Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P18353
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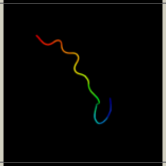
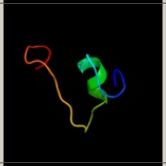
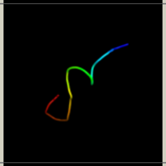
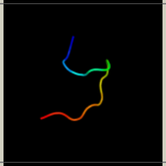
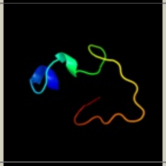
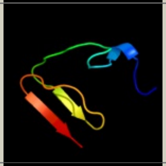
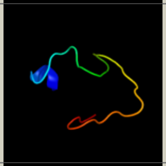
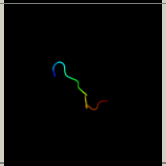
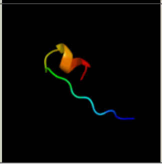
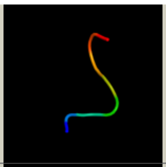
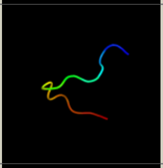
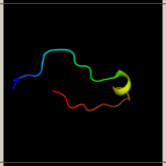
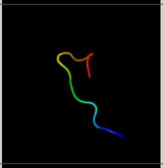
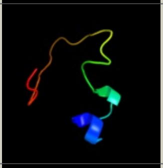
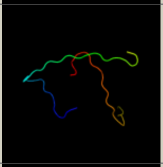
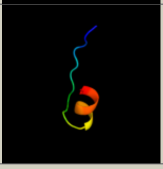
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w5cL_	Alignment		22.3	54	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**cytochrome b559 beta subunit; **PDBTitle:** photosystem ii from thermosynechococcus elongatus
2	d2axtf1	Alignment		21.8	54	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome b559 subunits **Family:**Cytochrome b559 subunits
3	d1c2aa1	Alignment		19.2	36	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Bowman-Birk inhibitor, BBI **Family:**Bowman-Birk inhibitor, BBI
4	d1fl2a2	Alignment		15.0	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
5	d1j83a_	Alignment		14.3	38	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 17 carbohydrate binding module, CBM17
6	d2fj8a1	Alignment		13.8	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Bowman-Birk inhibitor, BBI **Family:**Bowman-Birk inhibitor, BBI
7	d1efva2	Alignment		11.1	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
8	c1efpC_	Alignment		11.0	24	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**protein (electron transfer flavoprotein); **PDBTitle:** electron transfer flavoprotein (etf) from paracoccus2 denitrificans
9	d1efpa2	Alignment		10.9	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
10	c1tx6J_	Alignment		10.9	50	**PDB header:**hydrolase/protein binding **Chain:** J: **PDB Molecule:**bowman-birk type trypsin inhibitor; **PDBTitle:** trypsin:bbi complex
11	c2bi8A_	Alignment		10.6	39	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** udp-galactopyranose mutase from klebsiella pneumoniae with2 reduced fad

12	c1w1nA_	Alignment		9.5	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase tor1; **PDBTitle:** the solution structure of the fatc domain of the protein2 kinase tor1 from yeast
13	d1pbia_	Alignment		9.4	29	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Bowman-Birk inhibitor, BBI **Family:**Bowman-Birk inhibitor, BBI
14	c2qn5B_	Alignment		7.6	42	**PDB header:**hydrolase inhibitor/hydrolase **Chain:** B: **PDB Molecule:**bowman-birk type bran trypsin inhibitor; **PDBTitle:** crystal structure and functional study of the bowman-birk2 inhibitor from rice bran in complex with bovine trypsin
15	c2zylA_	Alignment		7.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible oxidoreductase; **PDBTitle:** crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
16	c2pd0D_	Alignment		7.3	38	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** protein cgd2_2020 from cryptosporidium parvum
17	d3clsd2	Alignment		7.3	27	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
18	c2fqcA_	Alignment		6.9	80	**PDB header:**toxin **Chain:** A: **PDB Molecule:**conotoxin pl14a; **PDBTitle:** solution structure of conotoxin pl14a
19	c1zq1D_	Alignment		6.7	8	**PDB header:**lyase **Chain:** D: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit e; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
20	d2bi7a1	Alignment		6.7	37	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**UDP-galactopyranose mutase, N-terminal domain
21	d2d6fc3	Alignment	not modelled	6.6	21	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
22	d1cqxa2	Alignment	not modelled	6.2	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
23	d1u97a_	Alignment	not modelled	6.1	46	**Fold:**Cysteine alpha-hairpin motif **Superfamily:**Cysteine alpha-hairpin motif **Family:**COX17-like
24	d1pm6a_	Alignment	not modelled	5.9	20	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
25	d1qmva_	Alignment	not modelled	5.8	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
26	c3fnvB_	Alignment	not modelled	5.8	40	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**cdgsh iron sulfur domain-containing protein 2; **PDBTitle:** crystal structure of miner1: the redox-active 2fe-2s protein causative2 in wolfram syndrome 2
27	c2pnvA_	Alignment	not modelled	5.5	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
28	c2rnbA_	Alignment	not modelled	5.4	54	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cytochrome c oxidase copper chaperone; **PDBTitle:** solution structure of human cu(i)cox17

29	d2v1ra1	Alignment	not modelled	5.3	31	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain