Phyre2

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Description	RVBD0283_(-)_344022_345638
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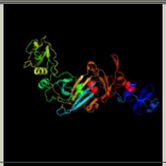
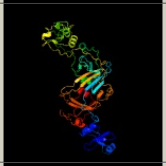
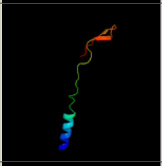
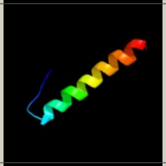
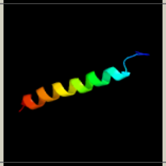
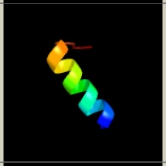
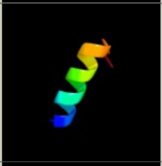
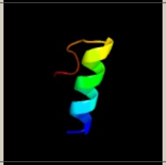
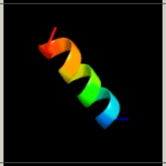
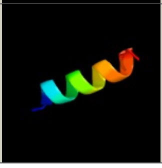
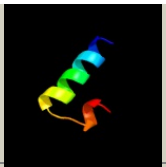
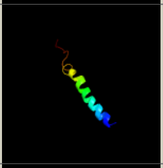
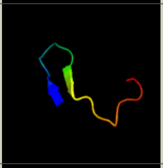
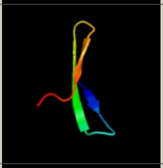
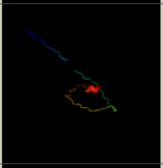
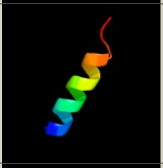
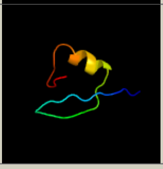
Unique Job ID	5d77b21f6d72add7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4kk7A_	Alignment		100.0	37	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**esx-1 secretion system protein eccb1; **PDBTitle:** structure of eccb1 from the type vii (esx-1) secretion system of2 mycobacterium tuberculosis.
2	c5cyuA_	Alignment		100.0	37	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**conserved membrane protein; **PDBTitle:** structure of the soluble domain of eccb1 from the mycobacterium2 smegmatis esx-1 secretion system.
3	d2fb5a1	Alignment		49.7	10	**Fold:**YojJ-like **Superfamily:**YojJ-like **Family:**YojJ-like
4	c6navl_	Alignment		42.4	20	**PDB header:**structural protein **Chain:** l: **PDB Molecule:**m9ud72; **PDBTitle:** cryo-em reconstruction of sulfolobus islandicus lal14/1 pilus
5	c2k9yA_	Alignment		32.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
6	c2k9yB_	Alignment		32.7	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
7	d1vh6a_	Alignment		18.7	24	**Fold:**Four-helical up-and-down bundle **Superfamily:**Flagellar export chaperone FliS **Family:**Flagellar export chaperone FliS
8	c1vh6A_	Alignment		18.7	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flis; **PDBTitle:** crystal structure of a flagellar protein
9	c5xefA_	Alignment		18.6	5	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**flagellar protein flis; **PDBTitle:** crystal structure of flagellar chaperone from bacteria
10	c5gzbA_	Alignment		18.4	40	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**transcriptional enhancer factor tef-3; **PDBTitle:** crystal structure of transcription factor tead4 in complex with m-cat2 dna
11	c2hzdA_	Alignment		17.4	40	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**transcriptional enhancer factor tef-1; **PDBTitle:** nmr structure of the dna-binding tea domain and insights2 into tef-1 function

12	c3k1iA_	Alignment		17.2	5	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**flagellar protein; **PDBTitle:** crystal strcture of flis-hp1076 complex in h. pylori
13	c6f0kA_	Alignment		16.3	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** alternative complex iii
14	c2ciuA_	Alignment		14.8	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**import inner membrane translocase subunit tim21 **PDBTitle:** structure of the ims domain of the mitochondrial import2 protein tim21 from s. cerevisiae
15	c3c1zA_	Alignment		14.4	8	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna integrity scanning protein disa; **PDBTitle:** structure of the ligand-free form of a bacterial dna damage sensor2 protein
16	c6gyyB_	Alignment		14.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diadenylate cyclase; **PDBTitle:** crystal structure of daca from staphylococcus aureus, n166c/t172c2 double mutant
17	c2lxfA_	Alignment		14.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a potential acylphosphatase from giardia2 lamblia, seattle structural genomics center for infectious disease3 target gilaa.01396.a
18	c6cfwE_	Alignment		13.8	18	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**mbh subunit; **PDBTitle:** cryoem structure of a respiratory membrane-bound hydrogenase
19	c3hshA_	Alignment		13.0	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**collagen alpha-1(xviii) chain; **PDBTitle:** crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)
20	d2zjru1	Alignment		13.0	20	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
21	c2a7oA_	Alignment	not modelled	11.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**huntingtin interacting protein b; **PDBTitle:** solution structure of the hset2/hypb sri domain
22	c3n3fB_	Alignment	not modelled	10.3	9	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**collagen alpha-1(xv) chain; **PDBTitle:** crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
23	c6ch3B_	Alignment	not modelled	10.2	14	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**flagellar secretion chaperone flis,flagellin; **PDBTitle:** crystal structure of the cytoplasmic domain of flha and flis-flic2 complex
24	d1gado2	Alignment	not modelled	10.0	21	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
25	c1zzaA_	Alignment	not modelled	9.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**stannin; **PDBTitle:** solution nmr structure of the membrane protein stannin
26	d1iioa_	Alignment	not modelled	9.5	24	**Fold:**EF Hand-like **Superfamily:**Hypothetical protein MTH865 **Family:**Hypothetical protein MTH865
27	c2l02B_	Alignment	not modelled	8.9	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
28	d2i5nh1	Alignment	not modelled	8.8	26	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**Photosynthetic reaction centre, H-chain, cytoplasmic domain

29	d1y7ma1	Alignment	not modelled	8.7	7	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
30	c1k6nH_	Alignment	not modelled	8.7	20	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**photosynthetic reaction center h subunit; **PDBTitle:** e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
31	c4rv7C_	Alignment	not modelled	8.4	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diadenylate cyclase; **PDBTitle:** characterization of an essential diadenylate cyclase
32	c6hraD_	Alignment	not modelled	8.0	42	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**potassium-transporting atpase kdpf subunit; **PDBTitle:** cryo-em structure of the kdpfabc complex in an e1 outward-facing state2 (state 1)
33	c5mrwD_	Alignment	not modelled	8.0	42	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**potassium-transporting atpase kdpf subunit; **PDBTitle:** structure of the kdpfabc complex
34	c5mrwH_	Alignment	not modelled	8.0	42	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**potassium-transporting atpase kdpf subunit; **PDBTitle:** structure of the kdpfabc complex
35	c6hrbD_	Alignment	not modelled	8.0	42	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**potassium-transporting atpase kdpf subunit; **PDBTitle:** cryo-em structure of the kdpfabc complex in an e2 inward-facing state2 (state 2)
36	c5mrwL_	Alignment	not modelled	8.0	42	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**potassium-transporting atpase kdpf subunit; **PDBTitle:** structure of the kdpfabc complex
37	c2kncA_	Alignment	not modelled	7.5	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
38	c2lf3A_	Alignment	not modelled	7.4	56	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**effector protein hopab3; **PDBTitle:** solution nmr structure of hoppmal_281_385 from pseudomonas syringae2 pv. maculicola str. es4326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4 pst2a
39	c2i5nH_	Alignment	not modelled	7.2	26	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**reaction center protein h chain; **PDBTitle:** 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
40	c2dzqA_	Alignment	not modelled	7.1	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
41	c2dn5A_	Alignment	not modelled	7.0	41	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
42	d1ixsa_	Alignment	not modelled	6.7	29	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
43	c2d99A_	Alignment	not modelled	6.6	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
44	d1q60a_	Alignment	not modelled	6.4	36	**Fold:**GTF2I-like repeat **Superfamily:**GTF2I-like repeat **Family:**GTF2I-like repeat
45	c2ed2A_	Alignment	not modelled	6.3	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
46	c2e3lA_	Alignment	not modelled	6.3	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor gtf2ird2 beta; **PDBTitle:** solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna
47	c5zjiO_	Alignment	not modelled	6.3	22	**PDB header:**membrane protein **Chain:** O: **PDB Molecule:**16kda membrane protein; **PDBTitle:** structure of photosystem i supercomplex with light-harvesting2 complexes i and ii
48	c2ejeA_	Alignment	not modelled	5.9	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
49	c2l8sA_	Alignment	not modelled	5.5	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-1; **PDBTitle:** solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
50	c2dn4A_	Alignment	not modelled	5.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
51	c4jonA_	Alignment	not modelled	5.4	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**centrosomal protein of 170 kda; **PDBTitle:** crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom)
52	c2dzrA_	Alignment	not modelled	5.1	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-067, a gtf2i domain in

						human2 cdna
53	c1ohfB_	Alignment	not modelled	5.0	30	**PDB header:**virus **Chain:** B: **PDB Molecule:**nudaurelia capensis omega virus capsid protein; **PDBTitle:** the refined structure of nudaurelia capensis omega virus
54	c2k1kB_	Alignment	not modelled	5.0	42	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
55	c2k1kA_	Alignment	not modelled	5.0	42	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
56	c2k1lB_	Alignment	not modelled	5.0	42	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3