Phyre2

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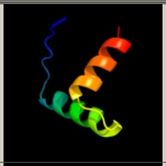
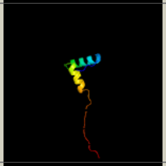
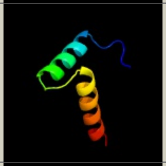
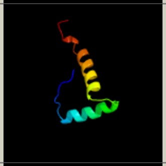
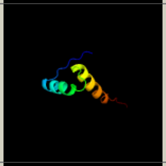
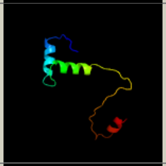
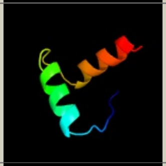
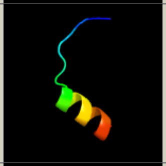
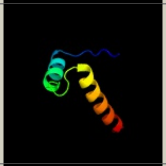
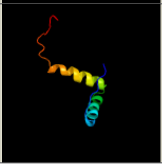
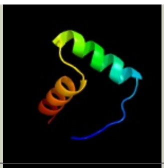
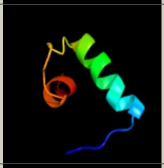
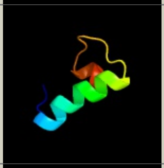
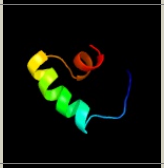
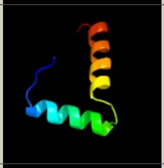
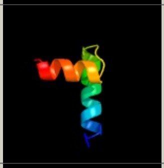
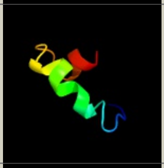
Description	RVBD2493_(-)_2808093_2808314
Date	Wed Aug 7 12:50:12 BST 2019
Unique Job ID	8ad7aec981188e3b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kk4B_	Alignment		90.8	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
2	c5x3tA_	Alignment		89.4	31	**PDB header:**antitoxin/toxin **Chain:** A: **PDB Molecule:**antitoxin vapb26; **PDBTitle:** vapbc from mycobacterium tuberculosis
3	d2bsqe1	Alignment		88.8	15	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Trafficking protein A-like
4	c2h1oH_	Alignment		88.5	15	**PDB header:**gene regulation/dna complex **Chain:** H: **PDB Molecule:**trafficking protein a; **PDBTitle:** structure of fitab bound to ir36 dna fragment
5	c2bj3D_	Alignment		86.1	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
6	c1q5vB_	Alignment		82.8	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
7	c2ca9B_	Alignment		78.6	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
8	d2bj7a1	Alignment		78.0	11	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
9	c6a7vU_	Alignment		77.3	33	**PDB header:**toxin/antitoxin **Chain:** U: **PDB Molecule:**antitoxin vapb11; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
10	d2hzaa1	Alignment		67.6	23	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
11	c2k5jB_	Alignment		66.7	18	**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

12	d2hzab1	Alignment		50.7	27	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
13	d1xrxa1	Alignment		41.8	32	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like
14	c1xrxD_	Alignment		41.8	32	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
15	c4aaiB_	Alignment		24.7	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**orf e73; **PDBTitle:** thermostable protein from hyperthermophilic virus ssv-rh
16	c4a1qB_	Alignment		24.7	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**orf e73; **PDBTitle:** solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
17	c2k29A_	Alignment		23.4	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
18	c3h87D_	Alignment		21.5	26	**PDB header:**toxin/antitoxin **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
19	c2mdvB_	Alignment		18.2	18	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of beta alpha alpha 38
20	c1t01B_	Alignment		17.0	42	**PDB header:**cell adhesion, structural protein **Chain:** B: **PDB Molecule:**talin 1; **PDBTitle:** vinculin complexed with the vbs1 helix from talin
21	c1syqB_	Alignment	not modelled	14.5	42	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**talin 1; **PDBTitle:** human vinculin head domain vh1, residues 1-258, in complex with human2 talin's vinculin binding site 1, residues 607-636
22	c5x7fA_	Alignment	not modelled	12.3	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative o-methyltransferase rv1220c; **PDBTitle:** structure of a o-methyltransferase from mycobacterium tuberculosis at2 2.0 resolution
23	c1ea4K_	Alignment	not modelled	12.1	27	**PDB header:**gene regulation/dna **Chain:** K: **PDB Molecule:**transcriptional repressor copg; **PDBTitle:** transcriptional repressor copg/22bp dsdna complex
24	d2cpga_	Alignment	not modelled	12.1	27	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
25	c5htlA_	Alignment	not modelled	12.1	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**msha biogenesis protein mshe; **PDBTitle:** structure of mshe with cdg
26	c6ejfQ_	Alignment	not modelled	11.1	7	**PDB header:**motor protein **Chain:** Q: **PDB Molecule:**type iv pilus assembly protein pilf; **PDBTitle:** thermus thermophilus pilf atpase (apoprotein form)
27	c2gpyB_	Alignment	not modelled	10.5	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**o-methyltransferase; **PDBTitle:** crystal structure of putative o-methyltransferase from bacillus2 halodurans
28	c3fmtF_	Alignment	not modelled	9.1	13	**PDB header:**replication inhibitor/dna **Chain:** F: **PDB Molecule:**protein seqa; **PDBTitle:** crystal structure of seqa bound to dna
29	c4hv0B	Alignment	not modelled	9.0	16	**PDB header:**transcription, viral protein **Chain:** B: **PDB Molecule:**avtr;

29	c4nv0B_	Alignment	not modelled	9.0	10	**PDBTitle:** structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus
30	c2c4rL_	Alignment	not modelled	8.6	40	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
31	c2an7A_	Alignment	not modelled	8.3	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein pard; **PDBTitle:** solution structure of the bacterial antidote pard
32	c4dbgB_	Alignment	not modelled	7.9	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ring finger protein 31; **PDBTitle:** crystal structure of hoil-1l-ubl complexed with a hoip-uba derivative
33	c1dl5A_	Alignment	not modelled	7.2	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** protein-l-isoaspartate o-methyltransferase
34	c2jr6A_	Alignment	not modelled	6.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein nma0874; **PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
35	d1v71a1	Alignment	not modelled	6.5	11	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
36	c2qezC_	Alignment	not modelled	6.3	32	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ethanolamine ammonia-lyase heavy chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase heavy chain2 (yp_013784.1) from listeria monocytogenes 4b f2365 at 2.15 a3 resolution
37	c2o8xA_	Alignment	not modelled	5.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
38	d1p1ca_	Alignment	not modelled	5.6	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
39	c3t98A_	Alignment	not modelled	5.4	24	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup54; **PDBTitle:** molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
40	c3ntvB_	Alignment	not modelled	5.3	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mw1564 protein; **PDBTitle:** crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus
41	c6gbrA_	Alignment	not modelled	5.2	67	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**polymerase cofactor vp35; **PDBTitle:** crystal structure of the oligomerization domain of vp35 from reston2 virus, mercury derivative
42	c6iyaD_	Alignment	not modelled	5.2	29	**PDB header:**antitoxin **Chain:** D: **PDB Molecule:**transcriptional regulator copg family; **PDBTitle:** structure of the dna binding domain of antitoxin copaso
43	c5h2sA_	Alignment	not modelled	5.2	50	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**piscidin-4; **PDBTitle:** solution structure of tilapia piscidin 4 (tp4) from oreochromis2 niloticus
44	d1s4ka_	Alignment	not modelled	5.2	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**YdiL-like
45	c1zw2B_	Alignment	not modelled	5.1	28	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**talin; **PDBTitle:** vinculin head (0-258) in complex with the talin rod2 residues 2345-2369