Phyre^2

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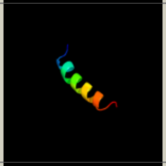
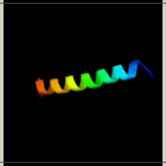
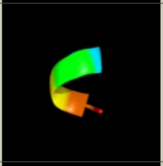
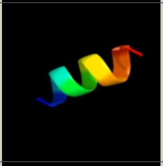
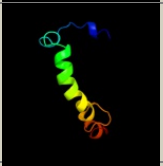
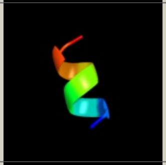
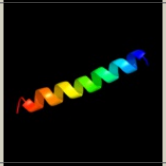
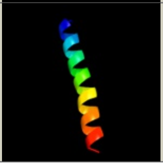
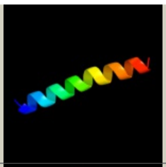
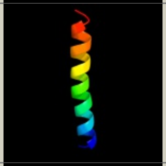
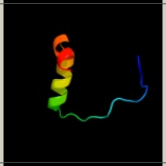
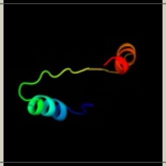
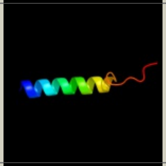
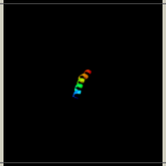
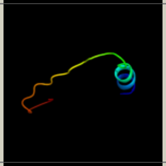
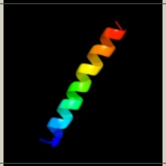
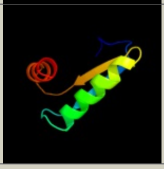
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kncA_	Alignment		18.3	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
2	d1z6na1	Alignment		13.5	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
3	d1kqfb2	Alignment		12.1	26	**Fold:**Single transmembrane helix **Superfamily:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor **Family:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
4	d1whqa_	Alignment		11.9	67	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
5	c2ap8A_	Alignment		10.1	42	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bombinin h4; **PDBTitle:** solution structure of bombinin h4 in dpc micelles
6	d2es9a1	Alignment		10.0	50	**Fold:**YoaC-like **Superfamily:**YoaC-like **Family:**YoaC-like
7	c2ap7A_	Alignment		9.9	42	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bombinin h2; **PDBTitle:** solution structure of bombinin h2 in dpc micelles
8	c2k21A_	Alignment		9.5	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
9	c2zcpA_	Alignment		9.3	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dehydrosqualene synthase; **PDBTitle:** crystal structure of the c(30) carotenoid dehydrosqualene2 synthase from staphylococcus aureus complexed with3 farnesyl thiopyrophosphate
10	c3a0bX_	Alignment		8.9	35	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
11	c3a0hx_	Alignment		8.9	35	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex

12	c3a0hX_	Alignment		8.9	35	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
13	c3a0bx_	Alignment		8.9	35	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
14	c3go5A_	Alignment		8.3	24	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**multidomain protein with s1 rna-binding domains; **PDBTitle:** crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
15	d2ifqa1	Alignment		8.1	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
16	c2k1aA_	Alignment		8.0	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
17	d1rhzb_	Alignment		7.9	19	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
18	d1a8la2	Alignment		7.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
19	c1s5lx_	Alignment		7.6	35	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem ii psbx protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
20	c2xpdC_	Alignment		7.5	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol peroxidase; **PDBTitle:** reduced thiol peroxidase (tpx) from yersinia pseudotuberculosis
21	d1j08a2	Alignment	not modelled	7.2	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
22	d1t56a2	Alignment	not modelled	7.1	13	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
23	d1u3em2	Alignment	not modelled	7.0	59	**Fold:**DNA-binding domain of intron-encoded endonucleases **Superfamily:**DNA-binding domain of intron-encoded endonucleases **Family:**DNA-binding domain of intron-encoded endonucleases
24	d2pf1a2	Alignment	not modelled	6.7	67	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
25	c2ww9B_	Alignment	not modelled	6.6	25	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
26	c2ariA_	Alignment	not modelled	6.5	45	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope polyprotein gp160; **PDBTitle:** solution structure of micelle-bound fusion domain of hiv-12 gp41
27	d1f9ma_	Alignment	not modelled	6.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
28	d2fkla1	Alignment	not modelled	6.4	50	**Fold:**Dodecin subunit-like **Superfamily:**Amyloid beta a4 protein copper binding domain (domain 2) **Family:**Amyloid beta a4 protein copper binding domain (domain 2)
						Fold: Single transmembrane helix

29	d2e74d2	Alignment	not modelled	5.8	46	**Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
30	d1q90d_	Alignment	not modelled	5.5	31	**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)
31	c2kb1A_	Alignment	not modelled	5.4	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**wsk3; **PDBTitle:** nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsa
32	d1rh5b_	Alignment	not modelled	5.3	19	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
33	c3c5tB_	Alignment	not modelled	5.3	50	**PDB header:**signaling protein/signaling protein **Chain:** B: **PDB Molecule:**exendin-4; **PDBTitle:** crystal structure of the ligand-bound glucagon-like peptide-1 receptor2 extracellular domain
34	c1ddxA_	Alignment	not modelled	5.2	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (prostaglandin h2 synthase-2); **PDBTitle:** crystal structure of a mixture of arachidonic acid and prostaglandin2 bound to the cyclooxygenase active site of cox-2: prostaglandin3 structure
35	d1m7ta_	Alignment	not modelled	5.2	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase