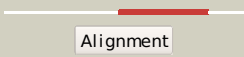
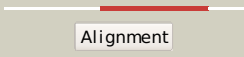
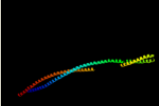
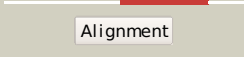
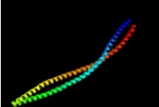
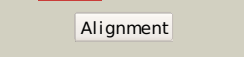
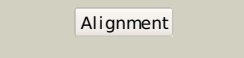
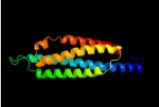
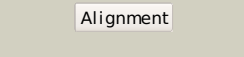
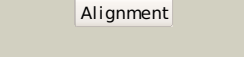
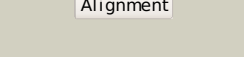
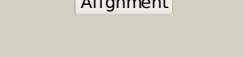
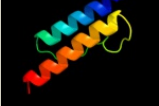
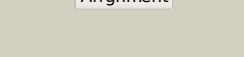
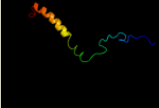
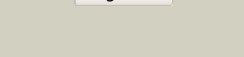
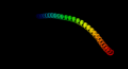
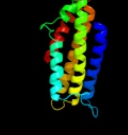
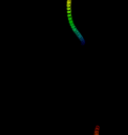
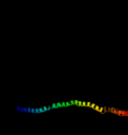
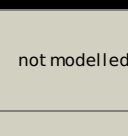


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qu7A_	 Alignment		99.9	99	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
2	c2ch7A_	 Alignment		99.7	26	PDB header: chemotaxis Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
3	c3g67A_	 Alignment		99.4	20	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
4	c2d4uA_	 Alignment		98.9	99	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: crystal structure of the ligand binding domain of the bacterial serine2 chemoreceptor tsr
5	d2liga_	 Alignment		98.2	36	Fold: Four-helical up-and-down bundle Superfamily: Aspartate receptor, ligand-binding domain Family: Aspartate receptor, ligand-binding domain
6	d2asra_	 Alignment		97.8	35	Fold: Four-helical up-and-down bundle Superfamily: Aspartate receptor, ligand-binding domain Family: Aspartate receptor, ligand-binding domain
7	c3lnrA_	 Alignment		97.7	13	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
8	d1vlta_	 Alignment		97.4	36	Fold: Four-helical up-and-down bundle Superfamily: Aspartate receptor, ligand-binding domain Family: Aspartate receptor, ligand-binding domain
9	d2asxa1	 Alignment		96.8	23	Fold: HAMP domain-like Superfamily: HAMP domain-like Family: HAMP domain
10	c2rm8A_	 Alignment		96.4	20	PDB header: signaling protein Chain: A: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
11	c1sj8A_	 Alignment		94.3	11	PDB header: structural protein Chain: A: PDB Molecule: talín 1; PDBTitle: crystal structure of talin residues 482-789

12	c2wpqA_	Alignment		94.2	7	PDB header: membrane protein Chain: A: PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
13	c3zrwB_	Alignment		93.6	18	PDB header: signaling protein Chain: B: PDB Molecule: af1503 protein, osmolarity sensor protein envz; PDBTitle: the structure of the dimeric hamp-dhp fusion a291v mutant
14	c2kbbA_	Alignment		77.1	13	PDB header: structural protein Chain: A: PDB Molecule: talín-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
15	c3dyjA_	Alignment		75.8	8	PDB header: structural protein Chain: A: PDB Molecule: talín-1; PDBTitle: crystal structure a talin rod fragment
16	c2qihA_	Alignment		73.5	12	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis
17	c1degF_	Alignment		68.5	8	PDB header: PDB COMPND:
18	c3ojaB_	Alignment		68.5	9	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
19	c1ei3C_	Alignment		63.3	6	PDB header: PDB COMPND:
20	c1degO_	Alignment		61.1	16	PDB header: PDB COMPND:
21	c3gvmA_	Alignment	not modelled	56.3	14	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
22	c1ei3E_	Alignment	not modelled	56.0	12	PDB header: PDB COMPND:
23	c2vs0B_	Alignment	not modelled	50.2	14	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
24	c1urqA_	Alignment	not modelled	43.6	19	PDB header: transport protein Chain: A: PDB Molecule: m-tomosyn isoform; PDBTitle: crystal structure of neuronal q-snares in complex with2 r-snare motif of tomosyn
25	c3ipdB_	Alignment	not modelled	39.1	10	PDB header: exocytosis Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
26	c3b5nF_	Alignment	not modelled	37.4	12	PDB header: membrane protein Chain: F: PDB Molecule: protein sso1; PDBTitle: structure of the yeast plasma membrane snare complex
27	c2kseA_	Alignment	not modelled	34.0	10	PDB header: transferase Chain: A: PDB Molecule: sensor protein qsec; PDBTitle: backbone structure of the membrane domain of e. coli2 histidine kinase receptor qsec, center for structures of3 membrane proteins (csm) target 4311c
28	c2ieqC_	Alignment	not modelled	32.8	14	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein

29	c1sfcJ_	Alignment	not modelled	32.0	10	PDB header: transport protein Chain: J: PDB Molecule: protein (syntaxin 1a); PDBTitle: neuronal synaptic fusion complex
30	c1n7sB_	Alignment	not modelled	30.2	11	PDB header: transport protein Chain: B: PDB Molecule: syntaxin 1a; PDBTitle: high resolution structure of a truncated neuronal snare2 complex
31	c3ok8A_	Alignment	not modelled	29.3	8	PDB header: protein binding Chain: A: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: i-bar of pinkbar
32	c1i49A_	Alignment	not modelled	25.3	16	PDB header: signaling protein Chain: A: PDB Molecule: arfaptin 2; PDBTitle: crystal structure analysis of arfaptin
33	c3hd7A_	Alignment	not modelled	24.9	22	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
34	c2npsB_	Alignment	not modelled	23.5	14	PDB header: transport protein Chain: B: PDB Molecule: syntaxin 13; PDBTitle: crystal structure of the early endosomal snare complex
35	c1sfcJ_	Alignment	not modelled	21.6	21	PDB header: transport protein Chain: I: PDB Molecule: protein (synaptobrevin 2); PDBTitle: neuronal synaptic fusion complex
36	c1nafA_	Alignment	not modelled	21.3	15	PDB header: signaling protein, membrane protein Chain: A: PDB Molecule: adp-ribosylation factor binding protein gga1; PDBTitle: crystal structure of the human gga1 gat domain
37	d1eq1a_	Alignment	not modelled	20.5	11	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III
38	c3b5nE_	Alignment	not modelled	19.3	15	PDB header: membrane protein Chain: E: PDB Molecule: synaptobrevin homolog 1; PDBTitle: structure of the yeast plasma membrane snare complex
39	c2d4yA_	Alignment	not modelled	19.2	10	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
40	c2bezC_	Alignment	not modelled	19.2	14	PDB header: viral protein Chain: C: PDB Molecule: e2 glycoprotein; PDBTitle: structure of a proteolitically resistant core from the2 severe acute respiratory syndrome coronavirus s2 fusion3 protein
41	c1gl2A_	Alignment	not modelled	18.9	13	PDB header: membrane protein Chain: A: PDB Molecule: endobrevin; PDBTitle: crystal structure of an endosomal snare core complex
42	c2npsA_	Alignment	not modelled	18.0	26	PDB header: transport protein Chain: A: PDB Molecule: vesicle-associated membrane protein 4; PDBTitle: crystal structure of the early endosomal snare complex
43	c1n7sA_	Alignment	not modelled	15.9	22	PDB header: transport protein Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: high resolution structure of a truncated neuronal snare2 complex
44	c3ghgK_	Alignment	not modelled	15.9	9	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
45	c1zvaA_	Alignment	not modelled	14.5	14	PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
46	d1wa8a1	Alignment	not modelled	13.6	11	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
47	c1bf5A_	Alignment	not modelled	13.4	7	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: tyrosine phosphorylated stat-1/dna complex
48	d1oxza_	Alignment	not modelled	13.0	14	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
49	c1oxzA_	Alignment	not modelled	13.0	14	PDB header: membrane protein Chain: A: PDB Molecule: adp-ribosylation factor binding protein gga1; PDBTitle: crystal structure of the human gga1 gat domain
50	d1wr6a1	Alignment	not modelled	12.6	8	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
51	c1kmiZ_	Alignment	not modelled	12.5	10	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
52	d1ez3a_	Alignment	not modelled	12.3	10	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
53	c2d3eD_	Alignment	not modelled	12.2	10	PDB header: contractile protein Chain: D: PDB Molecule: general control protein gcn4 and tropomyosin 1 PDBTitle: crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
54	c2efrB_	Alignment	not modelled	12.2	9	PDB header: contractile protein Chain: B: PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
						Fold: Four-helical up-and-down bundle

55	d2b0ha1	Alignment	not modelled	12.0	18	Superfamily: alpha-catenin/vinculin-like Family: VBS domain
56	c2l7aA	Alignment	not modelled	11.6	16	PDB header: cell adhesion Chain: A: PDB Molecule: tal1n-1; PDBTitle: solution structure of the talin vbs2b domain
57	c1wywyB	Alignment	not modelled	11.1	15	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
58	c3arcl	Alignment	not modelled	11.0	39	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
59	d1wa8b1	Alignment	not modelled	10.0	12	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
60	dli4da	Alignment	not modelled	9.2	16	Fold: BAR/IMD domain-like Superfamily: BAR/IMD domain-like Family: Arfaptin, Rac-binding fragment
61	c3arcl	Alignment	not modelled	9.0	39	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
62	c3prqL	Alignment	not modelled	9.0	39	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
63	c3prrl	Alignment	not modelled	9.0	39	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
64	d2axtl1	Alignment	not modelled	9.0	39	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein L, PsbL Family: PsbL-like
65	c1s5lL	Alignment	not modelled	9.0	39	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
66	c2axtl	Alignment	not modelled	9.0	39	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
67	c2axtl	Alignment	not modelled	9.0	39	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
68	c3bz2L	Alignment	not modelled	9.0	39	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
69	c3a0hl	Alignment	not modelled	9.0	39	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
70	c3a0bl	Alignment	not modelled	9.0	39	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of br-substituted photosystem ii complex
71	c3a0bL	Alignment	not modelled	9.0	39	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of br-substituted photosystem ii complex
72	c3a0hL	Alignment	not modelled	9.0	39	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
73	c3kziL	Alignment	not modelled	9.0	39	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii
74	c1s5lL	Alignment	not modelled	9.0	39	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
75	c3bz1L	Alignment	not modelled	9.0	39	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
76	c1l4aD	Alignment	not modelled	9.0	10	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: s-snap25 fusion protein; PDBTitle: x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
77	c1sfcD	Alignment	not modelled	8.7	10	PDB header: transport protein Chain: D: PDB Molecule: protein (snap-25b); PDBTitle: neuronal synaptic fusion complex
78	c3e7kF	Alignment	not modelled	8.4	17	PDB header: membrane protein Chain: F: PDB Molecule: trpm7 channel; PDBTitle: crystal structure of an antiparallel coiled-coil tetramerization2 domain from trpm7 channels
79	c2kvpA	Alignment	not modelled	8.3	16	PDB header: structural protein Chain: A: PDB Molecule: tal1n-1; PDBTitle: nmr structure of the talin vbs3 domain, 1815-1973
80	c3dtpA	Alignment	not modelled	8.2	15	PDB header: contractile protein Chain: A: PDB Molecule: myosin 2 heavy chain chimera of smooth and PDBTitle: tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map Fold: Spectrin repeat-like

81	d1x79a_	Alignment	not modelled	8.1	15	Superfamily: GAT-like domain Family: GAT domain
82	c3gxvD_	Alignment	not modelled	7.9	23	PDB header: hydrolase/replication Chain: D: PDB Molecule: replicative dna helicase; PDBTitle: three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
83	c2fxmB_	Alignment	not modelled	7.6	5	PDB header: contractile protein Chain: B: PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
84	c2npsD_	Alignment	not modelled	7.6	5	PDB header: transport protein Chain: D: PDB Molecule: syntaxin-6; PDBTitle: crystal structure of the early endosomal snare complex
85	d1o3xa_	Alignment	not modelled	7.6	14	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
86	c1yvlB_	Alignment	not modelled	7.5	7	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
87	c3gxvC_	Alignment	not modelled	7.5	23	PDB header: hydrolase/replication Chain: C: PDB Molecule: replicative dna helicase; PDBTitle: three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
88	c1eboE_	Alignment	not modelled	7.4	18	PDB header: viral protein Chain: E: PDB Molecule: ebola virus envelope protein chimera consisting PDBTitle: crystal structure of the ebola virus membrane-fusion2 subunit, gp2, from the envelope glycoprotein ectodomain
89	d1wrda1	Alignment	not modelled	7.3	8	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
90	c2j7aC_	Alignment	not modelled	7.2	24	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome c quinol dehydrogenase nrhf; PDBTitle: crystal structure of cytochrome c nitrite reductase nrhf2 complex from desulfovibrio vulgaris
91	c2l9uA_	Alignment	not modelled	7.1	10	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
92	c1junB_	Alignment	not modelled	7.1	28	PDB header: transcription regulation Chain: B: PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
93	d1t01a1	Alignment	not modelled	7.1	12	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
94	d2h8pc1	Alignment	not modelled	6.8	11	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
95	c2b9cA_	Alignment	not modelled	6.8	15	PDB header: contractile protein Chain: A: PDB Molecule: striated-muscle alpha tropomyosin; PDBTitle: structure of tropomyosin's mid-region: bending and binding2 sites for actin
96	d1r0da_	Alignment	not modelled	6.8	15	Fold: I/LWEQ domain Superfamily: I/LWEQ domain Family: I/LWEQ domain
97	c1m1jA_	Alignment	not modelled	6.7	5	PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha subunit; PDBTitle: crystal structure of native chicken fibrinogen with two different2 bound ligands
98	c2l7nA_	Alignment	not modelled	6.7	9	PDB header: structural protein Chain: A: PDB Molecule: talin-1; PDBTitle: nmr structure of the b domain of talin
99	c1l7cA_	Alignment	not modelled	6.7	14	PDB header: cell adhesion Chain: A: PDB Molecule: alpha e-catenin; PDBTitle: alpha-catenin fragment, residues 385-651