Phyre^2

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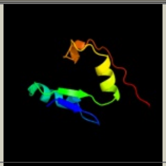
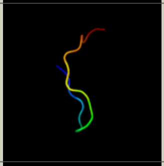
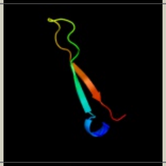
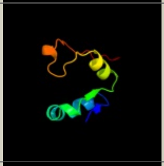
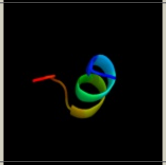
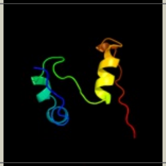
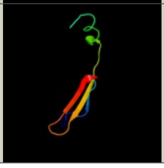
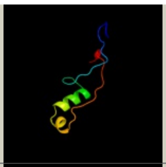
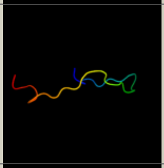
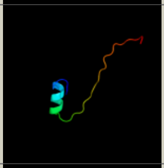
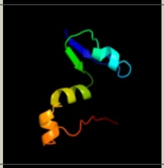
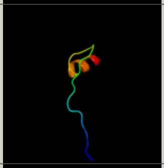
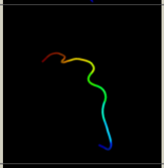
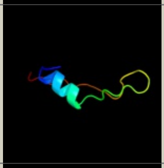
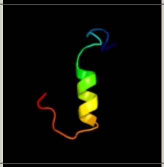
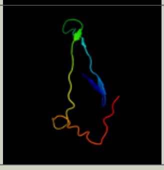
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3au9A_	Alignment		37.0	18	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase
2	d2ijra1	Alignment		22.7	24	**Fold:**Api92-like **Superfamily:**Api92-like **Family:**Api92-like
3	d1ei5a1	Alignment		19.7	30	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
4	d1zy9a1	Alignment		18.5	33	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**YicI N-terminal domain-like
5	c2jrbA_	Alignment		17.0	43	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**orf 1 protein; **PDBTitle:** c-terminal domain of orf1p from mouse line-1
6	d1smpi_	Alignment		15.1	23	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
7	c1r0lD_	Alignment		12.5	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
8	c1k5hB_	Alignment		9.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose-5-phosphate reductoisomerase
9	d2ctda1	Alignment		8.6	31	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
10	c2jcyA_	Alignment		8.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
11	d1ggla_	Alignment		7.4	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like

12	d1uowa_	Alignment		7.3	20	**Fold:**C2 domain-like **Superfamily:**C2 domain (Calcium/lipid-binding domain, CaLB) **Family:**Synaptotagmin-like (S variant)
13	c2x3bB_	Alignment		7.0	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
14	c1a6cA_	Alignment		6.8	15	**PDB header:**virus **Chain:** A: **PDB Molecule:**tobacco ringspot virus capsid protein; **PDBTitle:** structure of tobacco ringspot virus
15	c3a14B_	Alignment		6.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
16	d1j3na1	Alignment		6.5	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
17	c3monF_	Alignment		6.3	42	**PDB header:**sweet-tasting protein **Chain:** F: **PDB Molecule:**monellin; **PDBTitle:** crystal structures of two intensely sweet proteins
18	d1r0ka3	Alignment		6.2	17	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
19	d1bu2a2	Alignment		6.2	50	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
20	d1eg1a_	Alignment		6.1	22	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
21	c3hmhA_	Alignment	not modelled	5.5	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation factor tfiid 210 kda subunit; **PDBTitle:** crystal structure of the second bromodomain of human tbp-associated2 factor rna polymerase 1-like (taf1l)
22	c3p19A_	Alignment	not modelled	5.3	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative blue fluorescent protein; **PDBTitle:** improved nadph-dependent blue fluorescent protein
23	d1q0qa3	Alignment	not modelled	5.1	18	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
24	c2eghA_	Alignment	not modelled	5.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin