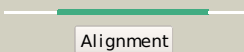
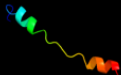
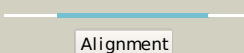
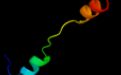
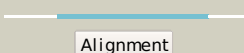
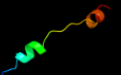
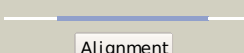

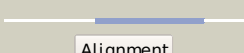

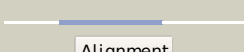
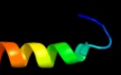
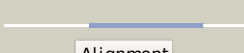

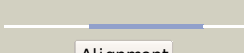






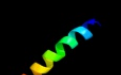

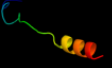

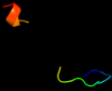
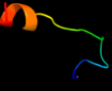
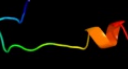





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2x2vG_	 Alignment		40.4	39	PDB header: membrane protein Chain: G: PDB Molecule: atp synthase subunit c; PDBTitle: structural basis of a novel proton-coordination type in an2 f1fo-atp synthase rotor ring
2	c1yceD_	 Alignment		32.0	36	PDB header: membrane protein Chain: D: PDB Molecule: subunit c; PDBTitle: structure of the rotor ring of f-type na+ -atpase from ilyobacter2 tartaricus
3	c2w5jM_	 Alignment		30.9	39	PDB header: hydrolase Chain: M: PDB Molecule: atp synthase c chain, chloroplastic; PDBTitle: structure of the c14-rotor ring of the proton translocating2 chloroplast atp synthase
4	c2wpdP_	 Alignment		29.3	39	PDB header: hydrolase Chain: P: PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: the mg.adp inhibited state of the yeast f1c10 atp synthase
5	c1shzF_	 Alignment		23.6	35	PDB header: signaling protein Chain: F: PDB Molecule: rho guanine nucleotide exchange factor 1; PDBTitle: crystal structure of the p115rhogef rgrgs domain in a2 complex with galpha(13):galpha(i1) chimera
6	c1wu0A_	 Alignment		21.6	42	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
7	d1htjF_	 Alignment		20.5	38	Fold: Regulator of G-protein signaling, RGS Superfamily: Regulator of G-protein signaling, RGS Family: Regulator of G-protein signaling, RGS
8	c1htjF_	 Alignment		20.5	38	PDB header: signaling protein Chain: F: PDB Molecule: kiaa0380; PDBTitle: structure of the rgs-like domain from pdz-rhogef
9	d1iapa_	 Alignment		18.9	35	Fold: Regulator of G-protein signaling, RGS Superfamily: Regulator of G-protein signaling, RGS Family: Regulator of G-protein signaling, RGS
10	c1ceuA_	 Alignment		17.4	36	PDB header: viral protein Chain: A: PDB Molecule: protein (hiv-1 regulatory protein n-terminal PDBTitle: nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
11	c2latA_	 Alignment		10.2	36	PDB header: membrane protein Chain: A: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: solution structure of a human minimembrane protein ost4

12	d1xmeh2	Alignment		9.6	43	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
13	c2xndK	Alignment		8.1	43	PDB header: hydrolase Chain: K: PDB Molecule: atp synthase lipid-binding protein, mitochondrial; PDBTitle: crystal structure of bovine f1-c8 sub-complex of atp2 synthase
14	c3bc1F	Alignment		8.1	56	PDB header: signaling protein/transport protein Chain: F: PDB Molecule: synaptotagmin-like protein 2; PDBTitle: crystal structure of the complex rab27a-slp2a
15	c1m8lA	Alignment		8.0	47	PDB header: viral protein Chain: A: PDB Molecule: vpr protein; PDBTitle: nmr structure of the hiv-1 regulatory protein vpr
16	c1sg7A	Alignment		8.0	42	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cation transport regulator chab; PDBTitle: nmr solution structure of the putative cation transport2 regulator chab
17	d1sg7a1	Alignment		8.0	42	Fold: ChaB-like Superfamily: ChaB-like Family: ChaB-like
18	c3h87D	Alignment		7.6	78	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
19	c3mwzA	Alignment		7.5	27	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: sialostatin I2; PDBTitle: crystal structure of the selenomethionine derivative of the I 22,47,2 100 m mutant of sialostatin I2
20	d1nekc	Alignment		6.8	15	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
21	d1c99a	Alignment	not modelled	6.3	24	Fold: Transmembrane helix hairpin Superfamily: F1F0 ATP synthase subunit C Family: F1F0 ATP synthase subunit C
22	c2o8gl	Alignment	not modelled	5.7	35	PDB header: hydrolase/inhibitor Chain: J: PDB Molecule: protein phosphatase inhibitor 2; PDBTitle: rat pp1c gamma complexed with mouse inhibitor-2