Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P39295
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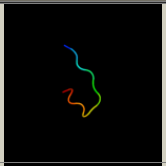
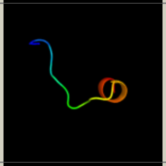
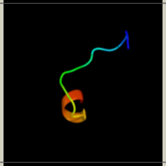
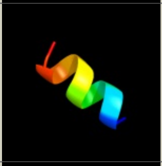
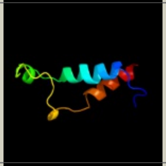
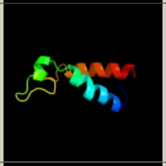
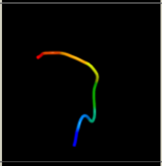
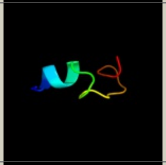
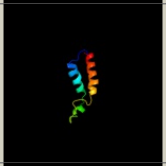
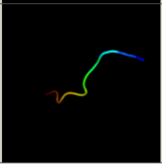
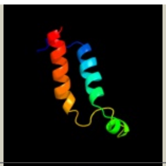
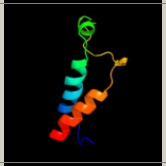
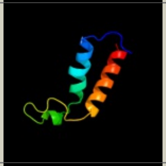
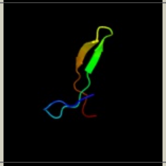
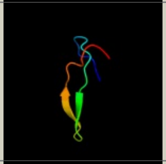
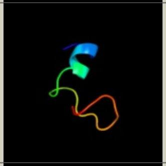
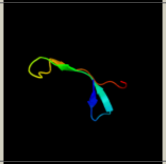
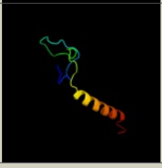
Unique Job ID	d915d6bc8b02c18e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1j3ba1	Alignment		23.2	38	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
2	d1i8na_	Alignment		16.7	29	**Fold:**Hairpin loop containing domain-like **Superfamily:**Hairpin loop containing domain-like **Family:**Anti-platelet protein
3	c1i8nA_	Alignment		16.7	29	**PDB header:**toxin **Chain:** A: **PDB Molecule:**anti-platelet protein; **PDBTitle:** crystal structure of leech anti-platelet protein
4	c2lbgA_	Alignment		15.3	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**major prion protein; **PDBTitle:** structure of the chr of the prion protein in dpc micelles
5	d1o0sa1	Alignment		11.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
6	c1yvyA_	Alignment		11.0	38	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxykinase [atp]; **PDBTitle:** crystal strucutre of anaerobiospirillum succiniciproducens2 phosphoenolpyruvate carboxykinase
7	c1gz3B_	Alignment		10.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent malic enzyme; **PDBTitle:** molecular mechanism for the regulation of human mitochondrial2 nad(p)+-dependent malic enzyme by atp and fumarate
8	c3ehwA_	Alignment		9.5	63	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dutp pyrophosphatase; **PDBTitle:** human dutpase in complex with alpha,beta-imido-dutp and mg2+:2 visualization of the full-length c-termini in all monomers and3 suggestion for an additional metal ion binding site
9	d1vjia_	Alignment		8.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
10	c2aw5A_	Alignment		8.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp-dependent malic enzyme; **PDBTitle:** crystal structure of a human malic enzyme
11	c1lj2D_	Alignment		7.9	30	**PDB header:**viral protein/ translation **Chain:** D: **PDB Molecule:**eukaryotic protein synthesis initiation factor; **PDBTitle:** recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization

12	d1gq2a1	Alignment		7.9	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
13	c1o0sB_	Alignment		7.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent malic enzyme; **PDBTitle:** crystal structure of ascaris suum malic enzyme complexed with nadh
14	d1pj3a1	Alignment		7.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
15	d2k7ia1	Alignment		7.5	20	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
16	c2k7iB_	Alignment		7.5	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0339 protein atu0232; **PDBTitle:** solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.
17	d1vyra_	Alignment		7.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
18	d1f7ra_	Alignment		7.1	71	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
19	d3bida1	Alignment		6.9	27	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
20	d1dosa_	Alignment		6.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
21	c1qr6A_	Alignment	not modelled	6.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme 2; **PDBTitle:** human mitochondrial nad(p)-dependent malic enzyme
22	d1oyaa_	Alignment	not modelled	5.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
23	d1icpa_	Alignment	not modelled	5.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
24	d1q45a_	Alignment	not modelled	5.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
25	c3lyiA_	Alignment	not modelled	5.6	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bromodomain-containing protein 1; **PDBTitle:** pwwp domain of human bromodomain-containing protein 1
26	c3l5aA_	Alignment	not modelled	5.4	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
27	c1ylhA_	Alignment	not modelled	5.3	38	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxykinase; **PDBTitle:** crystal structure of phosphoenolpyruvate carboxykinase from2 actinobaccilus succinogenes in complex with manganese and3 pyruvate
28	c2gq8A_	Alignment	not modelled	5.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, fmn-binding; **PDBTitle:** structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone

29	d1z41a1	Alignment	not modelled	5.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
30	c3gkaB_	Alignment	not modelled	5.1	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei