Phyre^2

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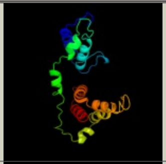
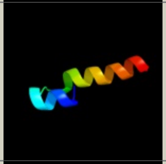
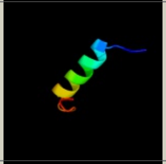
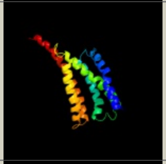
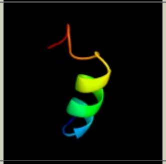
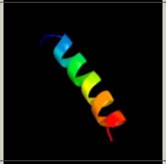
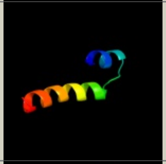
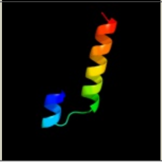
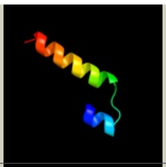
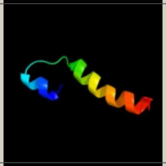
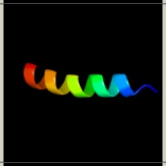
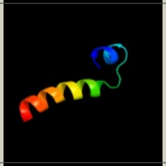
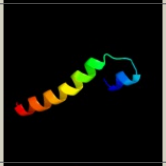
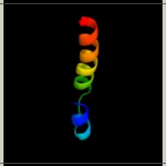
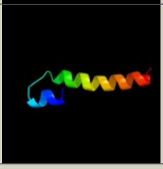
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zcdA_	Alignment		60.9	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**na(+)/h(+) antiporter 1; **PDBTitle:** crystal structure of the na+/h+ antiporter nhaa
2	c3lr4A_	Alignment		34.1	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
3	c2yvxD_	Alignment		24.3	11	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
4	c1wozA_	Alignment		21.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long conserved hypothetical protein (st1454); **PDBTitle:** crystal structure of uncharacterized protein st1454 from sulfolobus2 tokodaii
5	d2gkea2	Alignment		19.2	26	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase
6	d1pw4a_	Alignment		15.9	11	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
7	d1e3ha2	Alignment		14.4	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
8	c3efeC_	Alignment		13.8	32	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
9	c2idxA_	Alignment		13.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cob(i)yrinic acid a,c-diamide **PDBTitle:** structure of human atp:cobalamin adenosyltransferase bound2 to atp.
10	c1wy1B_	Alignment		12.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein ph0671; **PDBTitle:** crystal structure of the ph0671 protein from pyrococcus horikoshii ot3
11	d1noga_	Alignment		12.1	14	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase

12	c1nogA_	Alignment		12.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein ta0546; **PDBTitle:** crystal structure of conserved protein 0546 from thermoplasma2 acidophilum
13	d1zq1c1	Alignment		12.0	36	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
14	c2ah6B_	Alignment		11.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bh1595, unknown conserved protein; **PDBTitle:** crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution
15	c2g2dA_	Alignment		11.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:cobalamin adenosyltransferase; **PDBTitle:** crystal structure of a putative pduo-type atp:cobalamin2 adenosyltransferase from mycobacterium tuberculosis
16	d1rtya_	Alignment		11.1	21	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
17	c3f5dA_	Alignment		10.4	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from2 bacillus subtilis
18	c2nt8A_	Alignment		10.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase; **PDBTitle:** atp bound at the active site of a pduo type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri
19	c2zhzC_	Alignment		10.2	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**atp:cob(i)alamin adenosyltransferase, putative; **PDBTitle:** crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
20	c3ke4B_	Alignment		10.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical cytosolic protein; **PDBTitle:** crystal structure of a pduo-type atp:cob(i)alamin adenosyltransferase2 from bacillus cereus
21	d2fexa1	Alignment	not modelled	9.9	37	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
22	c3ci1A_	Alignment	not modelled	9.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase pduo-like protein; **PDBTitle:** structure of the pduo-type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri complexed3 with four-coordinate cob(ii)alamin and atp
23	d1fftb2	Alignment	not modelled	9.0	22	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
24	c2hp0A_	Alignment	not modelled	9.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ids-epimerase; **PDBTitle:** crystal structure of iminodisuccinate epimerase
25	d1rtyb_	Alignment	not modelled	8.8	21	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
26	c1wvtA_	Alignment	not modelled	7.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st2180; **PDBTitle:** crystal structure of uncharacterized protein st2180 from sulfolobus2 tokodaii
27	d1z96a1	Alignment	not modelled	7.8	35	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
28	c2g38A_	Alignment	not modelled	7.5	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium

						tuberculosis
29	d2g38a1	Alignment	not modelled	7.5	23	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PE
30	d1rfza_	Alignment	not modelled	7.3	14	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
31	d1tlqa_	Alignment	not modelled	6.7	7	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
32	c1tlqA_	Alignment	not modelled	6.7	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ypjq; **PDBTitle:** crystal structure of protein ypjq from bacillus subtilis, pfam duf64
33	d1szqa_	Alignment	not modelled	6.5	9	**Fold:**2-methylcitrate dehydratase PrpD **Superfamily:**2-methylcitrate dehydratase PrpD **Family:**2-methylcitrate dehydratase PrpD
34	c3mgkA_	Alignment	not modelled	6.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**intracellular protease/amidase related enzyme **PDBTitle:** crystal structure of probable protease/amidase from2 clostridium acetobutylicum atcc 824
35	c6rlxB_	Alignment	not modelled	6.1	42	**PDB header:**hormone(muscle relaxant) **Chain:** B: **PDB Molecule:**relaxin, b-chain; **PDBTitle:** x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
36	d1vf5b_	Alignment	not modelled	6.0	13	**Fold:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Superfamily:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
37	d3dtub2	Alignment	not modelled	5.9	16	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
38	d1sy7a1	Alignment	not modelled	5.1	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain