Phyre2

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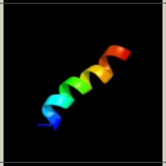
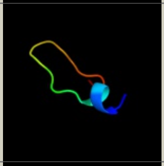
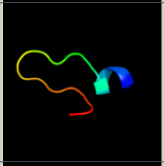
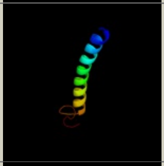
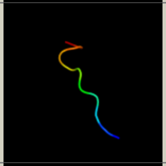
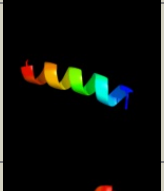
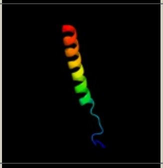
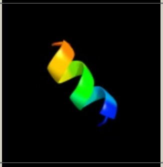
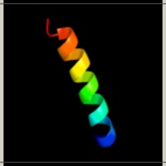
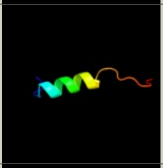
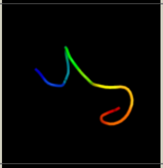
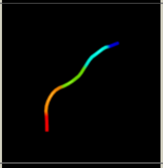
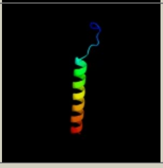
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l3oA_	Alignment		27.0	50	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**interleukin 3; **PDBTitle:** solution structure of murine interleukin 3
2	c2wwbB_	Alignment		15.5	11	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
3	d1rhzb_	Alignment		13.0	14	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
4	c1h4uA_	Alignment		12.1	11	**PDB header:**extracellular matrix protein **Chain:** A: **PDB Molecule:**nidogen-1; **PDBTitle:** domain g2 of mouse nidogen-1
5	d1gl4a1	Alignment		10.2	11	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Domain G2 of nidogen-1
6	c3bhpA_	Alignment		10.2	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** crystal structure of upf0291 protein ynzc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
7	c3kdvB_	Alignment		9.1	89	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage response b protein; **PDBTitle:** crystal structure of dna damage response b (ddrb) from deinococcus2 geothermalis
8	d1xrda1	Alignment		8.9	18	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
9	d1wu9a1	Alignment		8.8	6	**Fold:**EB1 dimerisation domain-like **Superfamily:**EB1 dimerisation domain-like **Family:**EB1 dimerisation domain-like
10	c1ujlA_	Alignment		8.6	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h **PDBTitle:** solution structure of the herg k+ channel s5-p2 extracellular linker
11	d1txqb1	Alignment		8.4	6	**Fold:**EB1 dimerisation domain-like **Superfamily:**EB1 dimerisation domain-like **Family:**EB1 dimerisation domain-like

12	c1txqB_	Alignment		8.4	6	**PDB header:**structural protein/protein binding **Chain:** B: **PDB Molecule:**microtubule-associated protein rp/eb family **PDBTitle:** crystal structure of the eb1 c-terminal domain complexed2 with the cap-gly domain of p150glued
13	c2kncA_	Alignment		8.4	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
14	c2qnaB_	Alignment		8.0	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of human importin-beta (127-876) in complex with the2 ibb-domain of snurportin1 (1-65)
15	c2latA_	Alignment		7.6	36	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** solution structure of a human minimembrane protein ost4
16	c2ys9A_	Alignment		7.6	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox and leucine zipper protein homez; **PDBTitle:** structure of the third homeodomain from the human homeobox2 and leucine zipper protein, homez
17	c2eqoA_	Alignment		7.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 3-interacting **PDBTitle:** solution structure of the stn_traf3ip1_nd domain of2 interleukin 13 receptor alpha 1-binding protein-1 [homo3 sapiens]
18	c2gzdC_	Alignment		7.3	18	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**rab11 family-interacting protein 2; **PDBTitle:** crystal structure of rab11 in complex with rab11-fip2
19	d2cpga_	Alignment		7.3	40	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
20	c2k1aA_	Alignment		6.9	21	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
21	c3a98B_	Alignment	not modelled	6.9	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**engulfment and cell motility protein 1; **PDBTitle:** crystal structure of the complex of the interacting regions of dock22 and elmo1
22	c3sojA_	Alignment	not modelled	6.8	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**pile; **PDBTitle:** francisella tularensis pilin pile
23	c2qx7A_	Alignment	not modelled	6.5	21	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
24	c2jvdA_	Alignment	not modelled	6.4	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynzc from bacillus subtilis. northeast3 structural genomics target sr384-1-46
25	c2wssT_	Alignment	not modelled	6.4	14	**PDB header:**hydrolase **Chain:** T: **PDB Molecule:**atp synthase subunit b, mitochondrial; **PDBTitle:** the structure of the membrane extrinsic region of bovine2 atp synthase
26	d1szia_	Alignment	not modelled	6.2	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain **Family:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
27	c2adlB_	Alignment	not modelled	6.1	60	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**ccda; **PDBTitle:** solution structure of the bacterial antitoxin ccda:2 implications for dna and toxin binding
28	c1jb0M_	Alignment	not modelled	6.1	29	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**photosystem 1 reaction centre subunit xii; **PDBTitle:** crystal structure of photosystem i: a photosynthetic

						reaction center2 and core antenna system from cyanobacteria
29	d1jb0m_	Alignment	not modelled	6.1	29	**Fold:**Single transmembrane helix **Superfamily:**Subunit XII of photosystem I reaction centre, PsaM **Family:**Subunit XII of photosystem I reaction centre, PsaM
30	d1fc2c_	Alignment	not modelled	6.0	30	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
31	c2q5dD_	Alignment	not modelled	5.9	10	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of human importin beta bound to the2 snurportin1 ibb-domain second crystal form
32	d1iq8a4	Alignment	not modelled	5.8	20	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Archaeosine tRNA-guanine transglycosylase, C2 domain
33	c2k6sB_	Alignment	not modelled	5.6	20	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**rab11fip2 protein; **PDBTitle:** structure of rab11-fip2 c-terminal coiled-coil domain
34	c3pvlB_	Alignment	not modelled	5.6	45	**PDB header:**motor protein/protein transport **Chain:** B: **PDB Molecule:**usher syndrome type-1g protein; **PDBTitle:** structure of myosin viia myth4-ferm-sh3 in complex with the cen1 of2 sans
35	d1nkzb_	Alignment	not modelled	5.6	13	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
36	c2hg5D_	Alignment	not modelled	5.6	13	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**kcsa channel; **PDBTitle:** cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
37	c3mtuD_	Alignment	not modelled	5.5	6	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**tropomyosin alpha-1 chain, microtubule-associated protein **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
38	d1lp1b_	Alignment	not modelled	5.5	30	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
39	c2pbdV_	Alignment	not modelled	5.5	71	**PDB header:**structural protein **Chain:** V: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** ternary complex of profilin-actin with the poly-pro-gab2 domain of vasp*
40	c2ww9B_	Alignment	not modelled	5.4	18	**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
41	d1prtf_	Alignment	not modelled	5.3	21	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
42	d2f2fa1	Alignment	not modelled	5.3	33	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like