

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
11 December 2008 (11.12.2008)

PCT

(10) International Publication Number
WO 2008/148493 A2

(51) International Patent Classification:
G01N 33/68 (2006.01)

(21) International Application Number:
PCT/EP2008/004238

(22) International Filing Date: 28 May 2008 (28.05.2008)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
07109522.8 4 June 2007 (04.06.2007) EP

(71) Applicant (for all designated States except US): **F. HOFFMAN-LA ROCHE AG** [CH/CH]; Grenzacherstrasse 124, CH-4070 Basel (CH).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **BERNDT, Peter** [DE/CH]; Mittlere Strasse 138, CH-4056 Basel (CH). **BOHRMANN, Bernd** [DE/CH]; Mohrhaldenstrasse 166B, CH-4125 Riehen (CH).

(74) Agent: **KUENG, Peter**; Grenzacherstrasse 124, CH-4070 Basel (CH).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM,

AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, NO, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

— of inventorship (Rule 4.17(iv))

Published:

— without international search report and to be republished upon receipt of that report
— with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

(54) Title: ANNEXIN A5 AND ANNEXIN A6 AS BIOMARKTER FOR ALZHEIMER'S DISEASE

(57) Abstract: The present invention relates to a method for assessing Alzheimer's disease in vitro comprising measuring in a sample (e.g. body fluid) the level of one or more proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof, wherein an altered level of said one or more proteins, or a variant thereof, is indicative that said individual suffers from Alzheimer's Disease. Furthermore, the present invention relates to a method for monitoring the progression of the Alzheimer's disease in vitro comprising measuring in a sample (e.g. body fluid) the level of one or more proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof, wherein an altered level of said one or more proteins, or a variant thereof, compared with an earlier measurement of the level of said one or more proteins, or a variant thereof, is indicative for the progression of Alzheimer's disease.



WO 2008/148493 A2

ANNEXIN A5 AND ANNEXIN A6 AS BIOMARKER FOR ALZHEIMER'S DISEASE

Alzheimer's disease (AD) is a complex neurodegenerative dementing illness. It is histopathologically characterized by the deposition of extracellular amyloid plaques mainly consisting of amyloid- β protein ($A\beta$) and the intracellular accumulation of hyperphosphorylated tau into neurofibrillary tangles.

5 In clinical practice, the diagnosis of AD is still largely based on cognitive tests and behavioral analysis. One of the most promising sources of biomarkers in AD is the cerebrospinal fluid (CSF). The CSF is, compared to the brain, more easily accessible and is in direct contact with the extracellular space of the central nervous system where biochemical changes in the brain could potentially be reflected. Therefore, a number of
10 putative biological markers of AD have been suggested, like CSF total tau (Andreasen, N., Vanmechelen, E., Van de Voorde, A., Davidsson, P., Hesse, C., Tarvonen, S., Raiha, I., Sourander, L., Winblad, B., and Blennow, K. (1998) J Neurol Neurosurg Psychiatry 64, 298-305) and phospho-tau levels (Andreasen, N., Sjogren, M., and Blennow, K. (2003) World J Biol Psychiatry 4, 147-155), CSF A β levels (Ida, N., Hartmann, T., Pantel, J., Schroder, J., Zerfass, R., Forstl, H., Sandbrink, R., Masters, C. L., and Beyreuther, K.
15 (1996) J Biol Chem 271, 22908-22914) or a combination thereof (Shoji, M., Matsubara, E., Kanai, M., Watanabe, M., Nakamura, T., Tomidokoro, Y., Shizuka, M., Wakabayashi, K., Igeta, Y., Ikeda, Y., Mizushima, K., Amari, M., Ishiguro, K., Kawarabayashi, T., Harigaya, Y., Okamoto, K., and Hirai, S. (1998) J Neurol Sci 158, 134-140). Yet, a
20 definitive diagnosis of AD can still only be made by a postmortem assessment of brain neuropathology and there is clearly a need for a reliable biomarker for AD.

Therefore, the present invention provides a method for assessing Alzheimer's Disease in vitro comprising measuring in a sample the level of one or more proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof in a sample
25 collected from an individual, wherein an altered level of said one or more proteins, or a variant thereof, is indicative that said individual suffers from Alzheimer's Disease.

Preferably, the level of said one or more proteins, or variants thereof, is increased in individuals suffering from Alzheimer's disease.

A sample may be a brain tissue sample (e.g. gray matter brain tissue) or a body fluid
30 sample. A body fluid is e.g. blood (whole blood, serum, plasma) or cerebrospinal fluid

(CSF). Preferably, the sample is a body fluid sample. More preferably, protein of interest is detected in CSF or blood. Methods for collecting tissue or fluid sample from an individual are well known to the skilled in the art.

The term "variants" in this context relates to proteins or peptides substantially similar to said proteins. The term "substantially similar" is well understood by the person skilled in the art. In particular, a variant may be an isoform or allele which shows amino acid exchanges compared to the amino acid sequence of the most prevalent peptide isoform in the human population. Preferably, such a substantially similar peptide has a sequence similarity to the most prevalent isoform of the protein or peptide of at least 80%, preferably at least 85%, more preferably at least 90%, most preferably at least 95%. Substantially similar are also precursor proteins and degradation products, e.g. proteolytic degradation products, which are still recognized by the diagnostic means or by ligands directed against the respective full-length protein or peptide. The term "variants" is also meant to relate to splice variants.

The term "variant" also relates to a post-translationally modified protein such as glycosylated protein. A "variant" is also a peptide which has been modified after collection of the sample, for example by covalent or non-covalent attachment of a label, particularly a radioactive or fluorescent label, to the protein.

The term "proteins of interest" as used herein refers to Annexin A5 (SEQ. ID NO: 1) or Annexin A6 (SEQ. ID NO: 2), or a variant thereof. Annexins are a family of structurally related proteins whose common property is calcium-dependent binding to phospholipids.

An altered protein level is a level of protein which is either decreased or increased compared to a reference level. A reference level can be a level measured in one or more healthy individual or a level measured in a sample collected at an earlier point in time.

The invention also includes the measuring of Annexin A5 and Annexin A6 in combination. Furthermore, Annexin A5 and/or Annexin A6 can be measured in combination with other biomarkers. The combined measurement can be simultaneously or non-simultaneously.

The present invention further provides a method for monitoring the progression of the Alzheimer's disease in vitro comprising measuring the level of one or more proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof in a sample collected from an individual, wherein an altered level of said one or more proteins, or a variant thereof, compared with an earlier measurement of the level of said one or more

proteins, or a variant thereof, is indicative for the progression of Alzheimer's Disease of said individual.

The sample can be a brain tissue sample (preferably, gray matter brain tissue) or a body fluid sample. Preferably, the sample is a body fluid sample. More preferably, the sample is cerebrospinal fluid (CSF) or blood sample.

The term "progression" of Alzheimer's disease refers to alteration of the stage of the disease. The stage of Alzheimer's disease is usually described in Braak stages. Braak has described six stages in Alzheimer's disease, the so-called Braak Stages I - VI, wherein Braak Stage I is the weakest manifestation of the disease and Braak stage VI is the most advanced stage (see H. Braak, E. Braak: Neuropathological staging of Alzheimer-related changes. *Acta Neuropathologica*, 1991, 82: 239-259; H. Braak, E. Braak, J. Bohl: Staging of Alzheimer-related cortical destruction. *European Neurology*, Basel, 1993, 33: 403-408). An alteration from e.g., Braak stage II to Braak stage IV means that the disease became worse. An alteration from e.g. Braak stage IV to Braak stage II means in improvement of the patient's condition.

If a protein is down-regulated in an AD patient, the measured protein level will further decrease (compared with an earlier measurement of the protein level) when the disease becomes more severe or worse. If a protein is up-regulated protein in an AD patient, the measured protein level will increase (compared with an earlier measurement of the protein level) when the disease becomes more severe. An alteration from e.g. Braak stage II to Braak stage IV means that the disease became worse. An alteration from e.g. Braak stage IV to Braak stage II means in improvement of the patient's condition. The above described method may also be used to test the efficacy of a treatment for Alzheimer's disease.

The term "earlier measurement" of the level of a protein as used herein refers to a measured level of a protein, or variant thereof, in a Alzheimer patient to an earlier time point.

In a preferred embodiment, a relative increase of the level of one or more proteins of interest indicates that the disease becomes worse and a relative decrease of the level of one or more proteins of interest indicates that the disease becomes less severe. The term "relative increase" as used herein refers to the comparative difference between a first measurement of a protein, or a variant thereof and second measurement of the protein, or a variant thereof, wherein the measured level of the second measurement is higher than the level of the first measurement. The term "relative decrease" means the

comparative difference between a first measurement of the level of a protein, or a variant thereof, and a second measurement of the protein, or a variant thereof, wherein the measured level of the second measurement is lower than the protein level of the first measurement.

5

Furthermore, the present invention provides the use of one or more proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof, as biomarker for Alzheimer's disease and/or for the progression of Alzheimer's disease in an individual.

The term "biomarker" as used herein refers to molecules in an individual which are
10 differentially present (i.e. present in increased or decreased levels) depending on presence or absence of a certain condition, disease, or complication. In particular, biochemical markers are gene expression products which are differentially present (e.g. through increased or decreased level of expression or turnover) in presence or absence of a certain condition, disease, or complication. A biomarker of the invention is a biochemical
15 marker. A biochemical marker is a protein, polypeptide or peptide. The level of a suitable biomarker can indicate the presence or absence of a particular condition, disease, or risk, and thus allow diagnosis or determination of the condition, disease or risk.

The term "normal level" as used herein refers to the normal range of the level of protein of interest in a body fluid sample of a control. A control is one or more
20 individuals not suffering from Alzheimer's disease. Preferably, the number of individuals is higher than 100, more preferably more than 500, most preferably more than 1000. The normal range is determined by methods well known to the skilled person in the art. A preferred method is for example to determine the range of the values between quantile 2.5 and quantile 97.5, which leaves 5% of "normal" values outside the normal range or in
25 other words, it covers 95% of all values of the control.

The pathological status is defined as deviation from the normal status. According to the invention this pathological status is indicated by a decreased or increased level of a biomarker. The term "decreased level" as used herein refers to the level of protein of interest in a body fluid sample which is significantly lower than the normal level.
30 Significantly lower means that the level is lower and that the difference to the normal level is statistically relevant ($p \leq 0.05$, preferably, $p \leq 0.01$). The term "increased level" as used herein refers to the level of protein of interest in a body fluid sample which is significantly higher than the normal level. Significantly higher means that the level is higher and that the difference to the normal level is statistically relevant ($p \leq 0.05$,
35 preferably, $p \leq 0.01$).

The person skilled in the art is familiar with different methods of measuring the level of a peptide or polypeptide. The term "level" relates to amount or concentration of a peptide or polypeptide in an individual or a sample taken from an individual.

In the context of the present invention, amount also relates to concentration. It is
5 evident, that from the total amount of a substance of interest in a sample of known size, the concentration of the substance can be calculated, and vice versa.

The term "measuring" according to the present invention relates to determining the amount or concentration, preferably semi-quantitatively or quantitatively. Measuring can be done directly or indirectly. Indirect measuring includes measuring of cellular
10 responses, bound ligands, labels, or enzymatic reaction products.

Measuring can be done according to any method known in the art. Preferred methods are described in the following:

In a preferred embodiment, the method for measuring the level of a protein of interest, comprises the steps of (a) contacting a cell with the protein for an adequate
15 period of time which is capable of a cellular response to the protein, (b) measuring the cellular response.

In another preferred embodiment, the method for measuring the level of a polypeptide of interest comprises the steps of (a) contacting a protein with a specifically binding ligand, (b) (optionally) removing non-bound ligand, (c) measuring the amount
20 of bound ligand.

Preferably, the protein is contained in a body fluid sample, and the amount of the protein in the sample is measured.

A body fluid may be blood (whole blood, blood serum, blood plasma) and cerebrospinal fluid. Preferably, a body fluid is cerebrospinal fluid (CSF). Samples of body
25 fluids can be obtained by any method known in the art.

If necessary, the samples may be further processed. Particularly, proteins may be purified from the sample according to methods known in the art, including filtration, centrifugation, or extraction methods such as chloroform/phenol extraction.

For measuring cellular responses, the sample or processed sample is added to a cell
30 culture and an internal or external cellular response is measured. The cellular response may include the expression of a reporter gene or the secretion of a substance, e.g., a protein, peptide, polypeptide, or a small molecule.

Other preferred methods for measurement may include measuring the amount of a ligand binding specifically to the protein, peptide or polypeptide of interest. Binding according to the present invention includes both covalent and non-covalent binding.

A ligand according to the present invention can be any protein, peptide, 5 polypeptide, nucleic acid, or other substance binding to the protein of interest. It is well known that proteins, if obtained or purified from the human or animal body, can be modified, e.g., by glycosylation. A suitable ligand according to the present invention may bind the protein exclusively or additionally via such sites.

Preferably, the ligand should bind specifically to the protein to be measured. 10 "Specific binding" according to the present invention means that the ligand should not bind substantially to ("cross-react" with) another protein or substance present in the sample investigated. Preferably, the specifically bound protein or isoform should be bound with at least 3 times higher, more preferably at least 10 times higher and even more preferably at least 50 times higher affinity than any other relevant protein, peptide 15 or polypeptide.

Non-specific binding may be tolerable, particularly if the investigated protein can still be distinguished and measured unequivocally, e.g., according to its size (such as on a Western Blot), or by its relatively higher abundance in the sample.

Binding of the ligand can be measured by any method known in the art. Preferably, 20 the method is semi-quantitative or quantitative. Suitable methods are described in the following.

First, binding of a ligand may be measured directly, e.g., by NMR or surface plasmon resonance.

Second, the ligand may be coupled covalently or non-covalently to a label allowing 25 detection and measurement of the ligand.

Labeling may be done by direct or indirect methods. Direct labeling involves coupling of the label directly (covalently or non-covalently) to the ligand. Indirect labeling involves binding (covalently or non-covalently) of a secondary ligand to the first ligand. The secondary ligand should specifically bind to the first ligand. Said secondary 30 ligand may be coupled with a suitable label and/or be the target (receptor) of tertiary ligand binding to the secondary ligand. The use of secondary, tertiary or even higher order ligands is often used to increase the signal. Suitable secondary and higher order ligands may include antibodies, secondary antibodies, and the well-known streptavidin-biotin system (Vector Laboratories, Inc.)

The ligand may also be "tagged" with one or more tags as known in the art.

Such tags may then be targets for higher order ligands. Suitable tags include biotin, digoxigenin, His-Tag, Glutathion-S-Transferase, FLAG, GFP, myc-tag, influenza A virus haemagglutinin (HA), maltose binding protein, and the like. In the case of a peptide or
5 polypeptide, the tag is preferably at the N-terminus and/or C-terminus.

Suitable labels are any labels detectable by an appropriate detection method. Typical labels include gold particles, latex beads, acridan ester, luminol, ruthenium, enzymatically active labels, radioactive labels, magnetic labels ("e.g., magnetic beads", including paramagnetic and superparamagnetic labels), and fluorescent labels.

10 Enzymatically active labels include e.g., horseradish peroxidase, alkaline phosphatase, beta-Galactosidase, Luciferase, and derivatives thereof. Suitable substrates for detection include di-amino-benzidine (DAB), 3,3'-5,5'-tetramethylbenzidine, NBT-BCIP (4-nitro blue tetrazolium chloride and 5-bromo-4-chloro-3-indolyl-phosphate, available as readymade stock solution from Roche Diagnostics), CDP-10 Star™
15 (Amersham Biosciences), ECF™ (Amersham Biosciences). A suitable enzyme-substrate combination may result in a colored reaction product, fluorescence or chemoluminescence, which can be measured according to methods known in the art (e.g., using a light-sensitive film or a suitable camera system).

Typical fluorescent labels include fluorescent proteins (such as GFP and its
20 derivatives), Cy3, Cy5, Texas Red, Fluorescein, and the Alexa dyes (e.g. Alexa 568). Further fluorescent labels are available, e.g., from Molecular Probes (Oregon). Also the use of quantum dots as fluorescent labels is contemplated.

Typical radioactive labels include 35S, 125I, 32P, 33P and the like. A radioactive label can be detected by any method known and appropriate, e.g. a light-sensitive film or
25 a phosphor imager.

Suitable measurement methods according the present invention also include precipitation (particularly immunoprecipitation), electrochemiluminescence (electro-generated chemiluminescence), RIA (radioimmunoassay), ELISA (enzyme-linked immunosorbent assay), sandwich enzyme immune tests, electrochemiluminescence
30 sandwich immunoassays (ECLIA), dissociation-enhanced lanthanide fluoro immuno assay (DELFA), scintillation proximity assay (SPA), turbidimetry, nephelometry, latexenhancedturbidimetry or nephelometry, solid phase immune tests, and mass spectrometry such as SELDI-TOF, MALDI-TOF, or capillary electrophoresis-mass spectrometry (CEMS).

Further methods known in the art (such as gel electrophoresis, e.g. 2D gel electrophoresis, SDS polyacrylamid gel electrophoresis (SDS-PAGE), Western Blotting), can be used alone or in combination with labelling or other detection methods as described above.

5 Preferred ligands include antibodies, nucleic acids, proteins, peptides or polypeptides, and aptamers, e.g., nucleic acid or peptide aptamers. Methods to such ligands are well-known in the art. For example, identification and production of suitable antibodies or aptamers is also offered by commercial suppliers. The person skilled in the art is familiar with methods to develop derivatives of such ligands with higher affinity or
10 specificity. For example, random mutations can be introduced into the nucleic acids, proteins, peptides or polypeptides. These derivatives can then be tested for binding according to screening procedures known in the art, e.g., phage display. Aptamers are chemically synthesized (usually short) strands of oligonucleotides (DNA or RNA) that can adopt highly specific three-dimensional conformations. Aptamers are designed to
15 have appropriate binding affinities and specificities towards certain target molecules.

The term "antibody" as used herein includes both polyclonal and monoclonal antibodies, as well as any modifications or fragments thereof, such as Fv, Fab and F(ab)₂ fragments that are capable of binding antigen or hapten.

The present invention also relates to a kit comprising a means or an agent for
20 measuring one or more proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof.

Such means or agent may be any suitable means or agent known to the person skilled in the art. Examples for such means or agents as well as methods for their use have been given in this specification. For example, a suitable agent may be any kind of ligand
25 or antibody specific for measuring said biomarkers. The kit may also comprise any other components deemed appropriate in the context of measuring the level(s) of the respective biomarkers, such as suitable buffers, filters, etc.

Optionally, the kit may additionally comprise a user's manual for interpreting the results of any measurement(s) with respect to determining whether an individual suffers
30 from Alzheimer's Disease and/or monitoring the progression of Alzheimer's Disease of an individual. Particularly, such manual may include information about what measured level corresponds to a decreased level or increased level.

The proteins of interest may also be used as target. Therefore, the present invention provides a method of screening for a compound which interacts with one or more

proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof. Such methods are well known in the art.

A suitable method is for example the method of screening for a compound which interacts with one or more proteins of the group consisting of Annexin A5 and Annexin
5 A6, or a variant thereof, comprising a) contacting said one or more proteins, or a variant thereof with a compound or a plurality of compounds under conditions which allow interaction of said compound or a plurality of compounds with said one or more proteins, or a variant thereof; and b) detecting the interaction between said compound or plurality of compounds with said one or more proteins, or variants thereof.

10 The protein(s) of interest may be immobilized prior step a) or between step a) and step b).

Having now generally described this invention, the same will become better understood by reference to the specific examples, which are included herein for purpose of illustration only and are not intended to be limiting unless otherwise specified, in
15 connection with the following figures.

Figures

Figure 1 shows histograms of protein identifications in dependence of the rank correlation P-value for the data with randomized label. X-axis: the distribution of log(P)-values; black: real data with randomized labels; white: simulated data set with randomized
5 labels. The high rank correlation values cannot be produced by chance in a dataset that contains all the real data that has randomly re-labeled.

Figure 2 shows a graphical representation of the Braak-stage dependent increase of peptide counts of Annexin A5. (y-axis: number of peptide counts, x-axis: Braak stage).

Figure 3 shows a graphical representation of the Braak-stage dependent increase of
10 peptide counts of Annexin A6. (y-axis: number of peptide counts, x-axis: Braak stage).

Examples:

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated.

5 Example 1:

Sample preparation

Grey matter brain tissue from Alzheimer patients with different Braak Stages (II; IV; V; VI) two in each case and grey matter brain tissue of two healthy controls, were investigated. For each brain, the following sample preparation procedure was carried out:

- 10 1. Grey matter tissue from frozen brain sections of the occipital association gyrus was mechanically dissected, and dried.
2. The tissue was solubilized in 2% SDS; 66mM Na₂CO₃,
3. A BCA Protein concentration test was performed to determine the protein concentration of each sample.
- 15 4. Proteinseperation step: After reduction and alkylation 38 µg Protein per Sample was loaded on a 4-12% Bis Tris Gel

Each Protein lane was cut into 19 sections. Each section was digested using an established in-gel digest procedure by which tryptic digests of the proteins were obtained and dried in the lyophilisator.

- 20 5. A fused silica column (75µm ID, 280 µm OD) packed with Magic C18 material was used as both the LC separation column and the electrospray tip.

6. The Peptides of each gel section were injected twice. They were concentrated on a C18 Trap Colomn and separated via nanoflow over the Magic C18 column by a Dionex Ultimate HPLC.

- 25 7. The separated peptides were analyzed on the fly by a Thermo LTQ Iontrap. Each MS Scan was set to acquire a full mass spectrum between 400 and 1500 Da followed by seven MS/MS scans between 400 and 2000 Da of the top seven ions from the preceding MS scan. Relative collision energy for CID was set to 35%. Dynamic exclusion was enabled with a repeat count of 2, a repeat duration of 60 seconds, and an exclusion

duration of 60 seconds. Altogether 38 LC-MS runs were performed for each Sample. Each run took 150 minutes.

Data Evaluation

5 Mass spectra data annotation

The acquired MS/MS spectra were searched by SEQUEST against a Human Genome derived Protein Database (humangp) containing more than 48000 different proteins, pig trypsin peptides were added as well. All accepted peptides had to have a Δ cn of at least 0.1 and a xCorr of 2.0 for +1 2.5 for +2 and 3.2 for +3 charges. At least two
10 *different peptides passing the above filter criteria have to be seen to consider a protein as a valid identification.* Furthermore only proteins which have been identified in both duplicates have been taken into account.

Peptide counts as protein quantifier

It has been attempted to use counts of detected peptides per protein identity as
15 *indicators for protein quantity. This approach has been applied for proteomics data generated from a mouse model of AD, and a similar approach has been recently published in peer-reviewed literature (Quantitative methods for proteomics data analysis: Lu P, Vogel C, Wang R, Yao X, Marcotte EM. Absolute protein expression profiling estimates the relative contributions of transcriptional and translational regulation. Nat*
20 *Biotechnol. 2007 Jan. 25(1):117-24; Benjamini, Yoav; Hochberg, Yosef (1995). "Controlling the false discovery rate: a practical and powerful approach to multiple testing". Journal of the Royal Statistical Society, Series B (Methodological) 57 (1): 289-300.). An estimation of the false discovery rate was used by simulation of random datasets by permutation of the labels in the experimental data. Marker candidates have to have P-*
25 *values larger than 10^{-2.5} and need to be at least one standard deviation separated from the bulk of the random P-values distribution as calculated by the FDR simulation.*

A reasonable estimate for a FDR statistic requires at least three samples in order to be able to estimate P-Values for T statistics. Thus, the samples per group could not be compared (as each group contains exactly two samples). However, the light could be
30 *combined to moderate AD pathology and the severe pathology groups to try to find the differences caused by disease severity.*

Rank order changes as robust estimator of changes

While peptide counts are a useful tool for the elucidation of expression differences in sets of experiments that have appropriate sample numbers, the experiment was conducted to include few repeats but many (four) categories of severity. Proteins that are robustly changing with disease severity were mainly interesting.

5 Spearman-rank order correlation coefficients were used to estimate the connection between Braak stage and protein expression (as estimated by peptide counts). The significance of a non-zero value of the Spearman rank order correlation coefficient were given by a t-Statistic (Rank order statistics: Press WH, Teukolky SA, Vetterling WT, Flannery BP. Numerical recipes in C - Second Edition. p 609-656, Cambridge University
10 Press 1992), and as usual, a simulation of the dataset with randomized labels allowed estimating an empirical false discovery rate at a given significance level (see Figure 1).

Results:

The histogram for the distribution of $\log(P)$ -value for the real data and a simulated
15 data set with randomized labels showed that $\log(P)$ values above 4 are almost absent from the randomly labeled dataset (figure 1). A protein with a $\log(P)$ value above 4 is therefore considered as significant.

Protein	Sequence	$\log(P)$
Annexin A5	SEQ. ID NO: 1	6.47
Annexin A6	SEQ. ID NO: 2	4.06

Table 1: $\log(P)$ values of Annexin A5 and Annexin A6.

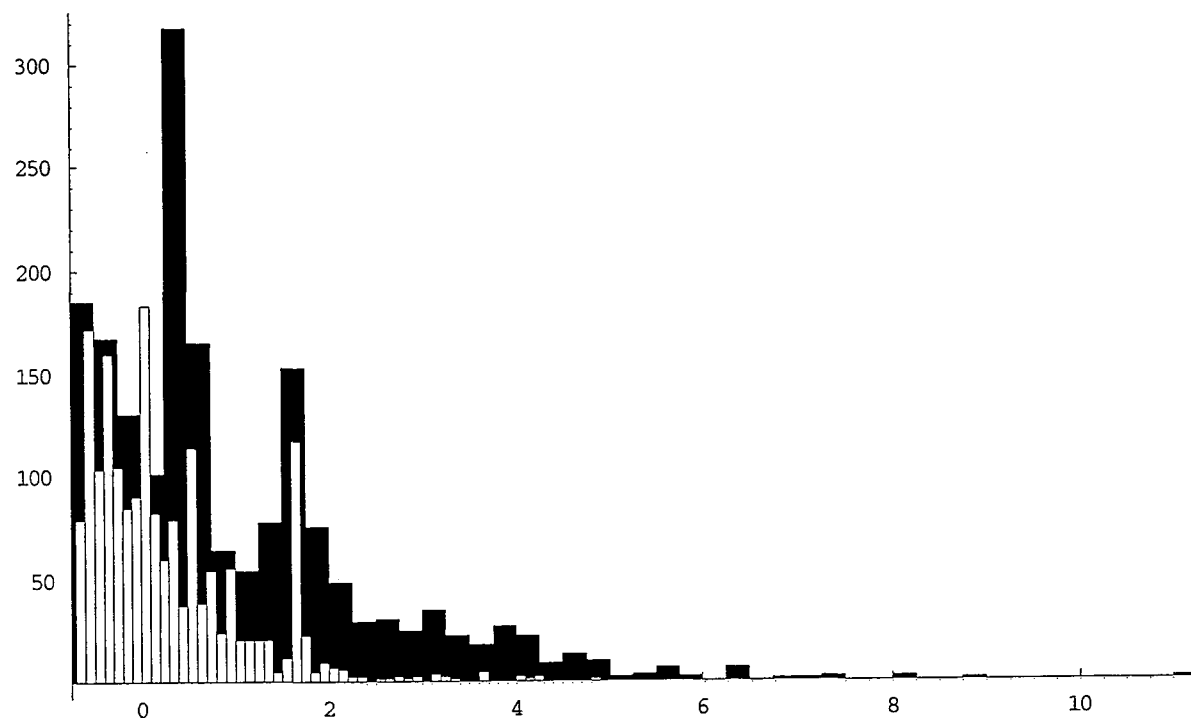
The peptide counts show a stage-dependent increase (see Figures 2 and 3).

20 The rather low $\log(P)$ value of Annexin A6 is caused through a single outlier and the manual inspection of the acquired data showed that the protein is significantly increased according to the disease state (see figures 3).

Claims

1. An in vitro method for assessing Alzheimer's disease comprising measuring in a sample the level of one or more proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof in a sample collected from an individual, wherein
5 an altered level of said one or more proteins, or a variant thereof, is indicative that said individual suffers from Alzheimer's disease.
2. The method according to claim 1 wherein the level of said one or more proteins, or a variant thereof, is increased.
3. An in vitro method for monitoring the progression of the Alzheimer's disease
10 comprising measuring the level of one or proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof in a sample collected from an individual, wherein an altered level of said one or more proteins, or a variant thereof, compared with an earlier measurement of the level of said one or more proteins, or a variant thereof, is indicative for the progression of Alzheimer's
15 Disease of said individual.
4. The method according to claim 3, wherein the level of Tubulin B6 or a variant thereof, is increased compared with the earlier measured level.
5. The method according to any one of the claims 1 to 4, wherein the sample is a body fluid sample, preferably a cerebrospinal fluid sample or a blood sample.
- 20 6. Use of one or more proteins of the group consisting of Annexin A5 and Annexin A6, or a variant thereof as biomarker for Alzheimer's Disease and/or for the progression of Alzheimer's Disease in an individual.
7. A kit comprising a means or an agent for measuring of Annexin A5 or Annexin A6, or a variant thereof.
- 25 8. The kit according to claim 7 wherein the kit further comprises a user's manual for interpreting the results of any measurement with respect to determining the risk of an individual suffering from Alzheimer's disease and/or monitoring the progression of Alzheimer's disease of an individual.
9. Use of a kit according to claim 7 or 8 in a method according to any one of claims 1
30 to 5.
10. Methods, uses and kits substantially as herein before described especially with reference to the foregoing examples***

Figure 1:



5 Figure 2

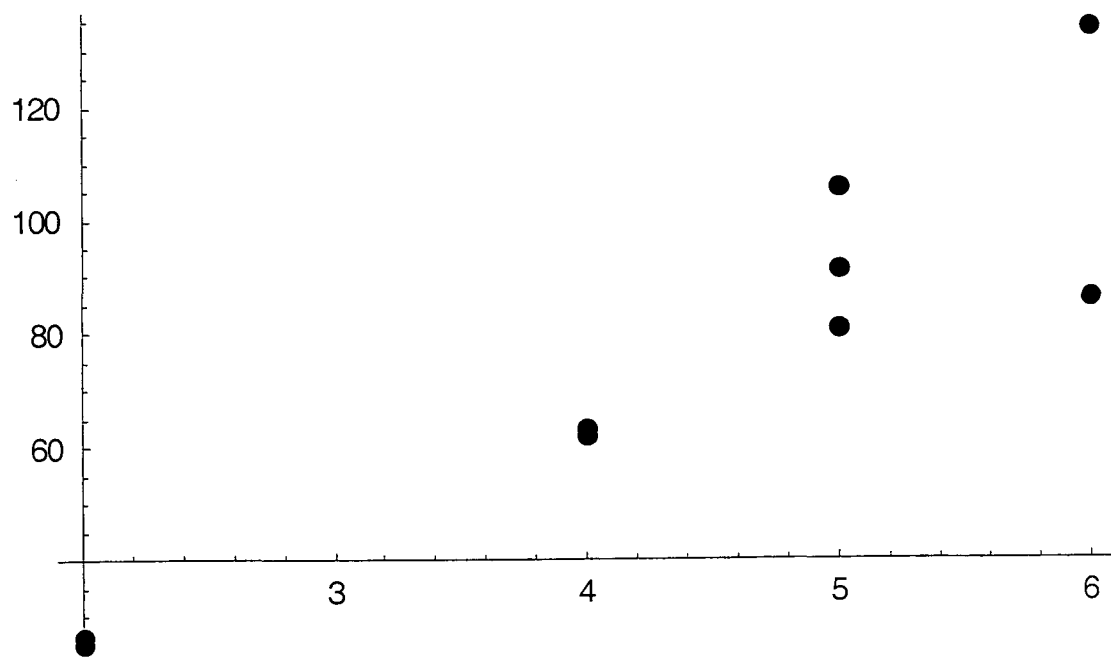


Figure 3

