Phyre^2

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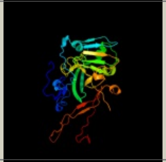
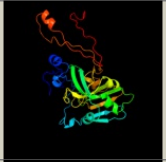
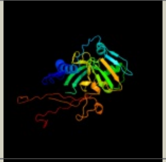
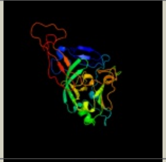
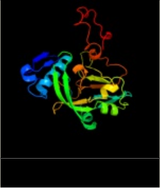
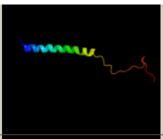
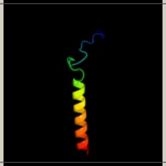
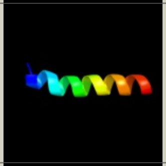
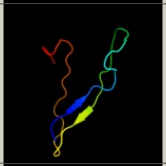
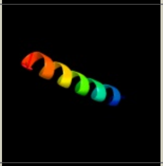
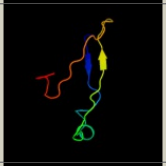
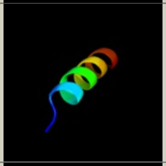
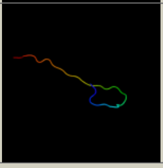
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xdya_	Alignment		100.0	100	**Fold:**Oxidoreductase molybdopterin-binding domain **Superfamily:**Oxidoreductase molybdopterin-binding domain **Family:**Oxidoreductase molybdopterin-binding domain
2	c1xdyC_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**bacterial sulfite oxidase; **PDBTitle:** structural and biochemical identification of a novel2 bacterial oxidoreductase, w-containing cofactor
3	c2xtsC_	Alignment		100.0	20	**PDB header:**oxidoreductase/electron transport **Chain:** C: **PDB Molecule:**sulfite dehydrogenase; **PDBTitle:** crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
4	c1soxB_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite oxidase; **PDBTitle:** sulfite oxidase from chicken liver
5	c2bihA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrate reductase [nadph]; **PDBTitle:** crystal structure of the molybdenum-containing nitrate2 reducing fragment of pichia angusta assimilatory nitrate3 reductase
6	c2bpbA_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit a; **PDBTitle:** sulfite dehydrogenase from starkeya novella
7	c2biiA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrate reductase [nadph]; **PDBTitle:** crystal structure of nitrate-reducing fragment of2 assimilatory nitrate reductase from pichia angusta
8	c2a9dB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite oxidase; **PDBTitle:** crystal structure of recombinant chicken sulfite oxidase with arg at2 residue 161
9	c1ogpD_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**sulfite oxidase; **PDBTitle:** the crystal structure of plant sulfite oxidase provides2 insight into sulfite oxidation in plants and animals
10	d1ogpa2	Alignment		100.0	21	**Fold:**Oxidoreductase molybdopterin-binding domain **Superfamily:**Oxidoreductase molybdopterin-binding domain **Family:**Oxidoreductase molybdopterin-binding domain
11	d2a9da2	Alignment		100.0	22	**Fold:**Oxidoreductase molybdopterin-binding domain **Superfamily:**Oxidoreductase molybdopterin-binding domain **Family:**Oxidoreductase molybdopterin-binding domain

12	c2e76D_	Alignment		77.3	17	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
13	c1p84E_	Alignment		53.8	22	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
14	c2fyuE_	Alignment		34.5	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
15	d1ogpa1	Alignment		28.0	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
16	c2fynO_	Alignment		22.0	9	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
17	d1r6oc1	Alignment		21.2	18	**Fold:**ClpS-like **Superfamily:**ClpS-like **Family:**Adaptor protein ClpS (YljA)
18	d2a9da1	Alignment		13.5	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
19	c3h3gB_	Alignment		12.9	29	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**parathyroid hormone-related protein; **PDBTitle:** crystal structure of the extracellular domain of the human parathyroid2 hormone receptor (pth1r) in complex with parathyroid hormone-related3 protein (pthrp)
20	d2axwa1	Alignment		12.0	12	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
21	d2evea1	Alignment	not modelled	11.8	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
22	c3dnjB_	Alignment	not modelled	11.5	9	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease adapter protein clps; **PDBTitle:** the structure of the caulobacter crescentus clps protease2 adaptor protein in complex with a n-end rule peptide
23	c3ffdP_	Alignment	not modelled	10.7	31	**PDB header:**immune system/hormone **Chain:** P: **PDB Molecule:**parathyroid hormone-related protein; **PDBTitle:** structure of parathyroid hormone-related protein complexed2 to a neutralizing monoclonal antibody
24	d1l7la_	Alignment	not modelled	9.9	38	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**PA-IL, galactose-binding lectin 1
25	d1pd0a2	Alignment	not modelled	9.4	16	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**beta-sandwich domain of Sec23/24 **Family:**beta-sandwich domain of Sec23/24
26	c2inpE_	Alignment	not modelled	7.9	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**phenol hydroxylase component pho; **PDBTitle:** structure of the phenol hydroxylase-regulatory protein2 complex
27	d2g2xa1	Alignment	not modelled	7.8	27	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
28	c1r8oA_	Alignment	not modelled	7.1	22	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kunitz trypsin inhibitor; **PDBTitle:** crystal structure of an unusual kunitz-type trypsin inhibitor from2 copaifera langsdorffii seeds
						PDB header:oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase

29	c3diiB_	Alignment	not modelled	6.8	16	sdr; **PDBTitle:** crystal structure of a carbohydrate specific scor enzyme2 from clostridium thermocellum, ligand-free form
30	d1zud21	Alignment	not modelled	6.3	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
31	d2huha1	Alignment	not modelled	6.2	18	**Fold:**C2 domain-like **Superfamily:**Smr-associated domain-like **Family:**Smr-associated domain
32	c2fvnA_	Alignment	not modelled	6.0	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein afad; **PDBTitle:** the fibrillar tip complex of the afa/dr adhesins from2 pathogen e. coli displays synergistic binding to 5 1 and v3 3 integrins
33	d1qo7a_	Alignment	not modelled	5.7	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
34	d2ar1a1	Alignment	not modelled	5.5	18	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
35	d1pgw21	Alignment	not modelled	5.5	22	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
36	d2hkja1	Alignment	not modelled	5.3	22	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Topoisomerase VI-B subunit middle domain
37	d1pgl21	Alignment	not modelled	5.3	22	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
38	d1ny721	Alignment	not modelled	5.2	26	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP