Phyre^{2}

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Description	RVBD0239_(-)_289104_289337
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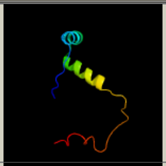
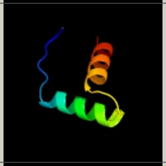
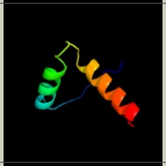
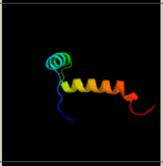
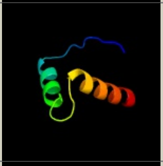
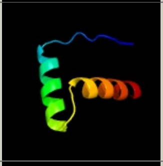
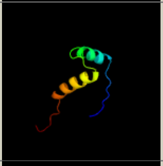
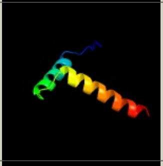
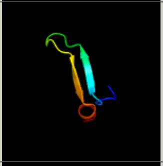
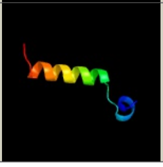
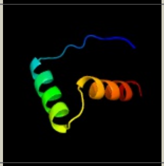
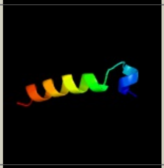
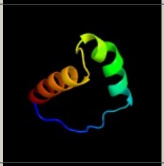
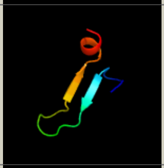
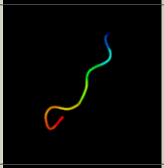
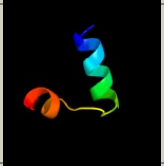
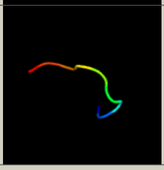
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5jB_	Alignment		97.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	c5x3tA_	Alignment		93.4	38	**PDB header:**antitoxin/toxin **Chain:** A: **PDB Molecule:**antitoxin vapb26; **PDBTitle:** vapbc from mycobacterium tuberculosis
3	d2bj7a1	Alignment		84.3	17	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
4	c2bj3D_	Alignment		82.7	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
5	c4me7E_	Alignment		79.4	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** E: **PDB Molecule:**antitoxin endoai; **PDBTitle:** crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
6	c2ca9B_	Alignment		77.5	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
7	c2rbfB_	Alignment		64.6	15	**PDB header:**oxidoreductase/dna **Chain:** B: **PDB Molecule:**bifunctional protein puta; **PDBTitle:** structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
8	c1q5vB_	Alignment		64.3	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
9	c6iyaD_	Alignment		46.4	16	**PDB header:**antitoxin **Chain:** D: **PDB Molecule:**transcriptional regulator copg family; **PDBTitle:** structure of the dna binding domain of antitoxin copaso
10	d1wgea1	Alignment		39.6	27	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
11	c3obcB_	Alignment		34.0	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pyrophosphatase; **PDBTitle:** crystal structure of a pyrophosphatase (af1178) from archaeoglobus2 fulgidus at 1.80 a resolution

12	c6bwqB_	Alignment		33.3	19	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel **PDBTitle:** larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
13	c2k29A_	Alignment		30.3	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
14	d2a3qa1	Alignment		29.5	19	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
15	c2q4pA_	Alignment		29.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
16	c5cegC_	Alignment		29.4	15	**PDB header:**toxin **Chain:** C: **PDB Molecule:**addiction module antidote protein, copg/arc/metj family; **PDBTitle:** x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
17	d1ywsa1	Alignment		26.6	15	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
18	c2lkmA_	Alignment		23.2	78	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 12; **PDBTitle:** structural basis for molecular interactions involving mrg domains:2 implications in chromatin biology
19	c2mqkA_	Alignment		21.9	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent target dna activator b; **PDBTitle:** solution structure of n terminal domain of the mub aaa+ atpase
20	c2l9sA_	Alignment		19.4	78	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 12; **PDBTitle:** solution structure of pf1 sid1-msin3a pah2 complex
21	c4hv0B_	Alignment	not modelled	17.5	28	**PDB header:**transcription, viral protein **Chain:** B: **PDB Molecule:**avtr; **PDBTitle:** structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus
22	c5frgA_	Alignment	not modelled	17.1	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**formin-binding protein 1-like; **PDBTitle:** the nmr structure of the cdc42-interacting region of toca1
23	c2jr7A_	Alignment	not modelled	16.9	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**dph3 homolog; **PDBTitle:** solution structure of human desr1
24	c2k9iB_	Alignment	not modelled	14.7	25	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**uncharacterized protein orf56; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from sulfolobus2 islandicus
25	c3di4A_	Alignment	not modelled	14.5	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf1989; **PDBTitle:** crystal structure of a duf1989 family protein (spo0365) from2 silicibacter pomeroyi dss-3 at 1.60 a resolution
26	c2jmkA_	Alignment	not modelled	13.3	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein ta0956; **PDBTitle:** solution structure of ta0956
27	c5abxB_	Alignment	not modelled	13.0	35	**PDB header:**translation **Chain:** B: **PDB Molecule:**4e-binding protein mextli; **PDBTitle:** complex of c. elegans eif4e-3 with the 4e-binding protein2 mextli and cap analog
28	c3kk4B_	Alignment	not modelled	12.5	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
						PDB header:biosynthetic protein

29	c3lzcA_	Alignment	not modelled	11.5	35	**Chain:** A: **PDB Molecule:**dph2; **PDBTitle:** crystal structure of dph2 from pyrococcus horikoshii
30	d1qh4a1	Alignment	not modelled	11.3	24	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
31	c2uvaI_	Alignment	not modelled	11.1	60	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
32	c1x93B_	Alignment	not modelled	10.8	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hypothetical protein hp0222; **PDBTitle:** nmr structure of helicobacter pylori hp0222
33	d1x93a1	Alignment	not modelled	10.8	24	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
34	c1u9pA_	Alignment	not modelled	10.1	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
35	c1tu3J_	Alignment	not modelled	9.8	33	**PDB header:**protein transport **Chain:** J: **PDB Molecule:**rab gtpase binding effector protein 1; **PDBTitle:** crystal structure of rab5 complex with rabaptin5 c-terminal2 domain
36	c5waqA_	Alignment	not modelled	9.1	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein assembly factor bamd; **PDBTitle:** structure of bamd from neisseria gonorrhoeae
37	c2vkzH_	Alignment	not modelled	9.0	47	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
38	c1y9qA_	Alignment	not modelled	9.0	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
39	c5fujB_	Alignment	not modelled	8.9	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**mroupo; **PDBTitle:** crystallization of a dimeric heme peroxygenase from the2 fungus marasmius rotula
40	d2hzaa1	Alignment	not modelled	8.8	19	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
41	d1g0wa1	Alignment	not modelled	8.8	24	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
42	c4v1ag_	Alignment	not modelled	8.8	33	**PDB header:**ribosome **Chain:** G: **PDB Molecule:** **PDBTitle:** structure of the large subunit of the mammalian mitoribosome, part 22 of 2
43	c3lr4A_	Alignment	not modelled	8.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
44	c2h1oH_	Alignment	not modelled	8.4	15	**PDB header:**gene regulation/dna complex **Chain:** H: **PDB Molecule:**trafficking protein a; **PDBTitle:** structure of fitab bound to ir36 dna fragment
45	d1i0ea1	Alignment	not modelled	8.0	24	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
46	d1u6ra1	Alignment	not modelled	7.7	24	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
47	d2bsqe1	Alignment	not modelled	7.5	15	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Trafficking protein A-like
48	c4b3yB_	Alignment	not modelled	7.5	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase; **PDBTitle:** cryo-em structure of the mycobacterial fatty acid synthase
49	d1vrpa1	Alignment	not modelled	7.1	17	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
50	c3c19A_	Alignment	not modelled	6.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mk0293; **PDBTitle:** crystal structure of protein mk0293 from methanopyrus kandleri av19
51	d2hzab1	Alignment	not modelled	6.6	19	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
52	d1p94a_	Alignment	not modelled	6.6	16	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
53	c2ke4A_	Alignment	not modelled	6.4	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
54	c1ceuA_	Alignment	not modelled	6.4	41	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hiv-1 regulatory protein n-terminal **PDBTitle:** nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein

55	d1ei5a2	Alignment	not modelled	6.3	37	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
56	d2gaxa1	Alignment	not modelled	6.3	20	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
57	c2auwB_	Alignment	not modelled	6.2	30	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
58	c4fxeB_	Alignment	not modelled	6.2	22	**PDB header:**toxin/toxin inhibitor **Chain:** B: **PDB Molecule:**antitoxin relb; **PDBTitle:** crystal structure of the intact e. coli relbe toxin-antitoxin complex
59	d1au1a_	Alignment	not modelled	6.2	20	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
60	c3qoqC_	Alignment	not modelled	6.0	23	**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
61	d1mnta_	Alignment	not modelled	5.9	14	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
62	d1v9wa_	Alignment	not modelled	5.8	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
63	d1l5aa2	Alignment	not modelled	5.7	7	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
64	c6bxnB_	Alignment	not modelled	5.7	33	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**diphthamide biosynthesis enzyme dph2; **PDBTitle:** crystal structure of candidatus methanoperedens nitroreducens dph22 with 4fe-4s cluster and sam
65	d1qk1a1	Alignment	not modelled	5.5	17	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
66	c1xrxD_	Alignment	not modelled	5.4	22	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
67	d1xrxa1	Alignment	not modelled	5.4	22	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like
68	d1b5la_	Alignment	not modelled	5.3	20	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
69	d2j5pa1	Alignment	not modelled	5.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like