Phyre^2

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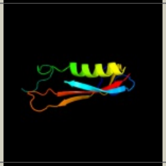
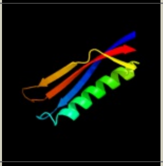
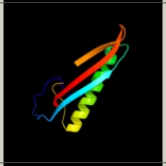
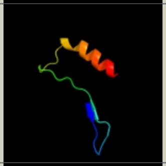
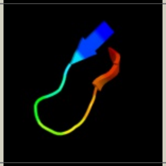
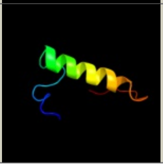
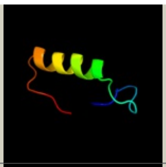
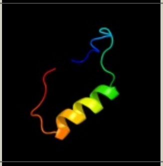
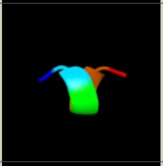
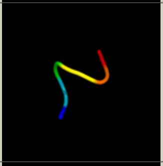
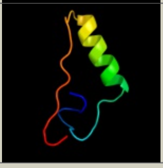
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y1bA_	Alignment		97.9	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein, signal; **PDBTitle:** crystal structure of the e. coli outer membrane lipoprotein2 rcsf
2	c1y2iC_	Alignment		96.9	21	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein s0862; **PDBTitle:** crystal structure of mcsg target apc27401 from shigella2 flexneri
3	d1y2ia_	Alignment		96.9	21	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
4	d1vr4a1	Alignment		95.4	13	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
5	c3qkbB_	Alignment		95.3	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
6	c2hl2A_	Alignment		34.6	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
7	d2noca1	Alignment		21.0	28	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
8	d1m5wa_	Alignment		20.9	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
9	c3cqrB_	Alignment		17.9	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**violaxanthin de-epoxidase, chloroplast; **PDBTitle:** crystal structure of the lipocalin domain of violaxanthin2 de-epoxidase (vde) at ph5
10	c2opdA_	Alignment		9.5	36	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**pilx; **PDBTitle:** structure of the neisseria meningitidis minor type iv pilin,2 pilx
11	d1xlma_	Alignment		9.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase

12	d1fcqa_	Alignment		9.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Bee venom hyaluronidase
13	c1fcuA_	Alignment		8.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase
14	c2v7sA_	Alignment		8.8	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable conserved lipoprotein lppa; **PDBTitle:** crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
15	c2kxhB_	Alignment		8.6	30	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**peptide of far upstream element-binding protein 1; **PDBTitle:** solution structure of the first two rrm domains of fir in the complex2 with fbp nbox peptide
16	d3e9va1	Alignment		8.4	50	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
17	d2z15a1	Alignment		7.9	33	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
18	d1nyta2	Alignment		7.8	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
19	c1zzaA_	Alignment		7.6	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**stannin; **PDBTitle:** solution nmr structure of the membrane protein stannin
20	c2atmA_	Alignment		7.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure of the recombinant allergen ves v 2
21	d1p77a2	Alignment	not modelled	7.3	12	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
22	d2jnaa1	Alignment	not modelled	6.9	26	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
23	c2im9A_	Alignment	not modelled	6.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460
24	d2im9a1	Alignment	not modelled	6.8	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Lpg0564-like
25	d1fcda2	Alignment	not modelled	6.2	31	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
26	c3iclA_	Alignment	not modelled	6.1	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**eal/ggdef domain protein; **PDBTitle:** x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
27	d1npya2	Alignment	not modelled	6.0	11	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
28	d1gpua1	Alignment	not modelled	5.8	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
						PDB header:isomerase, metal-binding protein

29	c2i56A_	Alignment	not modelled	5.7	13	**Chain:** A: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
30	d1w25a3	Alignment	not modelled	5.7	35	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
31	d2oufa1	Alignment	not modelled	5.5	11	**Fold:**HP0242-like **Superfamily:**HP0242-like **Family:**HP0242-like
32	d1ryia1	Alignment	not modelled	5.3	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain