

Supplementary Information for:

Binding of Congo red to amyloid protofibrils of the Alzheimer A β ₉₋₄₀ peptide probed by molecular dynamics simulations by Chun Wu, Justin Scott and Joan-Emma sheal

Table S1 This table list the initial contact residues and the final binding mode between the protofibril and the two CRs (one binds to the N-terminal (Nt) sheet-layer and the other binds to the C-terminal (Ct) sheet-layer) in the first seven trajectories. Only cases in which no CR dimers are formed are considered here (Figure S4).

Traj. ID	Binding to Nt- sheet-layer		Binding to Ct-sheet-layer	
	Initial Contact residues	Final binding mode	Initial Contact residues	Final binding mode
1	K16	Groove F20_V18_K16	I31	Parallel to β -stand
2	K16	Groove K16_H14_V12	A30,I31,M35	Parallel to β -stand
3	K16, F20	Groove F20_V18_K16	M35	Groove I31_M35
4	K16	Groove H14_V12	G37	Groove G20_I31
5	K16	Parallel to β -stand	V40	Sheet edges
6	K16	Groove F20_V18_K16	G38	Parallel to β -stand
7	K16, H14	Groove K16_H14_V12	V39	Sheet edges

Figure S1 the constructed starting structure for the binding simulations.

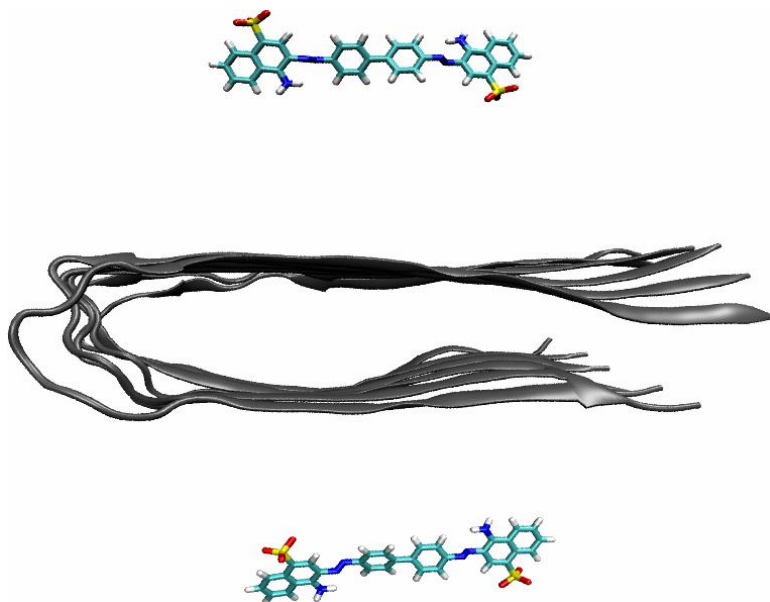


Figure S2 C α RMSD of the A β ₉₋₄₀ protofibril in all 8 trajectories.

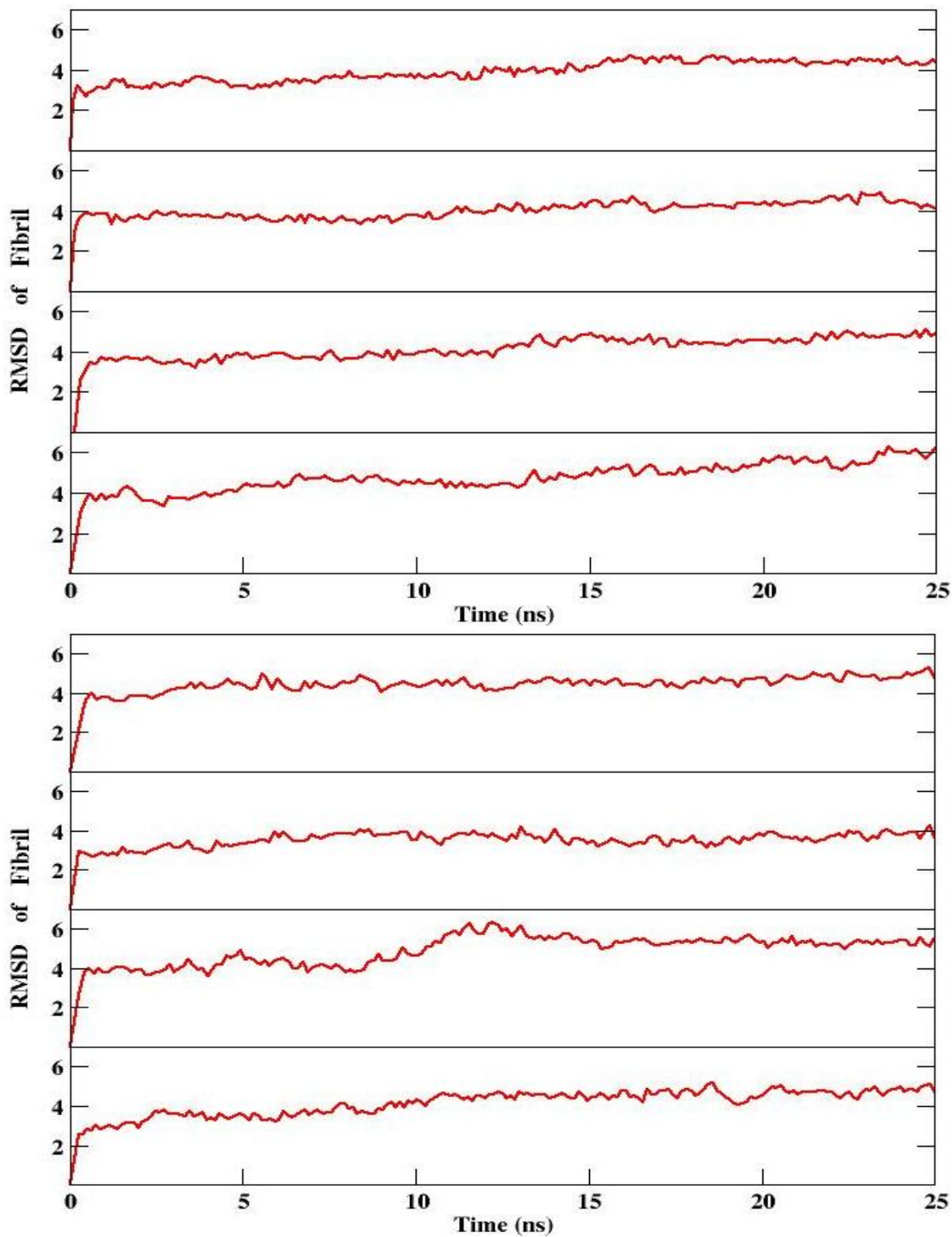


Figure S3 Binding of two CR molecules (red and black line) to the A β ₉₋₄₀ protofibril in for 8 trajectories. The distance cutoff for atom contacts between dye and the cross- β -subunit is set to be 3 Å. If the number of atom contacts is bigger than 20, then the system is designated as being in the bound state, otherwise it belongs the unbound state.

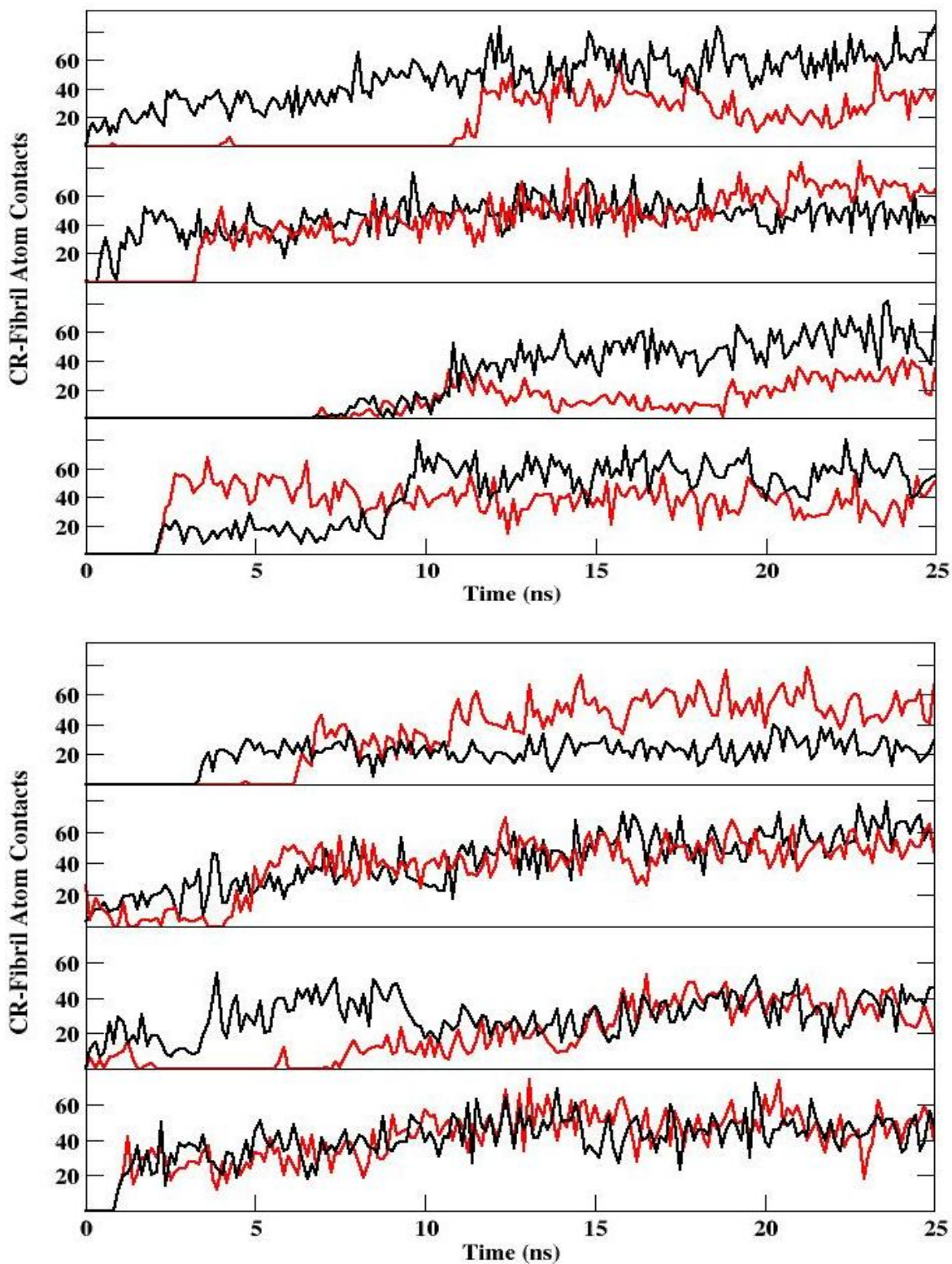
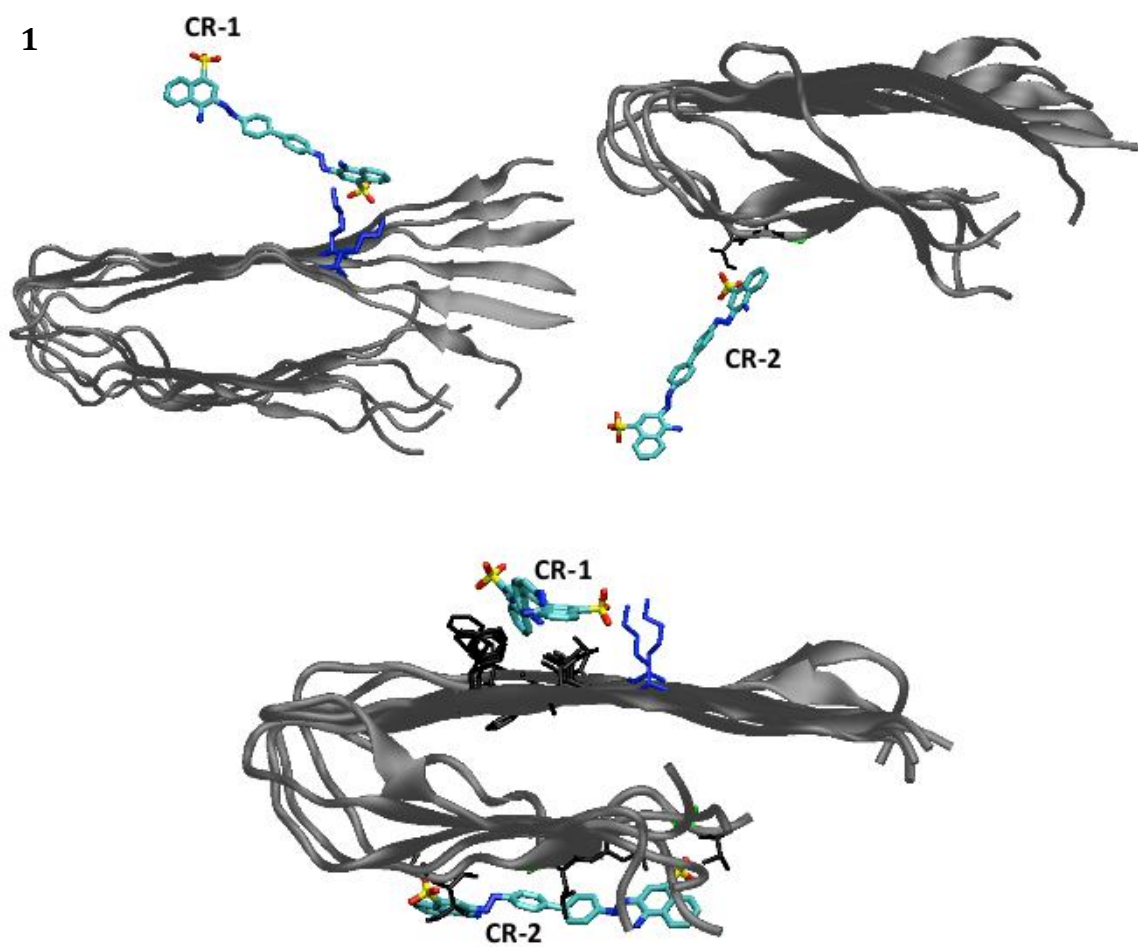
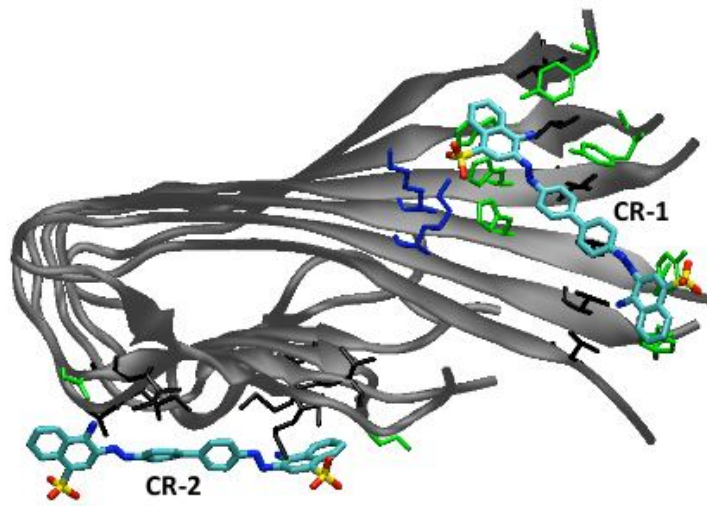
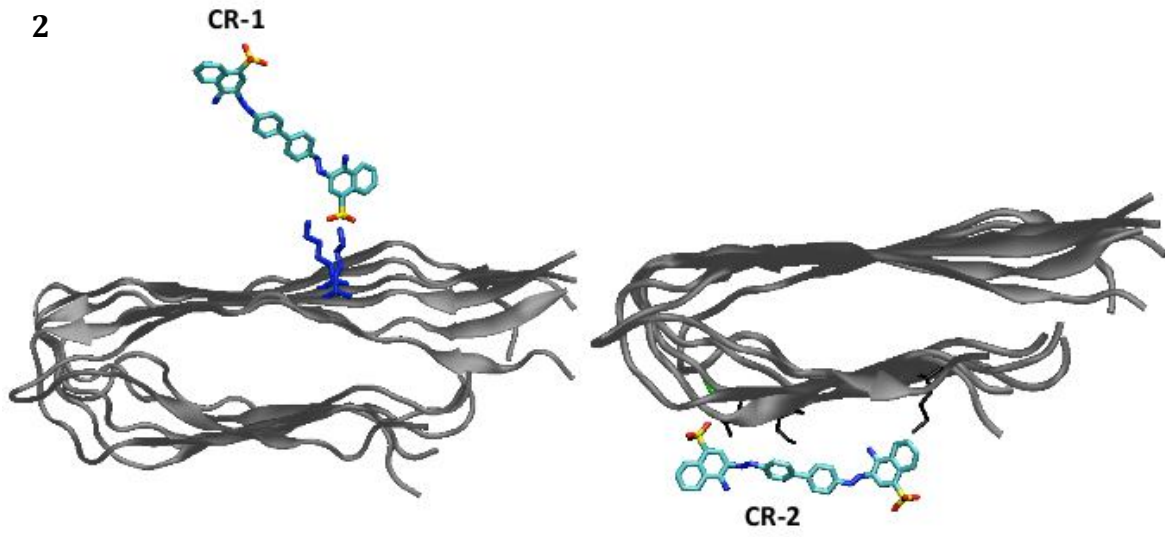


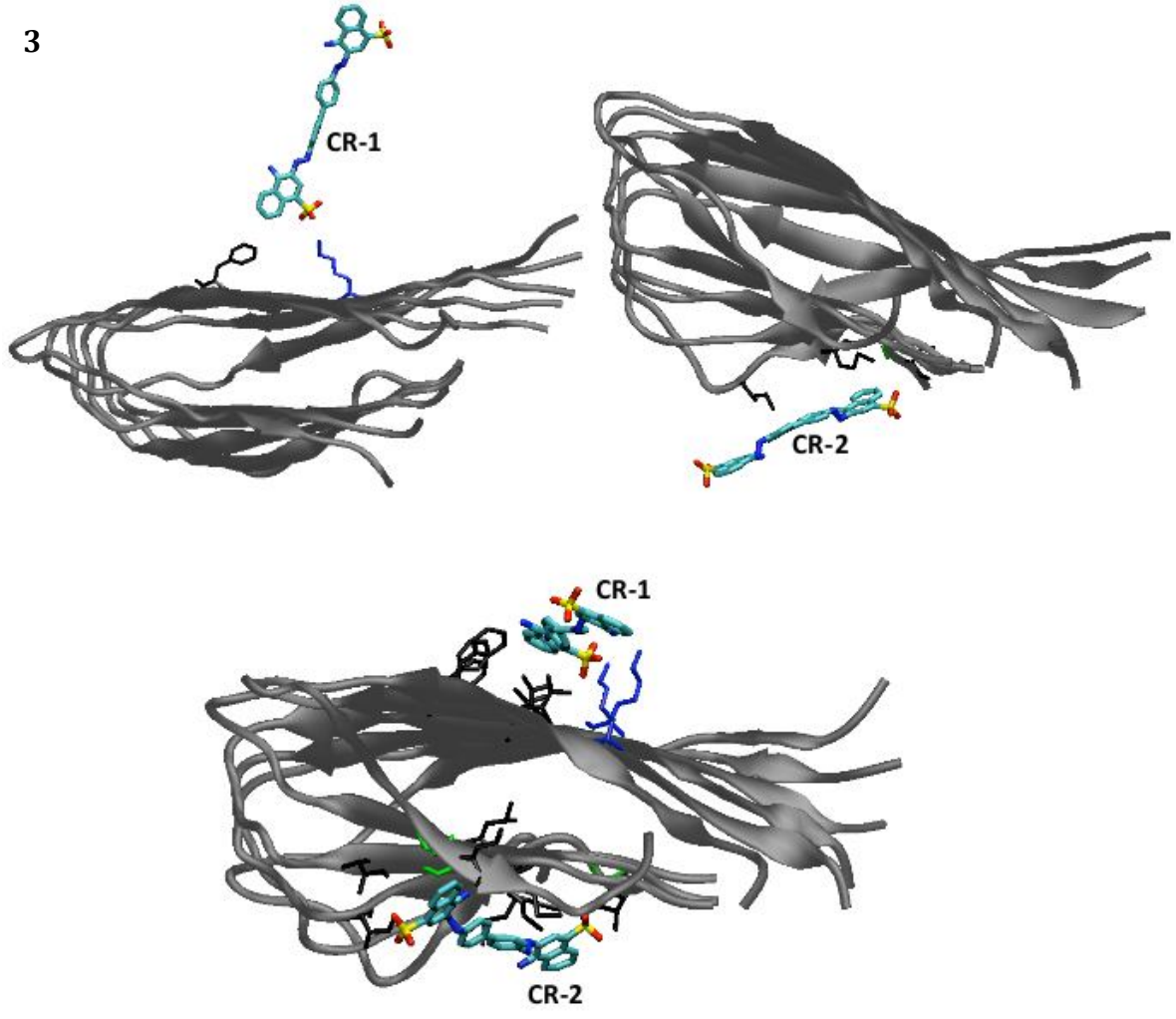
Figure S4 The initial and final contacts between the protofibril and two CRs in the eight trajectories.



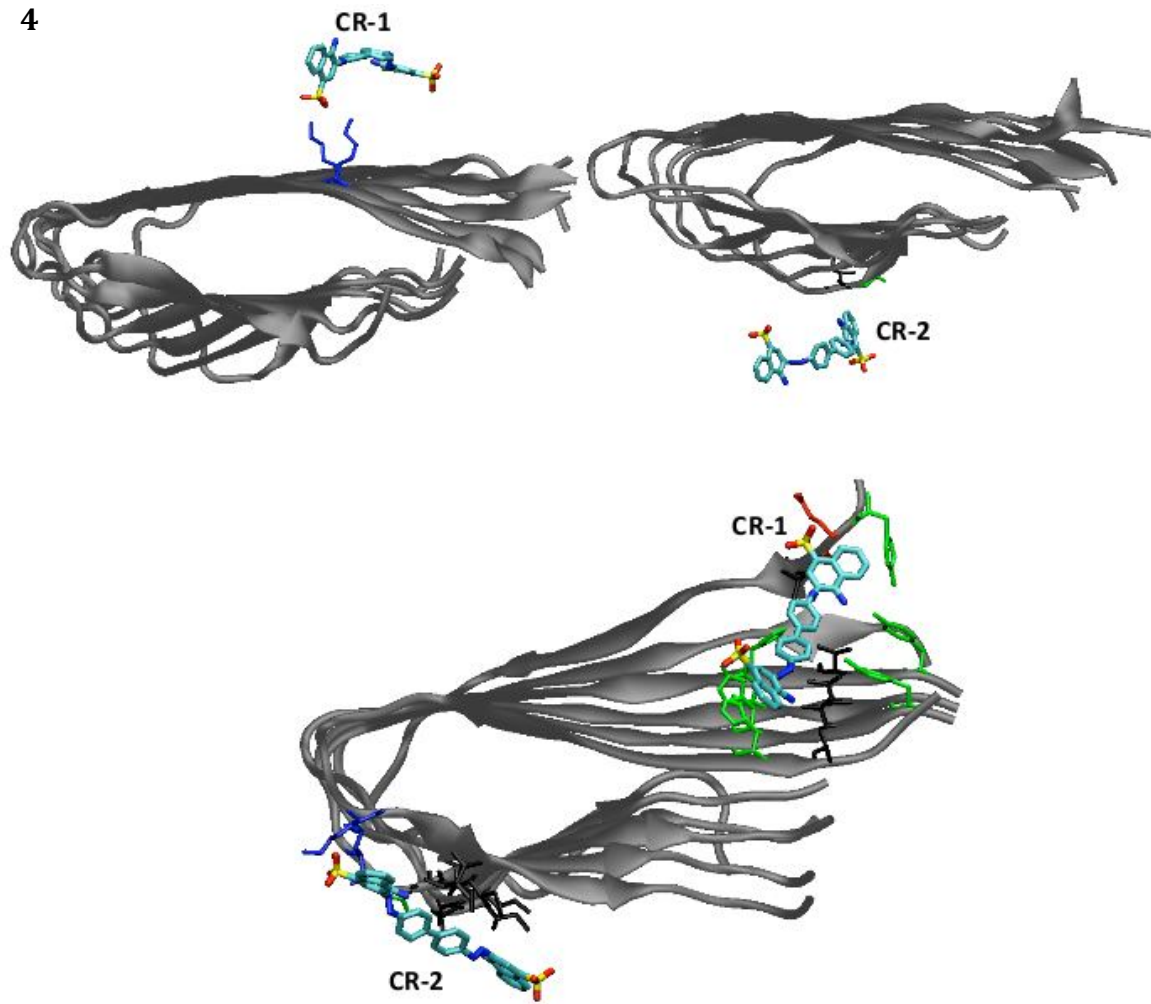
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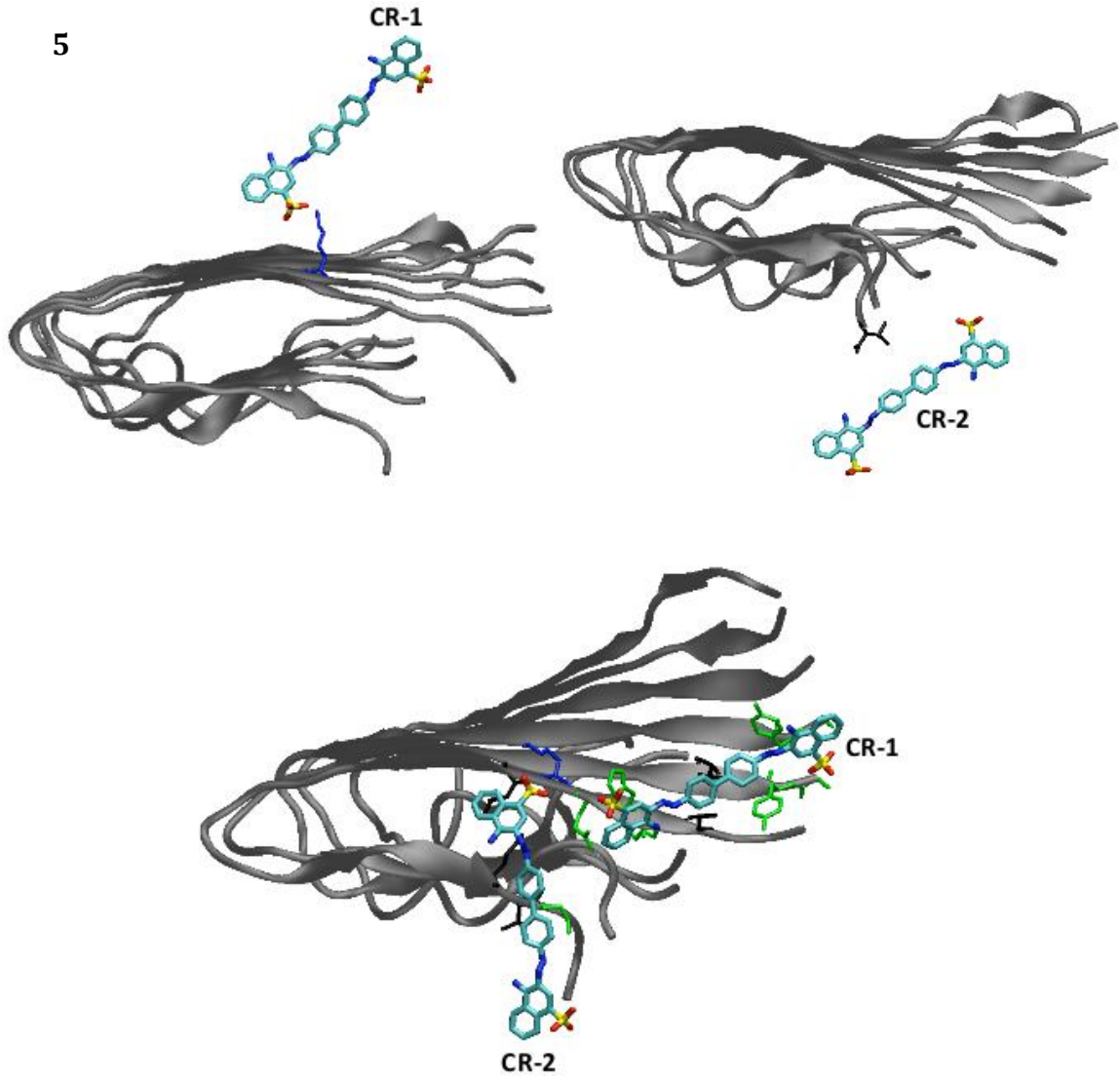
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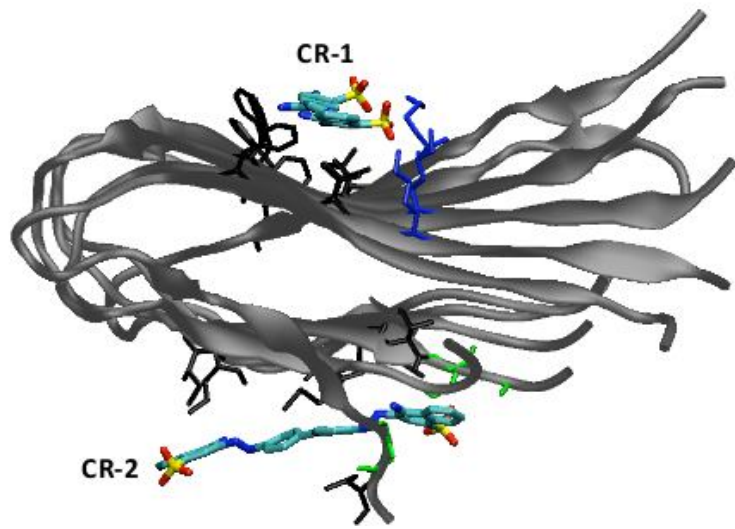
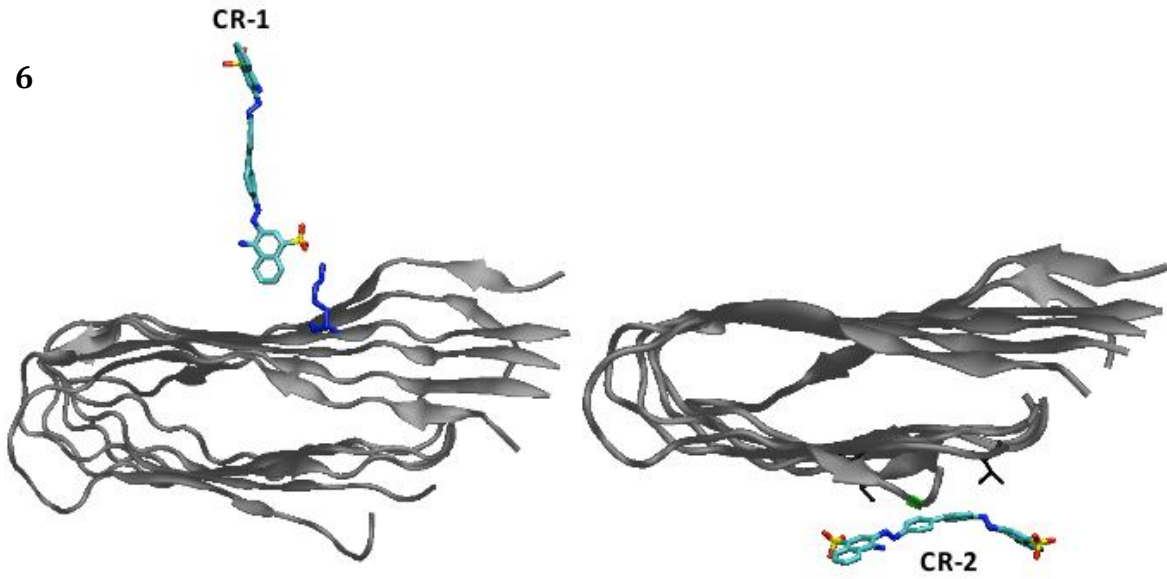
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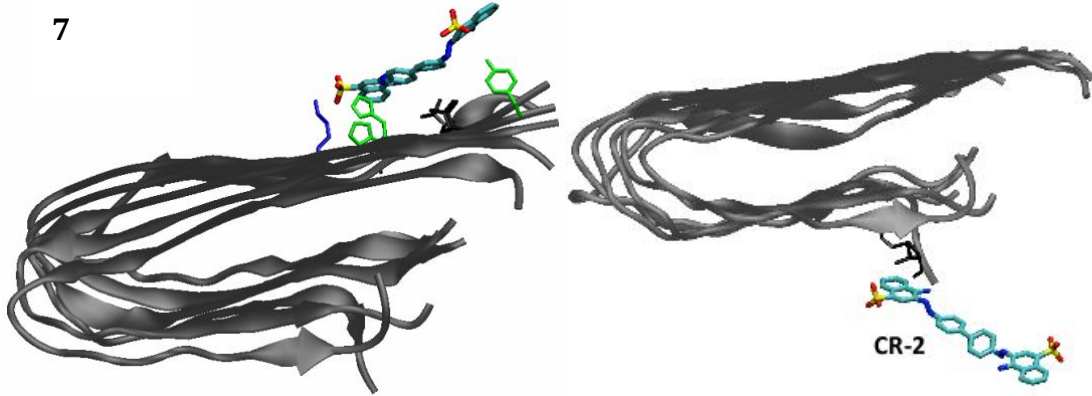
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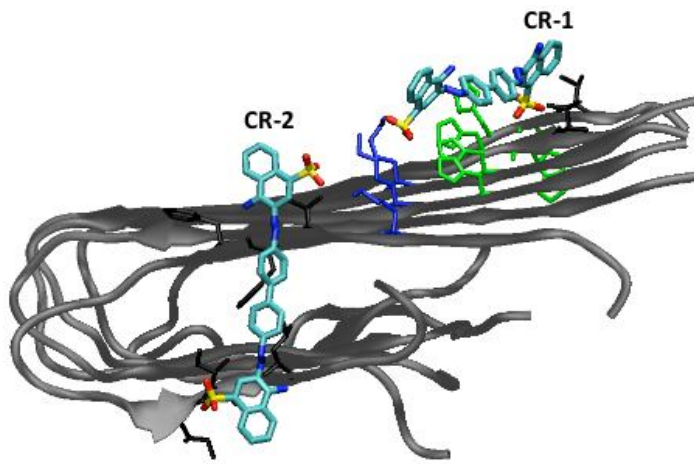
6



7



CR-2



CR-1

CR-2

8

CR Dimer

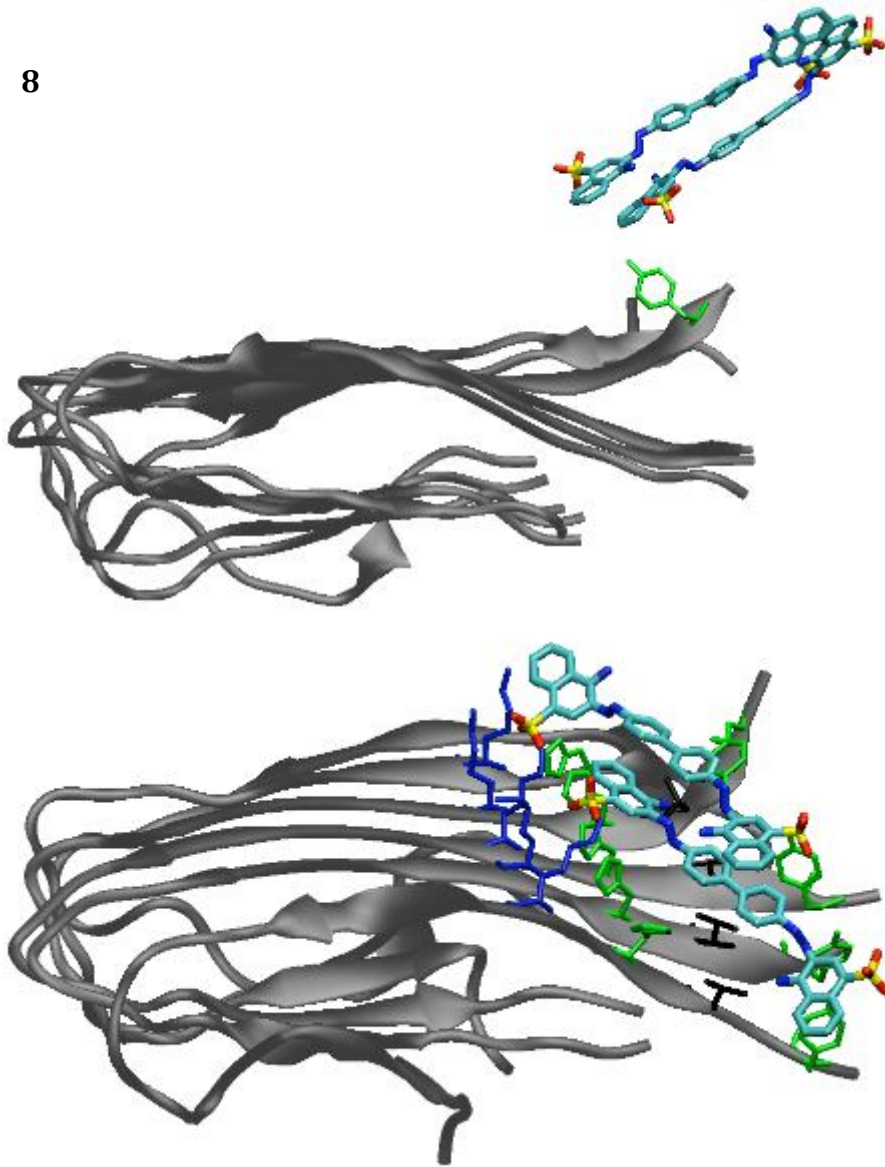
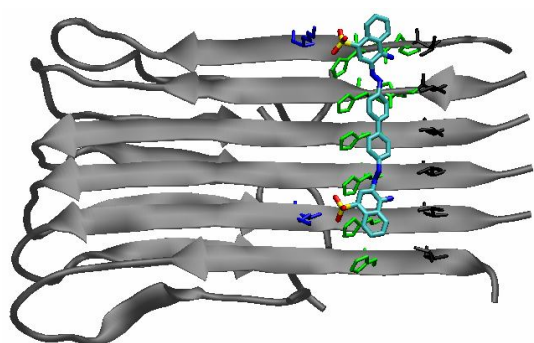
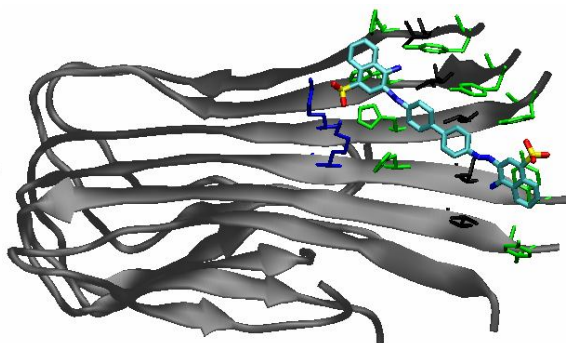


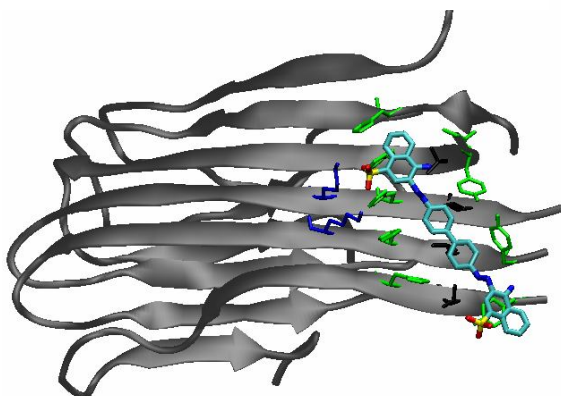
Figure S5 The centroid structures from the clustering. The centroids are further merged into different binding types (Type I-VII) based on binding sites.



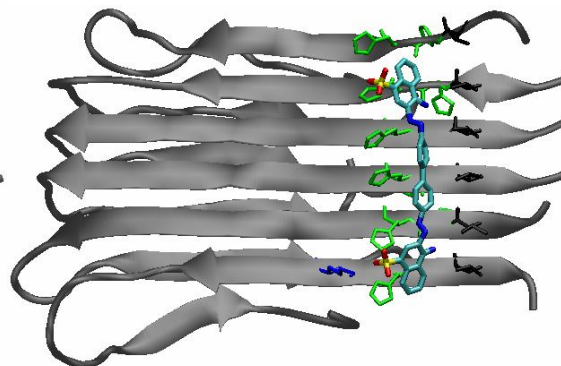
Type I 13.98%



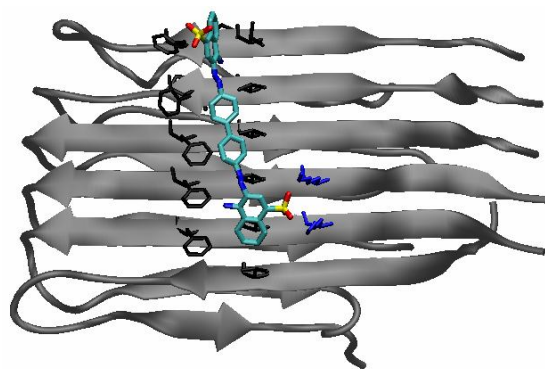
Type I 5.98%



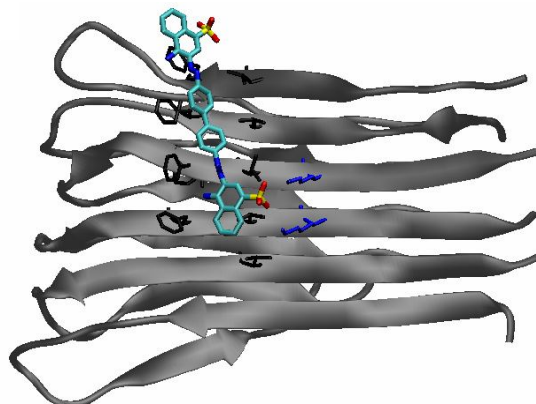
Type I 4.81%



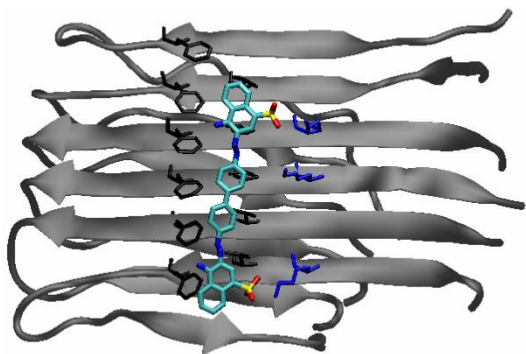
Type I 1.93%



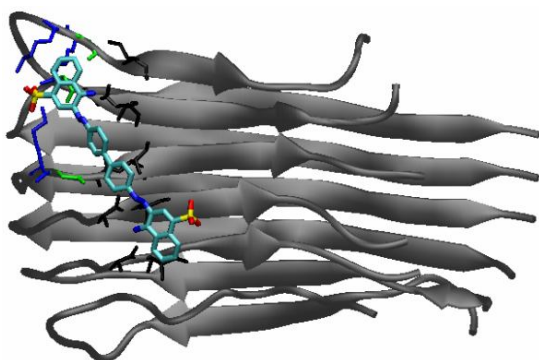
Type II 14.3%



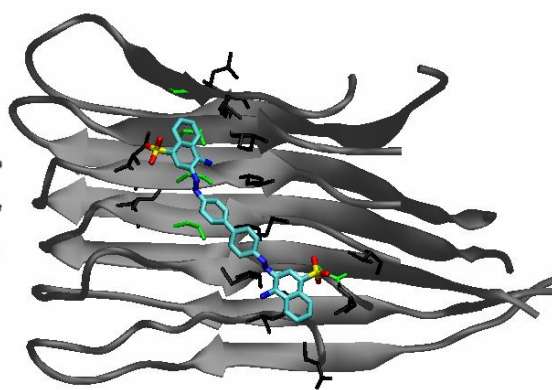
Type II 7.15%



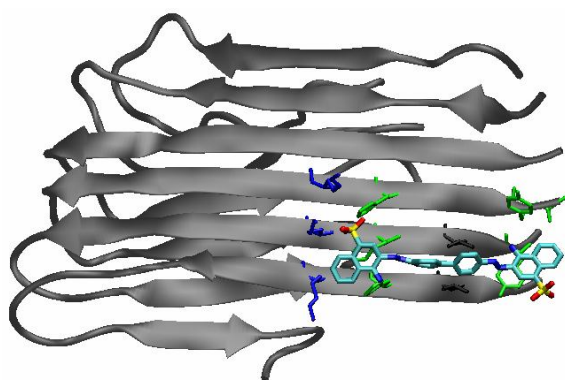
Type II 2.74%



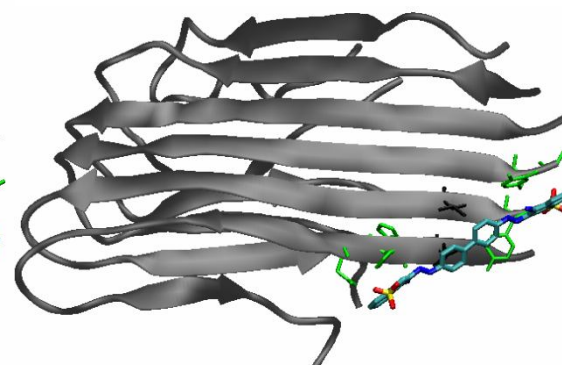
Type III 5.76%



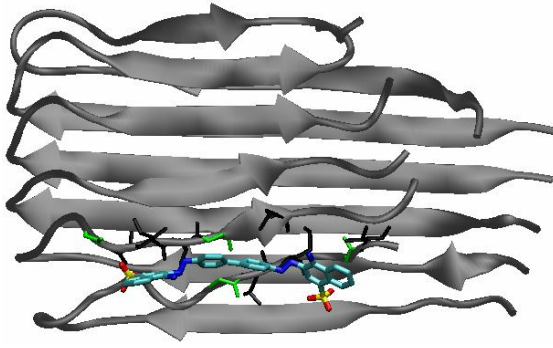
Type IV 4.79%



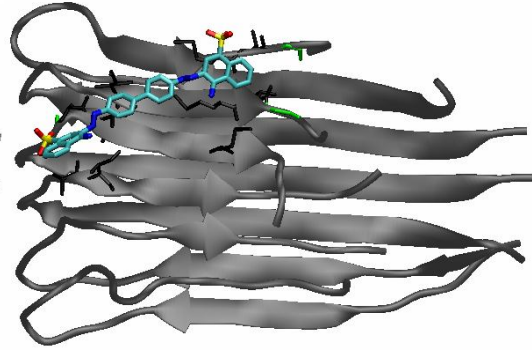
Type V 3.10%



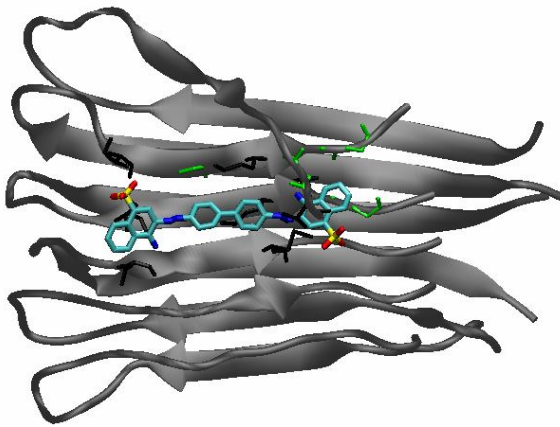
Type V 1.51 %



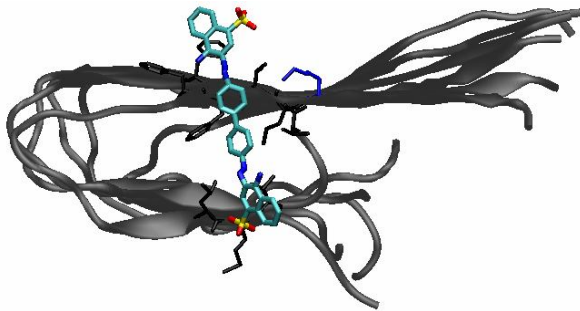
Type VI 8.09%



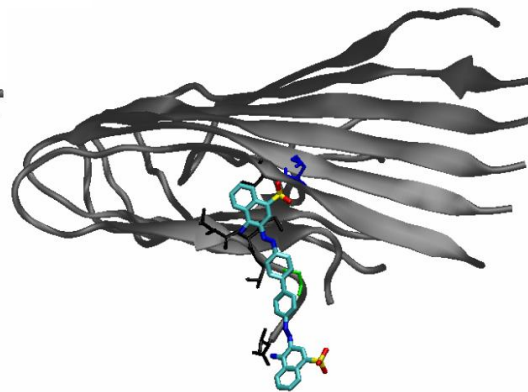
Type VI 6.29%



Type VI 1.93%

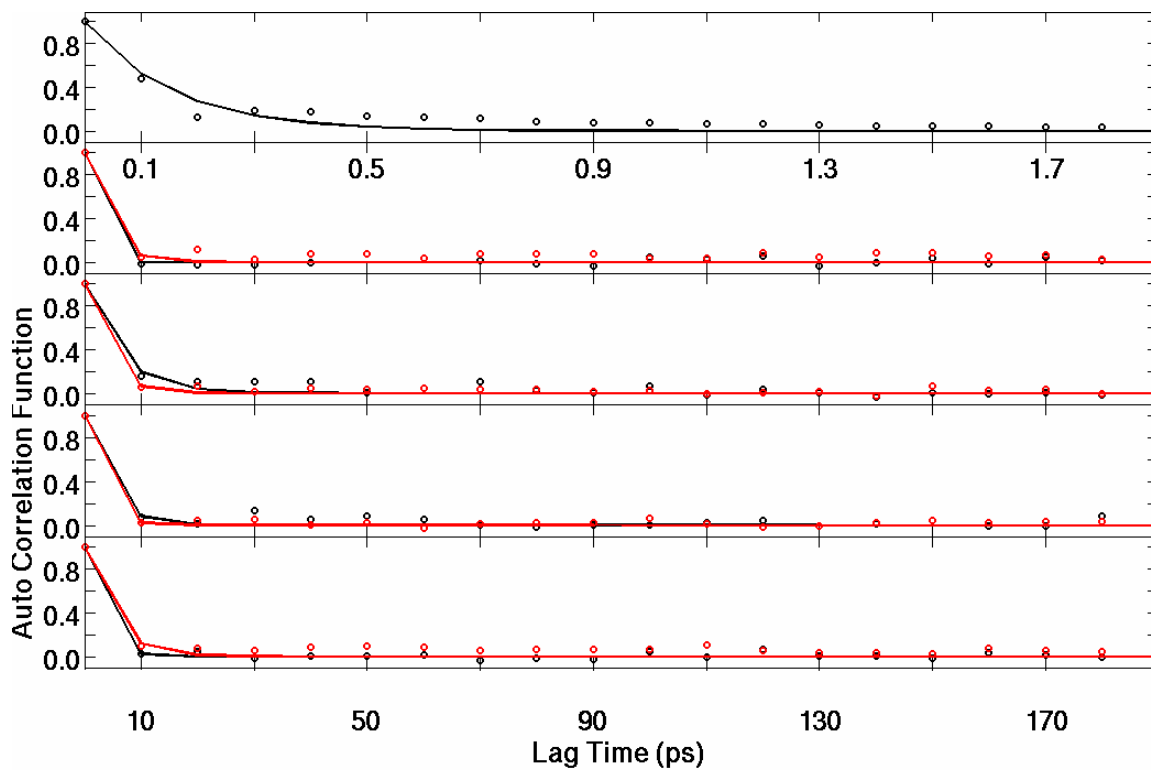


Type VII 10.16%



Type VII 2.47%

Figure S6 Auto-correlation function of the Central torsion angle of CR. Top 1: One free CR Top 2-4: Two CR molecules (red and black) bound to the $A\beta_{9-40}$ protofibril. The fitted lines to exponential decay are in solid, the data points are in cycles.



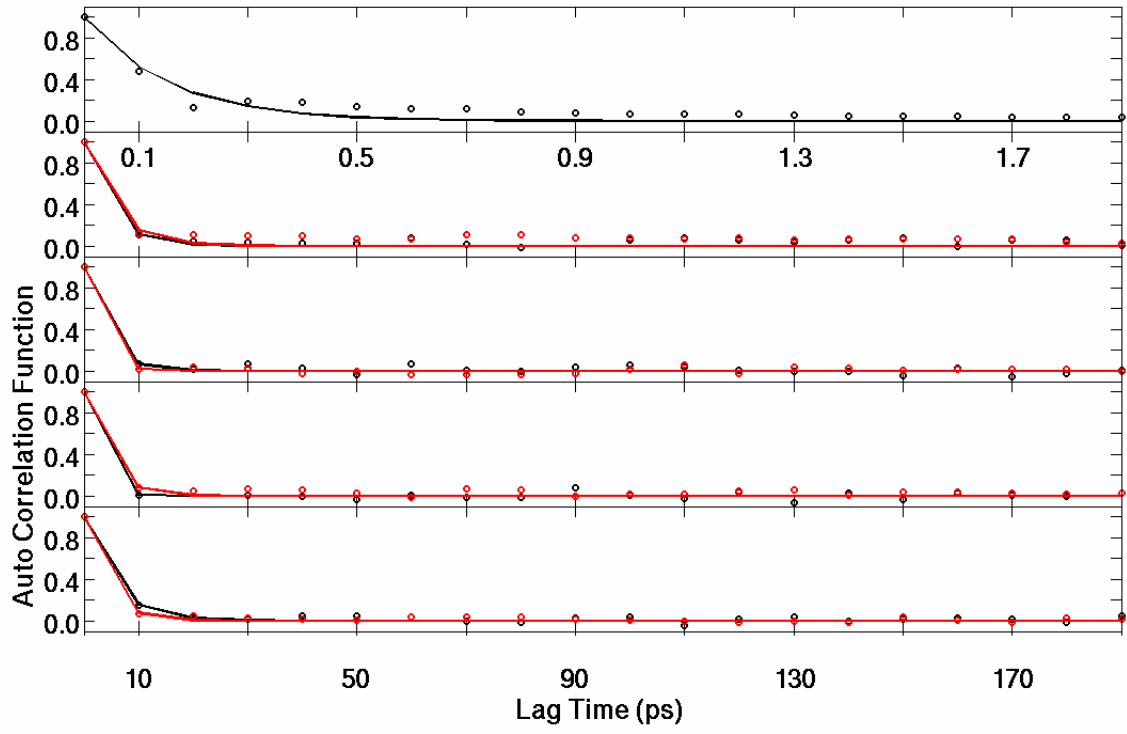
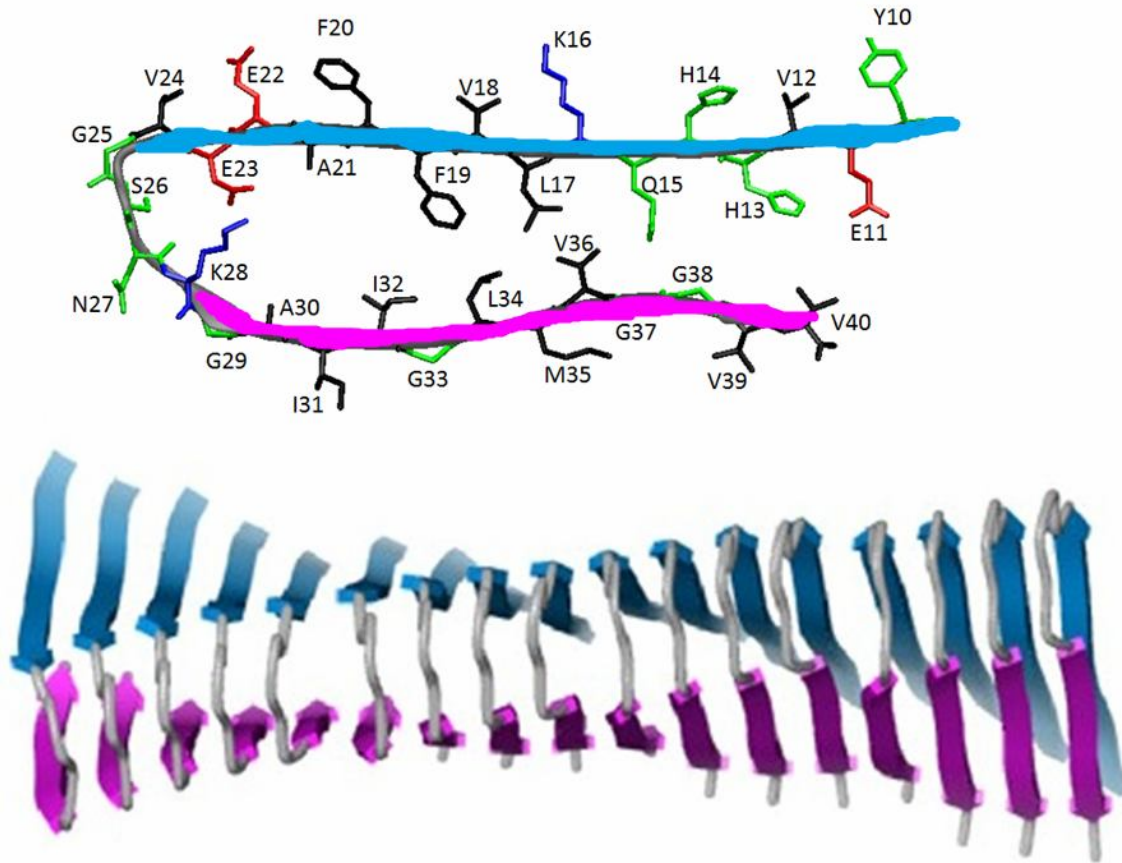


Figure S7 Long range twisting of A β ₉₋₄₀ fibril.



The fibril structure is adapted from reference 1

Reference

1. Kajava, A. V., U. Baxa, and A. C. Steven. 2010. β -arcades: recurring motifs in naturally occurring and disease-related amyloid fibrils. *Faseb Journal* 24:1311-1319.

Appendix A the force field of acidic Congo red molecule in MOL2 format

@<TRIPOS>MOLECULE

CRA

68 73 1 0 1

SMALL

USER_CHARGES

@<TRIPOS>ATOM

1	C9	3.536914	1.422858	-0.000002	ca	1	CRA	-0.0885	****
2	C10	4.956279	1.392528	0.061005	ca	1	CRA	0.0362	****
3	C1	5.732216	2.522086	0.500030	ca	1	CRA	-0.1512	****
4	S1	4.948198	4.068812	0.990089	sy	1	CRA	1.1310	****
5	O1	6.050543	4.933870	1.355071	o	1	CRA	-0.6604	****
6	O2	4.220306	4.491489	-0.193051	o	1	CRA	-0.6604	****
7	O3	4.082160	3.703296	2.096742	o	1	CRA	-0.6604	****
8	C2	7.076907	2.424663	0.546015	ca	1	CRA	-0.0825	****
9	H1	7.652192	3.263577	0.877937	ha	1	CRA	0.0944	****
10	H5	3.030305	2.323749	0.272951	ha	1	CRA	0.1423	****
11	C8	2.830146	0.327778	-0.391921	ca	1	CRA	-0.1353	****
12	H4	1.754774	0.374754	-0.427927	ha	1	CRA	0.1231	****
13	C7	3.488250	-0.869679	-0.735836	ca	1	CRA	-0.2128	****
14	H3	2.917042	-1.736536	-1.018780	ha	1	CRA	0.1337	****
15	C6	4.846301	-0.929113	-0.693838	ca	1	CRA	-0.1513	****
16	H2	5.344154	-1.852353	-0.919892	ha	1	CRA	0.1282	****
17	C5	5.613347	0.202582	-0.313748	ca	1	CRA	0.0508	****
18	C4	7.047269	0.148283	-0.301753	ca	1	CRA	0.1944	****
19	N3	7.684422	-1.032419	-0.701728	nh	1	CRA	-0.8470	****
20	H21	7.338134	-1.383010	-1.569584	hn	1	CRA	0.3410	****
21	H22	8.673659	-0.909502	-0.749753	hn	1	CRA	0.3410	****
22	C3	7.751272	1.239686	0.134274	ca	1	CRA	0.0598	****
23	N1	9.154672	1.116319	0.111270	ne	1	CRA	-0.1008	****
24	N2	9.802728	2.060286	0.538160	nf	1	CRA	-0.0748	****
25	C11	11.210626	1.906979	0.491164	ca	1	CRA	0.1248	****
26	C16	11.950411	3.026196	0.839110	ca	1	CRA	-0.1583	****
27	C15	13.334853	2.990780	0.822102	ca	1	CRA	-0.1306	****
28	H8	13.888410	3.866109	1.110198	ha	1	CRA	0.1311	****
29	H9	11.425493	3.919624	1.125244	ha	1	CRA	0.1191	****
30	C12	11.879813	0.738241	0.139162	ca	1	CRA	-0.1583	****
31	H6	11.318324	-0.135027	-0.127891	ha	1	CRA	0.1191	****
32	C13	13.258403	0.706832	0.127160	ca	1	CRA	-0.1306	****
33	H7	13.759994	-0.197069	-0.167786	ha	1	CRA	0.1311	****
34	C14	14.015577	1.832643	0.464268	cp	1	CRA	0.0019	****
35	C17	15.503704	1.789414	0.437264	cp	1	CRA	0.0019	****

36 C19	16.203782	0.698677	0.942302	ca	1 CRA	-0.1306	****
37 C21	17.587700	0.660263	0.903311	ca	1 CRA	-0.1583	****
38 H13	18.127495	-0.183080	1.294488	ha	1 CRA	0.1191	****
39 H11	15.667503	-0.121027	1.385152	ha	1 CRA	0.1311	****
40 C18	16.240667	2.843698	-0.107694	ca	1 CRA	-0.1306	****
41 H10	15.722954	3.684959	-0.531815	ha	1 CRA	0.1311	****
42 C20	17.619910	2.814284	-0.142709	ca	1 CRA	-0.1583	****
43 H12	18.166428	3.626374	-0.579756	ha	1 CRA	0.1191	****
44 C22	18.308172	1.717269	0.370420	ca	1 CRA	0.1248	****
45 N4	19.718677	1.571885	0.378406	ne	1 CRA	-0.0748	****
46 N5	20.352544	2.572670	0.078530	nf	1 CRA	-0.1008	****
47 C23	21.756362	2.464335	0.073513	ca	1 CRA	0.0598	****
48 C25	22.441076	3.595375	-0.285395	ca	1 CRA	0.1944	****
49 N6	21.781714	4.771413	-0.662458	nh	1 CRA	-0.8470	****
50 H19	22.149161	5.583020	-0.210486	hn	1 CRA	0.3410	****
51 H20	20.800293	4.703598	-0.500524	hn	1 CRA	0.3410	****
52 C24	22.451446	1.276891	0.440407	ca	1 CRA	-0.0825	****
53 H14	21.891063	0.408797	0.718405	ha	1 CRA	0.0944	****
54 C26	23.800355	1.230425	0.468394	ca	1 CRA	-0.1512	****
55 S2	24.614042	-0.293756	0.980244	sy	1 CRA	1.1310	****
56 O4	23.525743	-1.203803	1.275235	o	1 CRA	-0.6604	****
57 O5	25.402130	0.092585	2.136947	o	1 CRA	-0.6604	****
58 O6	25.421481	-0.676097	-0.164379	o	1 CRA	-0.6604	****
59 C28	24.555062	2.393675	0.087461	ca	1 CRA	0.0362	****
60 C27	23.874738	3.563645	-0.311601	ca	1 CRA	0.0508	****
61 C29	24.620597	4.692021	-0.740579	ca	1 CRA	-0.1513	****
62 H15	24.101806	5.560321	-1.101670	ha	1 CRA	0.1282	****
63 C31	25.980469	4.673581	-0.737585	ca	1 CRA	-0.2128	****
64 H17	26.533926	5.533746	-1.071616	ha	1 CRA	0.1337	****
65 C32	26.662420	3.517221	-0.309736	ca	1 CRA	-0.1353	****
66 H18	27.738342	3.505231	-0.304730	ha	1 CRA	0.1231	****
67 C30	25.975651	2.410187	0.084150	ca	1 CRA	-0.0885	****
68 H16	26.500259	1.532213	0.395129	ha	1 CRA	0.1423	****

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8	4	5	1
9	4	6	1

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12 8 22 1
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@<TRIPOS>SUBSTRUCTURE

1 CRA 1 **** 0 **** **