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## Amyloid-beta oligomerization is associated with the generation of a typical peptide fragment fingerprint

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36 **Author contributions:** AWS conceived the project, designed experiments and directed the  
37 study. AWS, CF, CD and SZ performed mass spectrometry analysis. DD performed electron  
38 Microscopy imaging. AWS, CF and CD performed biochemical studies. PO and OM  
39 performed CSF analysis. NR performed immunohistochemistry. AH and TLS performed  
40 array tomography. MPF performed histological examination of brain tissue. BTH, MPF, NR,  
41 PO and OM provided biological samples. AWS, CF, NR, SZ, MM and BTH wrote the paper.  
42 All authors discussed the results and commented on the paper.

43

44 **Conflict of interest:** none

45

## 46 **ABSTRACT**

47

48 Amyloid-beta ( $A\beta$ ) peptide oligomerization plays a central role in the pathogenesis of  
49 Alzheimer's disease (AD) and  $A\beta$  oligomers are collectively considered an appealing  
50 therapeutic target for the treatment of AD. However, the molecular mechanisms leading to  
51 the pathological accumulation of oligomers are unclear and the exact structural composition  
52 of oligomers is being debated. Using targeted and quantitative mass spectrometry, we reveal  
53 site-specific  $A\beta$  autocleavage during the early phase of aggregation, producing a typical  $A\beta$   
54 fragment signature and that truncated  $A\beta$  peptides can form stable oligomeric complexes with  
55 full-length  $A\beta$  peptide. We show that the use of novel anti- $A\beta$  antibodies raised against these  
56 truncated  $A\beta$  isoforms allows for monitoring and targeting the accumulation of truncated  $A\beta$   
57 fragments. Antibody-enabled screening of transgenic models of AD, as well as human post-  
58 mortem brain tissue and cerebrospinal fluid revealed that, aggregation-associated  $A\beta$   
59 cleavage is a highly relevant clinical feature of AD.

60

61 **1. INTRODUCTION**

62

63 Alzheimer disease (AD) is a progressive neurodegenerative disorder that is manifested as  
64 a gradual decline in memory and cognitive function. A number of studies indicate that  
65 soluble oligomers might account for the AD-associated decline in synaptic plasticity [1, 2]  
66 and that inhibition of natural A $\beta$  oligomerization rescues deficits in long-term potentiation  
67 (LTP) [3]. Several types of A $\beta$  assemblies of dimeric and trimeric [4] [1] [2] or dodecameric  
68 (A $\beta$ \* 56) [5] nature have been observed *in vitro* and *in vivo* in transgenic mouse models,  
69 human cerebrospinal fluid (CSF) [6], and post-mortem AD brain extracts [7] [8], with the  
70 higher molecular weight species being considered the main neurotoxic culprit associated with  
71 cognitive dysfunction. Collectively A $\beta$  oligomers can be considered as an appealing  
72 diagnostic and therapeutic target. However, the general morphological heterogeneity and, to  
73 some extent, metastable structure renders an antibody based targeting and detection of  
74 oligomers difficult. Therefore, the development of specific anti-oligomeric based therapeutics  
75 remains challenging.

76 Cerebrospinal fluid (CSF) analyses from AD patients indicate that the presence of A $\beta$   
77 oligomers correlates with a concomitant decrease in A $\beta$ 42 levels. CSF levels of total and  
78 phosphorylated Tau protein [9], tissue transglutaminase (tTGase) [10], ubiquitin [11], A $\beta$   
79 oligomers [12] as well as changes in A $\beta$ 1-42 concentration, together with the presence of  
80 particular A $\beta$  truncations [13] have been collectively suggested as useful biomarkers in AD.

81 Previously, mass spectrometry (MS) based analysis of CSF revealed a specific A $\beta$  peptide  
82 fragment signature in sporadic AD patients [14-16] and it has been reported that truncated A $\beta$   
83 is known to represent more than 60% of all A $\beta$  species found in non-demented as well as in  
84 AD individuals [17]. These findings may suggest that A $\beta$  oligomers could consist of a  
85 heterogeneous morphological entity of full-length A $\beta$ 40 and A $\beta$ 42 as well as truncated A $\beta$

86 isoforms, of which the latter may serve as an important molecular seed during peptide  
87 aggregation [18]. Similarly, a recent report showed that the aqueous phase of human AD  
88 brain extracts contained SDS-stable A $\beta$  species of a molecular weight range of 6-7kDa and  
89 that these A $\beta$  species may form part of larger A $\beta$  aggregates [19].

90 In this work we sought to identify a “molecular crosstalk” during the lag phase of A $\beta$   
91 peptide aggregation that typically precedes the pathological accumulation of neurotoxic  
92 oligomers. Here, we have identified site specific autocleavage of A $\beta$  peptide and report a  
93 typical peptide fragment fingerprint, which may be associated with the early nucleation  
94 process of A $\beta$  aggregation. Using targeted and quantitative MS, we reveal a highly  
95 reproducible A $\beta$  fragment signature with a significant abundance of C-terminal peptide  
96 amidation. Moreover, we show that these truncated A $\beta$  peptides have a particularly high  
97 propensity in forming SDS-stable low molecular weight oligomers of dimeric and trimeric  
98 nature. These findings have enabled us to develop novel neo-epitope antibodies that  
99 selectively bind to the gradual accumulation of truncated A $\beta$  isoforms during the early phase  
100 of peptide aggregation. Our targeted analysis of human brain tissue extracts and CSF  
101 revealed that A $\beta$  cleavage within the peptide’s  $\beta$ -turn region is a highly relevant feature  
102 observed in AD.

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111 **2. METHODS**

112 **2.1 A $\beta$  peptide preparation.**

113 Full-length wild type (wt) A $\beta$  peptides A $\beta$ 1-40, arctic mutant A $\beta$ 1-40 (Arc) and A $\beta$ 1-42  
114 A $\beta$  (Dr. James I. Elliott, Yale University, USA) were dissolved in 1,1,1,3,3,3-Hexafluoro-2-  
115 propanol (HFIP) at a concentration of 1mg/ml, followed by a 10-min sonication to break any  
116 preformed aggregates. HFIP solution was evaporated under a ventilated fume hood by  
117 applying a light stream of N<sub>2</sub> gas. The HFIP film containing the A $\beta$  peptide was either  
118 directly re-suspended in 100% DMSO and further diluted to 1% DMSO in a new buffer or  
119 stored dry at -20 °C until use. A $\beta$  peptide fragments comprising of residues: 1-15, 1-22, 1-23,  
120 1-24-NH<sub>2</sub>, 1-25, 1-25-NH<sub>2</sub>, 26-40, 24-40, (purity of  $\geq$  97%) were purchased from GenicBio  
121 Ltd. (Shanghai, China). A $\beta$  peptide concentrations were determined by UV absorbance using  
122 the peptide's molar extinction coefficient at 280nm.

123 **2.2 Size Exclusion Chromatography of A $\beta$ 42 ADDLs and transgenic mouse brain tissue**  
124 **extracts.**

125 Size exclusion chromatography (SEC) fractionation was carried out using an ÄKTA  
126 Explorer FPLC (GE Healthcare) placed inside a cold (4 °C) chamber. A Superdex 200  
127 10/300 GL column (GE Healthcare) was used and samples were eluted with either 25 mM  
128 ammonium acetate (pH 8.5) or a Superdex 75 10/300GL with 20mM Tris 20mM NaCl  
129 (pH7,5) (for aggregated A $\beta$ 1-25), at a flow rate of 0.5 ml/min. Prior to injection, samples  
130 were centrifuged at 4°C 16,000  $\times$  g for 20 min and 0.5ml of sample supernatant was injected  
131 onto the column. Aggregated A $\beta$ 1-25 peptide was filtered using 0.22 $\mu$ m filter devices prior to  
132 injection to prevent from injecting any large, fibrillary aggregates. Peptide elution was  
133 detected by absorbance at 280 nm, 275nm and 215nm and 0.5 ml fraction volumes were

134 collected. Eluted fractions were either used immediately or aliquoted (50ul) and stored at -  
135 80°C. Where indicated, samples volumes were concentrated approximately 10x in a speed  
136 vacuum.

### 137 **2.3 Matrix assisted Laser Desorption/Ionization Time-of-flight Mass Spectrometry** 138 **(MALDI TOF/TOF).**

139 Aliquots (2 µl) of samples were used for MALDI-TOF/TOF MS (ABI 4800 model,  
140 Applied Biosystems) measurements. Matrix solution of  $\alpha$ -cyano-4-hydroxycinnamic acid (7  
141 mg/ml in ACN/0.1% TFA (1:1, v/v)) was used for sample deposition. The sample (1 µl) was  
142 mixed with 1 µl of matrix solution and then 1 µl of this mixture was deposited in duplicates  
143 on the target plate and allowed to air dry. Samples were analyzed in reflectron positive mode.

144

### 145 **2.4 Digestion of A $\beta$ peptides.**

146 Proteolytic digestion using LysN (2ng/ul) was performed overnight at 37 °C in 50 mM  
147 ammonium bicarbonate, pH 10 (LysN buffer). For in-gel digestions, coomassie stained gel  
148 bands were cut at the migration level of LMW A $\beta$  oligomers (range: 6kDa - 14kDa) as  
149 revealed by their immunoreactive bands in WB. Gel bands were destained and dried in a  
150 speed vacuum prior to resuspension in Lys-N buffer containing 2ng/ul Lys-N protease  
151 followed by overnight digestion at 37°C. Following digestion, the solution was recovered and  
152 pooled with the peptides extracted from gels and concentrated by speed vacuum prior to LC-  
153 MS measurements. Immunoprecipitated samples (IP), were reduced and alkylated followed  
154 by in-solution digestion at 37°C using standard LysN buffer (50ul) and approximately 70ng  
155 of LysN. Dried samples were resuspended in 10% DMSO and 5% FA as described below,  
156 followed by LC-MS/MS or LC-SRM analysis.

157 **2.5 Liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS).**

158 For high resolution LC-MS/MS analysis, peptides were resuspended in 2% ACN, 0.1%  
159 FA and separated by reversed-phase chromatography on a Dionex Ultimate 3000 RSLC  
160 nanoUPLC system connected in-line with an Orbitrap Elite (Thermo Fischer Scientific,  
161 Waltham, MA, USA). The instrument was operated in an information-dependent mode where  
162 peptide masses for light and heavy lysine (K) labelled fragments A $\beta$ 16-23, A $\beta$ 16-24-NH<sub>2</sub>,  
163 A $\beta$ 16-25 and A $\beta$ 16-27 (purchased from Sigma Aldrich, Germany) were selected for  
164 collision-induced dissociation (CID) to generate tandem mass spectra using a normalized  
165 collision energy (CE) of 35. Samples were first captured on a homemade capillary pre-  
166 column (Magic C18; 3  $\mu$ m-200Å; 2 cm  $\times$  100  $\mu$ m) prior to analytical separation. A 80-min  
167 biphasic gradient was run starting from 100% A solvent (2% acetonitrile, 0.1% formic acid)  
168 to 90% B solvent (100% acetonitrile, 0.1% formic acid) on capillary column (Nikkyo C18; 3  
169  $\mu$ m-100 Å; 15 cm  $\times$  75 $\mu$ m inner diameter at 250 nl/min).

170 **2.6 Quantitation of A $\beta$  peptide fragments using Selected Reaction Monitoring (SRM)**  
171 **mass spectrometry.**

172 All samples were analysed on a TSQ-Vantage triple quadrupole mass spectrometer  
173 (Thermo Fisher Scientific). A 0.7-FWHM-resolution window for both Q1 and Q3 was set for  
174 parent- and product-ion isolation. Fragmentation of parent ions was performed in Q2 at 1.5  
175 mTorr, using collision energies calculated with the Pinpoint software (v1.1). Cycle times of  
176 0.5s-1s were used for SRM runs with a minimum dwell time of 20ms.

177 Parent-ion selection was set for Lys-N digested peptides on the positively-charged parent  
178 ions. CID fragmentation energies and the best transition selection were tested manually by  
179 infusion on the TSQ using the synthetic peptide standards listed below. Mouse or human



180 brain and CSF samples were extracted and prepared for digestion as outlined below.  
181 Following overnight digestion at 37°C, samples were dried using a speed vacuum and stored  
182 at –20°C until analyses were performed. For A $\beta$  peptide quantitation studies, a mixture of  
183 accurately quantified (by amino acid analysis) heavy isotope (lysine, K) labelled peptide  
184 standards (Sigma Aldrich, Germany) comprising of residues: A $\beta$ 16-23, A $\beta$ 16-25, A $\beta$ 16-27,  
185 A $\beta$ 28-38, A $\beta$ 28-40, A $\beta$ 28-42 and A $\beta$ 28-43, were spiked into each tube after resuspension of  
186 samples in the Lys-N digestion buffer. A $\beta$  peptide fragments were initially resuspended in a  
187 solution containing 20% DMSO & 10% formic acid (FA) and further diluted to 5% DMSO &  
188 2.5% FA prior to injection and analysis by LC-SRM. This solution provided maximum long-  
189 term stability of all peptide standards. Nano-LC-SRM parameters: Dried peptide aliquots  
190 were resuspended in 20 $\mu$ l DMSO (10%) with 5% FA. This preparation provided peptide  
191 solubility over two weeks without any significant changes in overall peptide recovery.  
192 Following resuspension, samples were briefly sonicated (3min) and allowed to settle for 1h to  
193 increase overall peptide solubility before analysis. Typically, 5 $\mu$ l of sample was loaded and  
194 captured on a homemade capillary precolumn (C18; 3  $\mu$ m, 200 Å; 2 cm  $\times$  250  $\mu$ m) before  
195 analytical LC separation (ACQUITY UPLC, Waters). Samples were separated using a 60min  
196 biphasic gradient starting from 100% solvent A (100% acetonitrile, 0.1% formic acid) to 90%  
197 solvent B (100% acetonitrile, 0.1% formic acid) on a Nikkyo (Nikkyo Technology) nano-  
198 column (C18; 3  $\mu$ m, 100 Å; 150mm length and 100 $\mu$ m inner diameter; flow of 0.5 $\mu$ l/min).  
199 The gradient was followed by a wash for 8 min at 90% solvent B and column re-equilibration  
200 for 15 min at 100%.

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204 **2.7 SDS-PAGE and Immunoblotting.**

205 Dried amples were mixed using standard SDS Lämmli sample buffer, Novex SDS sample  
206 buffer and heated at 80°C for 5 min prior to loading onto gels. Three different commercially  
207 available gels were used in order to compare the migration behaviour of A $\beta$  peptide  
208 fragments: Novex 16% Tris-Tricine gels, 1mm (Invitrogen), Biorad 10-20% Tricine gels  
209 (Biorad, Switzerland) and Novex Nupage 4-12% Bis-Tris gels, 1mm (Invitrogen), of which  
210 the latter type gels were used throughout the study. The following commercially available  
211 running buffers were used: Novex Nupage Mes-SDS buffer (Invitrogen), Novex Tricine-SDS  
212 buffer (Invitrogen) and Biorad Tricine buffer (Biorad, Switzerland). PAGE separated samples  
213 were electroblotted onto nitrocellulose (0.22 $\mu$ m) membranes using standard protocols as  
214 provided by the manufactures. Membranes were blocked for 1h at room temperature under  
215 constant rocking using Odyssey blocking buffer (Li-COR Biosciences, Bad Homburg,  
216 Germany) diluted 1:1 in PBS. Following blocking, membranes were incubated at 4 °C with  
217 constant rocking overnight using the primary rabbit polyconal neo-epitope antibodies N-5ns,  
218 N-5s, N-4, N-3s, D-4s, or D-6ns (0.28-0.5 $\mu$ g /ml), or the commercially available mouse  
219 monoclonal antibodies 6E10 and 4G8 (0.5 $\mu$ g /ml) (Enzo, Life Sciences, Switzerland).  
220 Membranes were washed four times with PBS-Tween (PBS containing 0.01% Tween 20),  
221 followed by incubation with a goat anti-rabbit or anti-mouse secondary IgG antibody (highly  
222 cross-adsorbed) (dilution, 1:5000) conjugated to Alexa Fluor 680 or 800 and scanned in a LI-  
223 COR scanner at a wavelength of 700 nm and 800 nm respectively.

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227 **2.8 Dotblotting.**

228 Typically, 1ul samples were spotted onto a nitrocellulose membrane, which corresponded  
229 to a total peptide load of 100ng (A $\beta$ 1-40) and 50ng (A $\beta$ 1-42) unless otherwise stated in the  
230 figures. Samples were left to dry for 15min followed by blocking of the membrane (30min)  
231 with LICOR buffer. Membrane strips were incubated with primary antibodies either for 2hrs  
232 at room temperature or overnight at 4°C on a shaker. Identical solutions, antibody  
233 concentrations and revelation procedures with secondary antibodies were used as described  
234 for immunoblotting above.

235

236 **2.9 Generation of polyclonal antibodies.**

237 Briefly, a hepta to deca peptide sequence corresponding to the target neo-epitope  
238 sequence of human A $\beta$  peptide was conjugated to a KLH-linker and used for immunization  
239 of rabbits (e.g. A $\beta$ 1-25: C+GG-VFFAEDVG-COOH). Antibodies (Table 1) were raised in  
240 rabbits against a peptide identical to C-terminal residues Gly25 (N-5ns & N-5s), Asp23 (N-  
241 3s), Val24-NH<sub>2</sub> (N-4), or N-terminal residues Val24 (D-4) and Ser26 (D-6) of human A $\beta$   
242 peptide. All polyclonal antibodies were affinity-purified against the target A $\beta$  neo-epitope  
243 sequence using the carboxy- and amidated C-terminal form of the peptide sequence.  
244 Antibody specificity and affinity was validated using direct ELISA with surface immobilized  
245 (cross-linked to BSA) A $\beta$  peptide sequences of normal and amidated C-terminus. All neo-  
246 epitope antibodies were prepared by Eurogentec SA, (Liege, Belgium).

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251 **2.10 In vitro A $\beta$  peptide aggregation studies.**

252 HFIP (1,1,1,3,3,3-Hexafluoro-2-propanol) (Sigma-Aldrich, Switzerland) dried A $\beta$  peptide  
253 films were solubilized in DMSO and further diluted with PBS (or 30mM Tris, 150mM NaCl)  
254 to a final concentration of 0.1mg/ml for A $\beta$ 1-40 and 0.05mg/ml for A $\beta$ 1-42. Samples were  
255 incubated at 37°C and left for spontaneous aggregation during either 0-20 hrs (short-term), 1-  
256 5 days (intermediate) or 1-10 wk (long-term). Aggregated sample aliquots were drawn at  
257 different time points and either analysed immediately using MS and/or DB or snap frozen in  
258 liquid nitrogen and stored at -80°C. Typically, one microliter was spotted onto a  
259 nitrocellulose membrane for dotblotting (50ng to 100ng / spot) or mixed with alpha-cyano  
260 matrix for MALDI-TOF/TOF analysis. For heavy water (H<sub>2</sub><sup>18</sup>O, 97.0%, Cambridge Isotope  
261 laboratories Inc., MA, USA) peptide aggregation studies, HFIP dried A $\beta$  peptide films were  
262 resuspended in anhydrous DMSO and diluted with H<sub>2</sub><sup>18</sup>O (containing Tris-NaCl  
263 10mM/150mM) to a final DMSO concentration of  $\leq 1\%$ . The heavy H<sub>2</sub><sup>18</sup>O part of the final  
264 reaction solution was estimated at approximately  $\geq 95\%$ .

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266 **2.11 Immunoprecipitation of mouse and human brain tissue.**

267 Mouse and human brain tissue samples were serially extracted using TBS, 2% SDS or  
268 formic acid (70-90%FA) as stated in the text. Briefly, tissue samples were homogenized (20  
269 strokes on ice) in TBS and 5mM EDTA with protease inhibitor complex (Roche,  
270 Switzerland) using a Teflon homogenizer. Samples were then subjected to centrifugation  
271 (150,000g) during 45min and the supernatant was recovered as the TBS soluble fraction.  
272 Protein pellets were subjected to an additional extraction using either SDS (2%) or FA (70%)  
273 followed by centrifugation. Typically, pellets were extracted with FA overnight at 4°C (to  
274 minimize formylation adducts) followed by centrifugation. SDS fractions were diluted to

275  $\leq 0.1\%$  SDS final concentration and FA fractions were neutralized to pH 7.5 with 5M sodium  
276 hydroxide (NaOH) solution prior to IP. All samples were initially depleted of endogenous  
277 IgG's using a mixture of protein A&G agarose beads (Roche AG, Switzerland). Typically, 2-  
278 4ug/ml rabbit polyclonal antibody (N-3s, N-4 or N-5ns) or 3-5ug/ml of 6E10 or 4G8 mouse  
279 monoclonal was used for overnight IP under continues rotation (4rpm/min) at 4°C. Samples  
280 were eluted with 40% ACN /H<sub>2</sub>O & 0.1% TFA and dried in a speed vacuum. IP'ed samples  
281 were either directly analysed by WB or MALDI-TOF/TOF or split and further digested  
282 overnight using LysN proteolysis for LC-MS/MS or SRM analysis as outlined above. Human  
283 CSF samples (500ul) were IP'ed with either N-5ns, or a mixture of the two commercial  
284 antibodies 6E10 and 4G8.

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299 **3. RESULTS**

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301 **3.1 In vitro A $\beta$  peptide aggregation is associated with autocleavage within the peptide's**  
302  **$\beta$ -turn vicinity resulting in the generation of a typical peptide fragment signature.**

303 We examined the aggregation behavior of synthetic A $\beta$ 42 peptide using MS and observed  
304 that peptide aggregation is associated with a time dependent appearance of a typical peptide  
305 fragment signature *in vitro*. To rule out the possibility of artefactual peptide hydrolysis during  
306 sample preparation or MS analysis, we carried out aggregation studies using normal and  
307 heavy oxygen labelled water (H<sub>2</sub><sup>18</sup>O) to determine whether peptide cleavage is the result of  
308 aggregation-induced peptide hydrolysis.

309 MS analysis of A $\beta$ 42 aggregation in both, normal and heavy (<sup>18</sup>O) labeled water produced  
310 identical MS spectra (Fig. 1A), revealing a highly reproducible A $\beta$  peptide fragment  
311 signature following short term (t=12h) aggregation. Under heavy water labelled conditions,  
312 the majority of N-terminal fragment masses were shifted by 2 mass units as a result of a  
313 hydrolysis induced <sup>18</sup>O atom incorporation at the newly formed C-terminus, as shown with  
314 one of the most abundant N-terminal fragment of residues A $\beta$ 1-25 (Fig. 1A-G). A $\beta$ 1-25  
315 represents one typical truncated A $\beta$  isoform from a selection of several large N-terminal  
316 fragments (Fig. 1B), where the monoisotopic peak was found to be shifted by 2.0012Da  
317 (0.5003Da for m/z = 734.3513 [M+4H]<sup>4+</sup>) as compared to the monoisotopic peak of normal  
318 (m/z= 733.8463 [M+4H]<sup>4+</sup>) (Fig. 1C, left) experimental conditions. No difference in mass  
319 shift was observed for the complementary C-terminal fragment of residues 26-42 indicating  
320 that hydrolysis-induced peptide cleavage resulted in stable <sup>18</sup>O incorporation only at the neo-  
321 C-terminal residue Gly<sub>25</sub> (Fig. 1C, right).

322 We also observed substantial C-terminal amidation (CONH<sub>2</sub>) within the same isotopic  
323 cluster of A $\beta$ 1-25, where the mass shift between the unmodified monoisotopic peak (m/z=

324 733.8509 [M+4H]<sup>4+</sup>) and the amidated monoisotopic peak ( $m/z= 733.6037$  [M+4H]<sup>4+</sup>)  
325 accounted for 0.988 Da (theoretical  $\Delta$  mass = 0.984 Da) (Fig. 1C, right). The estimated  
326 relative abundance of C-terminal amidation of fragment A $\beta$ 1-25-NH<sub>2</sub> has been estimated to  
327 account of approximately 20% of the normal, carboxy C-terminal population (data not  
328 shown).

329 Interestingly, A $\beta$ 1-24 was found to be predominantly amidated (A $\beta$ 1-24-NH<sub>2</sub>) and only  
330 minor levels of the normal carboxy C-terminus were detected (data not shown). Overall, we  
331 observed that the gradual accumulation of the A $\beta$  fragments of residues A $\beta$ 1-23, A $\beta$ 1-24-  
332 NH<sub>2</sub>, A $\beta$ 1-25 or A $\beta$ 1-25-NH<sub>2</sub> reflect a typical fragment signature during the early phase of  
333 peptide aggregation because these large N-terminal fragments could be readily detected  
334 following short term aggregation ( $\leq 1$ h) and typically preceded the accumulation of earlier  
335 reported A $\beta$  isoforms such as A $\beta$ 1-15 (Supplemental Fig.1). We also observed that some N-  
336 terminal fragments have increased aggregation propensities, as seen by the rapid formation of  
337 MS stable entities of dimeric and trimeric nature (Supplemental Fig.1 A&B) and that this in  
338 turn may affect LC-MS analysis. Therefore, to monitor the generation of these A $\beta$  isoforms  
339 in a more reproducible manner, we processed samples using Lys-N proteolysis, which  
340 generates the proteolytic cleavage product of residues A $\beta$ 16-25[20]. Lys-N digestion of A $\beta$   
341 peptides resulted in highly increased solution stabilities and MS detection (100 fold) of the  
342 proteolytic cleavage products as compared to non-digested A $\beta$ 1-25 (Supplemental Fig. 1D).  
343 The change in overall charge distribution from multiply charged ions ([M+2H]<sup>2+</sup> to  
344 [M+5H]<sup>5+</sup>) for A $\beta$ 1-25 to a predominantly double charged ion ([M+2H]<sup>2+</sup>) for the Lys-N  
345 fragment A $\beta$ 16-25 would generally account for this significantly improved detection.

346 Quantitative MS analysis, using a spiked-in heavy lysine (K16) labelled surrogate peptide  
347 indicated, that the relative abundance of fragment A $\beta$ 1-25 accounts for approximately 5% of  
348 full-length A $\beta$ 42 (Fig. 1D). However, the absolute abundance of the here identified truncated

349 A $\beta$  isoforms of A $\beta$ 1-23, A $\beta$ 1-24-NH<sub>2</sub> and A $\beta$ 1-25 as well as the C-terminal amidated form  
350 would clearly exceed this level.

351 To further confirm a hydrolysis-induced peptide cleavage during *in vitro* aggregation, we  
352 applied MS/MS using collision-induced dissociation (CID) to identify the site of stable <sup>18</sup>O  
353 incorporation. MS/MS analysis of the Lys-N digested A $\beta$ 1-25 (16-25) fragment allowed for  
354 unambiguous identification of the <sup>18</sup>O atom incorporation at Gly25 (Fig. 1E & F).

355

356

### 357 **3.2 N-terminal A $\beta$ peptide fragments are highly prone to oligomerization.**

358 To determine the biophysical properties of truncated A $\beta$  peptides, we investigated the  
359 aggregation properties of four large N-terminal fragments: A $\beta$ 1-23, A $\beta$ 1-24-NH<sub>2</sub>, A $\beta$ 1-25  
360 and A $\beta$ 1-25-NH<sub>2</sub>. Following *in vitro* aggregation of the synthetic A $\beta$  fragments (t=1wk) we  
361 observed significant changes in sodium dodecylsulfate polyacrylamide gel electrophoresis  
362 (SDS-PAGE) migration behavior as seen by the appearance of several low molecular weight  
363 (LMW) species in the range of 6kDa to 14kDa (Fig. 2A). High molecular weight (HMW)  
364 oligomers were observed in the 49kDa to 62kDa range and this oligomeric entity was found  
365 to be particularly characteristic for the amidated fragment A $\beta$ 1-25-NH<sub>2</sub>. Immunoblot analysis  
366 of some A $\beta$  isoforms remains challenging using the conventional antibody 6E10, as seen for  
367 A $\beta$ 1-23, which may result from conformation associated epitope masking [21], and therefore  
368 a decreased sensitivity for 6E10 when compared with 4G8.

369 MS detection of LMW oligomers was mainly achieved at the dimer and trimer level, such  
370 as shown with A $\beta$ 1-25, which may highlight the metastable structure found with soluble  
371 oligomers during LC-MS analysis (Supplementary Fig. 1A & B). Moreover, prolonged aging  
372 of the truncated A $\beta$  isoforms A $\beta$ 1-25 or A $\beta$ 1-25-NH<sub>2</sub> resulted in the generation of shorter N-  
373 terminal fragments such as the earlier reported fragments of residues A $\beta$ 1-14 and A $\beta$ 1-15



374 (Supplementary Fig. 1C & E). This observation was in agreement with prolonged A $\beta$ 42  
375 aggregation experiments (t=7d), showing a time dependent decrease in MS detection of A $\beta$ 1-  
376 25 together with the gradual appearance of shorter fragments, such as A $\beta$ 1-15  
377 (Supplementary Fig. 2A).

378 Transmission electron microscopy (TEM) imaging indicated that N-terminal fragments  
379 have a high propensity to form soluble, oligomeric aggregates following long-term  
380 incubation. A $\beta$ 1-25 preferentially formed homogenous spherical aggregates, which was less  
381 evident with the shorter N-terminal fragments of residues A $\beta$ 1-23 and A $\beta$ 1-24-NH<sub>2</sub> and only  
382 very few clusters of fibrils were observed with the amidated form A $\beta$ 1-25-NH<sub>2</sub> (Fig. 2A and  
383 Supplemental Fig. 2F). We further employed SEC (in Tris-NaCl) of aggregated A $\beta$ 1-25 and  
384 show that the LMW structures typically observed with these truncated A $\beta$  isoforms are true  
385 observations and can therefore exclude a SDS-PAGE induced migration artefact (Fig. 2B).  
386 SEC fractionation resulted in a clear separation of two A $\beta$  structures centered at the migration  
387 level of  $\leq$  6kDa (fraction: 12ml) and  $\leq$  3kDa (fraction: 15ml) and MS analysis of fraction  
388 volume 12ml revealed the presence of stable A $\beta$ 1-25 dimers and trimers, whereas monomers  
389 were mainly detected in fraction volume 15ml (data not shown). Because A $\beta$ 1-25 dimers  
390 (5.8kDa) and trimers (8.7kDa) were highly enriched in SEC fractions corresponding to a MW  
391 standard of  $\leq$ 14kDa, we speculated that LMW A $\beta$ 1-25 structures of may form part of larger  
392 A $\beta$  entities, which dissociate during SDS-PAGE analysis.

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398 **3.3 Monitoring A $\beta$  peptide aggregation using neo-epitope antibodies which specifically**  
399 **target truncated A $\beta$  isoforms.**

400 To create a simple analytical tool for the detection of site specific autocleavage during  
401 aggregation we set out to develop an antibody enabled proof-of-principle tool for monitoring  
402 A $\beta$  cleavage. We therefore developed a panel of rabbit polyclonal antibodies (Table 1) with  
403 high binding specificity for N-terminal fragments of residues A $\beta$ 1-23 (N-3s), A $\beta$ 1-24-NH<sub>2</sub>  
404 (N-4) and A $\beta$ 1-25 (N-5s & N-5ns) (Fig. 3 & Supplemental Fig 3A), as well as for two  
405 complementary C-terminal fragments: A $\beta$ 24-42 (D-4s) and A $\beta$ 26-42 (D-6ns) (Supplementary  
406 Fig. 3B).

407 Epitope binding was tested by dotblot (DB) using a repertoire of synthetic A $\beta$  peptide  
408 standards (1 $\mu$ g/spot) of different sequences or C-terminal endings and binding specificity was  
409 compared with the conventional antibodies 6E10 and 4G8. None of the neo-epitope  
410 antibodies detected full-length A $\beta$ 40 peptide, which highlights their unique binding  
411 specificity for cleaved A $\beta$  isoforms. Overall, 4G8 (17-24) showed higher specificity with  
412 respect to its binding epitope as compared to 6E10 (1-16) because detection of fragment A $\beta$ 1-  
413 15 was significantly reduced with 6E10, which is an observation reported before [22].

414 N-5s showed high specificity for the C-terminal Gly25 residue and N-3s selectively detected  
415 fragments ending with C-terminal residue Asp23. The N-5ns binding epitope was found to  
416 include residues spanning the neo-C-terminal region of residues 23-25, with preferential  
417 binding properties for C-terminal Gly25 (Supplemental Fig. 3A) and binding was  
418 significantly decreased or absent with the shorter fragments of A $\beta$ 1-22 and A $\beta$ 1-15  
419 respectively. Similarly, antibody N-4 revealed high binding specificity for the amidated C-  
420 terminal form of Val24 (A $\beta$ 1-24-NH<sub>2</sub>) (Fig. 3B). Because of the analytical limitations  
421 observed with DB (native conditions) we further compared the neo-epitope antibody  
422 selectivity to 6E10 using immunoprecipitation (IP) of an A $\beta$  fragment mixture along with

423 full-length A $\beta$ 40 (Fig. 3C) or in presence of a complex human proteome matrix (brain tissue  
424 extract) (Supplementary Fig. 4C & D). All neo-epitope antibodies showed high selectivity for  
425 their target fragments, whereas IP with 6E10 resulted in a pull-down of all A $\beta$  fragments  
426 together with full-length A $\beta$ 40.

427 The application of neo-epitope antibody N-5ns was further tested using ELISA and WB. At  
428 working concentrations of  $\leq 0.3\mu\text{g/ml}$ , N-5ns showed significantly lower affinity for the C-  
429 terminal amidated form A $\beta$ 1-25-NH<sub>2</sub> (Fig. 3D) and WB revealed high selectivity for the  
430 target fragments (Fig. 3E&F). In summary we can conclude that, by using a combination of  
431 different conventional techniques, we were able to show that the above mentioned neo-  
432 epitope antibodies have unique binding properties for truncated A $\beta$  isoforms and may serve as  
433 complementary tools for the analysis of biological samples.

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### 436 **3.4 A $\beta$ peptide cleavage is highly associated with changes in peptide secondary** 437 **structure.**

438 In order to understand the mechanisms associated with A $\beta$  peptide cleavage during  
439 aggregation we investigated peptide cleavage by stabilizing A $\beta$  secondary structure in  
440 different solutions. In PBS solution (or 40mM Tris: data not shown), A $\beta$ 40 showed a  
441 predominantly unordered structure with considerable decrease in signal amplitude over the  
442 time course of incubation, whereas incubation in 20% TFE solution induced a stable  $\alpha$ -helical  
443 structure during five days of incubation (Fig. 4A). Significant A $\beta$  cleavage was observed in  
444 PBS or Tris solutions, whereas cleavage was strongly attenuated in TFE (Fig. 4 B & C),  
445 indicating that A $\beta$  cleavage is highly associated with changes of the peptide's secondary  
446 structure as a result of peptide aggregation. This observation was also true for A $\beta$ 42 (data not  
447 shown).

448 Having established neo-epitope antibody specificity, we then selected and employed N-  
449 5ns to monitor *in vitro* A $\beta$ 42 aggregation using DB and MS. We observed a robust increase  
450 in N-5ns DB signal shortly after peptide incubation indicating a nearly instantaneous  
451 accumulation of diagnostic A $\beta$  fragments and TEM imaging of the peptide morphology  
452 indicated that there was a correlation between the N-5ns signal saturation by DB and the  
453 presence of typical oligomeric and protofibrillar aggregates (Fig. 4D).

454 We further studied the effects of different experimental conditions in A $\beta$  aggregation.  
455 Earlier findings provided strong evidence that the protein cross-linking activity of tissue  
456 transglutaminase (tTGase) plays an important role in AD pathogenesis [23] [24]. We  
457 therefore sought to investigate if tTGase induced A $\beta$  aggregation mirrors the accumulation of  
458 A $\beta$  fragment fingerprints. A $\beta$ 40 aggregation increased significantly in the presence of tTGase  
459 and was accompanied by the formation of low amounts of intra- and intermolecular cross-  
460 links (data not shown) as reported previously [25] [18]. This change in aggregation behavior  
461 could be detected by DB (Fig. 4E) and IP-MS analysis confirmed the presence of the N-5ns  
462 target fragments A $\beta$ 1-23 and A $\beta$ 1-25 in samples subjected to different aggregation conditions  
463 (Fig. 4F).

464 Since we were able to show that several peptide cleavage sites represent a typical hallmark  
465 of early aggregation, we argued that the sum of several cleavage products would increase  
466 overall DB screening sensitivity and showed, that the combination of several neo-epitope  
467 antibodies indeed increased detection sensitivity during *in vitro* peptide aggregation  
468 (Supplementary Fig. 4A). We further reasoned that neo-epitope antibody-based monitoring of  
469 A $\beta$  cleavage, prior to the accumulation of  $\beta$ -sheet enriched fibrils, would provide valuable  
470 information for future screening natural inhibitory compounds (Supplementary Fig. 4B) [26]  
471 [27] [28] [29]. This novel screening concept would be complementary to the typically  
472 employed Thioflavin-T fluorescence measurements, since N-5ns would allow identification

473 of aggregation inhibitory compounds targeting an oligomerization fate [21] [30] rather than  
474 advanced fibrillation.

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### 477 **3.5 A $\beta$ fragments form stable complexes with soluble oligomers.**

478 To better understand the biophysical properties of truncated A $\beta$  in peptide  
479 oligomerization, we investigated the aggregation kinetics of amyloid-derived diffusible  
480 ligands (ADDL's) using a combination of SEC, DB, WB and MS. Following 20hrs of A $\beta$ 42  
481 oligomerization, we observed a substantial increase in N-5ns signal using DB (Fig. 5A) and  
482 this positive signal was associated with the presence of a typical oligomeric morphology  
483 (data not shown). Following *in vitro* aggregation, the ADDL preparation was centrifuged in  
484 order to precipitate large insoluble aggregates (pellet) and the supernatant containing soluble  
485 A $\beta$  species was subjected to SEC fractionation. To identify SEC fractions containing  
486 truncated A $\beta$  isoforms, 50ul fractions were dried by speed vacuum and re-suspended in 5ul of  
487 PBS of which 1ul was spotted in duplicates onto a nitrocellulose membrane and probed by  
488 DB using N-5ns and 6E10 respectively. SEC fraction probing with N-5ns allowed  
489 identification of a substantial amount of truncated A $\beta$  within the oligomeric fractions (8ml -  
490 12ml) (Fig.5A). DB probing with 6E10 and N-5ns of the monomeric fraction (18ml)  
491 indicated that this fraction contained a mixture of both, A $\beta$ 42 monomers as well as truncated  
492 A $\beta$  isoforms and WB analysis of these SEC fractions was in line with the findings from DB  
493 (Fig. 5B). Moreover, WB also revealed the presence of HMW oligomers centered at the  
494 49kDa to 62kDa range. The presence of low amounts of this HMW entity observed in the  
495 monomeric fraction may indicate that truncated A $\beta$  fragments may favor the formation of  
496 these HMW structures as a result of sample concentration by speed-vacuum.

497 To further validate the N-5ns positive signals found by DB and WB, we analyzed  
498 oligomeric fractions using IP-MS. MS analysis of the “crude” fraction volume 8ml revealed  
499 that this fraction contained fragments A $\beta$ 1-23, A $\beta$ 1-24-NH<sub>2</sub>, A $\beta$ 1-25 and A $\beta$ 1-25-NH<sub>2</sub> along  
500 with some shorter fragments of A $\beta$ 1-17 to A $\beta$ 1-22 as well as full-length A $\beta$ 42 (Fig. 5C; top).  
501 Similarly, MS analysis of LMW A $\beta$  species extracted from SDS-PAGE gel bands ( $\leq$ 14kDa)  
502 confirmed the presence of different truncated A $\beta$  isoforms as well as their complementary C-  
503 terminal fragments (Supplementary Fig.5).

504 IP with N-4 resulted in a specific pull-down of fragment A $\beta$ 1-24-NH<sub>2</sub> (Fig. 5C; center)  
505 along with A $\beta$ 42 and N-5ns allowed a specific recovery of fragments A $\beta$ 1-25 but not A $\beta$ 1-  
506 25-NH<sub>2</sub>, as well as trace amounts of A $\beta$ 1-23 together with A $\beta$ 42 (Fig. 5C; bottom).

507 To further elucidate the importance of A $\beta$ 1-25 in oligomers, we analyzed two oligomeric  
508 (11.5ml and 14ml) and a monomeric fraction (18ml) using IP-MS (N-5ns) (Fig. 5D) and  
509 could identify A $\beta$ 1-25 in both, oligomeric and monomeric fractions. The relative abundance  
510 of this particular fragment varied considerably, which was in line with our DB and WB  
511 analysis. IP with N-5ns also resulted in a pull-down of A $\beta$ 42 indicating that oligomeric, as  
512 well as monomeric fractions contained metastable complexes of fragment A $\beta$ 1-25 and A $\beta$ 42,  
513 which may dissociate to a generally monomeric level during SDS-PAGE analysis. This data  
514 collectively confirms the above reported observation that truncated A $\beta$  can form stable  
515 entities with soluble oligomers.

516 To provide quantitative values for A $\beta$ 1-25 and A $\beta$ 42 we used IP combined with LC-SRM  
517 analysis. SEC fractions were split and one part was denatured with 70% FA over-night at 4°C  
518 to allow gradual dissociation of large oligomeric species. We reasoned that this approach  
519 would reduce the overall recovery (pull-down) of full-length A $\beta$ 42 stably bound to the  
520 surface of large oligomers and therefore allow more accurate quantitation of the A $\beta$ 1-25  
521 target fragment *per se*. SRM quantitation confirmed the significantly lower levels of A $\beta$ 1-25

522 (2-3pg/ul) (Fig. 5E) found in fraction volume 11.5ml as compared to the monomeric (18ml)  
523 fraction (21-23pg/ul), which is also in line with our WB analysis. Moreover, we found that  
524 FA dissociation of oligomers significantly reduced (40x) the amount of full-length A $\beta$ 42  
525 stably bound to fragment A $\beta$ 1-25. IP-MS of the monomeric fraction, using a combination of  
526 three different neo-epitope antibodies, revealed the presence of three truncated isoforms:  
527 A $\beta$ 1-23, A $\beta$ 1-24-NH<sub>2</sub> and A $\beta$ 1-25 together with A $\beta$ 42 (Fig. 5F).

528 Because our initial mock IP's of freshly prepared A $\beta$  fragment mixtures did not pull-down  
529 full-length A $\beta$ 40 or A $\beta$ 42, we sought to provide direct evidence that detection of A $\beta$ 42 within  
530 the monomeric fraction is the result of a collective pull-down due to stable interaction of  
531 truncated A $\beta$  and A $\beta$ 42. For this purpose, we denatured the first IP sample over-night using  
532 90% FA, followed by a second IP using the same antibody cocktail. MS analysis of the  
533 sequential IP (2<sup>nd</sup>) confirmed our assumption, because A $\beta$ 42 was no longer detected  
534 following FA treatment (Fig. 5G).

535 MS analysis of the insoluble, pellet fraction (from ADDL prep.) indicated that large  
536 insoluble aggregates also consist of heterogenic entities rich in N-terminal as well as C-  
537 terminal truncated A $\beta$  isoforms together with full-length A $\beta$ 42 (data not shown). This  
538 observation was further corroborated by the finding that IP with antibody N-5s or N-5ns of  
539 7M guanidine hydrochloride (GHC1) denatured A $\beta$ 42 fibrils, resulted in a specific recovery  
540 of A $\beta$ 1-25 together with trace amounts of A $\beta$ 42 (Supplementary Fig. 6A & B).

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546 **3.6 N-terminal A $\beta$  peptide fragments are present in the amyloid deposits in the human**  
547 **AD brain.**

548 Immunohistochemical staining (both chromogenic and fluorescent) of the frontal cortical  
549 tissue of human sporadic AD subjects (N = 6 AD cases and 3 age-matched non-demented  
550 controls) using N-5ns resulted in robust labeling of thioflavin-S-positive amyloid plaques and  
551 cerebral amyloid angiopathy (CAA) (Fig. 6A & B). Thioflavin-S-positive intraneuronal tau  
552 tangles were not labelled with N-5ns (Fig. 6B) and no non-specific labeling was detected in  
553 the control non-AD brains (Fig. 6C). Because one of the early and important effects of  
554 oligomeric A $\beta$  in AD is the binding of A $\beta$  to synapses and the resultant synaptic dysfunction  
555 and loss [31], we examined the presence of A $\beta$  neo-epitopes in synapses. Tissue from human  
556 subjects was prepared for high-resolution array tomography [32], allowing accurate detection  
557 of individual synapses. As seen with the immunostaining of paraffin sections, N-5ns labeled  
558 amyloid deposits that were positive for thioflavin-S and 6E10 (Fig. 6D). Both dense-core and  
559 diffuse plaques were immuno-positive for N-5ns. We also observed staining of N-5ns at  
560 individual pre- and postsynaptic puncta in the region of plaques, indicating that this A $\beta$   
561 fragment may be important in synapse degeneration (Fig. 6E).

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563

564 **3.7 Analysis of human AD brain and transgenic mice brain tissue highlights the**  
565 **significant abundance of A $\beta$  cleavage in AD.**

566 In order to further corroborate our *in vitro* observation on A $\beta$  cleavage, we analyzed  
567 human post-mortem brain tissue samples from human controls and AD subjects.

568 We employed IP-MS and WB analysis of TBS and FA tissue extractions to investigate  
569 presence of A $\beta$  truncation using the two conventional antibodies 6E10 and 4G8 and compared  
570 A $\beta$  peptide recovery with neo-epitope antibodies. IP with 6E10&4G8 resulted in the detection



571 of a band centered at the typical migration level of A $\beta$  monomers (>3kDa) (Fig. 7A, top blot:  
572 AD#1 lane: 1, AD#2 lane: 4), whereas IP with neo-epitope antibodies revealed a band  
573 centered at the migration level of  $\leq$ 6kDa for one AD subject (Fig. 7A top blot, lane: 5).  
574 Interestingly, re-probing the membrane with a neo-epitope antibody cocktail revealed a band  
575 centered at the migration level of  $\geq$ 3kDa (Fig. 7A bottom blot: AD#1 lane: 2, AD#2 lane: 5),  
576 indicating that both AD samples contained truncated A $\beta$  isoforms, whereas 4G8 failed to  
577 show similar specificity at this migration level, which is an observation also made with the  
578 synthetic A $\beta$  fragments (Fig. 3).

579 We further analyzed the same brain samples by MALDI-TOF/TOF MS. IP-MS (6E10&4G8)  
580 analysis of the AD#2 brain tissue extract (FA) resulted in a pull-down of large A $\beta$  fragments  
581 A $\beta$ 36, A $\beta$ 37, A $\beta$ 38 and A $\beta$ 40 together with several N-terminal fragments A $\beta$ 1-13-NH<sub>2</sub>, A $\beta$ 1-  
582 13, A $\beta$ 1-20, A $\beta$ 1-22, A $\beta$ 1-23, A $\beta$ 2-24-NH<sub>2</sub> A $\beta$ 1-24-NH<sub>2</sub> and A $\beta$ 1-25 (Fig. 7B). IP-MS  
583 analysis of the same AD brain, using a combination of three neo-epitope antibodies resulted  
584 in a specific pull-down of the target fragments (Fig. 7C). The same samples were also  
585 subjected to LC-MS/MS (Orbitrap) analysis for high resolution peptide mass confirmation  
586 (Fig. 7D & E).

587 Moreover show that, IP with N-5ns enables a specific recovery of fragment A $\beta$ 1-25 from  
588 Tg2576, APP/PS1 (Supplementary Fig. 6C & D) and 5xFAD (data not shown) transgenic  
589 mice brains. The use of SDS (Supplemental Fig. 7), TBS or FA (Supplementary Fig. 8A & B)  
590 extraction protocols all resulted in similar truncated A $\beta$  recovery, however, the levels of A $\beta$ 1-  
591 25 were found to be significantly increased in FA extracts as compared to TBS soluble  
592 fractions (Supplementary Fig. 8B). LC-SRM analysis of TBS and FA brain extracts from  
593 human controls indicated that the levels of cleaved A $\beta$  isoforms are significantly reduced or  
594 below the limit of detection (data not shown).

595

596 **3.8 Human CSF analysis reflects the accumulation of N-terminal fragments in AD**  
597 **brain.**

598 We first measured levels of A $\beta$ 42 and total Tau (T-Tau) in AD patients and non-demented  
599 (ND) controls using ELISA and observed significantly ( $p < 0.001$ ) decreased levels of A $\beta$ 42 as  
600 well as increased T-Tau levels ( $p < 0.001$ ) (Supplementary Fig. 8C & D) in AD patients as  
601 compared to ND controls, which is in line with earlier reported measurements of human CSF  
602 samples [11, 33]. We were further interested in identifying A $\beta$  cleave by applying  
603 quantitative IP-SRM (N-5ns) to measure A $\beta$ 1-25 levels in CSF and could clearly confirm the  
604 presence of A $\beta$ 1-25 in both; AD patients and age matched controls subjects (Supplementary  
605 Fig. 8E). A large inter-subject variability of A $\beta$ 1-25 levels was generally observed in AD  
606 patients ( $n=16$ ) but the measured levels failed to show a statistical significant difference  
607 ( $p > 0.05$ ) when compared to control subjects ( $n=14$ ) (Supplementary Table II).

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611 **4. DISCUSSION**

612 The presence of particular A $\beta$  peptide fragments *in vitro* [34, 35] and *in vivo* [36, 37] has  
613 been reported before and the accumulation of some A $\beta$  isoforms is thought to be associated  
614 with a putative enzymatic activity [38-40]. Generally, it seems unlikely that either proteinases  
615 or exopeptidases are responsible for the generation of truncated A $\beta$  isoforms because *in vitro*  
616 peptide cleavage still occurs in the presence of a metalloprotease inhibitor [35] or  
617 bacteriostatic agents (data not shown). Overall, the exact mechanism associated with the  
618 putative concerted enzymatic cleavage of A $\beta$  still remains unclear. Regardless of proteinase  
619 activity, earlier reports show that *in vitro* A $\beta$ 40 aggregation resulted in peptide cleavage at  
620 residue Asp23 [41] and that the increased aggregation observed for A $\beta$ 40 in the presence of

621 tTGase was accompanied with significant cleavage at residues Glu22 and Gly25 respectively  
622 [18]. Moreover, it has been suggested that A $\beta$ 25-35 as well as full-length A $\beta$ 40 mediated  
623 toxicity may result from a peptide cleavage induced radicalisation of cell membranes, and  
624 that prolonged incubation resulted in significant A $\beta$  cleavage at the Gly25-Ser26 bond [42].  
625 The here reported occurrence of cleavage at residue Gly25 is of particular interest, because  
626 A $\beta$ 1-25 was earlier identified as a sphingolipid binding domain motif, which can be rapidly  
627 internalized by neuronal cells [43].

628 We report here new, additional A $\beta$  fragments and were able to demonstrate that the  
629 gradual appearance of fragments A $\beta$ 1-23, A $\beta$ 1-24-NH<sub>2</sub> A $\beta$ 1-25 and its amidated form A $\beta$ 1-  
630 25NH<sub>2</sub> can be associated with the early events of A $\beta$  aggregation, because MS detection of  
631 the aforementioned N-terminal fragments precedes the accumulation of shorter A $\beta$  isoforms  
632 (i.e A $\beta$ 1-15).

633 To our knowledge, the presence of substantial C-terminal amidation *in vitro* and *in vivo*  
634 has not been reported before, suggesting that A $\beta$  cleavage is the result of at least two distinct  
635 molecular mechanisms. More importantly, we show that A $\beta$  cleavage is strongly attenuated  
636 when stabilizing the peptide in an  $\alpha$ -helical structure. This suggests that the transition from an  
637 unstructured, random-coil conformation to a  $\beta$ -sheet ordered structure triggers the cleavage  
638 cascade typically observed during peptide aggregation. Moreover, the time-dependent  
639 increase in A $\beta$ 1-15 abundance may indicate that shorter N-terminal fragments represent  
640 cleavage products associated with a more advanced phase of aggregation, which is  
641 corroborated by the observation that long-term incubation of the here described fragment of  
642 A $\beta$ 1-25, or its more amyloidogenic form A $\beta$ 1-25-NH<sub>2</sub>, give rise to shorter A $\beta$  isoforms.  
643 Generally, the detection of a particular A $\beta$  fragment signature in different AD transgenic  
644 models as well as human AD brains; collectively highlight the need for further understanding

645 the presence of A $\beta$  fragment signatures in AD. Therefore, the exact molecular mechanism  
646 leading to site specific hydrolysis of A $\beta$  remains to be elucidated in future studies.

647 Soluble A $\beta$  oligomers play a central role in AD pathogenesis, with dimers [44] and  
648 dodecamers (A $\beta$ \* 56) having attracted most of the scientific attention in the past. We report  
649 here that IP of soluble A $\beta$ 40 or A $\beta$ 42 oligomers resulted in a specific recovery of A $\beta$   
650 assemblies with a gel migration range of  $\geq 6$ kDa, and that similar A $\beta$  assemblies could be  
651 detected in TBS and FA lysates from human AD brains. Given by our findings, it is  
652 conceivable that A $\beta$  assemblies of putative dimeric or trimeric nature consist of a mixture of  
653 truncated and full-length A $\beta$ , which may form metastable complexes with HMW structures,  
654 which is partly in agreement with earlier reports [19].

655 The detection of A $\beta$ 1-25 in CSF samples from human controls may suggest a significant  
656 abundance of A $\beta$  oligomers present in control subjects, which is in line with earlier reports  
657 [45]. Interestingly, Holtta et al. (2013) showed that CSF oligomers were significantly  
658 increased in patients with mild and moderate dementia when compared to controls, whereas  
659 no significant difference was found in patients with severe dementia [12]. The here observed  
660 lack of statistical significance in A $\beta$ 1-25 levels in AD patients may result from the relatively  
661 small sample size and hence statistical power. It is also conceivable that CSF sample freeze-  
662 thaw cycles together with other, earlier reported confounding factors[46, 47] may have  
663 collectively contributed to a rapid *ex vivo* A $\beta$  aggregation in these samples.

664 In conclusion, we argue that neo-epitope antibodies would serve as appealing capture  
665 antibodies for future ELISA developments because we were able to show that the here  
666 described A $\beta$  fragments can self-propagate to dimers and trimers or form stable entities with  
667 large oligomers. However, measuring changes in levels of truncated A $\beta$  isoforms merits  
668 additional, future analytical improvements. We believe that monitoring pathological changes  
669 in A $\beta$  levels in human CSF [39] or plasma [48] requires the use of multiplexed approaches,

670 where truncated A $\beta$  isoforms together with several earlier reported A $\beta$  fragments [49] as well  
671 as pathologically relevant post-translational modifications, such as pyroglutamate modified  
672 A $\beta$  [16], should be monitored simultaneously and longitudinally in human biofluids.

673

674

## 675 **RESEARCH IN CONTEXT**

676 **Systematic Review:** A $\beta$  dimers, trimers and dodecamers have received the most scientific  
677 attention in the past, because these entities have been suggested to form the building blocks of  
678 larger neurotoxic assemblies. However, the key molecular triggers associated with early A $\beta$   
679 oligomerization are poorly understood and to date, the exact molecular structure of LMW  
680 oligomers still remains a conundrum.

681 **Interpretation:** We have identified here new truncated A $\beta$  isoforms with high aggregation  
682 propensities, which may serve as seeding units during early peptide aggregation. We provide  
683 analytical evidence that these truncated A $\beta$  isoforms are highly abundant in A $\beta$  oligomers.

684 **Future directions:** We plan to further study the generation of truncated A $\beta$  isoforms as  
685 well as their significance to the pre-symptomatic accumulation of neurotoxic oligomers. The  
686 use typical A $\beta$  peptide fragment fingerprints for a pre-symptomatic diagnosis of subjects  
687 suffering from MCI or other forms of dementia will be of particular interest. Furthermore, we  
688 are interested in studying the structural properties and aggregation fate of the here described  
689 truncated A $\beta$  isoforms. This will help to identify and understand the structure homology  
690 found in A $\beta$  oligomers which in turn may improve the future development of oligomer  
691 specific antibodies.

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712 **SUPPLEMENTARY DATA**

713 Supplementary figures 1-8 and tables I & II.

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