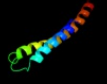
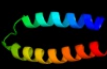
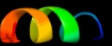
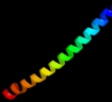


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1o5ha_	 Alignment		84.6	14	Fold: Methenyltetrahydrofolate cyclohydrolase-like Superfamily: Methenyltetrahydrofolate cyclohydrolase-like Family: Methenyltetrahydrofolate cyclohydrolase-like
2	c1tt9B_	 Alignment		77.1	12	PDB header: transferase, lyase Chain: B: PDB Molecule: formimidoyltransferase-cyclodeaminase PDBTitle: structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
3	d2asra_	 Alignment		55.7	8	Fold: Four-helical up-and-down bundle Superfamily: Aspartate receptor, ligand-binding domain Family: Aspartate receptor, ligand-binding domain
4	d1vlt_	 Alignment		54.4	16	Fold: Four-helical up-and-down bundle Superfamily: Aspartate receptor, ligand-binding domain Family: Aspartate receptor, ligand-binding domain
5	c1p68A_	 Alignment		49.8	14	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein s-824; PDBTitle: solution structure of s-824, a de novo designed four helix2 bundle
6	c2d4yA_	 Alignment		49.7	11	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
7	d1d2ta_	 Alignment		49.7	25	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Type 2 phosphatidic acid phosphatase, PAP2
8	d2j0aa1	 Alignment		48.2	19	Fold: IpaD-like Superfamily: IpaD-like Family: IpaD-like
9	c2j0oA_	 Alignment		48.2	19	PDB header: cell invasion Chain: A: PDB Molecule: invasin ipad; PDBTitle: shigella flexneri ipad
10	c2ym0B_	 Alignment		46.3	6	PDB header: cell invasion Chain: B: PDB Molecule: cell invasion protein sipd; PDBTitle: truncated sipd from salmonella typhimurium
11	c2d4uA_	 Alignment		43.5	15	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

12	d1q90m_	Alignment		41.8	50	Fold: Single transmembrane helix Superfamily: PetM subunit of the cytochrome b6f complex Family: PetM subunit of the cytochrome b6f complex
13	d1oqwa_	Alignment		41.4	13	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
14	d2liga_	Alignment		39.9	16	Fold: Four-helical up-and-down bundle Superfamily: Aspartate receptor, ligand-binding domain Family: Aspartate receptor, ligand-binding domain
15	d2pila_	Alignment		37.6	8	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
16	c3kdpG_	Alignment		36.8	38	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
17	c3kdpH_	Alignment		36.8	38	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
18	c2zzeG_	Alignment		34.9	46	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+ .pi2 state
19	c1gk6B_	Alignment		33.9	16	PDB header: vimentin Chain: B: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
20	c3ipdB_	Alignment		32.2	14	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
21	c1nfoA_	Alignment	not modelled	30.4	24	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein e2; PDBTitle: apolipoprotein e2 (apoE2, d154a mutation)
22	c2jo1A_	Alignment	not modelled	30.0	38	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
23	d1rhzb_	Alignment	not modelled	28.3	20	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
24	c1avoD_	Alignment	not modelled	27.1	11	PDB header: proteasome activator Chain: D: PDB Molecule: 11s regulator; PDBTitle: proteasome activator reg(alpha)
25	c2jp3A_	Alignment	not modelled	27.0	15	PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
26	c2xv5A_	Alignment	not modelled	26.9	19	PDB header: structural protein Chain: A: PDB Molecule: lamin-a/c; PDBTitle: human lamin a coil 2b fragment
27	c2cpbA_	Alignment	not modelled	26.1	24	PDB header: viral protein Chain: A: PDB Molecule: m13 major coat protein; PDBTitle: solution nmr structures of the major coat protein of2 filamentous bacteriophage m13 solubilized in3 dodecylphosphocholine micelles, 25 lowest energy structures
28	c1gk4A_	Alignment	not modelled	25.9	26	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2)

29	c2k9yB_	Alignment	not modelled	25.7	22	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
30	c2gl2B_	Alignment	not modelled	25.5	11	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
31	d2jaaa1	Alignment	not modelled	25.1	19	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
32	c2p7nA_	Alignment	not modelled	25.0	6	PDB header: cell invasion Chain: A: PDB Molecule: pathogenicity island 1 effector protein; PDBTitle: crystal structure of the pathogenicity island 1 effector2 protein from chromobacterium violaceum. northeast3 structural genomics consortium (nesgc) target cvr69.
33	c3n23E_	Alignment	not modelled	24.0	38	PDB header: hydrolase Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
34	c2xdjF_	Alignment	not modelled	23.9	20	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
35	d1f6ga_	Alignment	not modelled	23.8	17	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
36	c2k9yA_	Alignment	not modelled	22.3	22	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
37	c2jwaA_	Alignment	not modelled	19.3	21	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
38	d2axtj1	Alignment	not modelled	19.1	33	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, PsbJ Family: PsbJ-like
39	c1ei3E_	Alignment	not modelled	18.9	16	PDB header: PDB COMPND:
40	c1ei3C_	Alignment	not modelled	18.5	11	PDB header: PDB COMPND:
41	c1pi7A_	Alignment	not modelled	17.3	53	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
42	c2gohA_	Alignment	not modelled	17.3	53	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
43	c2gofA_	Alignment	not modelled	17.3	53	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
44	c1pi8A_	Alignment	not modelled	17.3	53	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
45	c1pjeA_	Alignment	not modelled	17.3	53	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
46	c2wvrB_	Alignment	not modelled	16.7	24	PDB header: replication Chain: B: PDB Molecule: geminin; PDBTitle: human cdt1:geminin complex
47	c3cvfA_	Alignment	not modelled	16.5	32	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
48	d2nwwa1	Alignment	not modelled	16.4	39	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
49	c3sokB_	Alignment	not modelled	16.3	11	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
50	c3b5nF_	Alignment	not modelled	15.8	16	PDB header: membrane protein Chain: F: PDB Molecule: protein sso1; PDBTitle: structure of the yeast plasma membrane snare complex
51	c2ww9B_	Alignment	not modelled	15.5	25	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sss1; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
52	c1n7sB_	Alignment	not modelled	15.4	14	PDB header: transport protein Chain: B: PDB Molecule: syntaxin 1a; PDBTitle: high resolution structure of a truncated neuronal snare2 complex
53	c2qdqA_	Alignment	not modelled	15.1	26	PDB header: structural protein Chain: A: PDB Molecule: talín-1; PDBTitle: crystal structure of the talin dimerisation domain
54	c2wwbB_	Alignment	not modelled	14.5	20	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sec61 subunit gamma; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome PDB header: protein transport

55	c3htuB_	Alignment	not modelled	14.4	15	Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 20; PDBTitle: crystal structure of the human vps25-vps20 subcomplex
56	c2ym9C_	Alignment	not modelled	13.7	6	PDB header: cell invasion Chain: C: PDB Molecule: cell invasion protein sipd; PDBTitle: sipd from salmonella typhimurium
57	d1kpla_	Alignment	not modelled	13.7	18	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
58	c2npsB_	Alignment	not modelled	13.5	16	PDB header: transport protein Chain: B: PDB Molecule: syntaxin 13; PDBTitle: crystal structure of the early endosomal snare complex
59	d1k1fa_	Alignment	not modelled	12.9	27	Fold: Bcr-Abl oncoprotein oligomerization domain Superfamily: Bcr-Abl oncoprotein oligomerization domain Family: Bcr-Abl oncoprotein oligomerization domain
60	c2jpxA_	Alignment	not modelled	12.7	50	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: a18h vpu tm structure in lipid bilayers
61	c2x2vG_	Alignment	not modelled	12.6	13	PDB header: membrane protein Chain: G: PDB Molecule: atp synthase subunit c; PDBTitle: structural basis of a novel proton-coordination type in an2 f1fo-atp synthase rotor ring
62	c3cveC_	Alignment	not modelled	12.6	30	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
63	c2zt9E_	Alignment	not modelled	12.3	18	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
64	c2hg5D_	Alignment	not modelled	12.0	22	PDB header: membrane protein Chain: D: PDB Molecule: kcsa channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
65	c1sfcJ_	Alignment	not modelled	11.9	11	PDB header: transport protein Chain: J: PDB Molecule: protein (syntaxin 1a); PDBTitle: neuronal synaptic fusion complex
66	c1lwuH_	Alignment	not modelled	11.9	10	PDB header: blood clotting Chain: H: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of fragment d from lamprey fibrinogen complexed with2 the peptide gly-his-arg-pro-amide
67	c2akcC_	Alignment	not modelled	11.8	25	PDB header: hydrolase Chain: C: PDB Molecule: class a nonspecific acid phosphatase phon; PDBTitle: crystal structure of tungstate complex of the phon protein2 from s. typhimurium
68	c2vv5D_	Alignment	not modelled	11.5	15	PDB header: membrane protein Chain: D: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: the open structure of msccs
69	c2qsgX_	Alignment	not modelled	11.1	21	PDB header: dna binding protein/dna Chain: X: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of rad4-rad23 bound to a uv-damaged dna
70	d1x3zb1	Alignment	not modelled	11.1	21	Fold: XPC-binding domain Superfamily: XPC-binding domain Family: XPC-binding domain
71	d1lotsa_	Alignment	not modelled	10.9	18	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
72	d1rh5b_	Alignment	not modelled	10.7	20	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
73	c1x8yA_	Alignment	not modelled	10.7	18	PDB header: structural protein Chain: A: PDB Molecule: lamin a/c; PDBTitle: human lamin coil 2b
74	c1wu0A_	Alignment	not modelled	10.6	24	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase c chain; PDBTitle: solution structure of subunit c of f1fo-atp synthase from2 the thermophilic bacillus ps3
75	c2ks1B_	Alignment	not modelled	10.6	44	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
76	c1deqO_	Alignment	not modelled	10.5	12	PDB header: PDB COMPND:
77	c3ck6E_	Alignment	not modelled	10.5	8	PDB header: structural protein Chain: E: PDB Molecule: putative membrane transport protein; PDBTitle: crystal structure of zntb cytoplasmic domain from vibrio2 parahaemolyticus rimd 2210633
78	c2hacA_	Alignment	not modelled	10.2	18	PDB header: membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
79	d1zuja1	Alignment	not modelled	9.4	19	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin
80	d2r6gf2	Alignment	not modelled	8.9	16	Fold: Metl-like Superfamily: Metl-like Family: Metl-like
81	c1fmhA_	Alignment	not modelled	8.8	20	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: nmr solution structure of a designed heterodimeric

						leucine2 zipper
82	d1q90b_	Alignment	not modelled	8.4	25	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
83	c1iflA_	Alignment	not modelled	8.4	28	PDB header: virus Chain: A: PDB Molecule: inovirus; PDBTitle: molecular models and structural comparisons of native and2 mutant class i filamentous bacteriophages ff (fd, f1, m13),3 if1 and ike
84	d1befa_	Alignment	not modelled	8.3	50	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
85	c2oarA_	Alignment	not modelled	8.2	20	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
86	c3jycA_	Alignment	not modelled	8.1	22	PDB header: metal transport Chain: A: PDB Molecule: inward-rectifier k+ channel kir2.2; PDBTitle: crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
87	c3lkwA_	Alignment	not modelled	8.0	30	PDB header: viral protein,hydrolase Chain: A: PDB Molecule: fusion protein of nonstructural protein 2b and PDBTitle: crystal structure of dengue virus 1 ns2b/ns3 protease active2 site mutant
88	c2kncB_	Alignment	not modelled	7.7	18	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIiB-beta3 transmembrane-cytoplasmic2 heterocomplex
89	d2ijob1	Alignment	not modelled	7.5	40	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
90	d2fomb1	Alignment	not modelled	7.5	50	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
91	d1q90L_	Alignment	not modelled	7.5	24	Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
92	c1q90L_	Alignment	not modelled	7.5	24	PDB header: photosynthesis Chain: L: PDB Molecule: cytochrome b6f complex subunit petI; PDBTitle: structure of the cytochrome b6f (plastoquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
93	d1c99a_	Alignment	not modelled	7.4	21	Fold: Transmembrane helix hairpin Superfamily: F1F0 ATP synthase subunit C Family: F1F0 ATP synthase subunit C
94	d1v54b2	Alignment	not modelled	7.4	14	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
95	d2axtl1	Alignment	not modelled	7.2	15	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein I, PsbI Family: PsbI-like
96	c2e74E_	Alignment	not modelled	7.1	26	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from m.laminosus
97	c1vf5E_	Alignment	not modelled	7.1	26	PDB header: photosynthesis Chain: E: PDB Molecule: protein pet I; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
98	c1vf5R_	Alignment	not modelled	7.1	26	PDB header: photosynthesis Chain: R: PDB Molecule: protein pet I; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
99	c2e75E_	Alignment	not modelled	7.1	26	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus