Phyre^2

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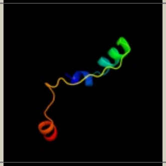
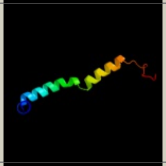
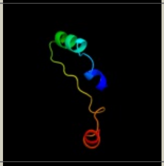
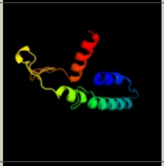
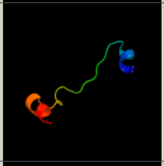
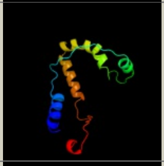
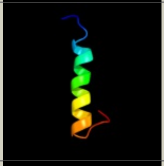
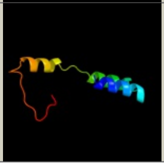
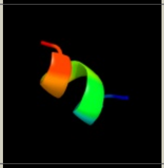
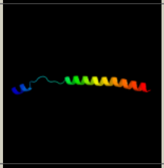
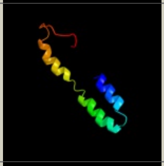
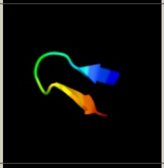
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sdia_	Alignment		100.0	100	**Fold:**YcfC-like **Superfamily:**YcfC-like **Family:**YcfC-like
2	c2xr1A_	Alignment		39.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
3	c2gejA_	Alignment		33.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol mannosyltransferase (pima); **PDBTitle:** crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
4	c2ycbA_	Alignment		30.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor; **PDBTitle:** structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
5	c2rdcA_	Alignment		27.0	22	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
6	c3af5A_	Alignment		22.9	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
7	d2fgea1	Alignment		21.5	17	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
8	c2k1vB_	Alignment		15.7	46	**PDB header:**hormone **Chain:** B: **PDB Molecule:**relaxin-3; **PDBTitle:** r3/i5 relaxin chimera
9	c2rpaA_	Alignment		15.1	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**katanin p60 atpase-containing subunit a1; **PDBTitle:** the solution structure of n-terminal domain of microtubule severing2 enzyme
10	c3fxdD_	Alignment		14.0	36	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**protein icmr; **PDBTitle:** crystal structure of interacting domains of icmr and icmq
11	c3cx3A_	Alignment		11.7	7	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure analysis of the streptococcus pneumoniae2 adcaii protein

12	c3mzkC_	Alignment		11.7	18	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**protein transport protein sec16; **PDBTitle:** sec13/sec16 complex, s.cerevisiae
13	c2rmsB_	Alignment		11.6	56	**PDB header:**transcription **Chain:** B: **PDB Molecule:**msin3a-binding protein; **PDBTitle:** solution structure of the msin3a pah1-sap25 sid complex
14	c2xdjF_	Alignment		10.4	22	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
15	c2h8bB_	Alignment		9.8	40	**PDB header:**hormone/growth factor **Chain:** B: **PDB Molecule:**insulin-like 3; **PDBTitle:** solution structure of insl3
16	c2ogwB_	Alignment		9.0	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua **PDBTitle:** structure of abc type zinc transporter from e. coli
17	c2r5uD_	Alignment		8.9	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the n-terminal domain of dnab helicase from2 mycobacterium tuberculosis
18	c2jufA_	Alignment		8.5	27	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**p53-associated parkin-like cytoplasmic protein; **PDBTitle:** nmr solution structure of parc cph domain. nesg target2 hr3443b/sgc-toronto
19	d1qi9a_	Alignment		8.3	29	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
20	c2fhdA_	Alignment		8.3	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
21	c3h25A_	Alignment	not modelled	8.2	32	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**replication protein b; **PDBTitle:** crystal structure of the catalytic domain of primase repb' in complex2 with initiator dna
22	c3hgkE_	Alignment	not modelled	8.2	20	**PDB header:**transferase **Chain:** E: **PDB Molecule:**effector protein hopab2; **PDBTitle:** crystal structure of effect protein avrptob complexed with2 kinase pto
23	d2jnga1	Alignment	not modelled	7.9	27	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**CPH domain
24	d1qhba_	Alignment	not modelled	7.7	18	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
25	d1vkea_	Alignment	not modelled	7.6	13	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
26	d1up8a_	Alignment	not modelled	7.5	14	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
27	c2o1eB_	Alignment	not modelled	7.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ycdh; **PDBTitle:** crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
28	d1u7ka_	Alignment	not modelled	7.2	33	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain

29	d2jeka1	Alignment	not modelled	7.1	20	**Fold:**Rv1873-like **Superfamily:**Rv1873-like **Family:**Rv1873-like
30	c1yv0T_	Alignment	not modelled	7.0	27	**PDB header:**contractile protein **Chain:** T: **PDB Molecule:**troponin t, fast skeletal muscle isoforms; **PDBTitle:** crystal structure of skeletal muscle troponin in the ca2+-2 free state
31	c1xouA_	Alignment	not modelled	7.0	24	**PDB header:**structural protein/chaperone **Chain:** A: **PDB Molecule:**espa; **PDBTitle:** crystal structure of the cesa-espa complex
32	d1xoua_	Alignment	not modelled	7.0	24	**Fold:**EspA/CesA-like **Superfamily:**EspA/CesA-like **Family:**EspA-like
33	d2v7qi1	Alignment	not modelled	6.7	60	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Epsilon subunit of mitochondrial F1F0-ATP synthase **Family:**Epsilon subunit of mitochondrial F1F0-ATP synthase
34	c2w9zA_	Alignment	not modelled	6.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**g1/s-specific cyclin-d1; **PDBTitle:** crystal structure of cdk4 in complex with a d-type cyclin
35	c3nrhA_	Alignment	not modelled	6.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bf1032; **PDBTitle:** crystal structure of protein bf1032 from bacteroides fragilis,2 northeast structural genomics consortium target bfr309
36	d1jwea_	Alignment	not modelled	6.2	18	**Fold:**N-terminal domain of DnaB helicase **Superfamily:**N-terminal domain of DnaB helicase **Family:**N-terminal domain of DnaB helicase
37	c1cosA_	Alignment	not modelled	6.2	29	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
38	c1cosB_	Alignment	not modelled	6.2	29	**PDB header:**alpha-helical bundle **Chain:** B: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
39	c1cosC_	Alignment	not modelled	6.2	29	**PDB header:**alpha-helical bundle **Chain:** C: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
40	c3imoC_	Alignment	not modelled	6.1	21	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass14
41	d1hula_	Alignment	not modelled	5.7	19	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
42	c2f59B_	Alignment	not modelled	5.5	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
43	d1b8za_	Alignment	not modelled	5.5	14	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
44	d2bs2b2	Alignment	not modelled	5.4	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
45	c3dlaD_	Alignment	not modelled	5.3	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
46	c3c4vB_	Alignment	not modelled	5.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted glycosyltransferases; **PDBTitle:** structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
47	c3lk2B_	Alignment	not modelled	5.0	18	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**f-actin-capping protein subunit beta isoforms 1 and 2; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil