

(51) International Patent Classification:
G01N 33/554 (2006.01)(21) International Application Number:
PCT/US2015/048504(22) International Filing Date:
4 September 2015 (04.09.2015)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/046,475 5 September 2014 (05.09.2014) US(71) Applicant: SYSTEM OF SYSTEMS ANALYTICS,
INC. [US/US]; 11250 Waples Mill Road, Suite 300, Fair-
fax, Virginia 22030 (US).(72) Inventors: CLIFF, Richard, O.; c/o SYSTEM OF SYS-
TEMS ANALYTICS, INC., Suite 300, Fairfax, Virginia
22030 (US). FLOWER, Robert W.; c/o SYSTEM OF
SYSTEMS ANALYTICS, INC., Suite 300, Fairfax, Vir-
ginia 22030 (US). MATVEEVA, Evgenia G.; c/o SYS-
TEM OF SYSTEMS ANALYTICS, INC., Suite 300, Fair-
fax, Virginia 22030 (US).(74) Agents: BRINCKERHOFF, Courtenay et al.; Foley &
Lardner LLP, 3000 K Street NW, Suite 600, Washington,
District of Columbia 20007 (US).(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, BN, BR, BW, BY,
BZ, CA, CH, CL, 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, IR, IS, JP, KE, KG, KN, KP, KR,
KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG,
MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM,
PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC,
SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, 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, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ,
TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU,
TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE,
DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU,
LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK,
SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

- as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))
- as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))

[Continued on next page]

(54) Title: METHODS FOR DETECTING AMYLOID BETA OLIGOMERS

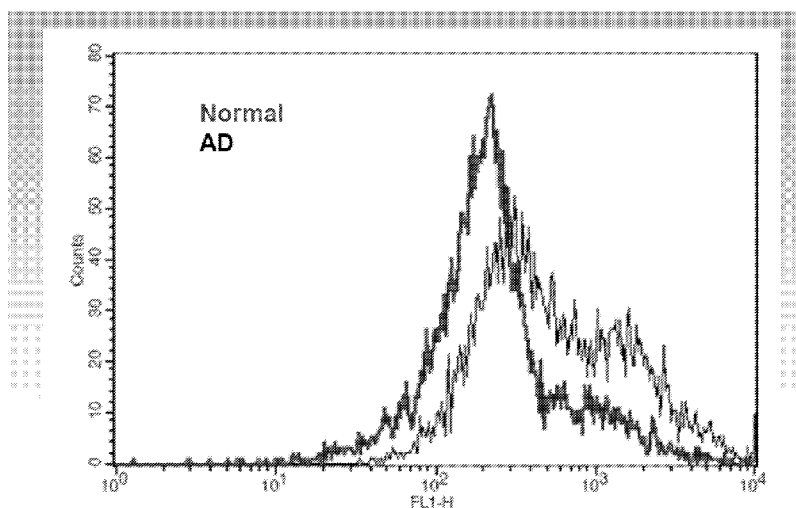


FIGURE 3

(57) Abstract: Methods of detecting A β oligomers, such as may be present in a biological sample are described. The methods include detection using flow cytometry, detection using synthetic A β oligomers and/or in vitro methods detecting A β oligomers associated with cells.



Published:

- *without international search report and to be republished
upon receipt of that report (Rule 48.2(g))*

METHODS FOR DETECTING AMYLOID BETA OLIGOMERS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefits of priority to U.S. Provisional Application No. 62/046,475, filed September 5, 2014, the entire contents of which are incorporated herein by reference.

5

BACKGROUND

The pathogenesis of misfolded protein disorders is characterized by the conversion of normal proteins into aggregation-prone β -sheet rich conformations. These conformations are implicated in amyloidogenic disease. In the case of Alzheimer's Disease (AD), self-assembly of amyloid beta (A β) protein into neurotoxic oligomers and fibrils is a leading postulation in regard to a major mechanism that causes AD.

10

Alzheimer's diseases is associated with a specific structural form of the A β protein (*e.g.*, a "misfolded protein" or a self-aggregated protein), while the protein in a different structural form (*e.g.*, a "normal protein") is not harmful. Misfolded A β protein form aggregates that self-assemble into non-branching fibrils with the common characteristic of a β -pleated sheet conformation. In the central nervous system (CNS), amyloid deposits can be present in cerebral and meningeal blood vessels (cerebrovascular deposits) and in brain parenchyma (plaques). Neuropathological studies in human and animal models indicate that cells proximal to amyloid deposits are disturbed in their normal functions. *See, e.g.*, Mandybur, *Acta Neuropathol.* 78:329-331, 1989; Kawai et al., *Brain Res.* 623:142-146, 1993; Martin et al., *Am. J. Pathol.* 145:1348-1381, 1994; Kalaria et al., *Neuroreport* 6:477-80, 1995; Masliah et al., *J. Neurosci.* 16:5795-5811, 1996. Other studies additionally indicate that amyloid fibrils may actually initiate neurodegeneration. *See, e.g.*, Lendon et al., *J. Am. Med. Assoc.* 277:825-831, 1997; Yankner, *Nat. Med.* 2:850-852, 1996; Selkoe, *J. Biol. Chem.* 271:18295-18298, 1996; Hardy, *Trends Neurosci.* 20:154-159, 1997.

15

20

25

While the underlying molecular mechanism that results in protein misfolding is still not completely understood, a common characteristic is the propensity to form aggregates and/or fibrils which exhibit a β -sheet structure or other conformations. Fibril formation and the subsequent formation of secondary β -sheet structures associated with plaque deposits, occurs via

a complex mechanism involving a nucleation stage, in which monomers of the protein associate to form oligomers, which associate to form fibrils, followed by extension of the fibrils at each end. For example, A β protein monomers can be found in various parts of healthy individuals, including body fluids (e.g., blood and cerebrospinal fluid) and tissue (e.g., brain). Disease
5 caused by misfolded A β protein appears to correlate with self-assembly of the monomers into oligomers (soluble aggregates), insoluble oligomers (e.g., insoluble amorphous self-aggregates), protofibrils, or fibrils, eventually forming into non-soluble, large aggregated deposits such as plaques found in diseased individuals.

Two abundant forms of A β protein found in amyloid plaques are A β_{1-40} (also referred to as
10 A β_{40}) and A β_{1-42} (also referred to as A β_{42}). Although A β_{40} is more abundant, A β_{42} is the more fibrillogenic and is the major component of the two in amyloid deposits of both AD and CAA. See, e.g., Wurth *et al.*, J. Mol. Biol. 319: 1279-90 (2002). In addition to the amyloid deposits in AD cases described above, AD cases can be associated with amyloid deposition in the vascular walls. See, e.g., Vinters H. V., Stroke Mar-Apr; 18(2):311-324, 1987; Itoh Y., *et al.*, Neurosci.
15 Lett. 155(2):144-147, Jun. 11, 1993.

There is a need, therefore, for methods of detecting A β oligomers, which can provide insight into the risk for, presence, progression, severity and prognosis of disease and/or the efficacy of therapeutic agents aimed at disrupting the formation of A β protein aggregates.

SUMMARY

20 Disclosed herein are methods for detecting A β oligomers in a biological sample.

In accordance with some embodiments, the methods comprise detecting A β oligomers in a biological sample obtained from a subject, comprising preparing a test sample comprising the biological sample and a peptide probe, wherein the peptide probe consists of from 10 to 34 amino acid residues comprising an amino acid sequence that is at least 70% identical to any one of SEQ
25 ID NOs:1-56 and 62-65, wherein the peptide probe preferentially binds to A β oligomers and is labeled with a fluorescent label capable of emitting a fluorescent signal, wherein the peptide probe forms complexes with any A β oligomer present in the biological sample; subjecting the test sample to flow cytometry to detect the fluorescent signal of the complexes; wherein the

fluorescent signal of the complexes is directly correlated with the presence and amount of A β oligomers in the biological sample.

Also disclosed are methods comprising determining the A β oligomer load of a subject by detecting A β oligomer associated with cells present in a biological sample obtained from the subject, comprising: preparing a first test sample comprising a biological sample from the subject that comprises cells and a peptide probe, wherein the peptide probe consists of from 10 to 34 amino acid residues comprising an amino acid sequence that is at least 70% identical to any one of SEQ ID NOs:1-56 and 62-65, wherein the peptide probe preferentially binds to A β oligomers and is labeled with a detectable label, wherein the peptide probe forms a first complex with A β oligomer associated with cells in the biological sample; detecting a signal of the first complex in the first test sample; preparing a second test sample comprising a biological sample from the subject that comprises cells, synthetic A β oligomer, and the peptide probe, wherein the peptide probe forms second complexes with A β oligomer associated with cells in the biological sample and with synthetic A β oligomer; detecting a signal of the second complexes in the second test sample; wherein a difference between the signal of the first complex in the first test sample and the signal of the second complexes in the second test sample is inversely correlated with the A β oligomer load of the subject. In some embodiments, the second test sample is prepared by combining the biological sample and synthetic A β oligomer, and subsequently introducing the peptide probe.

Also disclosed are *in vitro* methods of detecting A β oligomer associated with erythrocytes, comprising contacting erythrocytes with a peptide probe, wherein the peptide probe consists of from 10 to 34 amino acid residues comprising an amino acid sequence that is at least 70% identical to any one of SEQ ID NOs:1-56 and 62-65, wherein the peptide probe preferentially binds to A β oligomers and is labeled with a detectable label, wherein the peptide probe forms a complex with A β oligomer associated with erythrocytes; detecting a signal of the complex.

Also disclosed are *in vitro* method of detecting A β oligomer associated with platelets, comprising contacting platelets with a peptide probe, wherein the peptide probe consists of from 10 to 34 amino acid residues comprising an amino acid sequence that is at least 70% identical to any one of SEQ ID NOs:1-56 and 62-65, wherein the peptide probe preferentially binds to A β oligomers

and is labeled with a detectable label, wherein the peptide probe forms a complex with A β oligomer present on the surface of platelets; and detecting a signal of the complex.

In any of these methods, the detectable label may be a fluorescent label and the detecting steps may comprise subjecting the test samples to flow cytometry to detect a fluorescent signal of the complexes. In any of these methods, the fluorescent label may be an FITC label.

In any of these methods using a detectable label, the detectable label may be a fluorescent label and the detecting steps may comprise direct detection of the fluorescent signal of the complexes. In any of these methods using a detectable label, the detectable label may be a pyrene moiety and the detecting steps may comprise detecting pyrene excimer formation.

In any of these methods, the peptide probe may consist of SEQ ID NO:64 (Pep-11).

In any of these methods, the biological sample may comprise a sample of body fluid, such as blood, blood plasma, CSF, or brain homogenate. In any of these methods, the biological sample may comprise erythrocytes, including isolated erythrocytes. In any of these methods, the biological sample may comprise platelets, including isolated platelets. In some embodiments, the A β oligomer is associated with a cell, such as an erythrocyte and/or a platelet present in the biological sample. In some embodiments, the biological sample comprises erythrocytes and platelets and the methods comprise separately detecting A β oligomer associated with erythrocytes and A β oligomer associated with platelets.

In some embodiments, the complex formed and/or detected comprises peptide probe, A β oligomer, and an erythrocyte from the biological sample; peptide probe, A β oligomer, and a platelet from the biological sample, and/or peptide probe, synthetic A β oligomer, and an erythrocyte or platelet from the biological sample.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1 sets forth peptide probes useful in the methods described herein. Highlighting shows amino acid substitutions relative to the wildtype sequence and/or labels.

FIGURE 2 depicts (i) endogenous A β oligomer associated with erythrocytes in whole blood samples from normal subjects or subjects with Alzheimer's Disease and (ii) complexes comprising labeled peptide probe and endogenous A β oligomer.

FIGURE 3 depicts FITC signals from samples comprising whole blood samples containing erythrocytes from normal subjects or subjects with Alzheimer's Disease and PEP-11 peptide probe. The profiles reflect the amount of endogenous A β oligomer associated with erythrocytes in the sample.

FIGURE 4 depicts (i) endogenous A β oligomer associated with erythrocytes in whole blood samples from normal subjects or subjects with Alzheimer's Disease; (ii) samples with synthetic A β oligomer added; and (iii) complexes comprising labeled peptide probe and endogenous A β oligomer and complexes comprising labeled peptide probe and synthetic A β oligomer.

FIGURE 5 depicts FITC signals from samples comprising (i) whole blood samples containing erythrocytes from normal subjects or subjects with Alzheimer's Disease and (ii) synthetic A β oligomer and (iii) PEP-11 peptide probe. The profiles reflect the total amount of endogenous and synthetic A β oligomer associated with erythrocytes in the sample.

FIGURE 6 overlays the FITC signals from FIGURES 3 and 5. For normal subjects, the overlay shows a significant difference in the signal, reflecting a significant difference in the endogenous versus final (endogenous plus synthetic) A β oligomer loading of the erythrocytes in the sample. For subjects with Alzheimer's Disease, the overlay shows little difference in the signal, reflecting a small difference in the endogenous versus final A β oligomer loading of the erythrocytes in the sample.

FIGURE 7 depicts the overlay of FITC signals from a sample of whole blood from a normal human patient and PEP-11, without and with synthetic A β oligomer.

FIGURE 8 depicts different formats for Peptide Linked Immunosorbent Assay (PLISA).

FIGURE 9 depicts fluorescence values (O.D. absorbance) as a function of A β oligomer concentration for Peptide-Linked Immunosorbent Assay (PLISA) and Enzyme-Linked

Immunosorbent Assay (ELISA), and demonstrates that peptide probes can be used to detect A β oligomer with greater sensitivity.

FIGURE 10 depicts the signal ratio (%) of A β monomer/oligomer and A β fiber/oligomer for different A β monomer, oligomer, and fiber concentrations in buffer and 10% cerebrospinal fluid (CSF) when probed with peptide probe as described herein, and demonstrates that peptide probes preferentially detect A β oligomer.

FIGURE 11 depicts the ability of different peptide probes (Pep11-a, Pep11-b and Pep11-ds) to detect A β oligomer, A β monomer, or A β fiber by PLISA, and illustrates that the three peptide probes preferentially detect A β oligomer.

FIGURE 12 depicts the ability of labeled peptide probe to detect synthetic A β oligomer in cerebrospinal fluid.

FIGURE 13 depicts (i) gel electrophoresis bands depicting samples comprising (1) A β 42 biotinylated oligomer; (2) A β 42 biotinylated oligomer bound to beads via streptavidin; (3) peptide probe; (4) peptide probe bound to A β 42 biotinylated oligomer bound to beads via streptavidin; and (5) peptide probe and streptavidin-coated beads. The figure also depicts (ii) fluorescent anisotropy (milli-r) as a function of A β 42 oligomer concentration (nN). This information demonstrates that the peptide probes bind to A β oligomer with specificity and that the binding exhibits a dose-response profile.

FIGURE 14 depicts the ability of labeled peptide probe to distinguish between normal subjects and subjects having Mild Cognitive Impairment ($p \leq 0.012$) and between normal subjects and subjects suspected of having Alzheimer's Disease ($p \leq 0.030$), as determined by the peptide fluorescence of CSF samples probed with labeled peptide probe.

DETAILED DESCRIPTION

1. Definitions

As used herein, the singular forms "a," "an," and "the" designate both the singular and the plural, unless expressly stated to designate the singular only.

The term “about” and the use of ranges in general, whether or not qualified by the term about, means that the number comprehended is not limited to the exact number set forth herein, and is intended to refer to ranges substantially within the quoted range while not departing from the scope of the invention. As used herein, “about” will be understood by persons of ordinary skill
5 in the art and will vary to some extent on the context in which it is used. If there are uses of the term which are not clear to persons of ordinary skill in the art given the context in which it is used, “about” will mean up to plus or minus 10% of the particular term.

As used herein, “subject” denotes any animal including humans and domesticated animals, such as fish, cats, dogs, swine, cattle, sheep, goats, horses, rabbits, and the like. “Subject” also
10 includes experimental, laboratory animal models, such as transgenic animals used in biology and medical research. “Subject” also includes animals used in research settings, including fish, worms, mice and other small mammals, including vertebrates and non-vertebrates. A typical subject may be suspected of suffering from amyloidogenic disease, suspected of having been exposed to conditions creating a risk for amyloidogenic disease, have a genetic risk for
15 amyloidogenic disease (e.g., individuals with family members suffering from amyloidogenic disease or having ApoE4 allele variants), or may be desirous of determining risk or status with respect to amyloidogenic disease.

The term “biological sample” is used herein to refer to a sample from a subject. “Biological sample” includes body fluids, such as blood, cerebrospinal fluid, tissue homogenate, urine,
20 saliva, serum, and sweat. “Blood” includes whole blood, blood cells (including erythrocytes, platelets, and leukocytes) and plasma. “Plasma” includes platelet-rich plasma and platelet-poor plasma. “Tissue homogenate” includes brain homogenate, other neural tissue homogenate, eye tissue homogenate, vascular tissue homogenate, lung tissue homogenate, kidney tissue homogenate, heart tissue homogenate, liver tissue homogenate and other tissue homogenates.

25 “Endogenous,” “native,” and “naturally occurring” oligomers refer to oligomers present in a source occurring in or obtained from nature, such as a biological sample from a subject. An endogenous oligomer may include post-translational modifications, including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, acylation, farnesylation and cleavage.

As used herein, “A β protein” includes A β ₁₋₄₀ (also referred to as A β 40) and A β ₁₋₄₂ (also referred to as A β 42), which represent alternative carboxy-terminal truncations of APP. *See, e.g.,* Selkoe *et al.*, PNAS USA 85:7341-7345, 1988; Selkoe, *Trends Neurosci.* 16:403-409, 1993. A β 40 and A β 42 have identical amino acid sequences, with A β 42 having two additional residues (Ile and Ala) at its C terminus. The term also includes all naturally occurring mutants, including naturally occurring mutants known to exhibit increased tendency to form aggregates. Such mutants are known in the art, such as those disclosed in Murakami *et al.*, *J. Biol. Chem.* 46:46179-46187, 2003, which is incorporated herein by reference in its entirety.

The term “A β oligomer” is used herein to refer to an association of two or more A β monomers. Monomers may be associated covalently or non-covalently, *e.g.*, by covalent bonds, hydrogen bonds, ionic bonds, van der Waals interactions, etc. “A β oligomers” include, but are not limited to, for example, A β peptide dimers, trimers, tetramers, pentamers, hexamers, dodecamers, and higher order oligomers. An A β oligomer may comprise A β monomers having the same or different amino acid sequences. Typically, A β oligomers comprise A β proteins in the β -sheet conformation.

In some embodiments, the A β oligomer is a “soluble A β oligomer.” As used herein, the term “soluble A β oligomer” means soluble in aqueous and/or physiological conditions at temperatures in the range of 25 °C to 37 °C, such as about 25 °C, about 30 °C, about 35 °C, and about 37 °C. For example, a composition comprising a soluble A β oligomer would not have any particulate matter visible to the human eye and/or would not contain an appreciable amount of fibrillar particles as determined, for example, by ThT staining.

As used herein, “conformation” refers to the secondary or tertiary structure of a protein or peptide, for example, an alpha-helix, random coil or β -sheet secondary structure. A “conformation shift” means any change in the conformation of the non-primary structure of the protein, such as a change in the distance between the N- and C-termini (or between any other two points), folding more or less compactly, changing from predominantly one secondary structure to predominantly another secondary structure, such as from predominantly alpha helix/random coil to predominantly β -sheet, or any change in the relative amounts of different secondary

structures, such as a change in the relative amounts of alpha helix/random coil and β -sheet secondary structures even without a change in the predominant secondary structure.

“Probe” refers to a peptide or peptide mimic that binds to A β oligomer. As used herein, a probe may or may not undergo a conformation shift upon association with A β oligomer. In some
5 embodiments, the probe is a conformationally dynamic peptide based on the human A β protein sequence, as described in US 2010/0233095, the contents of which are incorporated herein by reference in their entirety. For convenience, the peptides and peptide mimics are referred to herein as “probes” without detracting from their utility in other contexts. These probes are discussed in more detail below.

10 “Peptide mimic” is also referred to as a peptidomimic or peptidomimetic or peptoid and refers to any molecule that mimics the properties of a peptide, such as peptide structure and certain physiochemical properties. Peptide mimics include polymeric molecules that mimic the folding and/or secondary structure of a specific peptide, as well as those that mimic the biological or chemical properties of a peptide. Peptide mimics may have an amino acid backbone and contain
15 non-natural chemical or amino acid substitutions. Peptoids may have side chains (R-groups) on the backbone amide nitrogen, instead of the alpha carbon as in peptides. This may serve one or more of several purposes: (1) peptoids may be resistant to proteolysis; (2) since peptoid secondary structure formation may not depend on hydrogen bonding, they may exhibit enhanced thermal stability as compared to peptides, and (3) the large number of available peptoid residues
20 allows for the production of a large variety of three-dimensional structures that may aid in assay development. Alternatively, peptide mimics may have different chemical backbones, such as β -peptides, anthranilamide oligomers, oligo (*m*-phenylene ethynylene), oligourea, oligopyrrolinones, azatides and N-substituted glycine oligomers. Peptide mimics may have
25 different chemical properties, such as resistance to proteases, while retaining peptide characteristics, such as peptide folding and peptide-peptide interactions (including, for example, interactions via hydrogen bonding, etc.). Any suitable peptide mimic can be used in the present invention, and include those designed and/or constructed as described in Chongsiriwatana, N. P, et al. *Proc Natl Acad Sci U S A* 2008, 105, (8), 2794-9; Kirshenbaum, K., et al. *Current Opinion in Structural Biology* 1999, 9, (4), 530-535; Lee, B. C., et al., *Journal of the American Chemical*

Society 2005, 127, (31), 10999-11009, which are each hereby incorporated by reference in their entirety.

“Similarity” between two peptides is determined by comparing the amino acid sequence of one peptide to the sequence of a second peptide. An amino acid of one peptide is similar to the
5 corresponding amino acid of a second peptide if it is identical or a conservative amino acid substitution. Conservative substitutions include those described in Dayhoff, M.O., ed., *The Atlas of Protein Sequence and Structure 5*, National Biomedical Research Foundation, Washington, D.C. (1978), and in Argos, P. (1989) *EMBO J.* 8:779-785. For example, amino acids belonging to one of the following groups represent conservative changes or substitutions:

10 -Ala, Pro, Gly, Gln, Asn, Ser, Thr:

-Cys, Ser, Tyr, Thr;

-Val, Ile, Leu, Met, Ala, Phe;

-Lys, Arg, His;

-Phe, Tyr, Trp, His; and

15 -Asp, Glu.

“Homology,” “homologs of,” “homologous,” “identity,” or “similarity” refers to sequence similarity between two peptides, with identity being a more strict comparison. Homology and identity may each be determined by comparing a position in each sequence that may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same
20 amino acid, then the molecules are identical at that position. A degree of identity of amino acid sequences is a function of the number of identical amino acids at positions shared by the amino acid sequences. A degree of homology or similarity of amino acid sequences is a function of the number of amino acids, *i.e.*, structurally related, at positions shared by the amino acid sequences. An “unrelated” or “non-homologous” sequence shares 10% or less identity, with one of the
25 sequences described herein. Related sequences share more than 10% sequence identity, such as at least about 15% sequence identity, at least about 20% sequence identity, at least about 30% sequence identity, at least about 40% sequence identity, at least about 50% sequence identity, at least about 60% sequence identity, at least about 70% sequence identity, at least about 80% sequence identity, at least about 90% sequence identity, at least about 95% sequence identity, or
30 at least about 99% sequence identity.

The term “percent identity” refers to amino acid sequence identity between two peptides. Identity may be determined by comparing a position in each sequence that is aligned for purposes of comparison. When an equivalent position in one compared sequence is occupied by the same amino acid in the other at the same position, then the molecules are identical at that position; 5 when the equivalent site occupied by the same or a similar amino acid residue (*e.g.*, similar in steric and/or electronic nature), then the molecules may be referred to as homologous (similar) at that position. Expression as a percentage of homology, similarity, or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. Various alignment algorithms and/or programs may be used, including FASTA, BLAST, or 10 ENTREZ, FASTA and BLAST are available as part of the GCG sequence analysis package (University of Wisconsin, Madison, Wis.), and may be used with, *e.g.*, default settings. ENTREZ is available through the National Center for Biotechnology Information, National Library of Medicine, NIH, Bethesda, Md.). In one embodiment, the percent identity of two sequences may be determined by the GCG program with a gap weight of 1, *e.g.*, each amino acid 15 gap is weighted as if it were a single amino acid mismatch between the two sequences. Other techniques for determining sequence identity are well known and described in the art.

2. Methods for detecting A β oligomer

Described herein are novel methods for detecting A β oligomer associated with Alzheimer’s Disease in biological samples from a subject. The methodologies use flow cytometry and/or 20 detect A β oligomer associated with cells present in or obtained from biological samples. The methods use peptide probes that preferentially bind to oligomeric forms of A β protein, such as soluble A β oligomers, as described in greater detail further below.

U.S. Patent No. 7,166,471 and U.S. Patent Application publications US 2006/0286672, US 2005/0026165, US 2008/0171341, US 2006/0057671, US 2008/0095706, and 25 US 2010/0233095 describe peptide probes useful for the detection of, for example, misfolded proteins, target protein having a predominantly β -sheet secondary structure, and target protein in a specific state of self-aggregation. The peptide probes described in these references can be used in the methods described herein. Thus, the entire contents each of these patent documents are incorporated herein by reference in their entirety.

In specific embodiments, the peptide probe consists of from 10 to 34 amino acid residues comprising an amino acid sequence that is at least 70% identical to any one of SEQ ID NOs:1-56 and 62-65, preferentially binds to A β oligomers, and is labeled with a detectable label. In further specific embodiments, the peptide probe consists of SEQ ID NO:64.

5 (i) Flow Cytometry

Flow cytometry is a fluid-based detection technique that passes cells or particles in a liquid biological sample through a detector, and permits the detection of the cells or particles. Once detected, the cells or particles can be sorted depending on size or any marker (e.g., fluorescent label) associated with the cell.

10 Prior to the present invention, it was not believed that flow cytometry could be used to detect complexes of peptide probes and A β oligomer because the complexes were thought to be too small to be detected. Where flow cytometry has been used to detect A β protein complexes, the complexes contained an antibody and/or a solid bead platform, which are much larger complexes. *See, e.g.*, Santos et al., Journal of Alzheimer's Disease, 11:117-125 (2007); EP
15 1882944; Santos et al., Journal of Alzheimer's Disease, 14:127-131 (2008). However, it was surprisingly discovered that flow cytometry can be used in the methods described herein.

Exemplary methods comprise preparing a test sample comprising the biological sample and a peptide probe as described herein, wherein the peptide probe is labeled with a detectable label and forms complexes with any A β oligomer present in the biological sample, and subjecting the
20 test sample to flow cytometry to detect the signal of any such complexes. In accordance with such methods, the signal of the complexes is directly correlated with the presence and amount of A β oligomers in the biological sample.

As noted above, the biological sample may comprise a sample of body fluid, such as whole blood, cerebrospinal fluid (CSF), and/or tissue homogenate (e.g., brain homogenate). In some
25 embodiments, the sample comprises blood plasma, including platelet rich or platelet poor blood plasma. In some embodiments, the sample comprises erythrocytes and/or may be a sample comprising isolated erythrocytes. In some embodiments, the sample comprises platelets and/or may be a sample comprising isolated platelets. In some embodiments, the sample comprises erythrocytes and platelets. In some embodiments, the sample does not include cells.

In some embodiments, the label of the peptide probe is a fluorescent label, such as an FITC label.

In some embodiments, the A β oligomer is associated with a cell present in the biological sample, such as with an erythrocyte or platelet present in the biological sample, as discussed in more detail below. In some embodiments, the complex comprises peptide probe, A β oligomer, and a
5 cell from the biological sample.

(ii) Cell-Associated A β Oligomer

While not wanting to be bound by any theory, it is believed that certain cells may be involved in the transport of A β protein *in vivo*, such as erythrocytes, platelets, and/or leukocytes, and that endogenous A β oligomers may be associated with such cells. Further, endogenous A β oligomers
10 may be associated with tissue cells, such as neurological tissue cells, such as brain tissue cells. For example, A β oligomer may be associated with such cells such as by being bound (covalently or otherwise) on the cell surface, in the cell membrane, or intracellularly.

The present invention provides *in vitro* methods of detecting A β oligomer associated with cells, such as erythrocytes, platelets, leukocytes and/or tissue cells. In some embodiments, the methods
15 comprise contacting cells *ex vivo* with a peptide probe that preferentially binds to A β oligomers and is labeled with a detectable label, such that the peptide probe forms a complex with A β oligomer associated with cells; and detecting a signal of the complex.

The label of the peptide probe can be any detectable label, and the signal can be detected by any suitable detection method, including flow cytometry, direct detection such as using fluorescence
20 microscopy, fluorescence-activated cell sorting and fluorescence spectroscopy. In some embodiment, the label is a fluorescent label, while in other embodiments, the label is another detectable label, such as an excimer-forming pyrene moiety, or any other suitable detectable label, such as the labels discussed in more detail below.

In specific embodiments, a sample, such as a biological sample from a subject, comprises
25 multiple cell types (e.g., erythrocytes and platelets) and is subjected to flow cytometry that separates complexes formed with each cell type, as noted above. For example, in some embodiments, the flow cytometry separately detects the signal of complex associated with

erythrocytes and the signal of complex associated with platelets, such as based on the different sizes of such complexes.

(iii) A β Oligomer Load

In some embodiments, the methods comprise determining an A β oligomer load of the subject.

5 As noted above, while not wanting to be bound by any theory, it is believed that certain cells may be involved in the transport of A β protein *in vivo*, such as erythrocytes, platelets, and/or leukocytes, and that such cells may be loaded with endogenous A β oligomers. Further, endogenous A β oligomers may be associated with tissue cells, such as neurological tissue cells, such as brain tissue cells. It is believed that by determining the degree of A β oligomer loading of
10 such cells, one can assess the risk, presence, progression, severity and/or prognosis of Alzheimer's disease in the subject, with higher loading generally being indicative of greater disease progression.

In some embodiments, A β oligomer load is determined by detecting A β oligomer associated with cells present in a biological sample obtained from a subject, such as by preparing a first test
15 sample comprising a biological sample from the subject that comprises cells and a peptide probe as described herein that is labeled with a detectable label and forms a first complex with A β oligomer associated with cells in the biological sample; detecting a signal of the first complex in the first test sample; preparing a second test sample comprising a biological sample from the subject that comprises cells, synthetic A β oligomer, and the peptide probe, wherein the peptide
20 probe forms second complexes with A β oligomer associated with cells in the biological sample and with synthetic A β oligomer; and detecting a signal of the second complexes in the second test sample.

In accordance with such methods, a difference between the signal of the first complex in the first test sample and the signal of the second complexes in the second test sample is inversely
25 correlated with the A β oligomer load of the subject. That is, if the second test sample exhibits a significantly greater signal than the first, that indicates that the cells were not fully loaded with endogenous A β oligomer, but were susceptible to further loading with synthetic A β oligomer, which resulted in the greater signal. On the other hand if the second test sample does not exhibit

a greater signal than the first, that indicates that the cells were loaded with endogenous A β oligomer, and so were not very susceptible to further loading with synthetic A β oligomer.

In accordance with these methods, any sample can be used that includes cells that may be loaded with endogenous A β oligomer, such as erythrocytes, platelets, leukocytes, or tissue cells, such as
5 cells from neurological tissue or brain.

In some embodiments, the second test sample is prepared by combining the biological sample and synthetic A β oligomer and then adding the labeled peptide probe. Such embodiments permit the synthetic A β oligomer to associate with cells in the biological sample before the peptide probe is added.

10 The label of the peptide probe can be any detectable label, and the signals can be detected by any suitable detection method, including flow cytometry, direct detection such as using fluorescence microscopy, fluorescence-activated cell sorting and fluorescence spectroscopy. In some embodiment, the label is a fluorescent label, while in other embodiments, the label is another detectable label, such as an excimer-forming pyrene moiety, or any other suitable detectable
15 label, such as the labels discussed in more detail below.

In some embodiments, different signals corresponding to A β oligomer associated with different cell types are detected, such as by flow cytometry as discussed above.

(iv) Additional Detection Methods

As noted above, in some embodiments detection methods other than flow cytometry are used in
20 the methods described herein. In some embodiments, assays similar to immunoassays but using a peptide probe as described herein instead of an antibody are used to detect A β oligomer in a biological sample. Such methods are referred to as a peptide-linked immunosorbent assay (i.e., "PLISA"). In specific embodiments, the PLISA can be a sandwich assay or a competitive assay. In some embodiments, the PLISA uses a solid-phase such as a plate that can be used in a
25 fluorescence detection apparatus, such as a fluorescence plate reader, or a bead with capture antibody or capture peptide attached thereto. Such methods are described in WO 2012/149145; WO 2011/149917; US 2012/0282169; US 2010/0233095; US 2008/0095706; US 8,372,593; and WO 2006/031644, the content of which are incorporated herein by reference in their entirety.

In some embodiments, a combination of detection methods is used to detect A β oligomer. In specific embodiments, a combination of flow cytometry and non-flow cytometry methods are used to detect A β oligomer.

3. Synthetic A β Oligomers

5 As noted above, some of the methods described herein use synthetic A β oligomers. Synthetic A β oligomers include stabilized synthetic A β oligomers as described in WO 2011/149917, the contents of which are incorporated herein by reference in their entirety. The synthetic A β oligomers can include covalent and/or noncovalent complexes of A β monomers, and may comprise several to several hundred monomer units. In some embodiments, the synthetic A β oligomers are about 5 to 50 amino acids, about 10 to 40, about 15-30, or about 20, including
10 about 5 to about 40, about 5 to about 30, about 5 to about 20, about 5 to about 15, about 5 to about 10, about 10 to about 50, about 10 to about 40, about 10 to about 30, about 10 to about 20, about 20 to about 50, about 20 to about 40, about 20 to about 30, about 30 to about 50, about 30 to about 40, or about 40 to about 50 amino acids. The monomers can comprise one or more of
15 A β 3-42, A β 37, A β 38, A β 39, A β 40 and A β 42.

4. Peptide Probes

As noted above, peptide probes described herein preferentially bind to A β oligomer, and thus are useful for detecting A β oligomer. In some embodiments, the peptide probe preferentially binds soluble A β oligomer, as compared to A β monomer and higher order A β protein aggregates such
20 as insoluble oligomers, insoluble amorphous self-aggregates, protofibrils or fibrils.

As noted above, U.S. Patent No. 7,166,471 and U.S. Patent Application publications US 2006/0286672, US 2005/0026165, US 2008/0171341, US 2006/0057671, US 2008/0095706, and US 2010/0233095 describe peptide probes that can be used in the methods described herein. In specific embodiments, the peptide probe consists of from 10 to 34 amino acid residues
25 comprising an amino acid sequence that is at least 70% identical to any one of SEQ ID NOs:1-56 and 62-65, preferentially binds to A β oligomers, and is labeled with a detectable label. In further specific embodiments, the peptide probe consists of SEQ ID NO:64.

In some embodiments the peptide probe does not include the full-length sequence of the A β protein, such as A β 40 or A β 42. In some embodiments, the peptide probe consists of from about 10 to about 34 amino acids, about 10 to about 30 amino acids, about 10 to about 25 amino acids, about 10 to about 20 amino acids, about 10 to about 15 amino acids, about 15 to about 34 amino acids, about 15 to about 30 amino acids, about 15 to about 25 amino acids, about 15 to about 20 amino acids, about 20 to about 34 amino acids, about 20 to about 30 amino acids, about 20 to about 25 amino acids, or any other range between about 10 to about 34 amino acids. In further embodiments, the probes about 10 amino acids, about 15 amino acids, about 20 amino acids, about 25 amino acids, about 30 amino acids, about 34 amino acids, or any other number between about 10 and about 34 amino acids. Probes of different lengths may exhibit different degrees of interaction and binding to A β oligomer, and suitable lengths can be selected by the skilled artisan guided by the teachings herein.

The probe may comprise a minimum number of contiguous amino acids of the A β protein, such as at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 11, at least about 12, at least about 13, at least about 14, at least about 15, at least about 16, at least about 17, at least about 18, at least about 19, at least about 20, at least about 21, at least about 22, at least about 23, at least about 24, at least about 25, at least about 30, at least about 34 contiguous amino acids of the A β protein, or any range between these numbers, such as about 10 to about 25 contiguous amino acids of the A β protein sequence.

The probe may comprise a maximum number of contiguous amino acids of the A β protein, such as up to about 5, up to about 6, up to about 7, up to about 8, up to about 9, up to about 10, up to about 11, up to about 12, up to about 13, up to about 14, up to about 15, up to about 16, up to about 17, up to about 18, up to about 19, up to about 20, up to about 21, up to about 22, up to about 23, up to about 24, up to about 25, up to about 30, or up to about 34 contiguous amino acids of the A β protein sequence, or any range between these numbers, such as about 10 to about 25 contiguous amino acids of the A β protein sequence.

In some embodiments, the probes may or may not undergo a conformation shift upon association with A β oligomer. In some embodiments, association of the peptide probe with A β oligomer is detected independently of any conformational shift that may or may not occur, such as by direct detection of probe associated with target oligomer, such as by detection of a detectable label on

probe associated with target oligomer. In some embodiments, the association is temporary, such as an initial association of the probe with the A β oligomer and a later dissociation of the probe from the A β oligomer. Detectable labels are described in greater detail below.

In some embodiments, the peptide probe comprises an amino acid sequence of the A β protein that undergoes a conformational shift, such as a shift from an α -helix/random coil conformation to a β -sheet conformation, or comprises a variant of such a sequence. For example, amino acids 16-35 of the A β protein are known to comprise a β -sheet forming region. Thus, the probe may comprise amino acids 16-35 or 17-35 of the A β protein, or an amino acid sequence that is a variant thereof. The probe may also comprise amino acids 3-35 or 5-42 of the A β protein, or an amino acid sequence that is a variant thereof. The amino acid sequence of the peptide probe may be designed, therefore, from the A β protein sequence, based on existing sequence and conformation information or, alternatively, may be readily determined experimentally.

In some embodiments, the peptide probes are capable of adopting both a primarily random coil/ α -helix conformation and a primarily β -sheet conformation, and adopt a primarily β -sheet conformation upon binding to target oligomer exhibiting a primarily β -sheet conformation. In some embodiments the peptide probe is provided in a primarily α -helix/random coil conformation, and undergoes a conformation shift to a primarily β -sheet conformation upon contact, binding, association and/or interaction with A β oligomer in a primarily β -sheet conformation. In other embodiments, the peptide probe shifts conformation by becoming more condensed, more diffuse, or adopting any different configuration. In some embodiments, the peptide probe more closely adopts the conformation of the A β oligomer. The probe may be provided in any physiologically acceptable solution. For example, the probe may be prepared as a trifluoroacetic salt and resuspended in an organic solvent, such as 100% hexafluoroisopropanol (HFIP) or 50% acetonitrile (ACN).

In some embodiments, the peptide probe comprises a variant sequence based on a corresponding region of the A β protein sequence. The variant sequence may comprise one or more amino acid additions, substitutions or deletions relative to the A β protein sequence, such that the variant sequence (or the peptide probe as a whole) has an amino acid sequence having at least 60%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% identity to the A β

protein sequence. In some embodiments, the peptide probe may have an amino acid sequence with one or more additional amino acids at either terminus, or at both termini, as compared to the reference sequence. Additions, substitutions, and deletions may also be made at an internal portion of the reference sequence, or both internally and terminally. In some embodiments, the peptide probe further comprises the addition of a lysine residue at the C-terminus, or another label to facilitate purification and/or labeling.

The reference sequence may comprise a minimum number of contiguous amino acids of the A β protein, such as at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 11, at least about 12, at least about 13, at least about 14, at least about 15, at least about 16, at least about 17, at least about 18, at least about 19, at least about 20, at least about 21, at least about 22, at least about 23, at least about 24, at least about 25, at least about 30, at least about 35 contiguous amino acids of the A β protein sequence, or any range between these numbers, such as about 10 to about 25 contiguous amino acids of the A β protein sequence.

The reference sequence may comprise a maximum number of contiguous amino acids of the A β protein, such as up to about 5, up to about 6, up to about 7, up to about 8, up to about 9, up to about 10, up to about 11, up to about 12, up to about 13, up to about 14, up to about 15, up to about 16, up to about 17, up to about 18, up to about 19, up to about 20, up to about 21, up to about 22, up to about 23, up to about 24, up to about 25, up to about 30, or up to about 34 contiguous amino acids of the A β protein sequence, or any range between these numbers, such as about 10 to about 25 contiguous amino acids of the A β protein sequence.

As disclosed above, the variant sequence optionally may adopt either a more- or less-ordered conformation upon binding to a target protein exhibiting a β -sheet conformation. In some embodiments, for example, the target protein is A β protein, and the variant sequence comprises one or more substitutions selected from the group consisting of G29H, G29R, G29K, and G33E. Additionally or alternatively, the β -sheet structure of the variant sequence may be less thermodynamically strong than that of the reference sequence. In specific embodiments, the variant sequence comprises one or more substitutions selected from the group consisting of I32S, F19S, S26D, H29D, I31D, L34D, and L34P.

Additionally or alternatively, the variant sequence may have an increased hydrophilicity and/or solubility in aqueous solutions than the reference sequence. In specific embodiments, the variant sequence comprises one or more amino acid additions or substitutions that introduce a glutamic acid residue and/or a d-arginine residue. Additionally or alternatively, the variant sequence may
5 be conjugated to a hydrophilic moiety, such as a soluble polyethylene glycol moiety.

In some embodiments, the variant sequence comprises the substitution of at least one residue with a glutamic acid residue. In some embodiments, the variant sequence comprises the substitution of at least one residue with a histidine residue. In some embodiments, the variant sequence comprises one or more substitutions selected from the group consisting of an isoleucine
10 residue with a serine residue; glutamic acid residue with either a proline residue, a glycine residue, a glutamine residue or a lysine residue; a phenylalanine residue with a serine residue; a leucine residue with a proline residue; an alanine residue with a glycine residue; and an aspartic acid residue with an asparagine residue.

In some embodiments, the peptide probes described herein bind to A β protein oligomer and
15 undergo a conformation shift upon such binding. The conformation shift may comprise a change in the distance between the N- and C-termini of the probe (or between any other two points), folding more or less compactly, changing from predominantly one secondary structure to predominantly another secondary structure, or any change in the relative amounts of different secondary structures, or any change in the relationship between any labels on the probes. In
20 some embodiments, the probes are conformationally dynamic peptides based on the human A β sequence, as described in US 2010/0233095.

Any of the probes described herein can be presented in D- or L-enantiomeric form. Additionally or alternatively,, the probes can be presented with an amino acid sequence in reverse order of the amino acid sequences described herein. For example, where a peptide probe is described as
25 having an amino acid sequence A-B-C-D, the reverse sequence would be D-C-B-A. In some embodiments, the probes are presented in D- or L-enantiomeric form, and/or in reverse order.

Any of the probes described herein may be end-capped at one or both of the C-terminus and the N-terminus with a small hydrophobic peptide ranging in size from about 1 to about 5 amino acids. In some embodiments, one or both of the C-terminus and N-terminus has a lysine residue,

such as to facilitate labeling. Additionally or alternatively, one or both of the C-terminus and N-terminus has a cysteine residue. Additionally or alternatively, any of the probes described herein may be modified by the substitution of a methionine residue with a residue resistant to oxidation, such as an alanine residue. Additionally or alternatively, any of the probes described herein may
5 be modified by the substitution of at least three consecutive residues of the reference sequence with alanine residues.

In some embodiments, the peptide probe is labeled with two pyrene labels, one on the N-terminal amine and the other on a side chain of a C-terminal lysine residue. In specific embodiments, the pyrene label is PBA. In some embodiments, the peptide probe contains a C-terminal amide in
10 place of the carboxyl group.

In accordance with any of the foregoing embodiments, the peptide probe may be conjugated to a biotin moiety, such as through a peptide linker. In specific embodiments, the peptide linker is selected from the group consisting of a flexible linker, a helical linker, a thrombin site linker and a kinked linker. In other embodiments, the peptide probe is conjugated to a biotin moiety
15 through a side chain of an internal lysine residue. Other appropriate peptide linkers are described in the art (*see, e.g.*, U.S. 6,448,087; Wurth et al., J. Mol. Biol. 319:1279-1290 (2002); and Kim et al., J. Biol. Chem. 280:35059-35076 (2005), which are incorporated herein by reference in their entireties). In some embodiments, suitable linkers may be about 8-12 amino acids in length. In further embodiments, greater than about 75% of the amino acid residues of the linker are selected
20 from serine, glycine, and alanine residues.

For example, biotinylation can be achieved through a helical linker such as EAAAK (SEQ ID NO:57) at the C-terminus, as illustrated by AD310 (SEQ ID NO:38). In general, a helical linker includes residues that form alpha helices, such as alanine residues. Alternatively, biotinylation can be achieved through a side chain on a lysine residue, including an internal or terminal lysine
25 residue, as illustrated by AD313 (SEQ ID NO:39). Alternatively, biotinylation can be achieved through a flexible linker (such as GSSGSSK (SEQ ID NO:58)) at the C-terminus, as illustrated by AD314 (SEQ ID NO:40). In general, a flexible linker includes one or more glycine and/or serine residues, or other residues that can freely rotate about their phi and psi angles.

Alternatively, biotinylation can be achieved through a thrombin site linker (such as a linker
30 comprising LVPRGS (SEQ ID NO:59), such as GLVPRGSGK (SEQ ID NO:60)) at the at the C-

terminus, as illustrated by AD317 (SEQ ID NO:41). Alternatively, biotinylation can be achieved through a kinked linker (such as PSGSPK (SEQ ID NO:61)) at the at the C-terminus, as illustrated by AD321 (SEQ ID NO:42). In general, kinked linkers comprise one or more proline residues, or other residues that have fixed phi and psi angles that rigidly project the biotin moiety
5 away from the peptide probe's protein-binding motif.

In some embodiments, the probes are selected from SEQ ID NOs:1-56, or from SEQ ID NOs:1-56 and 62-65. In some specific embodiments, the probes are selected from the group consisting of SEQ ID NOs:2, 22, 23, 41, 56, 62, 63, 64, or 65. In some embodiments, the probes are PEP-10, PEP-11 and PEP-12. Probes described in US 2008/0095706 for targeting A β protein, and
10 probes designed in accordance with US 2010/0233095, may be used as described herein. The contents of these applications are incorporated herein by reference in their entirety.

In specific embodiments, the probe may consist of two point mutations (e.g., SEQ ID NO:2; SEQ ID NO:62); the addition of two d-Arginine residues (r) (e.g., SEQ ID NO:22; SEQ ID NO:56; SEQ ID NO:62; SEQ ID NO:64); combinations of mutations described herein (e.g., SEQ ID
15 NO:23; SEQ ID NO:62); a naturally-occurring "Italian" mutant (SEQ ID NO:56); or addition of a linker and biotin (e.g., SEQ ID NO:41).

In some embodiments, the one or more amino acid additions, substitutions or deletions may introduce a salt bridge between two residues, such as between a glutamic acid residue and a histidine residue, a glutamic acid residue and an arginine residue, and/or a glutamic acid residue
20 and a lysine residue. Further, the amino acid additions, substitutions, or deletions may introduce an A β binding motif into the peptide probe, such as a GXXEG motif (SEQ ID NO:25).

Exemplary peptide probes designed in accordance with the principles described above are set forth in FIGURE 1. As shown by shading in the sequences in the figure, most of the peptide sequences are based on amino acids 16-35 of the A β peptide, which is a β -sheet forming region
25 of the A β peptide (others are based on longer portions of the A β peptide), with an added C-terminal lysine residue to facilitate labeling. Other peptide sequences are based on amino acids 17-35 of the A β peptide. The category (or categories) of the sequence variants are indicated in the table (e.g., modified to improve stability, provide a salt bridge, increase solubility, facilitate

alpha-helix formation, destabilize β -sheet structure, add an A β binding motif, etc.). Also illustrated are options for peptide probe labeling, including different label sites and label pairs.

The following abbreviations are used in FIGURE 1:

“PBA” = pyrene butyric acid

5 “r” = d-Arginine

“Dabcyl” = 4-(4-dimethylaminophenyl) diazenylbenzoic acid

“EDANS” = 5-(2'-aminoethyl)aminonaphthalene-1-sulfonic acid

“FAM” = 5(6)carboxyfluorescein

“Dansyl” = 5-dimethylaminonaphthalene-1-sulfonyl

10 “FITC” = Fluorescein isothiocyanate

“Ahx” = aminohexyl

The above features are optional for the peptide probes described herein. Although the probes in FIGURE 1 are depicted as having or not having these features, any of the probes listed in the figure and any of the probes described herein can have or lack one or more of these features.

15 The probe may alternatively be a peptide mimic (“peptoid”) of any of the peptide probes described herein. In some embodiments, the probe is a peptide mimic that has a natural peptide backbone but has non-natural amino acids or chemical moieties. In other embodiments, the probe is a peptide mimic that has a non-peptide backbone and comprises a chemical backbone, such as a polymeric backbone. In some embodiments, a peptide mimic exhibits increased
20 stability over the corresponding peptide.

Additional probes may be designed and tested for use in the present methods. Briefly, peptides and peptide mimics may be computationally designed to closely match hydrophobic topology and intramolecular pair contacts to wild type A β peptide and/or a probe with the desired characteristics as described above. Algorithms for designing such peptides and peptide mimics
25 are known in the art. *See, e.g.*, Mobley, D. L., et al., Structure 2009, 17, (4), 489-98; Fennell, C. J., et al., J Phys Chem B 2009; Voelz, V. A., et al., PLoS Comput Biol 2009, 5, (2), e1000281.; Shell, M. S., et al., Biophys J 2009, 96, (3), 917-24; Mobley, D. L., et al., J Chem Theory Comput 2007, 3, (4), 1231-1235; Wu, G. A., et al., Structure 2008, 16, (8), 1257-66; Chorny, I., et al., J Phys Chem B 2005, 109, (50), 24056-60.

5. Labels

As noted above, the peptide probes disclosed herein may comprise one or more detectable labels. For example, the peptide probe may be coupled or fused, either covalently or non-covalently, to a label, with or without a linker. Also as noted above, in some embodiments, the label is
5 detectable independent of the conformation of the probe and/or independent of any conformation shift or association with the A β oligomer.

In some embodiments, a label is selected to permit direct detection of probe associated with A β oligomer. Thus, for example, one or more labels may be detectable by direct detection, such as fluorescent labels, radioactive labels, etc. In some embodiments, the label is a fluorescent label,
10 such as FITC. In other embodiments, the label is pyrene, such as a pyrene excimer. Such association may be current probe association with A β oligomer or past probe association with A β oligomer. Additional labels are described below.

In some embodiments, a peptide probe may be labeled with a detectable label at the N-terminus, the C-terminus, both termini, or at one or more positions (including a side chain) that is
15 detectable independent of the conformation or conformational transition of the probe.

In some embodiments, a peptide probe may be labeled with a detectable label at the N-terminus, the C-terminus, both termini, or at one or more positions that generate a signal when the peptide associates with target protein or adopts a β -sheet conformation or undergoes a conformation change upon binding to target protein. Thus, for example, the label sites may be selected from
20 (i) the N-terminus and the C-terminus; (ii) the N-terminus and a separate site other than the C-terminus; (iii) the C-terminus and a separate site other than the N-terminus; and (iv) two sites other than the N-terminus and the C-terminus.

The peptide probe may be labeled with two or more labels, wherein the distance between two or more labels on the peptide probe when the peptide probe is bound to target protein is different
25 than the distance when the peptide probe is not bound to target protein. The peptide probe may additionally or alternatively be labeled with a detectable label pair selected from an excimer pair, a FRET pair and a fluorophore/quencher pair. When the peptide probe is labeled with an excimer pair, such as a pyrene pair, it may emit an excimer signal when the peptide probe exhibits a β -sheet conformation. When the peptide probe is labeled with a FRET pair, such as

DACIA-I/NBD, Marina Blue/NBD, Dansyl/Trp, and EDANS/FAM, it may emit a fluorescence resonance transfer (FRET) signal when the peptide probe exhibits a β -sheet conformation. When the peptide probe is labeled with a fluorophore/quencher pair, such as pyrene/Dabcyl, EDANS/Dabcyl and FAM/Dabcyl, the fluorophore signal may be quenched when the peptide probe exhibits a β -sheet conformation.

In some embodiments, the labels and label sites are selected such that the labels do or do not interact based on the conformation of the probe, for example, such that the labels do not interact when the probe is in its unassociated conformation and do interact when the probe undergoes a conformation shift upon association with target protein, to generate a detectable signal (including quenching), or vice versa. This may be accomplished by selecting label sites that are further apart or closer together depending on the associated state of the probe, *e.g.*, depending on whether the probe has undergone a conformation shift upon association with target protein. In some embodiments, the magnitude of the signal associated with the associated probe is directly correlated to the amount of target protein detected. Thus, the methods of the present invention permit detection and quantification of target protein.

For example, excimer, FRET or fluorophore/quencher label pairs may be used to permit detection of a specific conformation of the probe, such as the conformation adopted when the probe associates with A β protein aggregates associated with amyloidogenic disease. In these embodiments, the probe is labeled at separate sites with a first label and a second label, each being complementary members of an excimer, FRET or fluorophore/quencher pair.

For example, excimer-forming labels may emit their monomeric signals when the probe is in its unassociated state, and may emit their excimer signal when the probe undergoes a conformation shift that brings the labels in closer physical proximity, upon association with the target protein. Similarly, FRET labels may emit their FRET signal when the probe undergoes a conformation shift that brings the labels in closer physical proximity. On the other hand, fluorophore/quencher label pairs may emit the fluorophore signal when the probe is in its unassociated state, and that signal may be quenched when the probe undergoes a conformation shift that brings the labels in closer physical proximity. As noted above, the labels may be sited such that the opposite change in signal occurs when the probe undergoes a conformation shift upon association with the target protein.

In accordance with any of the foregoing, a detectable label may be conjugated to a side chain of a terminal lysine residue of the peptide probe, and/or to a side chain of an internal lysine residue of the peptide probe.

In some embodiments, the detectable label is attached to the probe by a linker. In specific
5 embodiments, the peptide linker is selected from the group consisting of a flexible linker, a
helical linker, a thrombin site linker and a kinked linker. In specific embodiments, the linker is
an aminohexyl linker. In other embodiments, the peptide probe is conjugated to a linking
through a side chain of an internal lysine residue. Other appropriate peptide linkers are described
in the art (*see, e.g.*, U.S. 6,448,087; Wurth et al., J. Mol. Biol. 319:1279-1290 (2002); and Kim et
10 al., J. Biol. Chem. 280:35059-35076 (2005), which are incorporated herein by reference in their
entireties). In some embodiments, suitable linkers may be about 8-12 amino acids in length. In
further embodiments, greater than about 75% of the amino acid residues of the linker are selected
from serine, glycine, and alanine residues.

Any of the probes described herein may include a dipyrrene butyrate (PBA) moiety at the N-
15 terminus and/or one extending from a lysine side chain near the C-terminus, and/or at any other
site suitable for labeling. Additionally or alternatively, any of the probes described herein may
have been modified to include an amide group at the C-terminus, in place of the naturally
occurring carboxyl group.

Moreover, while some of these embodiments have been described with reference to the use of
20 two labels per peptide probe, it should be understood that multiple labels could be used. For
example, one or more labels could be present at each labeling site, or multiple labels could be
present, each at different labeling sites on the probe. In these embodiments, the labels may
generate independent signals.

Exemplary labels for use in any of these embodiments include fluorescent agents (e.g.,
25 fluorophores, fluorescent proteins, fluorescent semiconductor nanocrystals), phosphorescent
agents, chemiluminescent agents, chromogenic agents, quenching agents, dyes, radionuclides,
metal ions, metal sols, ligands (e.g., biotin, streptavidin haptens, and the like), enzymes (e.g.,
beta-galactosidase, horseradish peroxidase, glucose oxidase, alkaline phosphatase, and the like),

enzyme substrates, enzyme cofactors (e.g., NADPH), enzyme inhibitors, scintillation agents, inhibitors, magnetic particles, oligonucleotides, and other moieties known in the art.

In specific embodiments, the fluorophore label is indocyanine green (ICG), Cypate, Cy3, Cy5, Cy7 or FITC. These and other directly detectable labels are useful in embodiments where the peptide probe may not undergo a conformational shift or transformation when associated with A β oligomer. In some embodiments, the directly detectable labels are detected using fluorescence microscopy, fluorescence-activated cell sorting or fluorescence spectroscopy.

As noted above, in some embodiments, the label comprises a pyrene moiety. As used herein, a pyrene moiety includes pyrene, which comprises four fused benzene rings or a derivative of pyrene. By pyrene derivative is meant a molecule comprising the four fused benzene rings of pyrene, wherein one or more of the pyrene carbon atoms is substituted or conjugated to a further moiety. Exemplary pyrene derivatives include alkylated pyrenes, wherein one or more of the pyrene carbon atoms is substituted with a linear or branched, substituted or unsubstituted, alkyl, alkenyl, alkynyl or acyl group, such as a C₁-C₂₀, linear or branched, substituted or unsubstituted alkyl, alkenyl, alkynyl or acyl group, where the group may be substituted with, for example, a moiety including an O, N or S atom (e.g., carbonyl, amine, sulfhydryl) or with a halogen. In some embodiments the pyrene derivative includes one or more free carboxyl groups and/or one or more free amine groups, each of which may be directly attached to a pyrene carbon atom or attached to any position on a linear or branched, substituted or unsubstituted, alkyl, alkenyl, alkynyl or acyl group as described above, such as being attached at a carbon atom that is separated from a pyrene carbon by 1 or more, such as 1 to 3, 1 to 5, or more, atoms. In some embodiments, the pyrene is substituted with one or more acetic acid moieties and/or one or more ethylamine moieties. In some embodiments, the pyrene derivative is substituted with a single methyl, ethyl, propyl or butyl group. In some embodiments, the pyrene is substituted with a short chain fatty acid, such as pyrene butyrate. In another embodiment, the pyrene is conjugated to albumin, transferrin or an Fc fragment of an antibody. In some embodiments, the substituent is attached to pyrene through a carbon-carbon linkage, amino group, peptide bond, ether, thioether, disulfide, or an ester linkage. In other embodiments, the pyrene derivative is PEGylated pyrene, i.e., pyrene conjugated to polyethylene glycol (PEG). Such pyrene derivatives may exhibit a

longer circulating half-life *in vivo*. In other embodiments, the pyrene derivative is pyrene conjugated to albumin.

In some embodiments, the label comprises a fluorescent protein which is incorporated into a peptide probe as part of a fusion protein. Fluorescent proteins may include green fluorescent proteins (e.g., GFP, eGFP, AcGFP, TurboGFP, Emerald, Azami Green, and ZsGreen), blue fluorescent proteins (e.g., EBFP, Sapphire, and T-Sapphire), cyan fluorescent proteins (e.g., ECFP, mCFP, Cerulean, CyPet, AmCyan1, and Midoriishi Cyan), yellow fluorescent proteins (e.g., EYFP, Topaz, Venus, mCitrine, YPet, PhiYFP, ZsYellow1, and mBanana), and orange and red fluorescent proteins (e.g., Kusabira Orange, mOrange, dTomato, dTomato-Tandem, DsRed, DsRed2, DsRed-Express (T1), DsRed-Monomer, mTangerine, mStrawberry, AsRed2, mRFP1, JRed, mCherry, HcRed1, mRaspberry, HcRed-Tandem, mPlum and AQ143). Other fluorescent proteins are described in the art (Tsien, R.Y., *Annual. Rev. Biochem.* 67:509-544 (1998); and Lippincott-Schwartz *et al.*, *Science* 300:87-91 (2003)). These and other directly detectable labels are useful in embodiments where the peptide probe may not undergo a conformational shift or transformation when associated with A β oligomer.

The fluorescent protein as part of a fusion protein may be coupled via a peptide linker as described in the art (U.S. 6,448,087; Wurth *et al.*, *J. Mol. Biol.* 319:1279-1290 (2002); and Kim *et al.*, *J. Biol. Chem.* 280:35059-35076 (2005), which are incorporated herein by reference in their entireties). In some embodiments, suitable linkers may be about 8-12 amino acids in length. In further embodiments, greater than about 75% of the amino acid residues of the linker are selected from serine, glycine, and alanine residues.

As used herein, a “fluorophore” is a chemical group that may be excited by light to emit fluorescence or phosphorescence. A “quencher” is an agent that is capable of quenching a fluorescent signal from a fluorescent donor. A first fluorophore may emit a fluorescent signal that excites a second fluorophore. A first fluorophore may emit a signal that is quenched by a second fluorophore. The probes disclosed herein may undergo fluorescence resonance energy transfer (FRET).

Fluorophores and quenchers may include the following agents (or fluorophores and quenchers sold under the following tradenames): 1,5 IAEDANS; 1,8-ANS; umbelliferone (e.g., 4-

Methylumbelliferone); acradimum esters, 5-carboxy-2,7-dichlorofluorescein; 5-Carboxyfluorescein (5-FAM); 5-Carboxytetramethylrhodamine (5-TAMRA) ; 5-FAM (5-Carboxyfluorescein); 5-HAT (Hydroxy Tryptamine) ; 5-Hydroxy Tryptamine (HAT); 5-ROX (carboxy-X-rhodamine); 5-TAMRA (5-Carboxytetramethylrhodamine); 6-Carboxyrhodamine
 5 6G; 6-CR 6G; 6-JOE; 7-Amino-4-methylcoumarin; 7-Aminoactinomycin D (7-AAD); 7-Hydroxy-4-methylcoumarin; 9-Amino-6-chloro-2-methoxyacridine; ABQ; Acid Fuchsin; ACMA (9-Amino-6-chloro-2-methoxyacridine); Acridine Orange; Acridine Red; Acridine Yellow; Acriflavin; Acriflavin Feulgen SITSA; Alexa Fluor 350™; Alexa Fluor 430™; Alexa Fluor 488™; Alexa Fluor 532™; Alexa Fluor 546™; Alexa Fluor 568™; Alexa Fluor 594™; Alexa
 10 Fluor 633™; Alexa Fluor 647™; Alexa Fluor 660™; Alexa Fluor 680™; Alizarin Complexon; Alizarin Red; Allophycocyanin (APC); AMC; AMCA-S; AMCA (Aminomethylcoumarin); AMCA-X; Aminoactinomycin D; Aminocoumarin; Aminomethylcoumarin (AMCA); Anilin Blue; Anthrocyl stearate; APC (Allophycocyanin); APC-Cy7; APTS; Astrazon Brilliant Red 4G; Astrazon Orange R; Astrazon Red 6B; Astrazon Yellow 7 GLL ; Atabrine; ATTO-TAG™
 15 CBQCA; ATTO-TAG™ FQ; Auramine; Aurophosphine G; Aurophosphine; BAO 9 (Bisaminophenylloxadiazole); Berberine Sulphate; Beta Lactamase; BFP blue shifted GFP (Y66H); Blue Fluorescent Protein; BFP/GFP FRET; Bimane; Bisbenzamide; Bisbenzimidazole (Hoechst); Blancophor FFG; Blancophor SV; BOBO™ -1; BOBO™ -3; Bodipy 492/515; Bodipy 493/503; Bodipy 500/510; Bodipy 505/515; Bodipy 530/550; Bodipy 542/563; Bodipy
 20 558/568; Bodipy 564/570; Bodipy 576/589; Bodipy 581/591; Bodipy 630/650-X; Bodipy 650/665-X; Bodipy 665/676; Bodipy FL; Bodipy FL ATP; Bodipy Fl-Ceramide; Bodipy R6G SE; Bodipy TMR; Bodipy TMR-X conjugate ; Bodipy TMR-X, SE; Bodipy TR; Bodipy TR ATP; Bodipy TR-X SE; BO-PRO™-1; BO-PRO™-3; Brilliant Sulphoflavin FF; Calcein; Calcein Blue ; Calcium Crimson™; Calcium Green; Calcium Orange; Calcofluor White; Carboxy-X-rhodamine (5-ROX); Cascade Blue™; Cascade Yellow; Catecholamine; CCF2
 25 (GeneBlazer); CFDA; CFP - Cyan Fluorescent Protein; CFP/YFP FRET; Chlorophyll; Chromomycin A; CL-NERF (Ratio Dye, pH); CMFDA; Coelenterazine f; Coelenterazine fcp; Coelenterazine h; Coelenterazine hcp; Coelenterazine ip; Coelenterazine n; Coelenterazine O; Coumarin Phalloidin; C-phycoerythrin; CPM Methylcoumarin; CTC; CTC Formazan; Cy2™; Cy3.1 8; Cy3.5™; Cy3™; Cy5.1 8; Cy5.5™; Cy5™; Cy7™; Cyan GFP; Cypate; cyclic AMP
 30 Fluorosensor (FiCRhR); Dabcyl; Dansyl; Dansyl Amine; Dansyl Cadaverine; Dansyl Chloride;

Dansyl DHPE; Dansyl fluoride; DAPI; Dapoxyl; Dapoxyl 2; Dapoxyl 3; DCFDA; DCFH
 (Dichlorodihydrofluorescein Diacetate); DDAO; DHR (Dihydrorhodamine 123); Di-4-ANEPPS;
 Di-8-ANEPPS (non-ratio); DiA (4-Di-16-ASP); Dichlorodihydrofluorescein Diacetate (DCFH);
 DiD - Lipophilic Tracer; DiD (DiIC18(5)); DIDS ; Dihydrorhodamine 123 (DHR); DiI
 5 (DiIC18(3)); Dinitrophenol; DiO (DiOC18(3)); DiR; DiR (DiIC18(7)); DNP; Dopamine; DsRed;
 DTAF; DY-630-NHS; DY-635-NHS; EBFP; ECFP; EGFP; ELF 97; EDANS; Eosin;
 Erythrosin; Erythrosin ITC ; Ethidium Bromide; Ethidium homodimer -1 (EthD-1); Euchrysin;
 EukoLight; Europium (III) chloride; EYFP; Fast Blue; FDA; Feulgen (Pararosaniline); FITC;
 Flazo Orange; Fluo-3; Fluo-4; Fluorescein (FITC); Fluorescein Diacetate; Fluoro-Emerald;
 10 Fluoro-Gold (Hydroxystilbamidine); Fluor-Ruby; FluorX; FM 1-43™; FM 4-46; Fura Red™;
 Fura Red™/Fluo-3; Fura-2; Fura-2/BCECF; Genacryl Brilliant Red B; Genacryl Brilliant Yellow
 10GF; Genacryl Pink 3G; Genacryl Yellow 5GF; GeneBlazer (CCF2); a fluorescent protein (e.g.,
 GFP (S65T); GFP red shifted (rsGFP); GFP wild type, non-UV excitation (wtGFP); GFP wild
 type, UV excitation (wtGFP); and GFPuv); Gloxalic Acid ; Granular Blue; Haematoporphyrin;
 15 Hoechst 33258; Hoechst 33342; Hoechst 34580; HPTS; Hydroxycoumarin; Hydroxystilbamidine
 (FluoroGold); Hydroxytryptamine; Indo-1; Indodicarbocyanine (DiD); Indocyanine Green
 (ICG); Indotricarbocyanine (DiR); Intrawhite Cf; JC-1; JO-JO-1; JO-PRO-1; Laurodan; LDS 751
 (DNA); LDS 751 (RNA); Leucophor PAF; Leucophor SF; Leucophor WS; Lissamine
 Rhodamine; Lissamine Rhodamine B ; Calcein/Ethidium homodimer; LOLO-1; LO-PRO-1;
 20 Lucifer Yellow; luminol, Lyso Tracker Blue; Lyso Tracker Blue-White; Lyso Tracker Green;
 Lyso Tracker Red; Lyso Tracker Yellow; LysoSensor Blue; LysoSensor Green; LysoSensor
 Yellow/Blue; Mag Green; Magdala Red (Phloxin B); Mag-Fura Red; Mag-Fura-2; Mag-Fura-5;
 Mag-Indo-1; Magnesium Green; Magnesium Orange; Malachite Green; Marina Blue; Maxilon
 Brilliant Flavin 10 GFF; Maxilon Brilliant Flavin 8 GFF; Merocyanin; Methoxycoumarin;
 25 Mitotracker Green FM; Mitotracker Orange; Mitotracker Red; Mitramycin ; Monobromobimane;
 Monobromobimane (mBBBr-GSH); Monochlorobimane; MPS (Methyl Green Pyronine Stilbene);
 NBD; NBD Amine; Nile Red; NED™; Nitrobenzoxadidole; Noradrenaline; Nuclear Fast Red;
 Nuclear Yellow; Nylosan Brilliant Iavin E8G; Oregon Green; Oregon Green 488-X; Oregon
 Green™; Oregon Green™ 488; Oregon Green™ 500; Oregon Green™ 514; Pacific Blue;
 30 Pararosaniline (Feulgen); PBFI; PE-Cy5; PE-Cy7; PerCP; PerCP-Cy5.5; PE-TexasRed [Red
 613]; Phloxin B (Magdala Red); Phorwite AR; Phorwite BKL; Phorwite Rev; Phorwite RPA;

Phosphine 3R; Phycoerythrin B [PE]; Phycoerythrin R [PE]; PKH26 (Sigma); PKH67; PMIA; Pontochrome Blue Black; POPO-1; POPO-3; PO-PRO-1; PO-PRO-3; Primuline; Procion Yellow; Propidium Iodid (PI); PyMPO; Pyrene; Pyronine; Pyronine B; Pyrozal Brilliant Flavin 7GF; QSY 7; Quinacrine Mustard; Red 613 [PE-TexasRed]; Resorufin; RH 414; Rhod-2; Rhodamine; Rhodamine 110 ; Rhodamine 123; Rhodamine 5 GLD; Rhodamine 6G; Rhodamine B; Rhodamine B 200; Rhodamine B extra; Rhodamine BB; Rhodamine BG; Rhodamine Green; Rhodamine Phallicidine; Rhodamine Phalloidine; Rhodamine Red; Rhodamine WT ; Rose Bengal; R-phycoerythrin; R-phycoerythrin (PE); RsGFP; S65A; S65C; S65L; S65T; Sapphire GFP; SBF1; Serotonin; Sevron Brilliant Red 2B; Sevron Brilliant Red 4G; Sevron Brilliant Red B; Sevron Orange; Sevron Yellow L; sgBFP™; sgBFP™ (super glow BFP); sgGFP™; sgGFP™ (super glow GFP); SITS; SITS (Primuline); SITS (Stilbene Isothiosulphonic Acid); SNAFL calcein; SNAFL-1; SNAFL-2; SNARF calcein; SNARF1; Sodium Green; SpectrumAqua; SpectrumGreen; SpectrumOrange; Spectrum Red; SPQ (6-methoxy-N-(3-sulfopropyl)quinolinium); Stilbene; Sulphorhodamine B can C; Sulphorhodamine G Extra; SYTO 11 ; SYTO 12; SYTO 13; SYTO 14; SYTO 15; SYTO 16; SYTO 17; SYTO 18; SYTO 20; SYTO 21; SYTO 22; SYTO 23; SYTO 24; SYTO 25; SYTO 40; SYTO 41; SYTO 42; SYTO 43; SYTO 44; SYTO 45; SYTO 59; SYTO 60; SYTO 61; SYTO 62; SYTO 63; SYTO 64; SYTO 80; SYTO 81; SYTO 82; SYTO 83; SYTO 84; SYTO 85; SYTOX Blue; SYTOX Green; SYTOX Orange; TET™; Tetracycline; Tetramethylrhodamine (TRITC); Texas Red™; Texas Red-X™ conjugate; Thiadicarbocyanine (DiSC3); Thiazine Red R; Thiazole Orange; Thioflavin 5; Thioflavin S; Thioflavin TCN; Thiolyte; Thiozole Orange; Tinopol CBS (Calcofluor White); TMR; TO-PRO-1; TO-PRO-3; TO-PRO-5; TOTO-1; TOTO-3; TriColor (PE-Cy5); TRITC TetramethylRhodamineIsoThioCyanate; True Blue; TruRed; Ultralite; Uranine B; Uvitex SFC; VIC®; wt GFP; WW 781; X-Rhodamine; XRITC; Xylene Orange; Y66F; Y66H; Y66W; Yellow GFP; YFP; YO-PRO-1; YO-PRO-3; YOYO-1; YOYO-3; and salts thereof.

6. Kits

Also provided are kits comprising the peptide probes, synthetic A β oligomers, and/or labels described herein. The kits may be prepared for practicing the methods described herein. Typically, the kits include at least one component or a packaged combination of components

useful for practicing a method. By “packaged combination” it is meant that the kits provide a single package that contains a combination of one or more components, such as probes, buffers, instructions for use, and the like. A kit containing a single container is included within the definition of “packaged combination.” The kits may include some or all of the components
5 necessary to practice a method disclosed herein. Typically, the kits include at least one probe in at least one container. The kits may include multiple probes which may be the same or different, such as probes comprising different sequences and/or different labels, in one or more containers. Multiple probes may be present in a single container or in separate containers, each containing a single probe.

10 EXAMPLES

EXAMPLE 1 – FLOW CYTOMETRY ASSAY ON WHOLE BLOOD

A. First Sample: without synthetic A β oligomer

A first sample containing whole blood is obtained from a subject by venipuncture and collected in EDTA tubes. Peptide probe labeled with FITC (PEP-11) stored in organic solvent is brought
15 to room temperature. The organic solvent is then removed by rotovaporation or air evaporation. The first sample is then diluted in HEPES-buffered saline and subsequently combined with the peptide probe solution. The resulting combination is stored in the dark at room temperature for up to an hour, in order to allow the labeled peptide probe to bind to (e.g., associate with and/or form a complex with) any A β oligomer associated with cells present in the first test sample.

20 B. Second Sample: with synthetic A β oligomer

A second sample containing whole blood is obtained in the same manner as described above. The second sample is then diluted in HEPES-buffered saline and subsequently combined with synthetic A β oligomer, allowing the synthetic A β oligomer to bind to cells (e.g., associate with and/or form a complex with) present in the second sample or any A β oligomer associated with
25 the cells. Peptide probe labeled with FITC (PEP-11) stored in organic solvent is brought to room temperature and diluted with saline. The organic solvent is then removed by rotovaporation or air evaporation. The peptide probe is then combined with the second sample containing whole blood and synthetic A β oligomer. The combination is stored in the dark at room temperature,

allowing the labeled peptide probe to bind to (e.g., associate with and/or form a complex with) any A β oligomer and synthetic A β oligomer associated with cells.

C. Flow Cytometry Analysis

After storage, the first and second samples are subjected to a FACScan flow cytometer in TruCount Tubes to isolate erythrocytes in the test samples. The erythrocytes in the test samples are gated in logarithmic forward/side scatter dot plots, and the fluorescence of the FITC labels are detected by appropriate bandpass filters.

EXAMPLE 2 – FLOW CYTOMETRY ASSAY ON ERYTHROCYTES IN WHOLE BLOOD

First and second samples are obtained from a normal subject (i.e., does not have Alzheimer's Disease) and a subject with Alzheimer's Disease. The samples are processed and analyzed in accordance with the procedure in EXAMPLE 1.

FIGURE 2 is a depiction of the first sample from each subject (i) before labeled peptide probe is added to the samples (left column); and (ii) after the labeled peptide probe is added to the samples (right column). As seen in the left column, endogenous A β oligomer is associated with erythrocytes to a greater degree in subjects with Alzheimer's disease. As seen in the right column, labeled peptide probe associates with (e.g., forms a complex with) A β oligomer associated with erythrocytes, permitting detection and quantification of endogenous A β oligomer associated with erythrocytes (e.g., by detection of peptide probe- A β oligomer-erythrocyte complexes).

FIGURE 3 shows FITC signals from the first samples (endogenous A β oligomer only) probed with PEP-11 peptide probe (SEQ ID NO:64). Complexes comprising labeled peptide probe-endogenous A β oligomer-erythrocytes are detected. The signal (fluorescence intensity) corresponding to the subject with Alzheimer's Disease is great than that corresponding to the normal subject, reflecting the greater amount of A β oligomer present in the sample from the subject with Alzheimer's Disease.

FIGURE 4 is a depiction of the second sample from each subject (i) before synthetic A β oligomer or labeled peptide probe is added to the samples (left column); (ii) after the

synthetic A β oligomer is added to the samples (middle column) and (iii) after the PEP-11 peptide probe is added to the samples (right column). As with FIGURE 2, as seen in the left column, endogenous A β oligomer is associated with erythrocytes to a greater degree in subjects with Alzheimer's disease. As seen in the middle column, synthetic A β oligomers associate with erythrocytes to a greater degree in the sample obtained from the normal subject as compared to the sample from the subject with Alzheimer's Disease. Without being bound by theory, it is believed that erythrocytes in subjects with Alzheimer's Disease already are associated with endogenous A β oligomer and thus have less capacity for association with synthetic A β oligomer. As seen in the right column, labeled peptide probe associates with endogenous and synthetic A β oligomers.

FIGURE 5 shows FITC signals from the second samples after the synthetic A β oligomer and labeled peptide probe are added to the samples. Complexes comprising labeled peptide probe-endogenous A β oligomer-erythrocytes and complexes comprising labeled peptide probe-synthetic A β oligomer-erythrocytes are detected. Comparing the figure to FIGURE 3, the signal for the subject with Alzheimer's Disease is roughly the same as in FIGURE 3, indicating that the amount of A β oligomer associated with erythrocytes is about the same before and after from the addition of synthetic A β oligomer. In contrast, the signal for the normal subject is significantly shifted to the right (e.g., a greater signal) in FIGURE 3, indicating that the amount of A β oligomer associated with erythrocytes is greater after the addition of synthetic A β oligomer.

FIGURE 6 overlays the signals from FIGURES 3 and 5 for the normal and AD subjects, and highlights the signal shift or "delta" (binding capacity) between the signal obtained with and without synthetic A β oligomer in the normal subject. It is believed that this signal shift is inversely correlated with the endogenous A β oligomer load of the erythrocytes, and thus the A β oligomer load of the subject, with a greater signal shift being correlated a low A β oligomer load and thus normal (non-AD) disease state, and a small signal shift being associated with a higher A β oligomer load and thus a higher risk of disease or more advanced disease state.

These data illustrate how the methods of EXAMPLE 1 and 2 can be used to distinguish between a normal subject and a subject with Alzheimer's Disease. Furthermore, this assay format could be used to provide a baseline A β oligomer load status of a normal subject that could be monitored over time for the risk or development of disease. Likewise, this assay format could be

used to provide a baseline A β oligomer load status of an AD subject that could be monitored over time for the progression of disease and/or success of therapeutic treatments.

A sample of whole blood was obtained from another normal subject and processed as indicated in EXAMPLE 1. FIGURE 7 depicts the delta shift (binding capacity) between the signal of the first (no synthetic A β oligomer) and second (synthetic A β oligomer) samples.

EXAMPLE 3 – FLOW CYTOMETRY ON PLATELETS IN PLASMA

A first sample containing platelet rich plasma (PRP) is obtained by separating whole blood or from a frozen sample of previously separated whole blood. The first sample is verified to contain PRP by flow cytometry (e.g., by detecting CD-41 as a surface marker). Peptide probe labeled with FITC (PEP-11) stored in organic solvent is brought to room temperature. The organic solvent is removed by rotovaporation or air evaporation. The first sample is diluted in HEPES-buffered saline and subsequently combined with the peptide probe solution. The resulting combination is stored in the dark at room temperature for up to an hour, in order to allow the labeled peptide probe to bind to any A β oligomer associated with platelets present in the first sample.

A second sample containing PRP is obtained in the same manner as described above. The second sample is diluted in HEPES-buffered saline and subsequently combined with synthetic A β oligomer, and the synthetic A β oligomer is allowed to bind to any A β oligomer associated with platelets present in the second sample. Peptide probe labeled with FITC (PEP-11) stored in organic solvent is brought to room temperature. The organic solvent is removed by rotovaporation or air evaporation. The peptide probe is combined with the second sample and the resulting combination is stored in the dark at room temperature, allowing the labeled peptide probe to bind to any A β oligomer (endogenous and synthetic) associated with platelets present in the samples.

The first and second samples are subjected to a FACScan flow cytometer in TruCount Tubes to isolate platelets in the test samples. The platelets in the test samples are gated in logarithmic forward/side scatter dot plots, and the fluorescence of the FITC labels are detected by appropriate bandpass filters. In the first sample, complexes comprising labeled peptide probe-endogenous A β oligomer-platelets will be detected, while in the second sample complexes comprising

labeled peptide probe-endogenous A β oligomer-platelets and complexes comprising labeled peptide probe-synthetic A β oligomer-platelets will be detected.

EXAMPLE 4 – FLOW CYTOMETRY ON CEREBROSPINAL FLUID

Cerebrospinal fluid (CSF) is obtained from a subject by either lumbar puncture or from a previously separated frozen sample (clinical collection). Peptide probe labeled with FITC (PEP-11) stored in organic solvent is brought to room temperature. The organic solvent is removed by rotovaporation or air evaporation. The CSF is diluted in HEPES-buffered saline and combined with the peptide probe solution. The resulting combination is stored in the dark at room temperature for up to an hour, in order to allow the labeled peptide probe to bind to any A β oligomer present in the first test sample.

The sample is subjected to a FACScan flow cytometer in TruCount Tubes. Any A β oligomer in the test sample is gated in logarithmic forward/side scatter dot plots, and the fluorescence of the FITC labels are detected by appropriate bandpass filters. Complexes comprising labeled peptide probe and A β oligomer are detected.

EXAMPLE 5 – PEPTIDE LINKED IMMUNOSORBENT ASSAY (PLISA)

FIGURE 8 depicts different formats for a PLISA as described herein. PLISA (A) depicts a sandwich format in which a target oligomer, such as an A β oligomer (SDS Oligo), binds to both surface-bound peptide probe (peptide) and peptide probe tagged with a label (Tag). The complex is detected using a labeled antibody (Anti-TagAb-label). PLISA (B) depicts a sandwich format in which the peptide probe tagged with a label is replaced by a labeled antibody (Ab-label) specific to the A β oligomer. PLISA (C) depicts a sandwich format in which the surface-bound peptide probe is replaced with an antibody specific to the A β oligomer (Ab-6E10). PLISA (D) depicts a competitive format in which A β oligomer in a biological sample competes with surface-bound A β oligomer for a labeled peptide probe. Each of PLISA (A)-(D) can use a solid-phase format (shown here as a bead, in which the bead is passed through an apparatus for detecting the labels).

EXAMPLE 6 – PLISA IS MORE SENSITIVE AND SELECTIVE COMPARED TO ELISA

Different concentrations of A β oligomer in solution are subjected to both PLISA and ELISA to determine the sensitivity of each assay, as measured by dose response curves. For the PLISA assay, the peptide probe used is AD317 (SEQ ID NO:41). For the ELISA, the antibody used is A β antibody 6E10 labeled with horse radish peroxidase. As shown in FIGURE 9, the PLISA is a more sensitive assay for detecting A β oligomer than the ELISA.

Three different concentrations (nN) of A β oligomer, A β monomer, and A β fiber in solution were subjected to both PLISA and ELISA, either in buffer or 10% CSF, to determine the selectivity of each assay for A β oligomer as compared to the other A β forms. Tables 1 and 2 in FIGURE 10 depict the results in buffer and 10% CSF, respectively, presented as a percent ratio of (monomer or fiber)/oligomer signal for the different oligomer concentrations. The data presented in both tables demonstrate a greater selectivity of PLISA for A β oligomer over both A β monomer and A β fiber, as compared to ELISA.

EXAMPLE 7 – PLISA USING PEP-11 DISTINGUISHES A β OLIGOMER FROM MONOMER AND FIBER

Different aggregate forms of A β protein (monomer, oligomer, and fiber) are subjected to PLISA using different PEP-11 peptide probe (Pep11-a, Pep11-b and Pep11-ds) and a control sample without PEP-11 peptide probe. Both Pep11-a and Pep11-b consist of SEQ ID NO:64, at a purity of 86% (standard) and 95% (high), respectively, as determined by high performance liquid chromatography (200 nm, C18, linear gradient). PEP-11ds is also represented by SEQ ID NO:64, but has a disulfide bridge at the two cysteines. High performance liquid chromatography (200 nm, C18, linear gradient) determined the purity of PEP-11ds to be 86.46%.

FIGURE 11 demonstrates that all of the PEP-11 peptides detect A β oligomer in a dose-dependent manner, and exhibit preferential binding to A β oligomer as compared to A β monomer or fiber. These results demonstrate that the PEP-11 peptide probe preferentially binds to A β oligomer and can distinguish A β oligomer from other types of A β protein aggregates.

EXAMPLE 8 – DETECTION OF A β OLIGOMER IN HUMAN CSF

Samples of CSF from a normal human subject are spiked with different concentrations of synthetic A β oligomer, and subjected to fluorescence detection assay using peptide probe AD315

(SEQ ID NO:65). The detection is performed in an assay with the following conditions: 10 mM HEPES buffer at pH 7.0; 0.005% NP-40; 10% normal human cerebrospinal fluid; 70 nM pyrenated peptide; and 37 °C incubation.

FIGURE 12 depicts the results, which show a linear, dose-dependent curve. The results demonstrate that the assay can be used to detect A β oligomer in cerebrospinal fluid.

EXAMPLE 9 – PEPTIDE PROBE BINDS A β 42 OLIGOMER

An assay is performed to analyze peptide probe binding to A β 42 oligomer. The peptide probe is the same as the probe in EXAMPLE 8. Five samples are analyzed: (1) A β 42 biotinylated oligomer as a positive control; (2) A β 42 biotinylated oligomer bound to a bead via streptavidin; (3) peptide positive control; (4) peptide probe bound to A β 42 biotinylated oligomer bound to a bead via streptavidin; and (5) peptide probe bound to a bead via streptavidin. Detection was by gel electrophoresis. Results are shown in FIGURE 13. As column 4 indicates by the presence of streptavidin, peptide probe can be used to detect A β 42 oligomer.

FIGURE 13 also shows a graph of fluorescent anisotropy (milli-r) as a function of A β 42 oligomer concentration (nN). The peptide probe used to produce this data is the same as the peptide probe for the gel electrophoresis data above. Anisotropy decreases as oligomer concentration increases.

The results of the assay, as presented by FIGURE 13, show that the peptide probes demonstrate specificity and sensitivity for the oligomeric form of A β protein.

EXAMPLE 10 – CLINICAL STUDY

Samples of human CSF from (1) subjects likely having Alzheimer's Disease (AD) (47 samples); (2) subjects having Mild Cognitive Impairment (MCI) (21 samples); and (3) normal subjects (i.e., not having AD or MCI) (32 samples) are subjected to an assay using pyrenated peptide. The purpose of the assay is to determine whether pyrenated peptide can accurately distinguish CSF samples based on the clinical condition of the subjects. The results of the assay are compared against results of commercially available ELISA kits that detect A β 42 oligomer, total tau and phosphorylated-tau.

FIGURE 14 demonstrates that peptide probe AD272 (SEQ ID NO: 22), can distinguish between MCI and normal subjects ($p \leq 0.012$) and between AD and normal subjects ($p \leq 0.030$) using fluorescence detection.

WHAT IS CLAIMED IS:

1. A method of detecting A β oligomers in a biological sample obtained from a subject, comprising:

preparing a test sample comprising the biological sample and a peptide probe,

wherein the peptide probe consists of from 10 to 34 amino acid residues comprising an amino acid sequence that is at least 70% identical to any one of SEQ ID NOs:1-56 and 62-65, wherein the peptide probe preferentially binds to A β oligomers and is labeled with a fluorescent label capable of emitting a fluorescent signal, wherein the peptide probe forms complexes with any A β oligomer present in the biological sample;

subjecting the test sample to flow cytometry to detect the fluorescent signal of the complexes;

wherein the fluorescent signal of the complexes is directly correlated with the presence and amount of A β oligomers in the biological sample.

2. A method of determining the A β oligomer load of a subject by detecting A β oligomer associated with cells present in a biological sample obtained from the subject, comprising:

preparing a first test sample comprising a biological sample from the subject that comprises cells and a peptide probe,

wherein the peptide probe consists of from 10 to 34 amino acid residues comprising an amino acid sequence that is at least 70% identical to any one of SEQ ID NOs:1-56 and 62-65, wherein the peptide probe preferentially binds to A β oligomers and is labeled with a detectable label, wherein the peptide probe forms a first complex with A β oligomer associated with cells in the biological sample;

detecting a signal of the first complex in the first test sample;

preparing a second test sample comprising a biological sample from the subject that comprises cells, synthetic A β oligomer, and the peptide probe, wherein the peptide probe forms second complexes with A β oligomer associated with cells in the biological sample and with synthetic A β oligomer;

detecting a signal of the second complexes in the second test sample;

wherein a difference between the signal of the first complex in the first test sample and the signal of the second complexes in the second test sample is inversely correlated with the A β oligomer load of the subject.

3. The method according to claim 2, wherein the second test sample is prepared by combining the biological sample and synthetic A β oligomer, and subsequently introducing the peptide probe.

4. An *in vitro* method of detecting A β oligomer associated with erythrocytes, comprising:

contacting erythrocytes with a peptide probe,

wherein the peptide probe consists of from 10 to 34 amino acid residues comprising an amino acid sequence that is at least 70% identical to any one of SEQ ID NOs:1-56 and 62-65, wherein the peptide probe preferentially binds to A β oligomers and is labeled with a detectable label, wherein the peptide probe forms a complex with A β oligomer associated with erythrocytes; and

detecting a signal of the complex.

5. An *in vitro* method of detecting A β oligomer present associated with platelets, comprising:

contacting platelets with a peptide probe,

wherein the peptide probe consists of from 10 to 34 amino acid residues comprising an amino acid sequence that is at least 70% identical to any one of SEQ ID NOs:1-56 and 62-65, wherein the peptide probe preferentially binds to A β oligomers and is labeled with a detectable label, wherein the peptide probe forms a complex with A β oligomer present on the surface of platelets; and

detecting a signal of the complex.

6. The method according to any one of the preceding claims, wherein the peptide probe consists of SEQ ID NO:64 (Pep-11).

7. The method according to any one of claims 2-6, wherein the detecting comprises subjecting the test samples to flow cytometry to detect a fluorescent signal of the complexes.
8. The method according to any one of claims one of claims 2-6, wherein the detectable label is a fluorescent label.
9. The method according to any one of the preceding claims, wherein the fluorescent label is an FITC label.
10. The method according to any one of claims 2-7, wherein the detectable label is a pyrene moiety and the detecting comprises detecting pyrene excimer formation.
11. The method according to any one of the preceding claims, wherein the detecting comprises direct detection of the fluorescent signal of the complex or complexes.
12. The method according to any one of claims 1-3 and 6-12, wherein the biological sample comprises a sample of body fluid.
13. The method according to claim 12, wherein the body fluid is selected from the group consisting of blood, blood plasma, CSF, and brain homogenate.
14. The method according to claim 13, wherein the body fluid comprises erythrocytes.
15. The method according to claim 14, wherein the erythrocytes are isolated erythrocytes.
16. The method according to claim 13, wherein the body fluid comprises platelets.
17. The method according to claim 16, wherein the platelets are isolated platelets.
18. The method according to any one of claims 1-3 and 6-17, wherein the A β oligomer is associated with one or more cells.

19. The method according to claim 18, wherein the one or more cells is selected from the group consisting of an erythrocyte, a platelet, a leukocyte or a tissue cell.
20. The method according to claim 19, wherein the one or more cells comprises an erythrocyte and a platelet.
21. The method according to claim 20, wherein the detecting comprises separately detecting A β oligomer associated with erythrocytes and A β oligomer associated with platelets.
22. The method according to any one of claims 1-3 and 6-21, wherein the complex formed and/or detected comprises peptide probe, A β oligomer, and an erythrocyte from the biological sample.
23. The method according to any one of claims 1-3 and 6-21, wherein the complex formed and/or detected comprises peptide probe, A β oligomer, and a platelet from the biological sample.
24. The method according to any one of claims 1-3 and 6-21, wherein the complex formed and/or detected comprises peptide probe, synthetic A β oligomer, and an erythrocyte or platelet from the biological sample.

FIGURE 1 (following pages)

SEQ ID NO:	Category	Name	Modification	Sequence
1	Wildtype	WT	Aβ protein residues 16-35, with added C-Terminal Lys	KL VFF AEDVG SNKGA IIGLM K
6	Stability	AD250	M35A to replace oxidizable methionine residue	KL VFF AEDVG SNKGA IIGLA K
2	Salt Bridge	P22	Salt bridge at G29H and G33E, also induce alpha-helix, and increase solubility	KL VFF AEDVG SNKHA IIELM K

SEQ ID NO:	Category	Name	Modification	Sequence
65		AD315	Salt bridge at G29H and G33E, also induce alpha-helix, and increase solubility; PBA and NH ₂ additions	PBA-KLVFF AEDVG SNKHA IIELM K(PBA)-NH ₂
14		P22 v.1	Salt bridge at G29R and G33E	KLVFF AEDVG SNKRA IIELM K
15		P22 v.2	Salt bridge at G29K and G33E	KLVFF AEDVG SNKKA IIELM K
3	Salt Bridge + Alpha Helix	P38	Salt bridge at G29H and G33E; Ala substitutions to increase alpha-helicity	KLVFF AEDAA AAKHA IIELM K

SEQ ID NO:	Category	Name	Modification	Sequence
4		P45	Salt bridge at G29H and G33E; Ala additions to increase alpha-helicity	KAAA KLVFF AEDVG SNKHA IIELM K
16	Salt Bridge + A β Binding Motif	P77	Salt bridge; Additional A β binding motif (GxxEG; SEQ ID NO:25); extended N-terminus	HHQ KLVFF AEDEG SRKHA IEGLM EG K
17		P59	Salt bridge; Additional A β binding motif (GxxEG; SEQ ID NO:25)	EAA KLVFF AEDEG SRKHA IEGLM EG K
19	Based on Naturally	Italian	P22, with E22K point mutation	KLVFF AKDVG SNKHA IIELM K

SEQ ID NO:	Category	Name	Modification	Sequence
20	Occurring Mutants	Dutch	P22, with E22Q point mutation	KLVFF AQDVG SNKHA I IELM K
21		Arctic	P22, with E22G point mutation	KLVFF AGDVG SNKHA I IELM K
22	Solubility	AD272	WT, with 2 C-terminal dArg residues, and alternate label site	(PBA)KLVFF AEDVG SNKGA I IGLM K(PBA)rr
23		AD316	P22, with 2 C-terminal dArg residues, and alternate label site	PBA-KLVFF AEDVG SNKHA I IELM K(PBA)rr

SEQ ID NO:	Category	Name	Modification	Sequence
24		AD305	P22, with 2 N-terminal dArg residues, 2 C-terminal E residues and alternate label site	rrK(PBA)LVFF AEDVG SNKHA IIELM K(PBA)EE
1		AD274	WT, with PEG10 at C-terminus	(PBA)KLVFF AEDVG SNKGA IIGLM K(PBA)PEG10
26		AD271	P45, with two dArg residues at C-terminus	(PBA)KAAA KLVFF AEDVG SNKHA IIELM K(PBA)rr
27		AD273	WT, with addition of Ala stretch (for alpha-helix formation) and dArg residues (for solubility)	(PBA)KAAA KLVFF AEDVG SNKGA IIGLM K(PBA)rr

SEQ ID NO:	Category	Name	Modification	Sequence
28	Reduce Stability of B-sheet	AD323	P22, with point mutations H29D and I31D	KLVFF AEDVG SNKDA DIELM K
29		AD325	P22, with point mutation S26D	KLVFF AEDVG DNKHA IIELM K
30		AD330	P22, with point mutation I31D	KLVFF AEDVG SNKHA DIELM K
31		AD329	P22, with point mutation L34D	KLVFF AEDVG SNKHA IEDM K
32		AD328	P22, with point mutation H29D	KLVFF AEDVG SNKDA IIELM K
33		AD327	P22, with point mutation S26D, I31D	KLVFF AEDVG DNKHA DIELM K
34		GM6	P22, with point mutations F19S, L34P	KLVSF AEDVG SNKHA IIEPM K
35		GM6 var.1	P22, with point mutation F19S	KLVSF AEDVG SNKHA IIELM K

SEQ ID NO:	Category	Name	Modification	Sequence
5, 18		I32S	Wildtype, with I32S point mutation	KLVFF AEDVG SNKGA ISGLM K
36	Label (PBA) Site	AD266	WT, with label on side chain of N-terminal Lys	K(PBA)LVFF AEDVG SNKGA IIGLM K(PBA)
37		AD268	WT, with label on side chain of near N-terminal Lys; addition of solubilizing dArg and E residues	EK(PBA)LVFF AEDVG SNKGA IIGLM K(PBA)rrr
38	Biotin	AD310	P22, biotin labeled with helical linker at C-terminus	(PBA)KLVFF AEDVG SNKHA IIGLM K(PBA)EAAAK(biotin)
39		AD313	P22, biotin labeled at side chain of internal Lys	(PBA)KLVFF AEDVG SNK(biotin)HA IIGLM K(PBA)

SEQ ID NO:	Category	Name	Modification	Sequence
40		AD314	P22, biotin labeled with flexible linker at C-terminus	(PBA)KLVFF AEDVG SNKHA IIELM K(PBA)GSSGSSK(biotin)
41		AD317	P22, biotin labeled with thrombin site linker, at C-terminus	(PBA)KLVFF AEDVG SNKHA IIELM K(PBA)GLVP RGSgK(biotin)
42		AD321	P22, biotin labeled with "kinked" linker at C-terminus	(PBA)KLVFF AEDVG SNKHA IIELM K(PBA)PSGSPK(biotin)
2, 43	Label/ Quenche r Pairs	AD326	P22, with pyrene and Dabcyl quencher	(PBA)KLVFF AEDVG SNKHA IIELM K(Dabcyl)

SEQ ID NO:	Category	Name	Modification	Sequence
44		AD309	WT, with EDANS and DabcyI quencher and solubilizing E residue	E(EDANS)LVFF AEDVG SNKGA IIGLM K(DabcyI)
45		AD306	Wildtype A β residues 5-42, with EDANS and DabcyI quencher and solubilizing E residue	E(EDANS)R HDSGY EVHHQ KLVFF AEDVG SNKGA IIGLM VGGVV IA K(DabcyI)
46		AD303	Wildtype A β residues 3-35, with EDANS and DabcyI quencher and solubilizing E residue	E(EDANS)EFR HDSGY EVHHQ KLVFF AEDVG SNKGA IIGLM K(DabcyI)

10/26

SEQ ID NO:	Category	Name	Modification	Sequence
47		AD302	P59, with EDANS and Dabcyl quencher and solubilizing E residue	E(EDANS)AAA KLVFF AEDEG SRKHA IEGLM EGK(Dabcyl)
48		AD301	P77, with EDANS and Dabcyl quencher and solubilizing E residue	E(EDANS)HHQ KLVFF AEDEG SRKHA IEGLM EGK(Dabcyl)
49		AD300	P22 with EDANS and Dabcyl quencher and solubilizing E residue	E(EDANS)LVFF AEDVG SNKHA IIELM K(Dabcyl)
50	FRET Pairs	AD295	P22, with Dansyl and Trp	(Dansyl)KLVFF AEDVG SNKHA IIELM W

SEQ ID NO:	Category	Name	Modification	Sequence
51		AD294	WT, with FAM and EDANS and solubilizing E residue	(FAM)KLVFF AEDVG SNKGA IIGLM E(EDANS)
52		AD293	P22, with FAM and EDANS and solubilizing E residue	(FAM)KLVFF AEDVG SNKHA IIGLM E(EDANS)
53		AD292	A β residues 3-35, with FAM and EDANS and solubilizing E residue	(FAM)EFR HD SGY EVHHQ KLVFF AEDVG SNKGA IIGLM E(EDANS)
54		AD291	P77, with FAM and EDANS and solubilizing E residue	(FAM)HHQ KLVFF AEDEG SRKHA IIGLM EGE(EDANS)

12/26

SEQ ID NO:	Category	Name	Modification	Sequence
55		AD290	P59, with FAM and EDANS, additional Ala, and solubilizing E residue	(FAM)EAA KLVFF AEDEG SRKHA IEGLM EGE(EDANS)
56		WT17-35	A β protein residues 17-35, with added N- and C-Terminal Cys	CLVFF AEDVG SNKGA IIGLMC
63		PEP-10	WT17-35 with FITC label	FITC-Ahx-CLVFF AEDVG SNKGA IIGLMC-NH ₂
64		PEP-11	WT17-35 with FITC and d-Arginine at C-Terminal	FITC-Ahx-CLVFF AEDVG SNKGA IIGLMCrr-NH ₂

SEQ ID NO:	Category	Name	Modification	Sequence
62		PEP-12	P-22 with FITC label, d-Arginine at C-Terminal and Histidine and Glutamic Acid substitutions	FITC-Ahx-CLVFF AEDVG SNKHA IIELMCrr-NH ₂

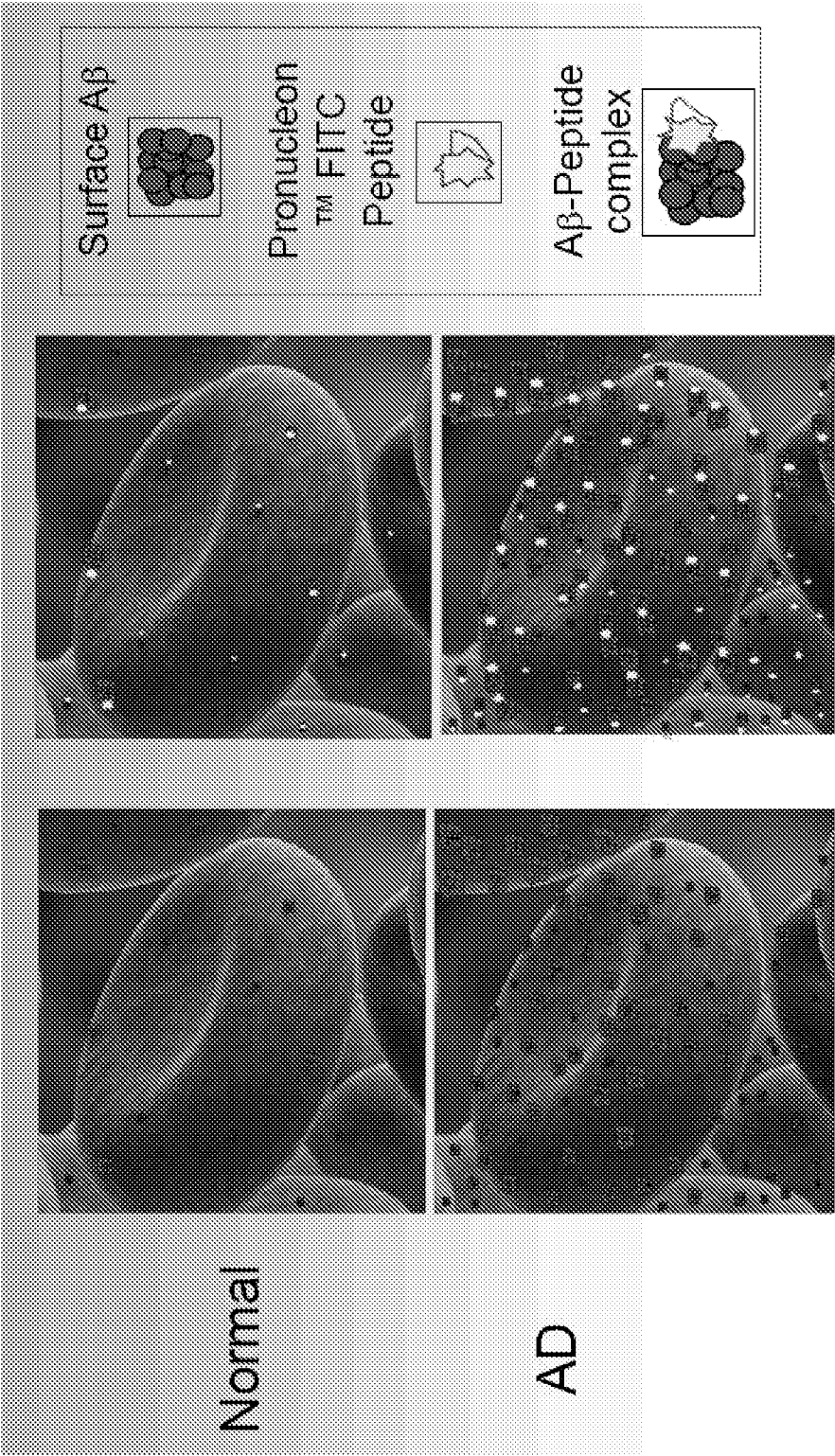


FIGURE 2

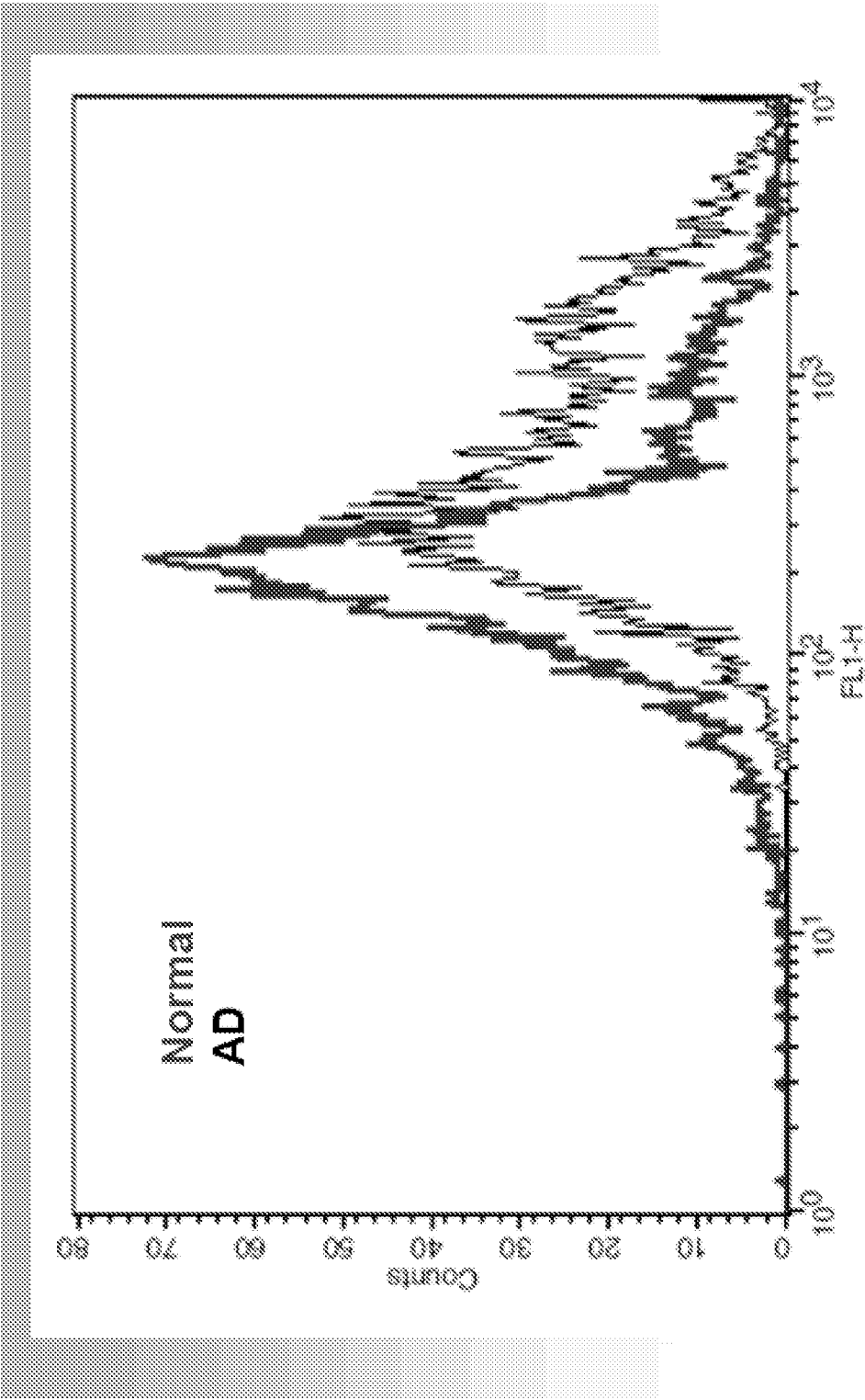


FIGURE 3

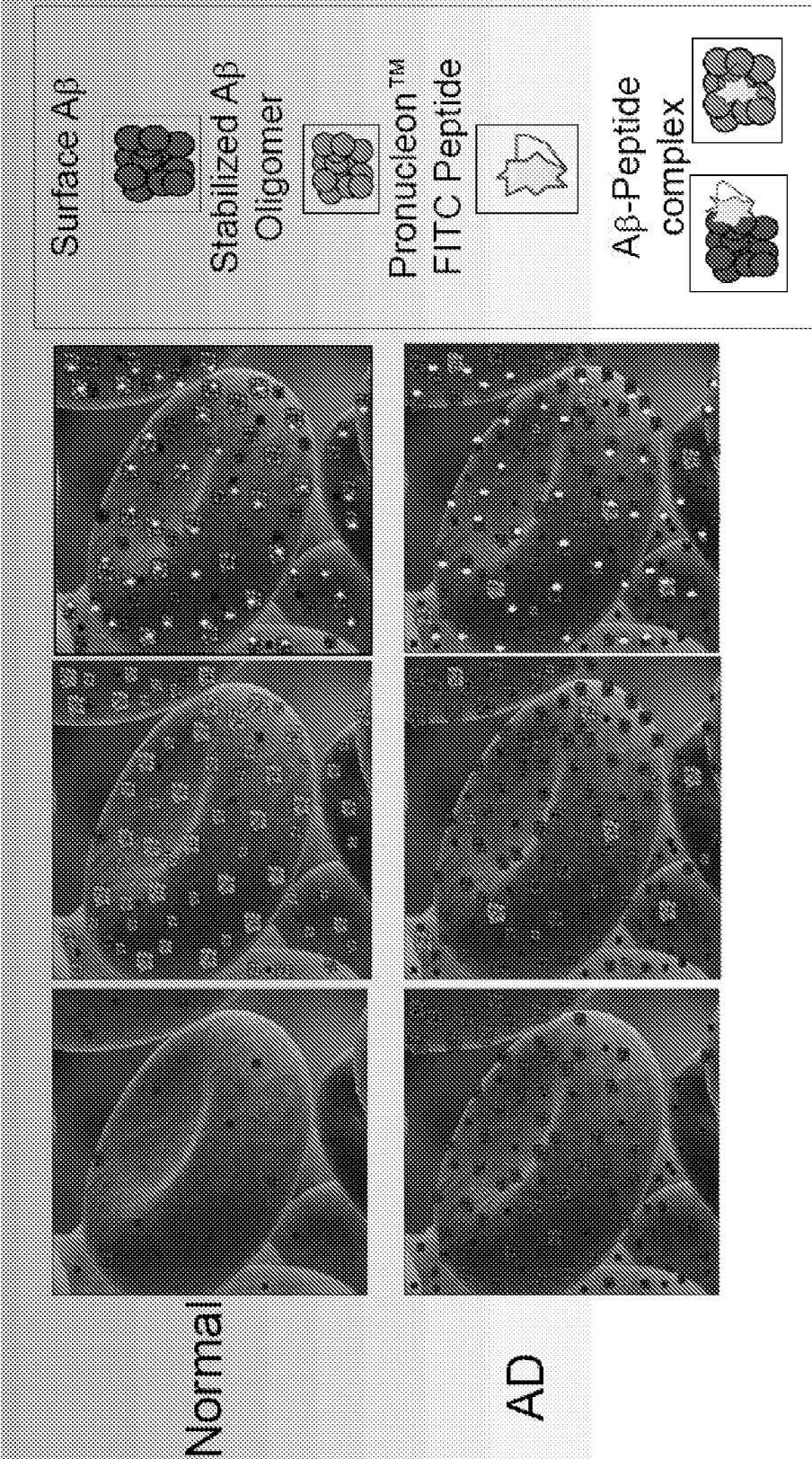


FIGURE 4

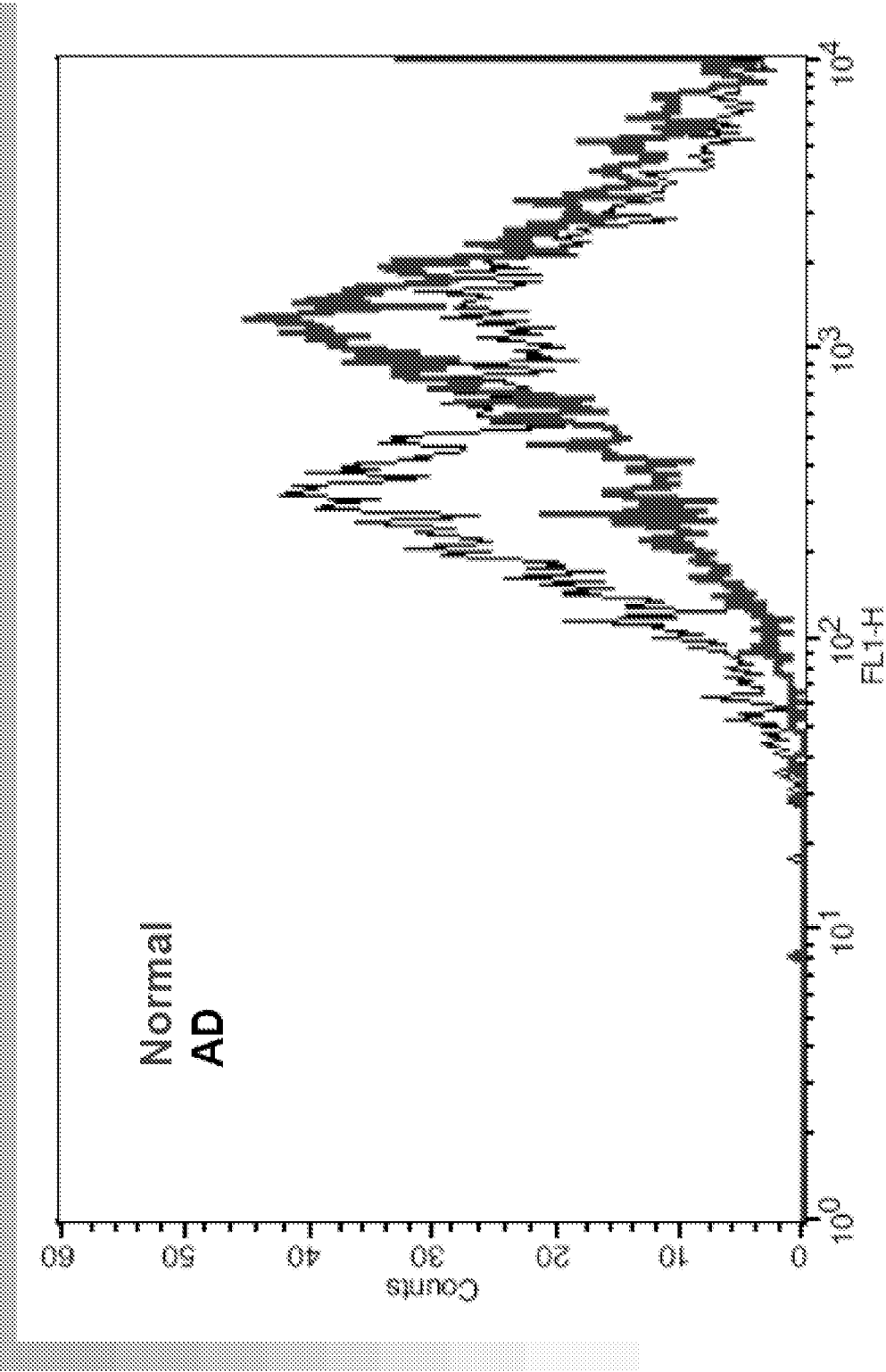


FIGURE 5

18/26

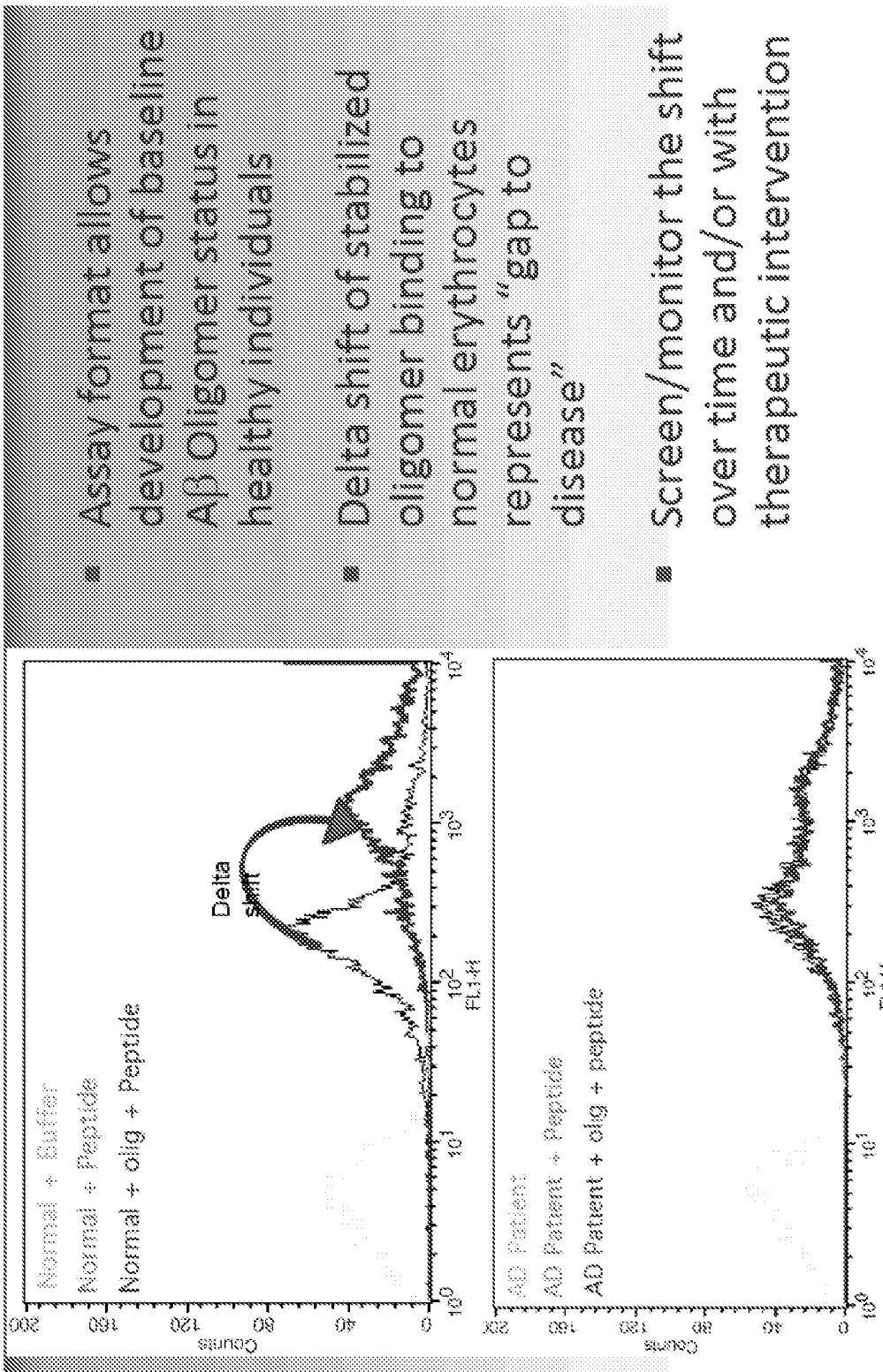
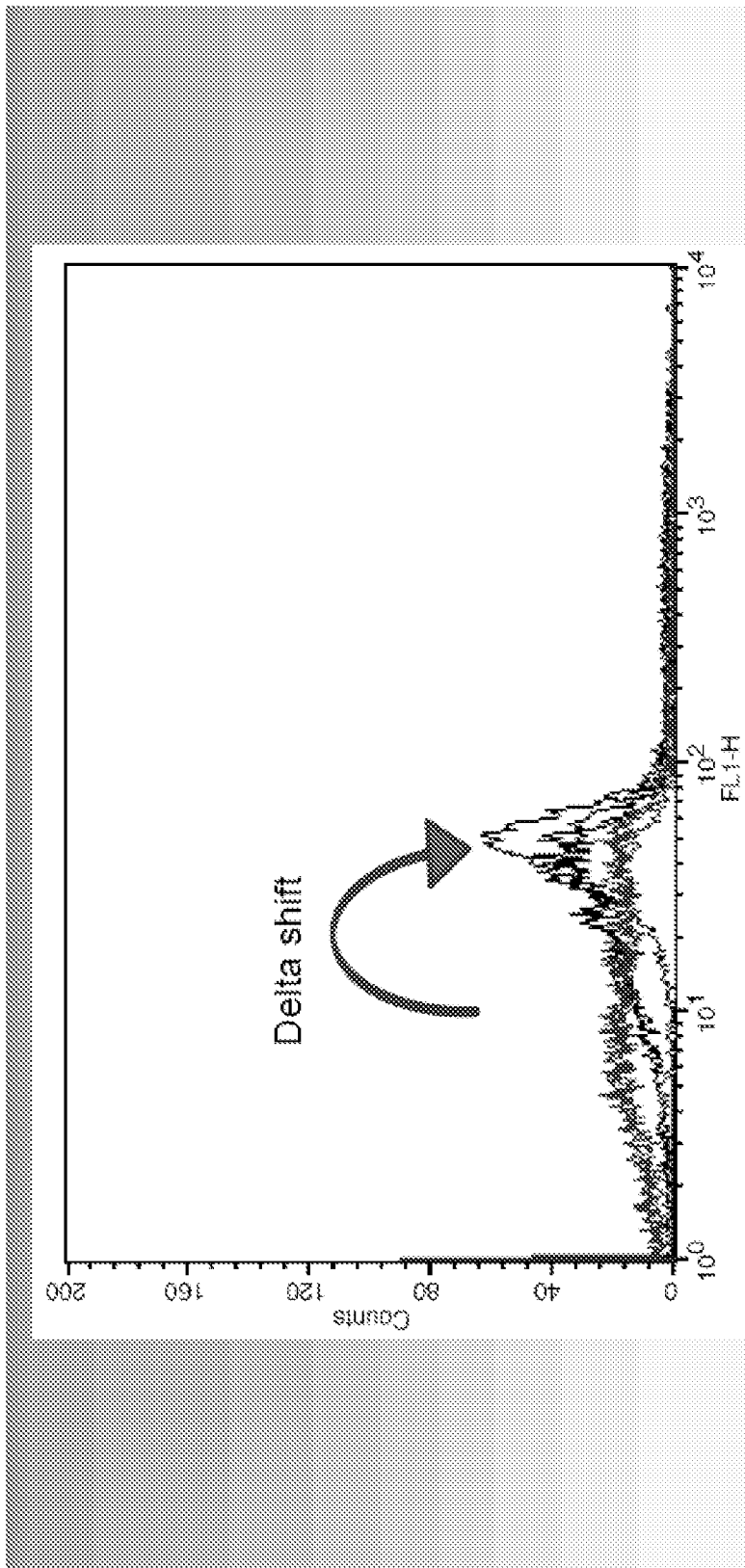


FIGURE 6

- Assay format allows development of baseline Aβ Oligomer status in healthy individuals
- Delta shift of stabilized oligomer binding to normal erythrocytes represents “gap to disease”
- Screen/monitor the shift over time and/or with therapeutic intervention



- Delta shift of stabilized oligomer binding to normal erythrocytes represents first attempt with healthy individual whole blood

FIGURE 7

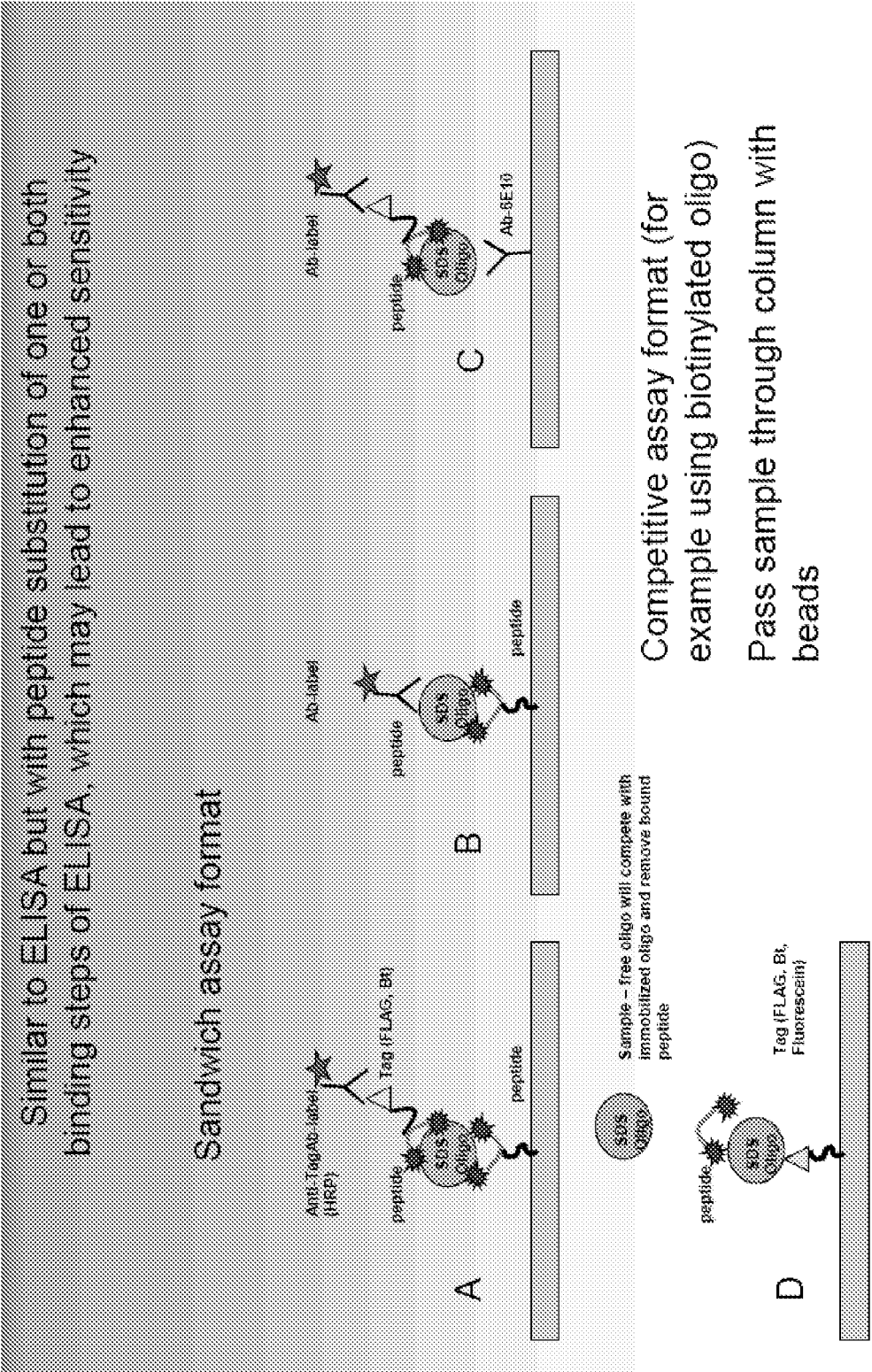


FIGURE 8

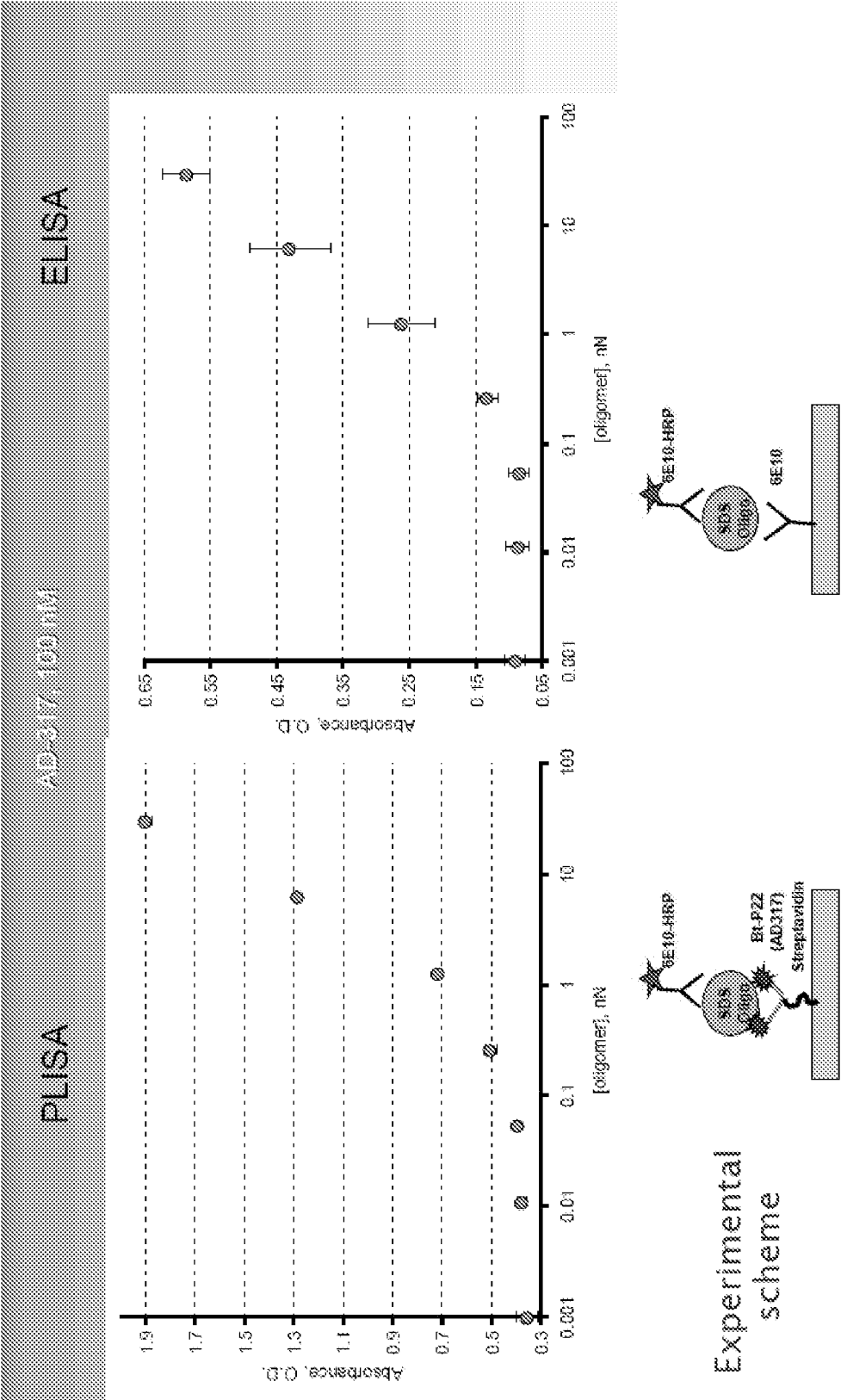


FIGURE 9

PLISA selectivity (compared to ELISA)

Table 1. Percentage of the spiked monomer and fiber signal (from ratio to the spiked oligomer signal) measured by PLISA versus ELISA (in buffer)*

[oligomer], nN	monomer/ oligomer signal in %		fiber / oligomer signal in %	
	PLISA	ELISA	PLISA	ELISA
150	19	80	12	37
50	6	70	12	40
16.7	11	60	22	41

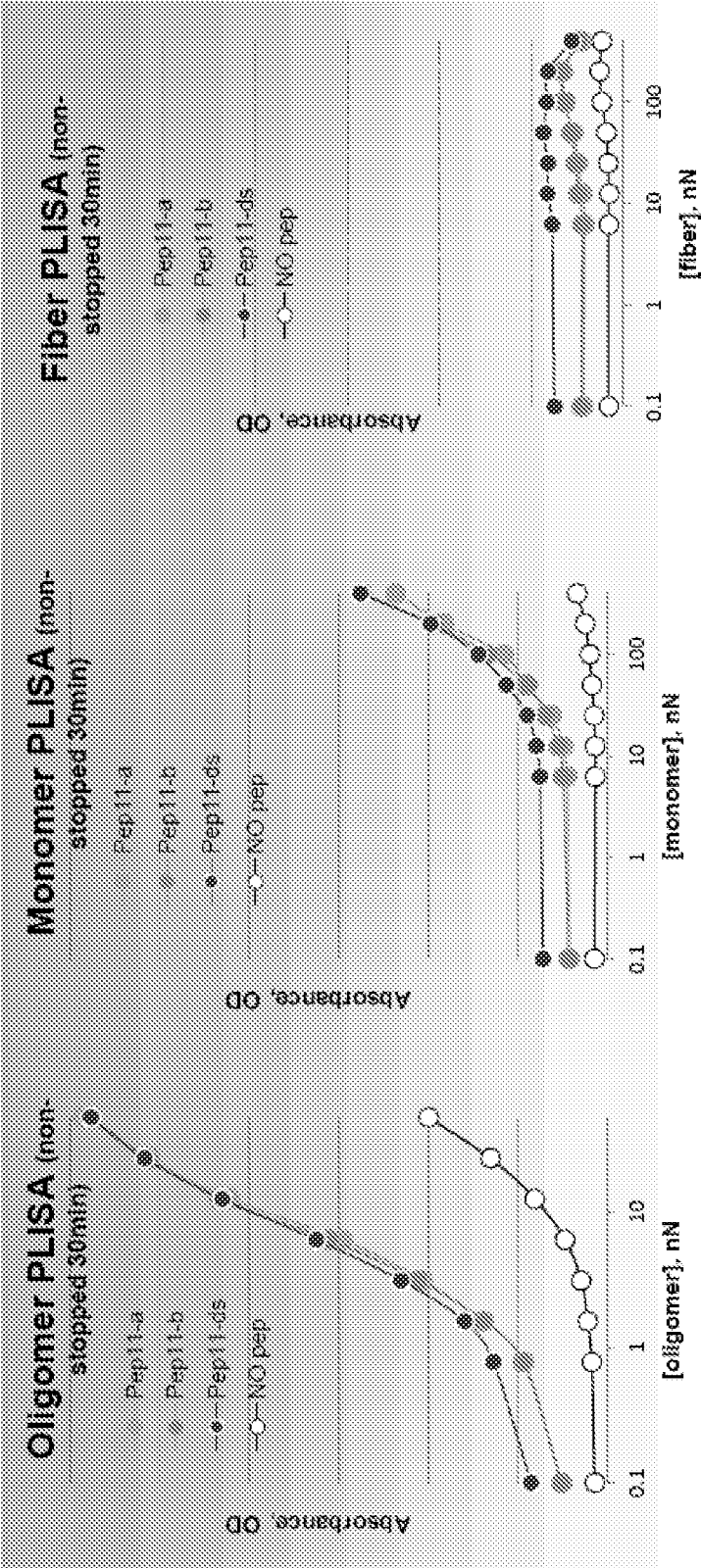
* Peptide: AD-317; blocking buffer TBST (TBS containing 0.05% Tween-20); buffer (20 mM Hepes, pH 7.0, containing 0.05% NP-40 and 1% fish gelatin) spiked with oligomer, or monomer, or fiber.

Table 2. Percentage of the spiked monomer signal (from ratio to the spiked oligomer signal) measured by PLISA versus ELISA (in 10% CSF)**

[oligomer], nN	monomer/ oligomer signal in %	
	PLISA	ELISA
30	17	112
6	14	111
1.2	N/A	113

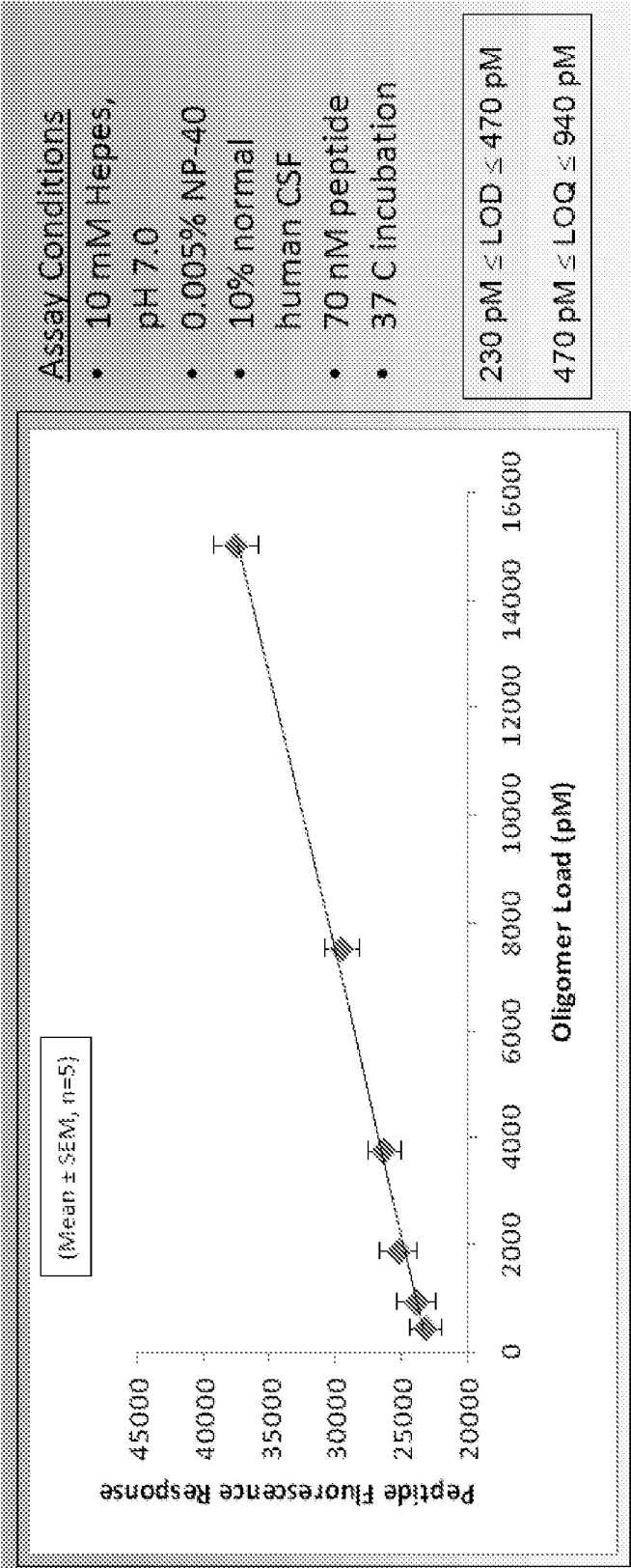
** Peptide: AD-317; blocking buffer TBST (TBS containing 0.05% Tween-20); CSF/buffer – mix of 10% CSF and 90% buffer (20 mM Hepes, pH 7.0, containing 0.05% NP-40 and 10% Superblock) spiked with oligomer, or monomer.

FIGURE 10



Pep11 recognizes Oligomer from Fiber

FIGURE 11



The peptide fluorescence response at 470 pM SDS oligomer is statistically distinguishable from control (0 pM) by t-test (p-value <0.05 at 18 hour time point)

FIGURE 12

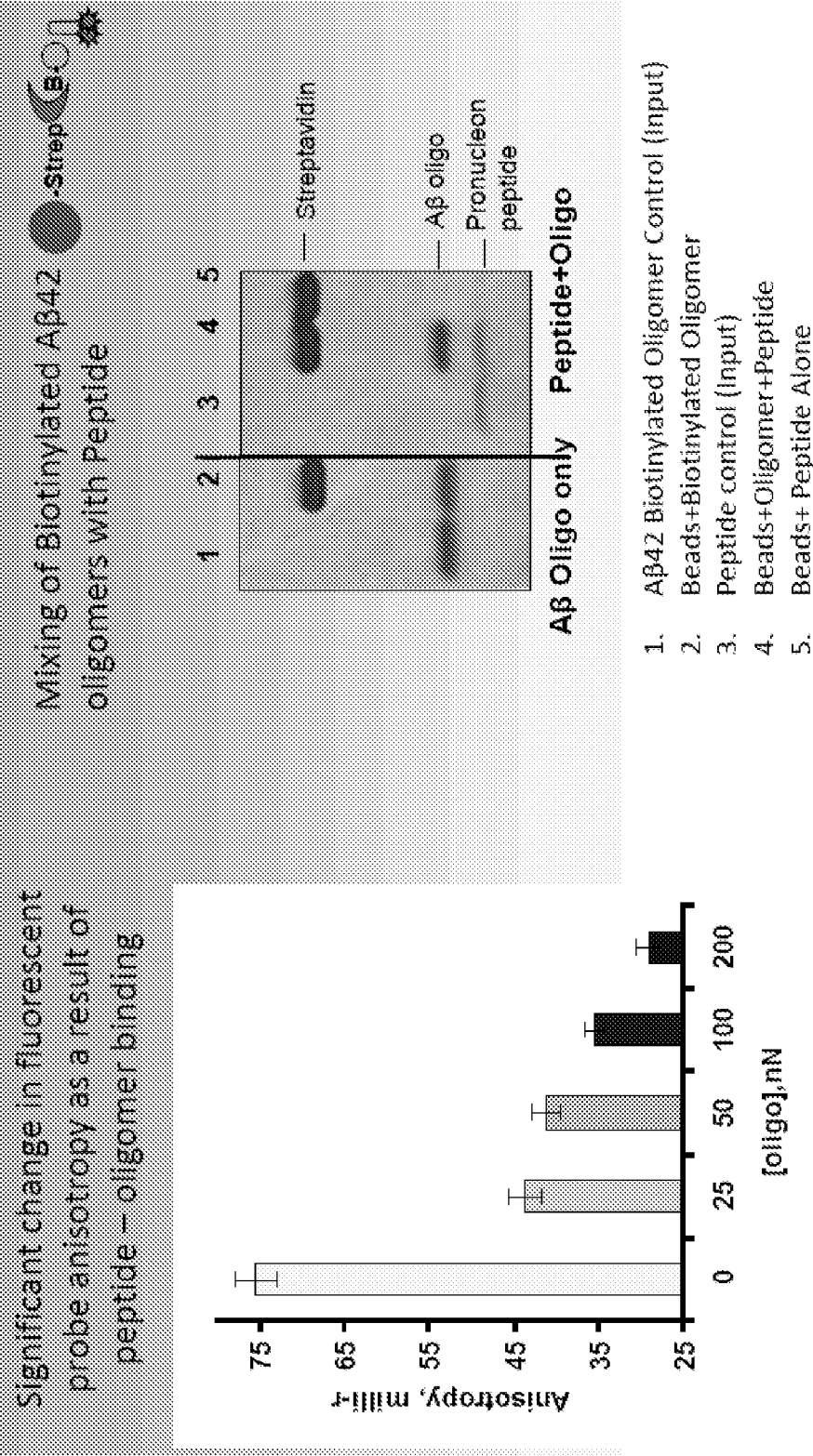
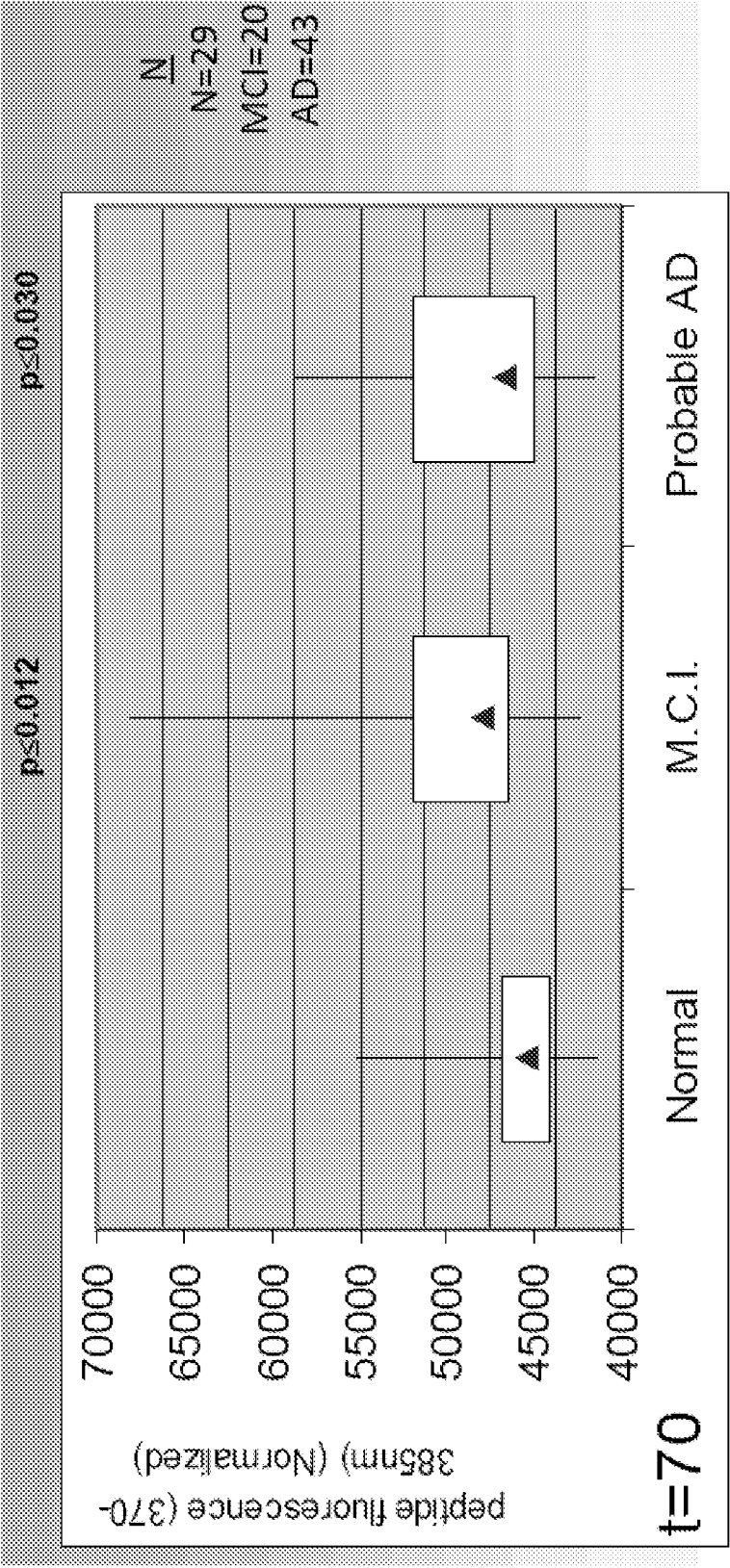


FIGURE 13



Categorization of Clinical CSF samples based on MMSE, CDR, and ASAD-cog cognitive testing scores

FIGURE 14