Phyre²

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Description	RVBD3165c_(-)_3533910_3534392
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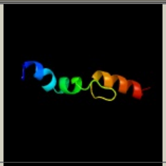
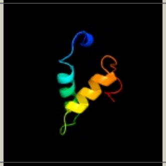
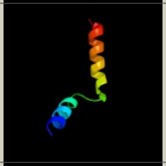
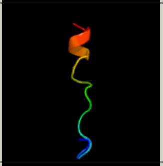
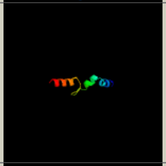
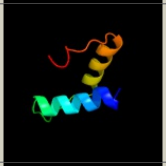
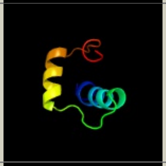
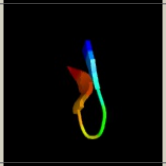
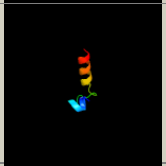
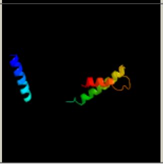
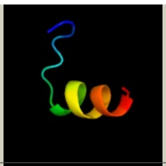
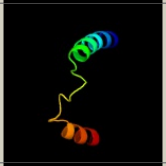
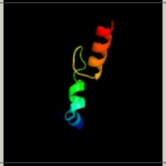
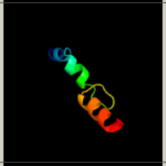
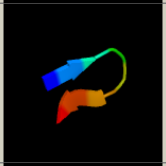
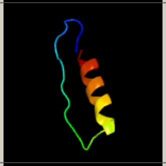
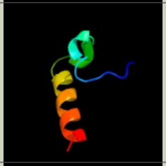
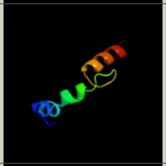
Unique Job ID	4db825a284af1b54

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6igaB_	Alignment		54.9	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**argininosuccinate lyase; **PDBTitle:** crystal structure of argininosuccinate lyase from mycobacterium2 tuberculosis
2	c1uusA_	Alignment		51.0	21	**PDB header:**signal transduction **Chain:** A: **PDB Molecule:**stat protein; **PDBTitle:** structure of an activated dictyostelium stat in its2 dna-unbound form
3	c3cm1C_	Alignment		31.2	25	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**ssga-like sporulation-specific cell division protein; **PDBTitle:** crystal structure of ssga-like sporulation-specific cell division2 protein (yp_290167.1) from thermobifida fusca yx-er1 at 2.60 a3 resolution
4	d1pzqa_	Alignment		28.3	47	**Fold:**Dimerisation interlock **Superfamily:**Docking domain A of the erythromycin polyketide synthase (DEBS) **Family:**Docking domain A of the erythromycin polyketide synthase (DEBS)
5	c6g3eA_	Alignment		23.4	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**argininosuccinate lyase; **PDBTitle:** crystal structure of edds lyase in complex with formate
6	c4y5wD_	Alignment		21.5	27	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**signal transducer and activator of transcription 6; **PDBTitle:** transcription factor-dna complex
7	c4y5uA_	Alignment		20.9	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription 6; **PDBTitle:** transcription factor
8	d3e9va1	Alignment		19.2	50	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
9	d2z15a1	Alignment		18.1	38	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
10	c4jqfA_	Alignment		17.8	32	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cst complex subunit stn1; **PDBTitle:** structure of the c-terminal domain of human telomeric stn1
11	c4xboA_	Alignment		17.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (cytidine/uridine-2'-o-)-methyltransferase trmj; **PDBTitle:** crystal structure of full length e.coli trmj in complex with sah

12	c2vxdA_	Alignment		16.9	33	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleophosmin; **PDBTitle:** the structure of the c-terminal domain of nucleophosmin
13	c1zjrA_	Alignment		16.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanosine-2'-o-)-methyltransferase; **PDBTitle:** crystal structure of a. aeolicus trmh/spou trna modifying enzyme
14	d1i0aa_	Alignment		15.9	13	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
15	d1hy0a_	Alignment		15.4	16	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
16	c5td6A_	Alignment		14.0	38	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**fog-3 protein; **PDBTitle:** c. elegans fog-3 btg/tob domain - h47n, c117a
17	c3drnB_	Alignment		12.7	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxiredoxin, bacterioferritin comigratory protein **PDBTitle:** the crystal structure of bcp1 from sulfolobus sulfataricus
18	c5cfiC_	Alignment		12.7	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bis(5'-nucleosyl)-tetraphosphatase (diadenosine **PDBTitle:** structural and functional attributes of malaria parasite ap4a2 hydrolase
19	d1k62a_	Alignment		12.1	10	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
20	c2llhA_	Alignment		11.9	50	**PDB header:**dna binding protein, chaperone **Chain:** A: **PDB Molecule:**nucleophosmin; **PDBTitle:** nmr structure of npm1_c70
21	d1tjva_	Alignment	not modelled	10.6	13	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
22	d1q7ha1	Alignment	not modelled	10.1	44	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
23	c3r90E_	Alignment	not modelled	9.8	30	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**malignant t cell-amplified sequence 1; **PDBTitle:** crystal structure of malignant t cell-amplified sequence 1 protein
24	c2f6aJ_	Alignment	not modelled	8.5	56	**PDB header:**cell adhesion/structural protein **Chain:** J: **PDB Molecule:**collagen; **PDBTitle:** collagen adhesin and collagen complex structure
25	d2j7pe1	Alignment	not modelled	8.4	70	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
26	c3dboA_	Alignment	not modelled	8.1	67	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
27	c2f6aF_	Alignment	not modelled	8.1	56	**PDB header:**cell adhesion/structural protein **Chain:** F: **PDB Molecule:**collagen; **PDBTitle:** collagen adhesin and collagen complex structure
28	c2f6aI_	Alignment	not modelled	8.1	56	**PDB header:**cell adhesion/structural protein **Chain:** I: **PDB Molecule:**collagen; **PDBTitle:** collagen adhesin and collagen complex structure
29	c2f6aE_	Alignment	not modelled	8.1	56	**PDB header:**cell adhesion/structural protein **Chain:** E: **PDB Molecule:**collagen;

						PDBTitle: collagen adhesin and collagen complex structure
30	c2f6aG_	Alignment	not modelled	8.1	56	**PDB header:**cell adhesion/structural protein **Chain:** G: **PDB Molecule:**collagen; **PDBTitle:** collagen adhesin and collagen complex structure
31	c2f6aH_	Alignment	not modelled	8.1	56	**PDB header:**cell adhesion/structural protein **Chain:** H: **PDB Molecule:**collagen; **PDBTitle:** collagen adhesin and collagen complex structure
32	c3iv1F_	Alignment	not modelled	8.0	43	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**tumor susceptibility gene 101 protein; **PDBTitle:** coiled-coil domain of tumor susceptibility gene 101
33	c2n5nA_	Alignment	not modelled	7.9	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 4; **PDBTitle:** structure of an n-terminal domain of chd4
34	c4bjqB_	Alignment	not modelled	7.9	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**penicillin binding protein transpeptidase domain protein; **PDBTitle:** crystal structure of e. coli penicillin binding protein 3,2 domain v88-s165
35	c3hfnA_	Alignment	not modelled	7.8	30	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**asl2047 protein; **PDBTitle:** crystal structure of an hfq protein from anabaena sp.
36	c2ch0A_	Alignment	not modelled	7.7	22	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**inner nuclear membrane protein man1; **PDBTitle:** solution structure of the human man1 c-terminal domain (residues 655-2 775)
37	d1okkd1	Alignment	not modelled	7.6	70	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
38	d1dbda_	Alignment	not modelled	7.5	27	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
39	c2e9fC_	Alignment	not modelled	7.2	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**argininosuccinate lyase; **PDBTitle:** crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine
40	d1z3eb1	Alignment	not modelled	7.2	44	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
41	c2k9yB_	Alignment	not modelled	7.0	46	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
42	c2k9yA_	Alignment	not modelled	7.0	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
43	c1y1uA_	Alignment	not modelled	7.0	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription 5a; **PDBTitle:** structure of unphosphorylated stat5a
44	c3kxyV_	Alignment	not modelled	6.9	56	**PDB header:**chaperone/transcription inhibitor **Chain:** V: **PDB Molecule:**exse; **PDBTitle:** crystal structure of the exsc-exse complex
45	c3qoqC_	Alignment	not modelled	6.8	43	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**alginate and motility regulator z; **PDBTitle:** crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
46	d1utca2	Alignment	not modelled	6.8	38	**Fold:**7-bladed beta-propeller **Superfamily:**Clathrin heavy-chain terminal domain **Family:**Clathrin heavy-chain terminal domain
47	c3d79A_	Alignment	not modelled	6.3	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph0734; **PDBTitle:** crystal structure of hypothetical protein ph0734.1 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
48	c3mgjA_	Alignment	not modelled	6.3	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1480; **PDBTitle:** crystal structure of the saccharop_dh_n domain of mj1480 protein from2 methanococcus jannaschii. northeast structural genomics consortium3 target mjr83a.
49	d1lb2b_	Alignment	not modelled	6.2	33	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
50	d1n8ja_	Alignment	not modelled	6.2	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
51	d1rj9a1	Alignment	not modelled	6.1	70	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
52	c1c9lA_	Alignment	not modelled	6.1	38	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**clathrin; **PDBTitle:** peptide-in-groove interactions link target proteins to the b-propeller2 of clathrin
53	c4ytgA_	Alignment	not modelled	6.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidylarginine deiminase; **PDBTitle:** crystal structure of porphyromonas gingivalis peptidylarginine2 deiminase (ppad) mutant c351a in complex with dipeptide met-arg.
54	c3cuxA_	Alignment	not modelled	5.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
						PDB header:oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide reductase/ thiol

55	c5enuB_	Alignment	not modelled	5.9	10	specific antioxidant/ **PDBTitle:** crystal structure of an alkyl hyroperoxide reductase from burkholderia2 ambifaria
56	d2daqa1	Alignment	not modelled	5.8	22	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
57	d2cvea1	Alignment	not modelled	5.7	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
58	c1q7hA_	Alignment	not modelled	5.6	44	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of a conserved pua domain protein from thermoplasma2 acidophilum
59	c2kgsA_	Alignment	not modelled	5.5	54	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** solution structure of the amino-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
60	c1zs7A_	Alignment	not modelled	5.5	56	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ape0525; **PDBTitle:** the structure of gene product ape0525 from aeropyrum pernix
61	c5he9E_	Alignment	not modelled	5.2	10	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**phage inhibitor protein; **PDBTitle:** bacterial initiation protein in complex with phage inhibitor protein
62	c2ysiA_	Alignment	not modelled	5.2	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**transcription elongation regulator 1; **PDBTitle:** solution structure of the first ww domain from the mouse2 transcription elongation regulator 1, transcription factor3 ca150
63	c4v14A_	Alignment	not modelled	5.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** structure and function analysis of mutt from the2 psychrofile fish pathogen aliivibrio salmonicida and the3 mesophile vibrio cholerae
64	d1g2ra_	Alignment	not modelled	5.1	16	**Fold:**YlxR-like **Superfamily:**YlxR-like **Family:**YlxR-like
65	d2csba3	Alignment	not modelled	5.0	86	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain