Theoretical study on the molecular determinants of the affibody protein $Z_{A\beta3}$ bound to an amyloid β peptide

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Figure S1. The RMSD values for $(Z_{A\beta3})_2$: A β heavy atoms in the three repeated MD runs.

1 0 2 1 2 0 0 mp			2 101 010 1001000 III (ΞΑβ3)2	
	$<\Delta\Delta E_{vdw>}^{sc}$	$<\Delta\Delta E_{elec>}^{sc}$	$<\!\!\Delta\Delta E_{elec,solv>}^{sc}$	$<\Delta\Delta G_{eff>}^{sc}$
Z _{Aβ3} Ile16	-1.71	-0.85	0.88	-1.68
$Z_{A\beta3}$ Val17	-1.01	-0.63	0.55	-1.09
$Z_{A\beta 3}$ Tyr18	-2.04	-9.80	6.88	-4.96
Z _{Aβ3} Leu19	-1.30	-0.30	0.46	-1.14
$Z_{A\beta3}$ Leu27	-1.06	0.01	0.17	-0.88
$Z_{A\beta 3}$ Phe30	-1.15	-0.06	0.44	-0.77
Z _{Aβ3} Ile31	-0.88	0.46	-0.34	-0.76
$Z_{A\beta3}$ Leu34	-1.36	0.85	-0.66	-1.17
$Z_{A\beta3}$ Leu45	-1.46	0.16	0.00	-1.30
$Z_{A\beta3}$ Ile16	-2.19	-2.80	2.55	-2.44
$Z_{A\beta3}$ Val17	-0.75	-1.83	1.54	-1.04
$Z_{A\beta3}$ Tyr18	-2.76	-0.40	1.46	-1.70
$Z_{A\beta3}$ Leu19	-1.57	-0.19	0.29	-1.47
$Z_{A\beta3}$ Leu27	-1.11	0.30	-0.21	-1.02
$Z_{A\beta3}$ Ile31	-0.95	-0.12	0.25	-0.82
$Z_{A\beta3}$ Leu34	-1.34	-0.49	0.61	-1.22
$Z_{A\beta3}$ Leu45	-2.23	-1.54	1.52	-2.25

Table S1. Decomposition of the side chain contribution to $\Delta\Delta G_{eff}$ for the resides in $(Z_{AB3})_2$

Only residues with side chains making a significant favorable contribution are listed ($\Delta\Delta G_{eff}^{sc} < -0.60$ kcal/mol). The energy unit is kcal/mol. Brackets denote the average over the last 10 ns of the MD trajectories.



Figure S2. Regression between the calculated $\Delta\Delta G_{eff}^{sc}$ values obtained from the per-residue decomposition method and the $\Delta\Delta G_{bind}$ values obtained from the computational alanine scanning for the wild type system. For the per-residue decomposition method, the polar solvation effect was not considered. The vibrational entropy was not included in both methods. The red cycles far away from the regression represent those of Tyr18 in the $Z_{A\beta3}$ subunit and Leu45 in the $Z_{A\beta3}$ subunit, respectively.



Figure S3 Evolution of the amide H-bond distance between $Z_{A\beta3}$ Glu15 and A β Asp23 obtained from the first MD simulation.



Simulation time (ns)

Figure S4. Intermolecular and intra-molecular H-bonds engaged in the stabilization of the β -sheet structure in the first MD simulation. (a) The side chain distance between the carboxyl carbon atom of A β Glu22 and the -OH group of $Z_{A\beta3}$ Tyr18. (b-d)Intermolecular H-bond distances between the $Z_{A\beta3}$ and A β residues. (f-h) Intermolecular H-bond distances between the $Z_{A\beta3}$ and A β residues. (f-h) Intermolecular H-bond distances between the

 $Z_{A\beta3}$ and A β residues. (i-p) Intra-molecular H-bond distances between the backbone atoms of A β residues.



Figure S5. The closest distance (R_{clo}) between any two heavy atoms of the aromatic rings. The R_{clo} values were measured for the aromatic pairs of $Z_{A\beta3}$ Tyr18 and A β Phe20, $Z_{A\beta3}$ Tyr18 and A β Phe20, and $Z_{A\beta3}$ Tyr18 and $Z_{A\beta3}$ Tyr18, respectively, using the 200-ns trajectory of the first MD simulation.