LMW_c	17	12	17	13	11	18	16	20	22	13
	P02790	Hemopexin precursor	LMW_b	2	5	3							
	P02790	Hemopexin precursor	whole serum	46.33	53.75	73.40	66.33	1.00	1.00	1.00	1.00	1.00	
	gi|11321561	Hemopexin	LMW_c	10	8	9	6	6	11	15	7	10	7
	P10109	Adrenodoxin, mitochondrial precursor (Adrenal ferredoxin)	whole serum	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.08	
	gi|20149498	Ferritin, light polypeptide	LMW_c	1	0	0	0	0	0	0	0	0	0
	gi|60499021	Ferrochelatase isoform a precursor	LMW_c	0	0	1	0	0	0	0	0	0	0
	Q04656	Copper-transporting ATPase 1 (ATP7A)	whole serum	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.20	0.00	
	Q9UJW0	Dynactin subunit 4	whole serum	0.00	0.00	0.60	0.75	0.00	0.00	0.00	0.40	0.50	
	Q92859	Neogenin precursor	whole serum	3.67	4.00	1.20	1.42	1.00	0.75	0.86	0.40	0.33	
NMDA receptor related proteins	Q5T2T0	Novel protein (with guanylate kinase II domain)	whole serum	0.00	0.00	0.00	1.08	0.00	0.00	0.00	0.00	0.50	
	Q92796	Presynaptic protein SAP10	whole serum	0.00	0.00	0.00	0.42	0.00	0.00	0.00	0.00	0.33	
	Q99996	A-kinase anchor protein 9	whole serum	0.67	0.50	0.00	0.00	0.33	0.50	0.43	0.00	0.00	
	Q13224	Glutamate [NMDA] receptor subunit epsilon 2 precursor	whole serum	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.20	0.00	
	Q12879	Glutamate [NMDA] receptor subunit epsilon 1 precursor	whole serum	0.00	0.25	0.40	0.58	0.00	0.25	0.14	0.40	0.42	
	gi|33356128	NMDA receptor regulated 1-like protein isoform 1	LMW_c	0	0	0	0	0	0	0	1	0	0

TABLE 11

Biomarker candidates for the differentiation between patients having microhemorrhages in the brain and patients without microhemorrhages

Proteins found in non-SH cases but not in SH cases

Accession	Name	Probability	MW	found in x % of samples on average		
				SH 0 (n = 16)	SH 1 + 2 (n = 3)	SH 3 (n = 5)
P35542	Serum amyloid A-4 protein precursor	9.09E−004	14797.3	0.50	0.00	0

Accession	Name	Probability	MW	found in x % of samples on average	
				PMCI non-SH (n = 8)	PMCI SH (n = 3)
	Proteins found in PMCI SH cases but not in PMCI non-SH cases				
P21817	Ryanodine receptor 1	8.02E−004	564813.8	0	1.00
Q9NVE5	Ubiquitin carboxyl-terminal hydrolase 40	3.65E−005	140041.1	0	0.67
Q5NV79	V5-4 protein (Fragment)	4.56E−005	10672	0	0.67
P51843	Nuclear receptor 0B1 (Nuclear receptor DAX-1)	4.77E−004	51683.9	0	0.67
Q96SU4	Oxysterol binding protein-related protein 9	4.96E−004	83132.4	0	0.67
P17706	Tyrosine-protein phosphatase, non-receptor type 2	5.85E−004	48497.5	0	0.67
O15013	Rho guanine nucleotide exchange factor 10	7.23E−004	127038.7	0	0.67
O75129	KIAA0634 protein (Fragment)	7.87E−004	145332	0	0.67
Q8N543	Hypothetical protein FLJ10826	8.10E−004	63206.2	0	0.67
Q96AE7	Tetratricopeptide repeat protein 17	8.61E−004	129476.8	0	0.67
	Proteins found in PMCI non-SH cases but not in PMCI SH cases				
P02747	Complement C1q subcomponent	8.22E−013	25757.1	0.88	0
P02775	Platelet basic protein precursor (PBP)	4.10E−009	13885.4	0.88	0
P35542	Serum amyloid A-4 protein precursor	9.09E−004	14797.3	0.88	0
P20929	Nebulin	2.48E−004	772742.8	0.63	0
Q4V312	Colony stimulating factor 2 receptor, alpha, low-affinity (Granulocyte-macrophage)	5.36E−005	46871.6	0.50	0
P02671	Fibrinogen alpha chain precursor	9.49E−005	94914.3	0.50	0
P13667	Protein disulfide-isomerase A4 precursor	2.62E−004	72887.1	0.50	0
Q15643	Thyroid receptor interacting protein 11	9.52E−004	227498.2	0.50	0

Accession	Name	Probability	MW	found in x % of samples on average		
				Normal non-SH (n = 5)	PMCI non-SH (n = 8)	PMCI SH (n = 3)
	Proteins found only in PMCI non-SH (but neither in Normal non-SH nor PMCI SH) cases					
Q4V312	Colony stimulating factor 2 receptor, alpha, low-affinity (Granulocyte-macrophage)	5.36E−005	46871.6	0	0.50	0
P13667	Protein disulfide-isomerase A4 precursor	2.62E−004	72887.1	0	0.50	0
	Proteins found only in PMCI SH (but neither in Normal non-SH nor PMCI non-SH) cases					
P21817	Ryanodine receptor 1 (Skeletal muscle-type ryanodine receptor)	8.02E−004	564813.8	0	0	1.00
Q9NVE5	Ubiquitin carboxyl-terminal hydrolase 40	3.65E−005	140041.1	0	0	0.67
P51843	Nuclear receptor 0B1 (Nuclear receptor DAX-1)	4.77E−004	51683.9	0	0	0.67
Q96SU4	Oxysterol binding protein-related protein 9 (OSBP-related protein 9) (ORP-9)	4.96E−004	83132.4	0	0	0.67
O15013	Rho guanine nucleotide exchange factor 10	7.23E−004	127038.7	0	0	0.67
O75129	KIAA0634 protein (Fragment)	7.87E−004	145332	0	0	0.67
Q8N543	Hypothetical protein FLJ10826	8.10E−004	63206.2	0	0	0.67

SH 0 no hemorrhages

SH 1 + 2 insignificant hemorrhages

SH 3 significant hemorrhages

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Ala Asn Asp Ser Gly Pro Arg Arg

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Val Phe Arg
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Val Val Thr Asn Pro Lys Glu
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Val Lys

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Asn Tyr Ile Ala Pro Glu Ile Leu Arg
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Arg

<210> SEQ ID NO 29
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<400> SEQUENCE: 34

Gly Met Gly Ser Asp Arg Thr Ala Leu Ser Leu Gln Gly Ala Trp Gly
1               5                   10                  15

Ile Phe Leu Ser Thr Phe Tyr Lys
            20


<210> SEQ ID NO 35
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 35

Cys Glu Val Asn Ala Glu Asp Lys Glu Asn Ser Gly Asp Tyr Ile Ser
1               5                   10                  15

Glu Asn Glu Asp Pro Glu Leu Gln Asp Tyr Arg
            20                  25


<210> SEQ ID NO 36
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 36

Lys Ala Tyr Ile Asn Thr Ile Ser Ser Leu Lys Asp Leu Ile Thr Lys
1               5                   10                  15


<210> SEQ ID NO 37
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 37

His Ser Gln Pro Ala Thr Pro Thr Pro Leu Gln Ser Arg
1               5                   10
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<210> SEQ ID NO 38
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 38

Asn Cys Tyr Ser Leu Leu Asn Leu Ala Glu Val Arg Ser Lys Tyr Leu
1 5 10 15

Gly Lys

<210> SEQ ID NO 39
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 39

Asn Cys Tyr Ser Leu Leu Asn Leu Ala Glu Val Arg Ser Lys Tyr Leu
1 5 10 15

Gly Lys

<210> SEQ ID NO 40
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

Val Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
1 5 10

<210> SEQ ID NO 41
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

Glu Asn Leu Glu Val Gly Tyr Glu Val Leu Thr Ile Arg Ala Ser Asp
1 5 10 15

Arg Asp Ser Pro Ile Asn Ala Asn Leu Arg
20 25

<210> SEQ ID NO 42
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 42

Glu Thr Lys Glu Thr His Val Leu Arg
1 5

<210> SEQ ID NO 43
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 43

Gln Phe Val Gly Cys Met Arg Asn Leu Ser Val Asp Gly Lys
1 5 10

<210> SEQ ID NO 44

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<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

Val Pro Gly Gly Thr Arg Ala Phe Ala Leu Arg Pro Gly Cys Thr Tyr
1 5 10 15

Ala Val Gly Ala Ala Cys Thr Pro Arg
20 25

<210> SEQ ID NO 45
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 45

Asp Gly Val Tyr Phe Leu Tyr Glu Ala Leu His Gly Pro Pro Lys Lys
1 5 10 15

<210> SEQ ID NO 46
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 46

Ala Thr Trp Ser Gly Ala Val Leu Ala Gly Arg
1 5 10

<210> SEQ ID NO 47
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 47

Ser Leu Pro Ala Pro Trp Leu Ser Met Ala Pro Val Ser Trp Ile Thr
1 5 10 15

Pro Gly Leu Lys
20

<210> SEQ ID NO 48
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48

Ser Trp Val Pro His Thr Phe Glu Ser Glu Leu Ser Asp Pro Val Glu
1 5 10 15

Leu Leu Val Ala Glu Ser
20

<210> SEQ ID NO 49
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 49

Thr Pro Gly Ala Ala Ala Asn Leu Glu Leu Ile Phe Val Gly Pro Gln
1 5 10 15

His Ala Gly Asn Tyr Arg
20

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<210> SEQ ID NO 50
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 50

Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg
1 5 10

<210> SEQ ID NO 51
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 51

Ala Val Leu Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr
1 5 10 15

Ala Val Lys

<210> SEQ ID NO 52
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala
1 5 10 15

Phe Thr Ser Lys
20

<210> SEQ ID NO 53
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

Ile Thr Leu Leu Ser Ala Leu Val Glu Thr Arg
1 5 10

<210> SEQ ID NO 54
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54

Asn Leu Ala Val Ser Gln Val Val His Lys
1 5 10

<210> SEQ ID NO 55
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 55

Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala Phe
1 5 10 15

Thr Ser Lys

<210> SEQ ID NO 56
<211> LENGTH: 9

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

Glu Trp Phe Ser Glu Thr Phe Gln Lys
1 5

<210> SEQ ID NO 57
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

Ile Lys Gln Ser Glu Leu Ser Ala Lys
1 5

<210> SEQ ID NO 58
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 58

Leu Lys Glu Phe Gly Asn Thr Leu Glu Asp Lys
1 5 10

<210> SEQ ID NO 59
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 59

Thr Pro Asp Val Ser Ser Ala Leu Asp Lys
1 5 10

<210> SEQ ID NO 60
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 60

Glu Ser Leu Ser Ser Tyr Trp Glu Ser Ala Lys
1 5 10

<210> SEQ ID NO 61
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 61

Leu Arg Asp Leu Tyr Ser Lys
1 5

<210> SEQ ID NO 62
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

Ser Thr Ala Ala Met Ser Thr Tyr Thr Gly Ile Phe Thr Asp Gln Val
1 5 10 15

Leu Ser Val Leu Lys
20

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<210> SEQ ID NO 63
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

Ser Thr Ala Ala Met Ser Thr Tyr Thr Gly Ile Phe Thr Asp Gln Val
1 5 10 15

Leu Ser Val Leu Lys Gly Glu Glu
20

<210> SEQ ID NO 64
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

Thr Ala Ala Gln Asn Leu Tyr Glu Lys
1 5

<210> SEQ ID NO 65
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

Thr Tyr Leu Pro Ala Val Asp Glu Lys
1 5

<210> SEQ ID NO 66
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66

Ala Trp Phe Leu Glu Ser Lys
1 5

<210> SEQ ID NO 67
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

Asp Gly Trp Gln Trp Phe Trp Ser Pro Ser Thr Phe Arg
1 5 10

<210> SEQ ID NO 68
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68

Glu Leu Leu Glu Thr Val Val Asn Arg
1 5

<210> SEQ ID NO 69
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 69

Ile Leu Gln Ala Asp Gln Glu Leu
1 5

<210> SEQ ID NO 70
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70

Leu Asn Ile Leu Asn Asn Asn Tyr Lys
1 5

<210> SEQ ID NO 71
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 71

Glu Glu Leu Ala Thr Phe Asp Pro Val Asp Asn Ile Val Phe Asn Met
1 5 10 15

Ala Ala Gly Ser Ala Pro Met Gln Leu His Leu Arg
20 25

<210> SEQ ID NO 72
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 72

Glu Phe Pro Glu Val His Leu Gly Gln Trp Tyr Phe Ile Ala Gly Ala
1 5 10 15

Ala Pro Thr Lys
20

<210> SEQ ID NO 73
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 73

Lys Trp Ile Tyr His Leu Thr Glu Gly Ser Thr Asp Leu Arg
1 5 10

<210> SEQ ID NO 74
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74

Met Lys Asp Gly Leu Cys Val Pro Arg
1 5

<210> SEQ ID NO 75
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 75

Ser Leu Thr Ser Cys Leu Asp Ser Lys
1 5

-continued

<210> SEQ ID NO 76
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 76

Glu Phe Thr Pro Pro Val Gln Ala Ala Tyr Gln Lys
1 5 10

<210> SEQ ID NO 77
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 77

Phe Phe Glu Ser Phe Gly Asp Leu Ser Thr Pro Asp Ala Val Met Gly
1 5 10 15

Asn Pro Lys

<210> SEQ ID NO 78
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 78

Phe Phe Glu Ser Phe Gly Asp Leu Ser Thr Pro Asp Ala Val Met Gly
1 5 10 15

Asn Pro Lys Val Lys
20

<210> SEQ ID NO 79
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 79

Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys
1 5 10

<210> SEQ ID NO 80
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 80

Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys Leu His Val
1 5 10 15

Asp Pro Glu Asn Phe Arg
20

<210> SEQ ID NO 81
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 81

Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn Leu
1 5 10 15

Lys

-continued

<210> SEQ ID NO 82
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 82

Leu His Val Asp Pro Glu Asn Phe Arg
1 5

<210> SEQ ID NO 83
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 83

Leu Leu Gly Asn Val Leu Val Cys Val Leu Ala His His Phe Gly Lys
1 5 10 15

<210> SEQ ID NO 84
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 84

Leu Leu Val Val Tyr Pro Trp Thr Gln Arg
1 5 10

<210> SEQ ID NO 85
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 85

Leu Leu Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly
1 5 10 15

Asp Leu Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys
20 25

<210> SEQ ID NO 86
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 86

Ser Ala Val Thr Ala Leu Trp Gly Lys
1 5

<210> SEQ ID NO 87
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 87

Ser Ala Val Thr Ala Leu Trp Gly Lys Val Asn Val Asp Glu Val Gly
1 5 10 15

Gly Glu Ala Leu Gly Arg
20

<210> SEQ ID NO 88
<211> LENGTH: 32

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 88

Ser Ala Val Thr Ala Leu Trp Gly Lys Val Asn Val Asp Glu Val Gly
1 5 10 15

Gly Glu Ala Leu Gly Arg Leu Leu Val Val Tyr Pro Trp Thr Gln Arg
20 25 30

<210> SEQ ID NO 89
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 89

Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn Leu Lys
1 5 10 15

<210> SEQ ID NO 90
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 90

Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg
1 5 10

<210> SEQ ID NO 91
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 91

Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys
1 5 10

<210> SEQ ID NO 92
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 92

Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys Tyr His
1 5 10

<210> SEQ ID NO 93
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 93

Leu Pro Ser Glu Gly Pro Arg Pro Ala His Val Val Val Gly Asp Val
1 5 10 15

Leu Gln Ala Ala Asp Val Asp Lys
20

<210> SEQ ID NO 94
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 94

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Asn Ile Val Ala Ala Met Lys
1               5


<210> SEQ ID NO 95
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 95

Pro Ala His Val Val Val Gly Asp Val Leu Gln Ala Ala Asp Val Asp
1               5                   10                  15

Lys


<210> SEQ ID NO 96
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 96

Thr Val Ala Gly Gln Asp Ala Val Ile Val Leu Leu Gly Thr Arg
1               5                   10                  15


<210> SEQ ID NO 97
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 97

Val Val Ala Cys Thr Ser Ala Phe Leu Leu Trp Asp Pro Thr Lys
1               5                   10                  15


<210> SEQ ID NO 98
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 98

Tyr Val Ala Val Met Pro Pro His Ile Gly Asp Gln Pro Leu Thr Gly
1               5                   10                  15

Ala Tyr Thr Val Thr Leu Asp Gly Arg
            20                  25


<210> SEQ ID NO 99
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 99

Glu Ile Ser Glu Ala Met Lys
1               5


<210> SEQ ID NO 100
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 100

Glu Ala Gln Gln Tyr Ser Glu Ala Leu Ala Ser Thr Arg
1               5                   10
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<210> SEQ ID NO 101
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 101

Gln Gln Lys Phe Tyr Leu Glu Thr Gln Ala Gly Lys
1 5 10

<210> SEQ ID NO 102
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 102

Glu Leu Leu Glu Ser Tyr Ile Asp Gly Arg
1 5 10

<210> SEQ ID NO 103
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 103

His Gln Asp Phe Asn Ser Ala Val Gln Leu Val Glu Asn Phe Cys Arg
1 5 10 15

<210> SEQ ID NO 104
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 104

Ile Val Glu Gly Ser Asp Ala Glu Ile Gly Met Ser Pro Trp Gln Val
1 5 10 15

Met Leu Phe Arg
20

<210> SEQ ID NO 105
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 105

Leu Ala Val Thr Thr His Gly Leu Pro Cys Leu Ala Trp Ala Ser Ala
1 5 10 15

Gln Ala Lys

<210> SEQ ID NO 106
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 106

Ser Glu Gly Ser Ser Val Asn Leu Ser Pro Pro Leu Glu Gln Cys Val
1 5 10 15

Pro Asp Arg

<210> SEQ ID NO 107
<211> LENGTH: 18
<212> TYPE: PRT

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 107

Ser Leu Glu Asp Lys Thr Glu Arg Glu Leu Leu Glu Ser Tyr Ile Asp
1 5 10 15

Gly Arg

<210> SEQ ID NO 108
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 108

Thr Ala Thr Ser Glu Tyr Gln Thr Phe Phe Asn Pro Arg
1 5 10

<210> SEQ ID NO 109
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 109

Thr Phe Gly Ser Gly Glu Ala Asp Cys Gly Leu Arg Pro Leu Phe Glu
1 5 10 15

Lys

<210> SEQ ID NO 110
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 110

Tyr Gly Phe Tyr Thr His Val Phe Arg
1 5

<210> SEQ ID NO 111
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 111

Asp Phe Ala Leu Leu Ser Leu Gln Val Pro Leu Lys
1 5 10

<210> SEQ ID NO 112
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 112

Asp Phe Ala Leu Leu Ser Leu Gln Val Pro Leu Lys Asp Ala Lys
1 5 10 15

<210> SEQ ID NO 113
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 113

Asp His Ala Val Asp Leu Ile Gln Lys
1 5

-continued

<210> SEQ ID NO 114
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 114

Glu Pro Phe Leu Ser Cys Cys Gln Phe Ala Glu Ser Leu Arg
1 5 10

<210> SEQ ID NO 115
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 115

Gly Leu Glu Glu Glu Leu Gln Phe Ser Leu Gly Ser Lys
1 5 10

<210> SEQ ID NO 116
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 116

Gly Pro Glu Val Gln Leu Val Ala His Ser Pro Trp Leu Lys
1 5 10

<210> SEQ ID NO 117
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 117

Lys Ala Asp Gly Ser Tyr Ala Ala Trp Leu Ser Arg
1 5 10

<210> SEQ ID NO 118
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 118

Leu His Leu Glu Thr Asp Ser Leu Ala Leu Val Ala Leu Gly Ala Leu
1 5 10 15

Asp Thr Ala Leu Tyr Ala Ala Gly Ser Lys
20 25

<210> SEQ ID NO 119
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 119

Ser Cys Gly Leu His Gln Leu Leu Arg
1 5

<210> SEQ ID NO 120
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 120

Thr Tyr Asn Val Leu Asp Met Lys
1 5

<210> SEQ ID NO 121
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 121

Val Asp Phe Thr Leu Ser Ser Glu Arg
1 5

<210> SEQ ID NO 122
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 122

Val Gly Leu Ser Gly Met Ala Ile Ala Asp Val Thr Leu Leu Ser Gly
1 5 10 15

Phe His Ala Leu Arg
20

<210> SEQ ID NO 123
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 123

Val Leu Ser Leu Ala Gln Glu Gln Val Gly Gly Ser Pro Glu Lys
1 5 10 15

<210> SEQ ID NO 124
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 124

Tyr Val Ser His Phe Glu Thr Glu Gly Pro His Val Leu Leu Tyr Phe
1 5 10 15

Asp Ser Val Pro Thr Ser Arg
20

<210> SEQ ID NO 125
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 125

Phe Gln Asn Ser Ala Ile Leu Thr Ile Gln Pro Lys
1 5 10

<210> SEQ ID NO 126
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 126

Met Val Glu Thr Thr Ala Tyr Ala Leu Leu Thr Ser Leu Asn Leu Lys
1 5 10 15

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<210> SEQ ID NO 127
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 127

Val Phe Gln Phe Leu Glu Lys
1 5

<210> SEQ ID NO 128
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 128

Tyr Ile Tyr Pro Leu Asp Ser Leu Thr Trp Ile Glu Tyr Trp Pro Arg
1 5 10 15

<210> SEQ ID NO 129
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 129

Ala Glu Ala Thr Thr Leu His Val Ala Pro Gln Gly Thr Ala Met Ala
1 5 10 15

Val Ser Thr Phe Arg
20

<210> SEQ ID NO 130
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 130

Ala Asn Phe Asp Ala Gln Gln Phe Ala Gly Thr Trp Leu Leu Val Ala
1 5 10 15

Val Gly Ser Ala Cys Arg
20

<210> SEQ ID NO 131
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 131

Gly Ala Val His Val Val Val Ala Glu Thr Asp Tyr Gln Ser Phe Ala
1 5 10 15

Val Leu Tyr Leu Glu Arg
20

<210> SEQ ID NO 132
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 132

Lys Leu Asp Gly Ile Cys Trp Gln Val Arg
1 5 10

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<210> SEQ ID NO 133
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 133

Leu Asp Gly Ile Cys Trp Gln Val Arg
1 5

<210> SEQ ID NO 134
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 134

Gln Leu Tyr Gly Asp Thr Gly Val Leu Gly Arg
1 5 10

<210> SEQ ID NO 135
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 135

Arg Pro Ala Ser Pro Ile Ser Thr Ile Gln Pro Lys
1 5 10

<210> SEQ ID NO 136
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 136

Ser Leu Pro Val Ser Asp Ser Val Leu Ser Gly Phe Glu Gln Arg
1 5 10 15

<210> SEQ ID NO 137
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 137

Val Gln Glu Ala His Leu Thr Glu Asp Gln Ile Phe Tyr Phe Pro Lys
1 5 10 15

<210> SEQ ID NO 138
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 138

Tyr Gly Phe Cys Glu Ala Ala Asp Gln Phe His Val Leu Asp Glu Val
1 5 10 15

Arg

<210> SEQ ID NO 139
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 139

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Glu Ile Met Glu Asn Tyr Asn Ile Ala Leu Arg
1               5                   10


<210> SEQ ID NO 140
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 140

Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg
1               5                   10


<210> SEQ ID NO 141
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 141

Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu
1               5                   10                  15

Gly Thr Gln Ala Ile Tyr Lys
            20


<210> SEQ ID NO 142
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 142

Ser Leu Gly Asn Val Ile Met Val Cys Arg
1               5                   10


<210> SEQ ID NO 143
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 143

Met Ala Lys Glu Ser Gly Ile Ser Leu Lys Glu Ile Gln Val Leu Ala
1               5                   10                  15

Arg


<210> SEQ ID NO 144
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 144

Glu Phe Thr Pro Gln Met Gln Ala Ala Tyr Gln Lys
1               5                   10


<210> SEQ ID NO 145
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 145

Gly Thr Phe Ser Gln Leu Ser Glu Leu His Cys Asp Lys
1               5                   10


<210> SEQ ID NO 146
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<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 146

Gly Thr Phe Ser Gln Leu Ser Glu Leu His Cys Asp Lys Leu His Val
1 5 10 15

Asp Pro Glu Asn Phe Arg
20

<210> SEQ ID NO 147
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 147

Leu Leu Gly Asn Val Leu Val Cys Val Leu Ala Arg
1 5 10

<210> SEQ ID NO 148
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 148

Leu Leu Val Val Tyr Pro Trp Thr Gln Arg
1 5 10

<210> SEQ ID NO 149
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 149

Thr Ala Val Asn Ala Leu Trp Gly Lys
1 5

<210> SEQ ID NO 150
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 150

Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn Leu Lys
1 5 10 15

<210> SEQ ID NO 151
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 151

Val Asn Val Asp Ala Val Gly Gly Glu Ala Leu Gly Arg
1 5 10

<210> SEQ ID NO 152
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 152

Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys

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1               5                   10


<210> SEQ ID NO 153
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 153

Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys Tyr His
1               5                   10


<210> SEQ ID NO 154
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 154

Ala Asn Ser Ser Ala Thr Glu Thr Ile Asn Lys
1               5                   10


<210> SEQ ID NO 155
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 155

Gly Phe Phe Asp Pro Asn Thr Glu Glu Asn Leu Thr Tyr Leu Gln Leu
1               5                   10                  15

Lys


<210> SEQ ID NO 156
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 156

Pro Gly Ser Pro Ala Cys Ser Pro Val Leu Gly Ser Gly Gly Arg Ala
1               5                   10                  15

Arg


<210> SEQ ID NO 157
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 157

Thr Phe Pro Gly Phe Phe Ser Pro Met Leu Gly Glu Phe Val Ser Glu
1               5                   10                  15

Thr Glu Ser Arg
            20


<210> SEQ ID NO 158
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 158

Val Thr Ser Gly Ser Thr Thr Thr Thr Arg
1               5                   10
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<210> SEQ ID NO 159
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 159

Glu Ser Ser Ser His His Pro Gly Ile Ala Glu Phe Pro Ser Arg
1 5 10 15

<210> SEQ ID NO 160
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 160

Glu Val Asp Leu Lys Asp Tyr Glu Asp Gln Gln Lys
1 5 10

<210> SEQ ID NO 161
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 161

Gly Leu Ile Asp Glu Val Asn Gln Asp Phe Thr Asn Arg
1 5 10

<210> SEQ ID NO 162
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 162

Gly Ser Glu Ser Gly Ile Phe Thr Asn Thr Lys
1 5 10

<210> SEQ ID NO 163
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 163

His Pro Asp Glu Ala Ala Phe Phe Asp Thr Ala Ser Thr Gly Lys
1 5 10 15

<210> SEQ ID NO 164
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 164

His Arg His Pro Asp Glu Ala Ala Phe Phe Asp Thr Ala Ser Thr Gly
1 5 10 15

Lys

<210> SEQ ID NO 165
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 165

Thr Phe Pro Gly Phe Phe Ser Pro Met Leu Gly Glu Phe Val Ser Glu

-continued

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1               5                   10                  15

Thr Glu Ser Arg
            20


<210> SEQ ID NO 166
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 166

Asp Ser Gln Glu Glu Glu Lys Thr Glu Ala Leu Thr Ser Ala Lys
1               5                   10                  15


<210> SEQ ID NO 167
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 167

Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr Phe Lys
1               5                   10                  15


<210> SEQ ID NO 168
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 168

Phe Asp Leu Val Pro Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr
1               5                   10                  15

Gly Asp Ala Tyr Val Ile Leu Lys
            20


<210> SEQ ID NO 169
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 169

His Val Val Pro Asn Glu Val Val Val Gln Arg
1               5                   10


<210> SEQ ID NO 170
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 170

Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys
1               5                   10


<210> SEQ ID NO 171
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 171

Arg Thr Thr Glu Met Met Pro Val Tyr Leu Asp Leu Asn Lys
1               5                   10


<210> SEQ ID NO 172
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<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 172

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
1 5 10

<210> SEQ ID NO 173
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 173

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
1 5 10

<210> SEQ ID NO 174
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 174

Ala Leu Asp Leu Ile Asn Lys Arg
1 5

<210> SEQ ID NO 175
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 175

Asp Gly Tyr Leu Phe Gln Leu Leu Arg
1 5

<210> SEQ ID NO 176
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 176

Asp Ser Pro Val Leu Ile Asp Phe Phe Glu Asp Thr Glu Arg
1 5 10

<210> SEQ ID NO 177
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 177

Gly Glu Val Leu Pro Leu Pro Glu Ala Asn Phe Pro Ser Phe Pro Leu
1 5 10 15

Pro His His Lys
20

<210> SEQ ID NO 178
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 178

His Pro Leu Lys Pro Asp Asn Gln Pro Phe Pro Gln Ser Val Ser Glu

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1               5                   10                  15

Ser Cys Pro Gly Lys
            20


<210> SEQ ID NO 179
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 179

Lys Gly Glu Val Leu Pro Leu Pro Glu Ala Asn Phe Pro Ser Phe Pro
1               5                   10                  15

Leu Pro His His Lys
            20


<210> SEQ ID NO 180
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 180

Leu Pro Pro Leu Arg
1               5


<210> SEQ ID NO 181
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 181

Arg Asp Gly Tyr Leu Phe Gln Leu Leu Arg
1               5                   10


<210> SEQ ID NO 182
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 182

Arg Pro Ser Glu Ile Val Ile Gly Gln Cys Lys
1               5                   10


<210> SEQ ID NO 183
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 183

Ser Gly Phe Pro Gln Val Ser Met Phe Phe Thr His Thr Phe Pro Lys
1               5                   10                  15


<210> SEQ ID NO 184
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 184

Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg
1               5                   10


<210> SEQ ID NO 185
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<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 185

Thr Pro Leu Thr Ala Thr Leu Ser Lys
1 5

<210> SEQ ID NO 186
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 186

Val Thr Val Ser Ser Ala Ser Pro Thr Ser Pro Lys
1 5 10

<210> SEQ ID NO 187
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 187

Ala Gly Val Glu Thr Thr Lys Pro Ser Lys
1 5 10

<210> SEQ ID NO 188
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 188

Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
1 5 10 15

Ala Asn Lys

<210> SEQ ID NO 189
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 189

Val Thr Val Leu Gly Gln Pro Lys
1 5

<210> SEQ ID NO 190
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 190

Thr Gly Tyr Tyr Trp Gly Trp Ile Arg
1 5

<210> SEQ ID NO 191
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 191

Gly Leu Glu Trp Val Ala Asn Ile Lys
1 5

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<210> SEQ ID NO 192
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 192

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
1 5 10

<210> SEQ ID NO 193
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 193

Ala Glu Ala Gln Ala Gln Tyr Ser Ala Ala Val Ala Lys
1 5 10

<210> SEQ ID NO 194
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 194

Ala Gly Phe Ser Trp Ile Glu Val Thr Phe Lys
1 5 10

<210> SEQ ID NO 195
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 195

Ala Asn Thr Val Gln Glu Ala Thr Phe Gln Met Glu Leu Pro Lys
1 5 10 15

<210> SEQ ID NO 196
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 196

Phe Ser Ser His Val Gly Gly Thr Leu Gly Gln Phe Tyr Gln Glu Val
1 5 10 15

Leu Trp Gly Ser Pro Ala Ala Ser Asp Asp Gly Arg
20 25

<210> SEQ ID NO 197
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 197

Gly Pro Asp Val Leu Thr Ala Thr Val Ser Gly Lys
1 5 10

<210> SEQ ID NO 198
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 198

Leu Trp Ala Tyr Leu Thr Ile Gln Gln Leu Leu Glu Gln Thr Val Ser
1 5 10 15

Ala Ser Asp Ala Asp Gln Gln Ala Leu Arg
20 25

<210> SEQ ID NO 199
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 199

Met Asn Phe Arg Pro Gly Val Leu Ser Ser Arg
1 5 10

<210> SEQ ID NO 200
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 200

Asn Val His Ser Gly Ser Thr Phe Phe Lys
1 5 10

<210> SEQ ID NO 201
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 201

Val Thr Ile Gly Leu Leu Phe Trp Asp Gly Arg
1 5 10

<210> SEQ ID NO 202
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 202

Ala Glu Ala Glu Ser Leu Tyr Gln Ser Lys
1 5 10

<210> SEQ ID NO 203
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 203

Ala Gln Tyr Glu Asp Ile Ala Gln Lys
1 5

<210> SEQ ID NO 204
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 204

Asp Tyr Gln Glu Leu Met Asn Thr Lys
1 5

<210> SEQ ID NO 205

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<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 205

Glu Gln Ile Lys Ser Leu Asn Asn Gln Phe Ala Ser Phe Ile Asp Lys
1 5 10 15

<210> SEQ ID NO 206
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 206

Phe Leu Glu Gln Gln Asn Gln Val Leu Gln Thr Lys
1 5 10

<210> SEQ ID NO 207
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 207

Phe Ser Ser Cys Gly Gly Gly Gly Gly Ser Phe Gly Ala Gly Gly Gly
1 5 10 15

Phe Gly Ser Arg
20

<210> SEQ ID NO 208
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 208

Gly Gly Gly Gly Gly Gly Tyr Gly Ser Gly Gly Ser Ser Tyr Gly Ser
1 5 10 15

Gly Gly Gly Ser Tyr Gly Ser Gly Gly Gly Gly Gly Gly Gly Arg
20 25 30

<210> SEQ ID NO 209
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 209

Ile Glu Ile Ser Glu Leu Asn Arg
1 5

<210> SEQ ID NO 210
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 210

Leu Ala Leu Asp Leu Glu Ile Ala Thr Tyr Arg
1 5 10

<210> SEQ ID NO 211
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 211

Leu Asn Asp Leu Glu Asp Ala Leu Gln Gln Ala Lys
1 5 10

<210> SEQ ID NO 212
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 212

Met Ser Gly Glu Cys Ala Pro Asn Val Ser Val Ser Val Ser Thr Ser
1 5 10 15

His Thr Thr Ile Ser Gly Gly Gly Ser Arg
20 25

<210> SEQ ID NO 213
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 213

Asn Lys Leu Asn Asp Leu Glu Asp Ala Leu Gln Gln Ala Lys
1 5 10

<210> SEQ ID NO 214
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 214

Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg
1 5 10

<210> SEQ ID NO 215
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 215

Asn Met Gln Asp Met Val Glu Asp Tyr Arg
1 5 10

<210> SEQ ID NO 216
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 216

Asn Met Gln Asp Met Val Glu Asp Tyr Arg
1 5 10

<210> SEQ ID NO 217
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 217

Gln Ile Ser Asn Leu Gln Gln Ser Ile Ser Asp Ala Glu Gln Arg
1 5 10 15

<210> SEQ ID NO 218

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<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 218

Ser Lys Ala Glu Ala Glu Ser Leu Tyr Gln Ser Lys
1 5 10

<210> SEQ ID NO 219
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 219

Ser Leu Asp Leu Asp Ser Ile Ile Ala Glu Val Lys
1 5 10

<210> SEQ ID NO 220
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 220

Thr His Asn Leu Glu Pro Tyr Phe Glu Ser Phe Ile Asn Asn Leu Arg
1 5 10 15

<210> SEQ ID NO 221
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 221

Thr Leu Leu Glu Gly Glu Glu Ser Arg
1 5

<210> SEQ ID NO 222

<400> SEQUENCE: 222

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<210> SEQ ID NO 223
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 223

Thr Asn Ala Glu Asn Glu Phe Val Thr Ile Lys
1 5 10

<210> SEQ ID NO 224
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 224

Trp Glu Leu Leu Gln Gln Val Asp Thr Ser Thr Arg
1 5 10

<210> SEQ ID NO 225
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 225

Tyr Glu Glu Leu Gln Ile Thr Ala Gly Arg
1 5 10

<210> SEQ ID NO 226
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 226

Gly Ser Ser Gly Gly Gly Cys Phe Gly Gly Ser Ser Gly Gly Tyr Gly
1 5 10 15

Gly Leu Gly Gly Phe Gly Gly Gly Ser Phe Arg
20 25

<210> SEQ ID NO 227
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 227

Ala Asp Leu Glu Met Gln Ile Glu Ser Leu Thr Glu Glu Leu Ala Tyr
1 5 10 15

Leu Lys

<210> SEQ ID NO 228
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 228

Ala Glu Thr Glu Cys Gln Asn Thr Glu Tyr Gln Gln Leu Leu Asp Ile
1 5 10 15

Lys

<210> SEQ ID NO 229
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 229

Ala Leu Glu Glu Ser Asn Tyr Glu Leu Glu Gly Lys
1 5 10

<210> SEQ ID NO 230
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 230

Asp Ala Glu Ala Trp Phe Asn Glu Lys
1 5

<210> SEQ ID NO 231
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 231

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Glu Leu Thr Thr Glu Ile Asp Asn Asn Ile Glu Gln Ile Ser Ser Tyr
1               5                   10                  15

Lys


<210> SEQ ID NO 232
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 232

Gly Ser Leu Gly Gly Gly Phe Ser Ser Gly Gly Phe Ser Gly Gly Ser
1               5                   10                  15

Phe Ser Arg


<210> SEQ ID NO 233
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 233

Gly Ser Ser Gly Gly Gly Cys Phe Gly Gly Ser Ser Gly Gly Tyr Gly
1               5                   10                  15

Gly Leu Gly Gly Phe Gly Gly Gly Ser Phe Arg
            20                  25


<210> SEQ ID NO 234
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 234

Ile Lys Glu Trp Tyr Glu Lys
1               5


<210> SEQ ID NO 235
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 235

Leu Ala Ser Tyr Leu Asp Lys
1               5


<210> SEQ ID NO 236
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 236

Leu Glu Asn Glu Ile Gln Thr Tyr Arg
1               5


<210> SEQ ID NO 237
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 237

Leu Lys Tyr Glu Asn Glu Val Ala Leu Arg
1               5                   10
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<210> SEQ ID NO 238
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 238

Asn Val Ser Thr Gly Asp Val Asn Val Glu Met Asn Ala Ala Pro Gly
1 5 10 15

Val Asp Leu Thr Gln Leu Leu Asn Asn Met Arg
20 25

<210> SEQ ID NO 239
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 239

Ser Lys Glu Leu Thr Thr Glu Ile Asp Asn Asn Ile Glu Gln Ile Ser
1 5 10 15

Ser Tyr Lys

<210> SEQ ID NO 240
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 240

Ser Leu Leu Glu Gly Glu Gly Ser Ser Gly Gly Gly Gly Arg
1 5 10

<210> SEQ ID NO 241
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 241

Ser Gln Tyr Glu Gln Leu Ala Glu Gln Asn Arg
1 5 10

<210> SEQ ID NO 242
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 242

Ser Gln Tyr Glu Gln Leu Ala Glu Gln Asn Arg Lys
1 5 10

<210> SEQ ID NO 243
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 243

Thr Ile Asp Asp Leu Lys Asn Gln Ile Leu Asn Leu Thr Thr Asp Asn
1 5 10 15

Ala Asn Ile Leu Leu Gln Ile Asp Asn Ala Arg
20 25

<210> SEQ ID NO 244

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<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 244

Val Leu Asp Glu Leu Thr Leu Thr Lys
1 5

<210> SEQ ID NO 245
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 245

Val Thr Met Gln Asn Leu Asn Asp Arg
1 5

<210> SEQ ID NO 246
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 246

Tyr Cys Val Gln Leu Ser Gln Ile Gln Ala Gln Ile Ser Ala Leu Glu
1 5 10 15

Glu Gln Leu Gln Gln Ile Arg
20

<210> SEQ ID NO 247
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 247

Tyr Glu Asn Glu Val Ala Leu Arg
1 5

<210> SEQ ID NO 248
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 248

Asp Ile Glu Asn Gln Tyr Glu Thr Gln Ile Thr Gln Ile Glu His Glu
1 5 10 15

Val Ser Ser Ser Gly Gln Glu Val Gln Ser Ser Ala Lys
20 25

<210> SEQ ID NO 249
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 249

Glu Ile Glu Thr Tyr His Asn Leu Leu Glu Gly Gly Gln Glu Asp Phe
1 5 10 15

Glu Ser Ser Gly Ala Gly Lys
20

<210> SEQ ID NO 250
<211> LENGTH: 13

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 250

Phe Ser Ser Ser Ser Gly Tyr Gly Gly Gly Ser Ser Arg
1 5 10

<210> SEQ ID NO 251
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 251

Gly Gly Gly Gly Ser Phe Gly Tyr Ser Tyr Gly Gly Gly Ser Gly Gly
1 5 10 15

Gly Phe Ser Ala Ser Ser Leu Gly Gly Gly Phe Gly Gly Gly Ser Arg
20 25 30

<210> SEQ ID NO 252
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 252

His Gly Val Gln Glu Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Lys
1 5 10 15

<210> SEQ ID NO 253
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 253

Ile Lys Phe Glu Met Glu Gln Asn Leu Arg
1 5 10

<210> SEQ ID NO 254
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 254

Ile Gln Asp Trp Tyr Asp Lys Lys
1 5

<210> SEQ ID NO 255
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 255

Leu Ala Ser Tyr Leu Asp Lys
1 5

<210> SEQ ID NO 256
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 256

Asn Tyr Ser Pro Tyr Tyr Asn Thr Ile Asp Asp Leu Lys Asp Gln Ile
1 5 10 15

-continued

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Val Asp Leu Thr Val Gly Asn Asn Lys
            20                  25


<210> SEQ ID NO 257
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 257

Ser Asp Leu Glu Met Gln Tyr Glu Thr Leu Gln Glu Glu Leu Met Ala
1               5                   10                  15

Leu Lys


<210> SEQ ID NO 258
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 258

Ser Gly Gly Gly Gly Gly Gly Gly Leu Gly Ser Gly Gly Ser Ile Arg
1               5                   10                  15


<210> SEQ ID NO 259
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 259

Ser Thr Met Gln Glu Leu Asn Ser Arg
1               5


<210> SEQ ID NO 260
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 260

Thr Leu Leu Asp Ile Asp Asn Thr Arg
1               5


<210> SEQ ID NO 261
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 261

Val Gln Ala Leu Glu Glu Ala Asn Asn Asp Leu Glu Asn Lys
1               5                   10


<210> SEQ ID NO 262
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 262

Tyr Cys Gly Gln Leu Gln Met Ile Gln Glu Gln Ile Ser Asn Leu Glu
1               5                   10                  15

Ala Gln Ile Thr Asp Val Arg
            20
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<210> SEQ ID NO 263
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 263

Ala Glu Thr Glu Cys Gln Asn Thr Glu Tyr Gln Gln Leu Leu Asp Ile
1 5 10 15

Lys Ile Arg

<210> SEQ ID NO 264
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 264

Gly Ser Leu Gly Gly Gly Phe Ser Ser Gly Gly Phe Ser Gly Gly Ser
1 5 10 15

Phe

<210> SEQ ID NO 265
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 265

Ile Leu Leu Gln Ile Asp Asn Ala Arg
1 5

<210> SEQ ID NO 266
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 266

Ile Arg Leu Glu Asn Glu Ile Gln Thr Tyr Arg
1 5 10

<210> SEQ ID NO 267
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 267

Ile Ser Ala Leu Glu Glu Gln Leu Gln Gln Ile Arg
1 5 10

<210> SEQ ID NO 268
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 268

Leu Ala Ala Asp Asp Phe Arg
1 5

<210> SEQ ID NO 269
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 269

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Leu Ala Ser Tyr Leu Asp Lys
1               5


<210> SEQ ID NO 270
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 270

Leu Glu Asn Glu Ile Gln Thr Tyr Arg
1               5


<210> SEQ ID NO 271
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 271

Leu Lys Tyr Glu Asn Glu Val Ala Leu Arg
1               5                   10


<210> SEQ ID NO 272
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 272

Asn Gln Ile Leu Asn Leu Thr Thr Asp Asn Ala Asn
1               5                   10


<210> SEQ ID NO 273
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 273

Asn Gln Ile Leu Asn Leu Thr Thr Asp Asn Ala Asn Ile Leu Leu Gln
1               5                   10                  15

Ile Asp Asn Ala Arg
            20


<210> SEQ ID NO 274
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 274

Asn Val Gln Ala Leu Glu Ile Glu Leu Gln Ser Gln Leu Ala Leu Lys
1               5                   10                  15


<210> SEQ ID NO 275
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 275

Arg Val Leu Asp Glu Leu Thr Leu Thr Lys
1               5                   10


<210> SEQ ID NO 276
<211> LENGTH: 20
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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 276

Ser Gly Gly Gly Gly Gly Gly Gly Gly Cys Gly Gly Gly Gly Gly Val
1 5 10 15

Ser Ser Leu Arg
20

<210> SEQ ID NO 277
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 277

Ser Lys Glu Leu Thr Thr Glu Ile Asp Asn Asn Ile Glu Gln Ile Ser
1 5 10 15

Ser Tyr Lys

<210> SEQ ID NO 278
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 278

Ser Leu Leu Glu Gly Glu Gly Ser Ser Gly Gly Gly Gly Arg
1 5 10

<210> SEQ ID NO 279
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 279

Val Gln Ala Leu Glu Ile Glu Leu Gln Ser Gln Leu Ala Leu Lys
1 5 10 15

<210> SEQ ID NO 280
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 280

Leu Glu Gln Glu Ile Ala Thr Tyr Arg
1 5

<210> SEQ ID NO 281
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 281

Glu Val Ala Thr Asn Ser Glu Leu Val Gln Ser Gly Lys
1 5 10

<210> SEQ ID NO 282
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 282

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Gly Ser Cys Gly Ile Gly Gly Gly Ile Gly Gly Gly Ser Ser Arg
1               5                   10                  15


<210> SEQ ID NO 283
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 283

Ile Ser Ser Val Leu Ala Gly Gly Ser Cys Arg
1               5                   10


<210> SEQ ID NO 284
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 284

Val Leu Asp Glu Leu Thr Leu Ala Arg
1               5


<210> SEQ ID NO 285
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 285

Ala Glu Ala Glu Ser Leu Tyr Gln Ser Lys
1               5                   10


<210> SEQ ID NO 286
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 286

Glu Leu Leu Gln Gln Val Asp Thr Ser Thr Arg
1               5                   10


<210> SEQ ID NO 287
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 287

Gly Gly Ser Gly Gly Gly Gly Gly Gly Ser Ser Gly Gly Arg Gly Ser
1               5                   10                  15

Gly Gly Gly Ser Ser Gly Gly Ser Ile Gly Gly Arg
            20                  25


<210> SEQ ID NO 288
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 288

Gly Ser Gly Gly Gly Ser Ser Gly Gly Ser Ile Gly Gly Arg
1               5                   10


<210> SEQ ID NO 289
<211> LENGTH: 16
<212> TYPE: PRT
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 289

Lys Gln Ile Ser Asn Leu Gln Gln Ser Ile Ser Asp Ala Glu Gln Arg
1 5 10 15

<210> SEQ ID NO 290
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 290

Leu Ala Leu Asp Leu Glu Ile Ala Thr Tyr Arg
1 5 10

<210> SEQ ID NO 291
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 291

Asn Lys Leu Asn Asp Leu Glu Asp Ala Leu Gln Gln Ala Lys
1 5 10

<210> SEQ ID NO 292
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 292

Asn Val Glu Ile Asp Pro Glu Ile Gln Lys
1 5 10

<210> SEQ ID NO 293
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 293

Ser Glu Ile Asp Asn Val Lys Lys
1 5

<210> SEQ ID NO 294
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 294

Ser Gly Gly Gly Phe Ser Ser Gly Ser Ala Gly Ile Ile Asn Tyr Gln
1 5 10 15

Arg

<210> SEQ ID NO 295
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 295

Ser Ile Ser Asp Ala Glu Gln Arg
1 5

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<210> SEQ ID NO 296
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 296

Ser Ile Ser Ile Ser Val Ala Arg Gly Gly Gly Arg
1 5 10

<210> SEQ ID NO 297
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 297

Ser Lys Ala Glu Ala Glu Ser Leu Tyr Gln Ser Lys
1 5 10

<210> SEQ ID NO 298
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 298

Ser Leu Asp Leu Asp Ser Ile Ile Ala Glu Val Lys
1 5 10

<210> SEQ ID NO 299
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 299

Ser Leu Asn Asn Gln Phe Ala Ser Phe Ile Asp Lys
1 5 10

<210> SEQ ID NO 300
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 300

Ser Leu Asn Asn Gln Phe Ala Ser Phe Ile Asp Lys Val Arg
1 5 10

<210> SEQ ID NO 301
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 301

Ser Leu Val Asn Leu Gly Gly Ser Lys
1 5

<210> SEQ ID NO 302
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 302

Thr His Asn Leu Glu Pro Tyr Phe Glu Ser Phe
1 5 10

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<210> SEQ ID NO 303
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 303

Thr His Asn Leu Glu Pro Tyr Phe Glu Ser Phe Ile Asn Asn Leu Arg
1 5 10 15

<210> SEQ ID NO 304
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 304

Thr Leu Leu Glu Gly Glu Glu Ser Arg
1 5

<210> SEQ ID NO 305
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 305

Thr Asn Ala Glu Asn Glu Phe Val Thr Ile Lys
1 5 10

<210> SEQ ID NO 306
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 306

Val Asp Gln Leu Lys Ser Asp Gln Ser Arg
1 5 10

<210> SEQ ID NO 307
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 307

Val Glu Ile Asp Pro Glu Ile Gln Lys
1 5

<210> SEQ ID NO 308
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 308

Trp Glu Leu Leu Gln Gln Val Asp Thr Ser Thr Arg
1 5 10

<210> SEQ ID NO 309
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 309

Tyr Glu Glu Leu Gln Ile Thr Ala Gly Arg
1 5 10

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<210> SEQ ID NO 310
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 310

Gly Phe Ser Ser Gly Ser Ala Val Val Ser Gly Gly Ser Arg
1 5 10

<210> SEQ ID NO 311
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 311

Ile Glu Ile Ser Glu Leu Asn Arg
1 5

<210> SEQ ID NO 312
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 312

Leu Ala Leu Asp Val Glu Ile Ala Thr Tyr Arg
1 5 10

<210> SEQ ID NO 313
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 313

Leu Asn Asp Leu Glu Glu Ala Leu Gln Gln Ala Lys
1 5 10

<210> SEQ ID NO 314
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 314

Asn Leu Asp Leu Asp Ser Ile Ile Ala Glu Val Lys
1 5 10

<210> SEQ ID NO 315
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 315

Asn Val Gln Asp Ala Ile Ala Asp Ala Glu Gln Arg
1 5 10

<210> SEQ ID NO 316
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 316

Val Asp Leu Leu Asn Gln Glu Ile Glu Phe Leu Lys

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1               5                   10


<210> SEQ ID NO 317
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 317

Tyr Glu Asp Glu Ile Asn Lys Arg
1               5


<210> SEQ ID NO 318
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 318

Tyr Glu Glu Leu Gln Val Thr Val Gly Arg
1               5                   10


<210> SEQ ID NO 319
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 319

Tyr Leu Asp Gly Leu Thr Ala Glu Arg
1               5


<210> SEQ ID NO 320
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 320

Pro Phe Leu Ser Ile Ile Ser Ala Arg Tyr Ser Pro His Gln Asp Ala
1               5                   10                  15

Asp Pro Leu Lys
            20


<210> SEQ ID NO 321
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 321

Thr Phe Val Pro Gly Cys Gln Pro Gly Glu Phe Thr Leu Gly Asn Ile
1               5                   10                  15

Lys


<210> SEQ ID NO 322
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 322

Val Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe Gln Gly Lys
1               5                   10                  15


<210> SEQ ID NO 323
<211> LENGTH: 12
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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 323

Gly Ile Ser Leu Ala Asn Trp Met Cys Leu Ala Lys
1 5 10

<210> SEQ ID NO 324
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 324

Leu Gly Met Asp Gly Tyr Arg
1 5

<210> SEQ ID NO 325
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 325

Gln Tyr Val Gln Gly Cys Gly Val
1 5

<210> SEQ ID NO 326
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 326

Arg Leu Gly Met Asp Gly Tyr Arg
1 5

<210> SEQ ID NO 327
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 327

Ser Thr Asp Tyr Gly Ile Phe Gln Ile Asn Ser Arg
1 5 10

<210> SEQ ID NO 328
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 328

Thr Pro Gly Ala Val Asn Ala Cys His Leu Ser Cys Ser Ala Leu Leu
1 5 10 15

Gln Asp Asn Ile Ala Asp Ala Val Ala Cys Ala Lys
20 25

<210> SEQ ID NO 329
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 329

Trp Glu Ser Gly Tyr Asn Thr Arg
1 5

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<210> SEQ ID NO 330
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 330

Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp Thr Glu Arg
1 5 10 15

<210> SEQ ID NO 331
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 331

Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln Arg
1 5 10

<210> SEQ ID NO 332
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 332

Asn Pro Ser Glu Leu Lys Gly Lys Phe Ile His Thr Lys
1 5 10

<210> SEQ ID NO 333
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 333

Ile Ser Phe Gly Thr Pro Ala Pro Gly Phe Ser Ser Met Leu Tyr Gly
1 5 10 15

Met Lys

<210> SEQ ID NO 334
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 334

Asp Lys Val Asn Gly Asp Lys
1 5

<210> SEQ ID NO 335
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 335

Ala Gly Lys Arg Gly Tyr Ile Ile Asp Thr Arg
1 5 10

<210> SEQ ID NO 336
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 336

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Gly Arg Pro Ala Val Cys Gln Pro Gln Gly Arg
1               5                   10


<210> SEQ ID NO 337
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 337

Ile Glu Ile Ser Ser Pro Cys Cys Pro Arg
1               5                   10


<210> SEQ ID NO 338
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 338

Arg Pro Ile Ser Ser Cys Ser Gln Arg
1               5


<210> SEQ ID NO 339
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 339

Leu Pro Glu Met Glu Pro Leu Val Pro Arg Val Lys Glu Val Lys
1               5                   10                  15


<210> SEQ ID NO 340
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 340

Ala Thr Ala Val Val Asp Gly Ala Phe Lys
1               5                   10


<210> SEQ ID NO 341
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 341

Glu Gly Gly Leu Gly Pro Leu Asn Ile Pro Leu Leu Ala Asp Val Thr
1               5                   10                  15

Arg


<210> SEQ ID NO 342
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 342

Glu Gly Gly Leu Gly Pro Leu Asn Ile Pro Leu Leu Ala Asp Val Thr
1               5                   10                  15

Arg


<210> SEQ ID NO 343
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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 343

Gly Leu Phe Ile Ile Asp Gly Lys
1 5

<210> SEQ ID NO 344
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 344

Lys Glu Gly Gly Leu Gly Pro Leu Asn Ile Pro Leu Leu Ala Asp Val
1 5 10 15

Thr Arg

<210> SEQ ID NO 345
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 345

Leu Ser Glu Asp Tyr Gly Val Leu Lys
1 5

<210> SEQ ID NO 346
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 346

Arg Leu Ser Glu Asp Tyr Gly Val Leu Lys
1 5 10

<210> SEQ ID NO 347
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 347

Thr Asp Glu Gly Ile Ala Tyr Arg
1 5

<210> SEQ ID NO 348
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 348

Ile Ala Ala Asp Met Ser Asn Ile Ile Glu Asn Leu Asp Thr Arg
1 5 10 15

<210> SEQ ID NO 349
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 349

Asp Thr Gly Thr Tyr Gly Phe Leu Leu Pro Glu Arg
1 5 10

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<210> SEQ ID NO 350
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 350

Ala Gly Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys
1 5 10 15

<210> SEQ ID NO 351
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 351

His Ile Thr Ser Leu Glu Val Ile Lys
1 5

<210> SEQ ID NO 352
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 352

Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys
1 5 10

<210> SEQ ID NO 353
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 353

Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys
1 5 10

<210> SEQ ID NO 354
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 354

Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys
1 5 10

<210> SEQ ID NO 355
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 355

Ala Asp Glu Val Ala Ala Ala Pro Glu Gln Ile Ala Ala Asp Ile Pro
1 5 10 15

Glu Val Val Val Ser Leu Ala Trp Asp Glu Ser Leu Ala Pro Lys
20 25 30

<210> SEQ ID NO 356
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 356

Ile Pro Ala Cys Ile Ala Gly Glu Arg
1 5

<210> SEQ ID NO 357
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 357

Arg Tyr Gly Thr Cys Ile Tyr Gln Gly Arg
1 5 10

<210> SEQ ID NO 358
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 358

Tyr Gly Thr Cys Ile Tyr Gln Gly Arg
1 5

<210> SEQ ID NO 359
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 359

His Met Lys Ile Lys Ser Leu Glu Glu Met Tyr Val Phe Ser Leu Pro
1 5 10 15

Met Lys

<210> SEQ ID NO 360
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 360

Cys Val Arg Ala Asp Glu Tyr Ser Leu Tyr Ala Lys Asn Glu Asn Thr
1 5 10 15

Gly Val Val Val Val Lys
20

<210> SEQ ID NO 361
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 361

Tyr Ser Ser Ala Gly Thr Val Glu Phe Leu Val Asp Ser Lys
1 5 10

<210> SEQ ID NO 362
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 362

Leu Gly Pro Gly Met Ala Asp Ile Cys Lys
1 5 10

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<210> SEQ ID NO 363
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 363

Ile Tyr Val Asp Asp Gly Leu Ile Ser Leu Gln Val Lys
1 5 10

<210> SEQ ID NO 364
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 364

Asp Leu Gly Gln Gly Ile Gln Asn Ser Val Thr Asp Arg Pro Glu Thr
1 5 10 15

Arg

<210> SEQ ID NO 365
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 365

Leu Gly Met Pro Gln Phe Leu Ser Pro Glu Ala Gln Ser Leu Leu Arg
1 5 10 15

Met Leu Phe Lys
20

<210> SEQ ID NO 366
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 366

Gln Thr Ser Gly Leu Gln Ala Thr Ser Ser Trp Gln Asn Leu Asp Ala
1 5 10 15

Lys

<210> SEQ ID NO 367
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 367

Pro Ile Ser Ser Ile Gly Gln Val Gln Ser Tyr Met Glu His Tyr Cys
1 5 10 15

Asn Ser Ser Thr Asp Arg Arg
20

<210> SEQ ID NO 368
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 368

Glu Asn Phe Pro Asn Phe Leu Ser Ala Cys Asp Lys
1 5 10

-continued

<210> SEQ ID NO 369
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 369

Gly Thr Asn Tyr Leu Ala Asp Val Phe Glu Lys
1 5 10

<210> SEQ ID NO 370
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 370

Ile Asp Phe Ser Glu Phe Leu Ser Leu Leu Gly Asp Ile Ala Thr Asp
1 5 10 15

Tyr His Lys

<210> SEQ ID NO 371
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 371

Lys Ile Asp Phe Ser Glu Phe Leu Ser Leu Leu Gly Asp Ile Ala Thr
1 5 10 15

Asp Tyr His Lys
20

<210> SEQ ID NO 372
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 372

Ile Asp Phe Ser Glu Phe Leu Ser Leu Leu Gly Asp Ile Ala Thr Asp
1 5 10 15

Tyr His Lys

<210> SEQ ID NO 373
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 373

Lys Ile Asp Phe Ser Glu Phe Leu Ser Leu Leu Gly Asp Ile Ala Thr
1 5 10 15

Asp Tyr His Lys
20

<210> SEQ ID NO 374
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 374

Leu Leu Leu Ser Ser Leu Gly Ile Pro Val Asn His Leu Ile Glu Gly
1 5 10 15

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Ser Gln Lys

<210> SEQ ID NO 375
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 375

Pro Val Ala Gln Pro Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly
1 5 10 15

Ala Gly Thr Leu Ala Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys
20 25 30

<210> SEQ ID NO 376
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 376

Ala Val Leu Thr Ile Asp Glu Lys
1 5

<210> SEQ ID NO 377
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 377

Phe Leu Glu Asn Glu Asp Arg
1 5

<210> SEQ ID NO 378
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 378

Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys
1 5 10 15

<210> SEQ ID NO 379
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 379

Gly Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser
1 5 10 15

Ile Pro Pro Glu Val Lys
20

<210> SEQ ID NO 380
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 380

Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg
1 5 10

<210> SEQ ID NO 381

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<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 381

Lys Leu Ser Ser Trp Val Leu Leu Met Lys
1 5 10

<210> SEQ ID NO 382
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 382

Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys
1 5 10 15

<210> SEQ ID NO 383
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 383

Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys
1 5 10

<210> SEQ ID NO 384
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 384

Leu Ser Ser Trp Val Leu Leu Met Lys
1 5

<210> SEQ ID NO 385
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 385

Ser Ala Ser Leu His Leu Pro Lys
1 5

<210> SEQ ID NO 386
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 386

Ser Pro Leu Phe Met Gly Lys
1 5

<210> SEQ ID NO 387
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 387

Ser Val Leu Gly Gln Leu Gly Ile Thr Lys
1 5 10

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<210> SEQ ID NO 388
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 388

Val Phe Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro
1 5 10 15

Leu Lys

<210> SEQ ID NO 389
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 389

Phe Met Phe Asp Leu Phe Gln Gln Phe Arg
1 5 10

<210> SEQ ID NO 390
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 390

Asp Pro Asn His Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
1 5 10

<210> SEQ ID NO 391
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 391

Glu Ala Asn Tyr Ile Gly Ser Asp Lys Tyr Phe His Ala Arg
1 5 10

<210> SEQ ID NO 392
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 392

Leu Thr Gly His Gly Ala Glu Asp Ser Leu Ala Asp Gln Ala Ala Asn
1 5 10 15

Lys

<210> SEQ ID NO 393
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 393

Arg Gly Pro Gly Gly Ala Trp Ala Ala Glu Val Ile Ser Asn Ala Arg
1 5 10 15

<210> SEQ ID NO 394
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 394

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Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala Arg
1               5                   10


<210> SEQ ID NO 395
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 395

Ala Tyr Trp Asp Ile Met Ile Ser Asn His Gln Asn Ser Asn Arg
1               5                   10                  15


<210> SEQ ID NO 396
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 396

Glu Ala Leu Gln Gly Val Gly Asp Met Gly Arg
1               5                   10


<210> SEQ ID NO 397
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 397

Phe Arg Pro Asp Gly Leu Pro Lys
1               5


<210> SEQ ID NO 398
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 398

Gly Pro Gly Gly Val Trp Ala Ala Lys
1               5


<210> SEQ ID NO 399
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 399

Ser Phe Phe Lys Glu Ala Leu Gln Gly Val Gly Asp Met Gly Arg
1               5                   10                  15


<210> SEQ ID NO 400
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 400

Ser Asn Glu Lys Ala Glu Glu Trp Gly Arg
1               5                   10


<210> SEQ ID NO 401
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
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<400> SEQUENCE: 401

Val Tyr Leu Gln Gly Leu Ile Asp Tyr Tyr Leu Phe Gly Asn Ser Ser
1 5 10 15

Thr Val Leu Glu Asp Ser Lys
20

<210> SEQ ID NO 402
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 402

Glu Met Val Ser Gln Leu Gln Arg Glu Cys Tyr Leu Lys
1 5 10

<210> SEQ ID NO 403
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 403

Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu
1 5 10 15

Tyr Glu Tyr Leu Arg
20

<210> SEQ ID NO 404
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 404

Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys
1 5 10

<210> SEQ ID NO 405
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 405

Leu Asn Pro Gly Ala Leu Leu Pro Val Leu Thr Asp Pro Ala Leu Asn
1 5 10 15

Asp Leu Tyr Val Ile Ser Thr Phe Lys
20 25

<210> SEQ ID NO 406
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 406

Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr Leu Asp Ala Gly Leu
1 5 10 15

Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu Lys Pro Val Val Ala
20 25 30

Glu Phe Tyr Gly Ser Lys
35

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<210> SEQ ID NO 407
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 407

Ala Ser Tyr Leu Asp Cys Ile Arg
1 5

<210> SEQ ID NO 408
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 408

Cys Ser Thr Ser Ser Leu Leu Glu Ala Cys Thr Phe Arg
1 5 10

<210> SEQ ID NO 409
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 409

Asp Asp Thr Val Cys Leu Ala Lys
1 5

<210> SEQ ID NO 410
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 410

Asp Gly Ala Gly Asp Val Ala Phe Val Lys
1 5 10

<210> SEQ ID NO 411
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 411

Asp Leu Leu Phe Arg Asp Asp Thr Val Cys Leu Ala Lys
1 5 10

<210> SEQ ID NO 412
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 412

Asp Ser Gly Phe Gln Met Asn Gln Leu Arg
1 5 10

<210> SEQ ID NO 413
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 413

Asp Tyr Glu Leu Leu Cys Leu Asp Gly Thr Arg
1 5 10

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<210> SEQ ID NO 414
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 414

Glu Asp Pro Gln Thr Phe Tyr Tyr Ala Val Ala Val Val Lys
1 5 10

<210> SEQ ID NO 415
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 415

His Ser Thr Ile Phe Glu Asn Leu Ala Asn Lys
1 5 10

<210> SEQ ID NO 416
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 416

Lys Ala Ser Tyr Leu Asp Cys Ile Arg
1 5

<210> SEQ ID NO 417
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 417

Lys Cys Ser Thr Ser Ser Leu Leu Glu Ala Cys Thr Phe Arg
1 5 10

<210> SEQ ID NO 418
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 418

Lys Asp Ser Gly Phe Gln Met Asn Gln Leu Arg
1 5 10

<210> SEQ ID NO 419
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 419

Lys Pro Val Glu Glu Tyr Ala Asn Cys His Leu Ala Arg
1 5 10

<210> SEQ ID NO 420
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 420

Asn Leu Asn Glu Lys Asp Tyr Glu Leu Leu Cys Leu Asp Gly Thr Arg
1 5 10 15

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<210> SEQ ID NO 421
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 421

Asn Pro Asp Pro Trp Ala Lys
1 5

<210> SEQ ID NO 422
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 422

Ser Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro
1 5 10 15

Glu Pro Arg

<210> SEQ ID NO 423
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 423

Ser Val Ile Pro Ser Asp Gly Pro Ser Val Ala Cys Val Lys
1 5 10

<210> SEQ ID NO 424
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 424

Trp Cys Ala Val Ser Glu His Glu Ala Thr Lys
1 5 10

<210> SEQ ID NO 425
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 425

Tyr Leu Gly Glu Glu Tyr Val Lys
1 5

<210> SEQ ID NO 426
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 426

Phe Leu Pro Glu Gly Cys Gln Pro Leu Val Ser Ser Ala Val Asp Arg
1 5 10 15

<210> SEQ ID NO 427
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 427

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Glu Asp Phe Thr Ser Leu Ser Leu Val Leu Tyr Ser Arg
1               5                   10


<210> SEQ ID NO 428
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 428

Glu Phe Ser His Leu Gly Lys Glu Asp Phe Thr Ser Leu Ser Leu Val
1               5                   10                  15

Leu Tyr Ser Arg
            20


<210> SEQ ID NO 429
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 429

Glu Leu Ser Ser Phe Ile Asp Lys
1               5


<210> SEQ ID NO 430
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 430

Phe Pro Ser Gly Thr Phe Glu Gln Val Ser Gln Leu Val Lys
1               5                   10


<210> SEQ ID NO 431
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 431

Lys Phe Pro Ser Gly Thr Phe Glu Gln Val Ser Gln Leu Val Lys
1               5                   10                  15


<210> SEQ ID NO 432
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 432

Leu Pro Asp Ala Thr Pro Thr Glu Leu Ala Lys
1               5                   10


<210> SEQ ID NO 433
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 433

Arg Thr His Leu Pro Glu Val Phe Leu Ser Lys
1               5                   10


<210> SEQ ID NO 434
<211> LENGTH: 22
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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 434

Val Pro Thr Ala Asp Leu Glu Asp Val Leu Pro Leu Ala Glu Asp Ile
1 5 10 15

Thr Asn Ile Leu Ser Lys
20

<210> SEQ ID NO 435
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 435

Tyr Thr Phe Glu Leu Ser Arg
1 5

<210> SEQ ID NO 436
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 436

Ile Tyr Ile Ser Gly Met Ala Pro Arg
1 5

<210> SEQ ID NO 437
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 437

Met Asp Trp Leu Val Pro Ala Thr Cys Glu Pro Ile Gln Ser Val Phe
1 5 10 15

Phe Phe Ser Gly Asp Lys
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<210> SEQ ID NO 438
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<400> SEQUENCE: 438

Arg Val Asp Thr Val Asp Pro Pro Tyr Pro Arg
1 5 10

<210> SEQ ID NO 439
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<400> SEQUENCE: 439

Ser Ile Ala Gln Tyr Trp Leu Gly Cys Pro Ala Pro Gly His Leu
1 5 10 15

<210> SEQ ID NO 440
<211> LENGTH: 10
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 440

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Val Asp Thr Val Asp Pro Pro Tyr Pro Arg
1               5                   10


<210> SEQ ID NO 441
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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 441

Glu Glu Gln Asn Phe Val Val Gln Asn Glu Ile Asn Asn Met Ser Phe
1               5                   10                  15

Leu Thr Ala Asp Asn Lys
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<210> SEQ ID NO 442
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Ile Gly Ile Ser Trp Asn Lys Lys
1               5


<210> SEQ ID NO 443
<211> LENGTH: 10
<212> TYPE: PRT
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Phe Ser Gly Ser Ser Ser Gly Ala Asp Arg
1               5                   10


<210> SEQ ID NO 444
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 444

Tyr Leu Pro Cys Phe Gln Val Leu Pro Leu Asp Gln Gln Leu Val Leu
1               5                   10                  15

Val Arg


<210> SEQ ID NO 445
<211> LENGTH: 17
<212> TYPE: PRT
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<400> SEQUENCE: 445

His Cys Ile Val Leu Leu Gln Ile Ala Lys Asp Gln Ser Asn Ala Glu
1               5                   10                  15

Lys


<210> SEQ ID NO 446
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 446

Val Lys Leu Gln Asn Ala Glu Asn Asp Tyr Ile Asn Ala Ser Leu Val
1               5                   10                  15
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Asp Ile Glu Glu Ala Gln Arg
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<210> SEQ ID NO 447
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 447

Tyr Ile Leu Gly Ser Val Val Asp Ser Glu Lys Asn Tyr Val Asp Ala
1               5                   10                  15

Leu Lys Arg


<210> SEQ ID NO 448
<211> LENGTH: 16
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 448

Glu Ala Phe Lys Ser Ala Leu Met Ser Ser Tyr Trp Cys Ser Gly Lys
1               5                   10                  15


<210> SEQ ID NO 449
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 449

Glu Pro His Ile Ser Thr Leu Arg Lys Ile Leu Phe Glu Asp Phe Arg
1               5                   10                  15


<210> SEQ ID NO 450
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 450

Ile His Ile Glu Glu Asn Glu Asp Arg Asp Thr Gly Leu Glu Gln Arg
1               5                   10                  15

His Asn Lys


<210> SEQ ID NO 451
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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 451

Gly Leu Arg Ile His Glu Leu Ser Ser Asp Asp Tyr Ser Thr Glu Glu
1               5                   10                  15

Glu Ala Gln Thr Pro Asp Cys Ser Ile Thr Asp Phe Arg
            20                  25
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-continued

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<210> SEQ ID NO 452
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 452

Ile Gln Gln Gln Val Asp Ser Pro Met Asn Leu Lys
1               5                   10
```

We claim:

1. A method for diagnosing a neurological condition in a patient comprising:

a) obtaining a biological sample from said patient; and

b) evaluating said sample for the abundance of at least one biomarker selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NOs:1-440,

wherein the abundance of said at least one biomarker is indicative of a neurological condition.

2. The method of claim **1**, wherein the abundance of said biomarker is greater than that of a control sample.

3. The method of claim **1**, wherein said the abundance of said biomarker is less than that of a control sample.

4. The method of claim **1**, further comprising, prior to the evaluation step, harvesting low molecular weight peptides from said sample to generate at least one fraction comprising said peptides.

5. The method of claim **1**, wherein said biomarker is a low molecular weight protein complexed with a carrier protein.

6. The method of claim **5**, wherein said low molecular weight protein is further purified from said carrier protein.

7. The method of claim **6**, wherein said low molecular weight protein is digested and optionally sequenced.

8. The method of claim **1**, wherein said biological sample is blood, serum or plasma.

9. The method of claim **1**, wherein the evaluation step comprises an assay selected from the group consisting of mass spectrometry, immunoassay, immuno-mass spectrometry and suspension bead array.

10. The method of claim **9**, wherein said immunoassay is an enzyme linked immunosorbent assay (ELISA).

11. The method of claim **9**, wherein said mass spectrometry comprises tandem mass spectroscopy (MSMS).

12. The method of claim **1**, wherein the neurodegenerative disease is selected from the group consisting of

a) Alzheimer's disease;

b) mild cognitive impairment;

c) stable mild cognitive impairment;

d) progressive mild cognitive impairment;

e) vascular dementia;

f) angiopathy black holes;

g) cerebral amyloid angiopathy; and

h) microhemorrages.

13. The method of claim **1**, further comprising obtaining a neuroimage of brain microvasculopathy.

14. The method of claim **13**, wherein said neuroimage is obtained by a method selected from the group consisting of

a) susceptibility weighted imaging; and

b) magnetic resonance spectroscopy.

15. A method for diagnosing Alzheimer's disease in a patient comprising:

a) obtaining a biological sample from said patient; and

b) evaluating said sample for the abundance of at least one biomarker selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NOs:1, 3-13, 15, 16, 21, 22, 24-28, 31-33, 37-44, 56-59, 66-68, 93-101, 111-128, 143-153, 156-1170, 172-183, 263-279, 310-335, 348, 355-359, 362, 363, 365, 372, 373, 376-402, 406-426 and 436-44;

wherein the abundance of said at least one biomarker is indicative of Alzheimer's disease.

16. The method of claim **15**, wherein the marker is a peptide:

(i) associated with inflammation and has the amino acid sequence of SEQ ID NOs:28, 368-373 and 390-401;

(ii) associated with vitamin D metabolism and bone mineralization and has the amino acid sequence of SEQ ID NOs:331 and 427-435;

(iii) associated with coagulation and platelet activity and has the amino acid sequence of SEQ ID NOs:24, 102-110, 157-165, 350-354 and 376-389;

(iv) associated with the complement cascade and has the amino acid sequence of SEQ ID NOs:117-120, 129-138, 139-142 and 330;

(v) associated with globin activity and has the amino acid sequence of SEQ ID NOs:76-92, 144-153;

(vi) are glycosylated /associated with glyscosylation and has the amino acid sequence of SEQ ID NOs: 23, 50-55, 46-49, 174-183, 193-201 and 376-389;

(vii) associated with protease inhibition and has the amino acid sequence of SEQ ID NOs:50-55, 193-201 and 376-389;

(viii) associated with keratins and related proteins and has the amino acid sequence of SEQ ID NOs:154-155, 202-319 and 336-338;

(ix) associated with heme degradation and has the amino acid sequence of SEQ ID NOs:93-98;

(x) associated with pyruvate metabolism and has the amino acid sequence of SEQ ID NO:363;

(xi) associated with calcium related proteins and has the amino acid sequence of SEQ ID NOs:14, 372-373 and 402;

(xii) associated with defensin and has the amino acid sequence of SEQ ID NOs:355-358;

(xiii) associated with gelsolin and has the amino acid sequence of SEQ ID NOs:166-170;

(xiv) associated with vitronectin and has the amino acid sequence of SEQ ID NOs:436-440;

(xv) associated with profilin and has the amino acid sequence of SEQ ID NO:360;

(xvi) associated with thrombospondin and has the amino acid sequence of SEQ ID NO:405;

(xvii) associated with peroxiredoxin or alcohol dehydrogenase and has the amino acid sequence of SEQ ID NOs:340-347;

(xviii) associated with apolipoproteins and has the amino acid sequence of SEQ ID NOs:66-75;

(xix) associated with iron and copper metabolism and has the amino acid sequence of SEQ ID NOs:406-425; or

(xx) associated with NMDA receptor-related proteins and has the amino acid sequence of SEQ ID NOs:35-36.

17. The method of claim **15**, wherein said biomarker is a peptide having the amino acid sequence selected from the group consisting of SEQ ID NOs:93-98, 139-142, 166-170, 348, 355-358, 402 and 406-425.

18. The method of claim **15**, wherein said the abundance of said biomarker is less than that of a control sample.

19. The method of claim **15**, wherein the abundance of said biomarker is greater than that of a control sample.

20. The method of claim **15**, further comprising obtaining a neuroimage of brain microvasculopathy associated with Alzheimer's Disease.

21. The method of claim **20**, wherein said neuroimage is obtained by a method selected from the group consisting of

a) susceptibility weighted imaging; and

b) magnetic resonance spectroscopy.

22. The method of claim **15**, further comprising, prior to the evaluation step, harvesting low molecular weight peptides from said sample to generate at least one fraction comprising said peptides.

23. The method of claim **15**, wherein said biomarker is a low molecular weight protein complexed with a carrier protein.

24. The method of claim **23**, wherein said low molecular weight protein is further purified from said carrier protein.

25. The method of claim **24**, wherein said low molecular weight protein is digested and optionally sequenced.

26. The method of claim **15**, wherein said biological sample is blood, serum or plasma.

27. The method of claim **15**, wherein the evaluation step comprises an assay selected from the group consisting of mass spectrometry, immunoassay, immuno-mass spectrometry and suspension bead array.

28. The method of claim **27**, wherein said immunoassay is an enzyme linked immunosorbent assay (ELISA).

29. The method of claim **27**, wherein said mass spectrometry comprises tandem mass spectroscopy (MSMS).

30. A method for diagnosing mild cognitive impairment in a patient comprising:

a) obtaining a biological sample from said patient; and

b) evaluating said sample for the abundance of at least one biomarker selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NOs:2, 4, 14, 17, 23, 29, 34, 45-55, 60-65, 69-92, 102-110, 129-142, 154, 155, 171, 184-191, 193-226, 248-279, 281-320, 333, 336-347, 349-354, 360, 361, 364, 366-371, 374, 375, 403-405 and 427-435;

wherein the abundance of said at least one biomarker is indicative of mild cognitive impairment.

31. The method of claim **30**, wherein said the abundance of said biomarker is less than that of a control sample.

32. The method of claim **30**, wherein the abundance of said biomarker is greater than that of a control sample.

33. The method of claim **30**, further comprising obtaining a neuroimage of brain microvasculopathy associated with Alzheimer's Disease.

34. The method of claim **33**, wherein said neuroimage is obtained by a method selected from the group consisting of

a) susceptibility weighted imaging; and

b) magnetic resonance spectroscopy.

35. The method of claim **30**, further comprising, prior to the evaluation step, harvesting low molecular weight peptides from said sample to generate at least one fraction comprising said peptides.

36. The method of claim **30**, wherein said biomarker is a low molecular weight protein complexed with a carrier protein.

37. The method of claim **36**, wherein said low molecular weight protein is further purified from said carrier protein.

38. The method of claim **37**, wherein said low molecular weight protein is digested and optionally sequenced.

39. The method of claim **30**, wherein said biological sample is blood, serum or plasma.

40. The method of claim **30**, wherein the evaluation step comprises an assay selected from the group consisting of mass spectrometry, immunoassay, immuno-mass spectrometry and suspension bead array.

41. The method of claim **40**, wherein said immunoassay is an enzyme linked immunosorbent assay (ELISA).

42. The method of claim **40**, wherein said mass spectrometry comprises tandem mass spectroscopy (MSMS).

43. A method for diagnosing brain microhemorrhages in a patient comprising:

a) obtaining a biological sample from said patient; and

b) evaluating said sample for the abundance of at least one biomarker selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NOs: 441-452

wherein the abundance of said at least one biomarker is indicative of microhemorrhages.

44. The method of claim **43**, wherein said the abundance of said biomarker is less than that of a control sample.

45. The method of claim **43**, wherein the abundance of said biomarker is greater than that of a control sample.

46. The method of claim **43**, further comprising obtaining a neuroimage of brain microvasculopathy associated with Alzheimer's Disease.

47. The method of claim **46**, wherein said neuroimage is obtained by a method selected from the group consisting of

a) susceptibility weighted imaging; and

b) magnetic resonance spectroscopy.

48. The method of claim **43**, further comprising, prior to the evaluation step, harvesting low molecular weight peptides from said sample to generate at least one fraction comprising said peptides.

49. The method of claim **43**, wherein said biomarker is a low molecular weight protein complexed with a carrier protein.

50. The method of claim **49**, wherein said low molecular weight protein is further purified from said carrier protein.

51. The method of claim **50**, wherein said low molecular weight protein is digested and optionally sequenced.

52. The method of claim **43**, wherein said biological sample is blood, serum or plasma.

53. The method of claim **43**, wherein the evaluation step comprises an assay selected from the group consisting of mass spectrometry, immunoassay, immuno-mass spectrometry and suspension bead array.

54. The method of claim **53**, wherein said immunoassay is an enzyme linked immunosorbent assay (ELISA).

55. The method of claim **53**, wherein said mass spectrometry comprises tandem mass spectroscopy (MSMS).

56. An antibody specific for a peptide selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NOs:1-440.

57. The antibody of claim **56**, wherein said antibody is a monoclonal antibody, polyclonal antibody or chimeric antibody.

58. A kit for detecting a neurological condition in a patient, comprising at least one antibody of claim **56** and instructions for the storage or use thereof.

* * * * *

专利名称(译)	神经系统疾病的生物标志物		
公开(公告)号	US20100159486A1	公开(公告)日	2010-06-24
申请号	US12/513032	申请日	2007-11-01
申请(专利权)人(译)	乔治·梅森知识产权，INC. 罗马琳达大学		
当前申请(专利权)人(译)	乔治·梅森知识产权，INC. 罗马琳达大学		
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CPC分类号	G01N33/6896 G01N2800/2871 G01N2800/2821		
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外部链接	Espacenet USPTO		

摘要(译)

已发现低分子量（LMW）肽指示神经病症，例如阿尔茨海默氏病（AD），认知障碍和脑微血管。评估患者样品中是否存在这种LMW肽是检测神经病症和监测疾病进展的有效手段。LMW肽特别适用于在早期阶段检测神经病症而无需侵入性操作。