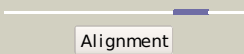
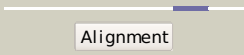
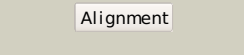
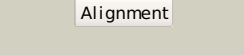
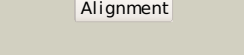
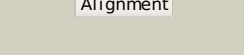
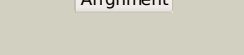
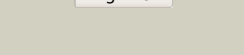
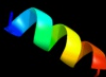
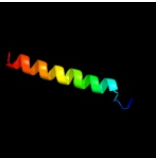
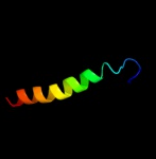
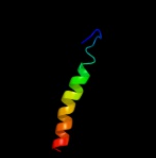
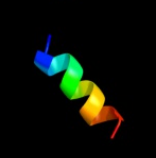
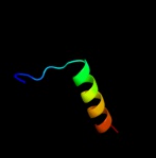
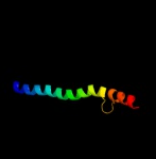
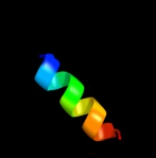


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p3xA_	 Alignment		15.0	46	PDB header: oxidoreductase Chain: A: PDB Molecule: polyphenol oxidase, chloroplast; PDBTitle: crystal structure of grenache (vitis vinifera) polyphenol2 oxidase
2	d1bt3a_	 Alignment		14.1	38	Fold: Di-copper centre-containing domain Superfamily: Di-copper centre-containing domain Family: Catechol oxidase
3	c2kncA_	 Alignment		12.6	10	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alpha-iiB-beta3 transmembrane-cytoplasmic2 heterocomplex
4	c3npvB_	 Alignment		11.0	38	PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosinase; PDBTitle: crystal structure of tyrosinase from bacillus megaterium soaked in2 cuso4
5	c3qngD_	 Alignment		10.6	47	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
6	c2y9xC_	 Alignment		10.1	46	PDB header: oxidoreductase Chain: C: PDB Molecule: polyphenol oxidase; PDBTitle: crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
7	c3lk2B_	 Alignment		9.4	50	PDB header: protein binding Chain: B: PDB Molecule: f-actin-capping protein subunit beta isoforms 1 and 2; PDBTitle: crystal structure of capz bound to the uncapping motif from carmil
8	c1js8A_	 Alignment		9.3	38	PDB header: oxygen storage/transport Chain: A: PDB Molecule: hemocyanin; PDBTitle: structure of a functional unit from octopus hemocyanin
9	c1hf9B_	 Alignment		8.4	25	PDB header: atpase inhibitor Chain: B: PDB Molecule: atpase inhibitor (mitochondrial); PDBTitle: c-terminal coiled-coil domain from bovine if1
10	d1iznb_	 Alignment		8.3	50	Fold: Subunits of heterodimeric actin filament capping protein Capz Superfamily: Subunits of heterodimeric actin filament capping protein Capz Family: Capz beta-1 subunit
11	d1js8a1	 Alignment		8.0	38	Fold: Di-copper centre-containing domain Superfamily: Di-copper centre-containing domain Family: Hemocyanin middle domain

12	c2k1kA_	Alignment		7.2	32	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
13	c2k1lB_	Alignment		7.2	32	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
14	c2k1kB_	Alignment		7.2	32	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
15	c2k1lA_	Alignment		7.2	32	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
16	c1wx2A_	Alignment		7.2	31	PDB header: oxidoreductase/metal transport Chain: A: PDB Molecule: tyrosinase; PDBTitle: crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of hydrogenperoxide
17	dlu1lA_	Alignment		6.3	4	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
18	c2kncB_	Alignment		6.1	18	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
19	c2fqcA_	Alignment		5.8	43	PDB header: toxin Chain: A: PDB Molecule: conotoxin pl14a; PDBTitle: solution structure of conotoxin pl14a
20	c1lnlB_	Alignment		5.7	38	PDB header: oxygen storage/transport Chain: B: PDB Molecule: hemocyanin; PDBTitle: structure of deoxygenated hemocyanin from rapana thomasiانا
21	c2fw9A_	Alignment	not modelled	5.6	4	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
22	dl1lna1	Alignment	not modelled	5.5	38	Fold: Di-copper centre-containing domain Superfamily: Di-copper centre-containing domain Family: Hemocyanin middle domain