Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A6M2
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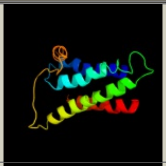
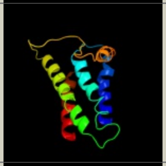
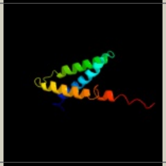
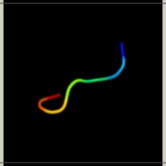
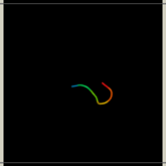
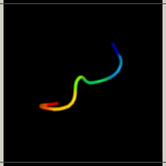
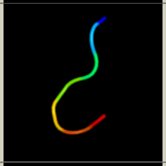
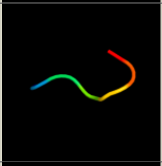
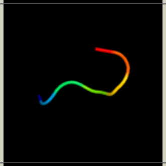
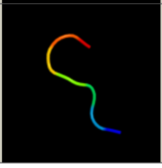
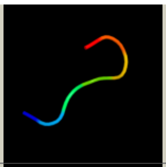
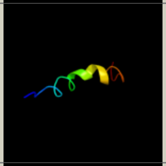
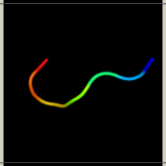
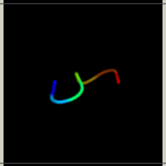
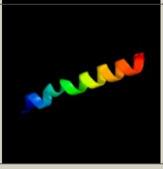
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hi7b1	Alignment		100.0	94	**Fold:**Bromodomain-like **Superfamily:**DsbB-like **Family:**DsbB-like
2	c3e9jC_	Alignment		100.0	94	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol/disulfide oxidoreductase dsbb; **PDBTitle:** structure of the charge-transfer intermediate of the2 transmembrane redox catalyst dsbb
3	c3kp9A_	Alignment		80.2	13	**PDB header:**blood coagulation,oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** structure of a bacterial homolog of vitamin k epoxide reductase
4	d2g84a1	Alignment		47.7	57	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
5	c3ocqA_	Alignment		46.9	71	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytosine/adenosine deaminase; **PDBTitle:** crystal structure of trna-specific adenosine deaminase from salmonella2 enterica
6	d1wkqa_	Alignment		45.3	43	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
7	d2b3ja1	Alignment		45.0	71	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
8	d1z3aa1	Alignment		44.4	71	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
9	d1wwra1	Alignment		41.9	57	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
10	c2nx8A_	Alignment		40.7	57	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna-specific adenosine deaminase; **PDBTitle:** the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
11	c3dh1D_	Alignment		39.4	43	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**trna-specific adenosine deaminase 2; **PDBTitle:** crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2

12	d1p6oa_	Alignment		38.6	57	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
13	d2a8na1	Alignment		36.9	57	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
14	c2l0lA_	Alignment		35.5	85	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**oxidoreductase that catalyzes reoxidation of dsba protein **PDBTitle:** dsbb2 peptide structure in 70% tfe
15	d2hxva2	Alignment		29.9	14	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
16	c2l0mA_	Alignment		28.5	85	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**oxidoreductase that catalyzes reoxidation of dsba protein **PDBTitle:** dsbb2 peptide structure in 100% tfe
17	c2o7pA_	Alignment		28.0	57	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
18	d1vq2a_	Alignment		25.5	57	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
19	c2hvwC_	Alignment		22.8	43	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** crystal structure of dcmp deaminase from streptococcus2 mutans
20	d1m56d_	Alignment		22.5	32	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
21	c2w4lC_	Alignment	not modelled	19.6	57	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** human dcmp deaminase
22	d2drpa2	Alignment	not modelled	16.5	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
23	d2a1ka1	Alignment	not modelled	12.3	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
24	c3pcqX_	Alignment	not modelled	10.3	25	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i 4.8k protein; **PDBTitle:** femtosecond x-ray protein nanocrystallography
25	d2eppa1	Alignment	not modelled	9.6	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
26	c1jb0X_	Alignment	not modelled	8.5	25	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i subunit psax; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
27	d1jb0x_	Alignment	not modelled	8.5	25	**Fold:**Single transmembrane helix **Superfamily:**Subunit PsaX of photosystem I reaction centre **Family:**Subunit PsaX of photosystem I reaction centre
28	d1qled_	Alignment	not modelled	7.5	29	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
29	d2akla2	Alignment	not modelled	7.3	57	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon

						Family: PhnA zinc-binding domain
30	c2aklA_	Alignment	not modelled	7.2	57	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
31	c2riqA_	Alignment	not modelled	6.5	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
32	c2jvnA_	Alignment	not modelled	6.1	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
33	d1eyfa_	Alignment	not modelled	5.6	38	**Fold:**Ada DNA repair protein, N-terminal domain (N-Ada 10) **Superfamily:**Ada DNA repair protein, N-terminal domain (N-Ada 10) **Family:**Ada DNA repair protein, N-terminal domain (N-Ada 10)