Phyre2

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Description	P0AFX4
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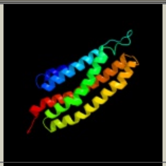
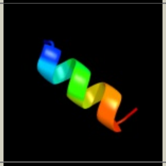
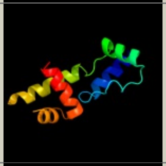
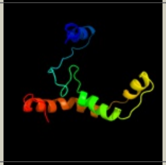
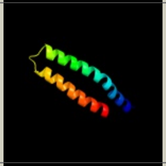
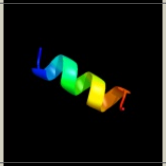
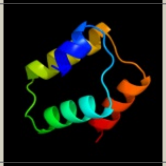
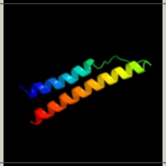
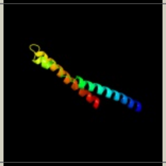
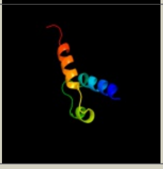
Unique Job ID	06d0808be6fe381c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p7vA_	Alignment		100.0	100	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulator of sigma d; **PDBTitle:** crystal structure of the escherichia coli regulator of sigma 70, rsd,2 in complex with sigma 70 domain 4
2	c2wvmA_	Alignment		44.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
3	d1p94a_	Alignment		39.8	55	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
4	c2plyB_	Alignment		30.5	19	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
5	c2zu8A_	Alignment		28.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
6	d1tlha_	Alignment		28.4	16	**Fold:**Anti-sigma factor AsiA **Superfamily:**Anti-sigma factor AsiA **Family:**Anti-sigma factor AsiA
7	c3k1tA_	Alignment		28.1	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha; **PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
8	c1wsuA_	Alignment		27.8	19	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** c-terminal domain of elongation factor selb complexed with2 secis rna
9	c3hosA_	Alignment		25.1	14	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
10	c1avoD_	Alignment		21.9	10	**PDB header:**proteasome activator **Chain:** D: **PDB Molecule:**11s regulator; **PDBTitle:** proteasome activator reg(alpha)
11	d1uoua1	Alignment		20.7	12	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain

12	d2o3aa1	Alignment		19.0	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
13	c2yy8B_	Alignment		17.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0106 protein ph0461; **PDBTitle:** crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
14	d1tjla1	Alignment		17.0	31	**Fold:**Long alpha-hairpin **Superfamily:**DnaK suppressor protein DksA, alpha-hairpin domain **Family:**DnaK suppressor protein DksA, alpha-hairpin domain
15	d2tpta1	Alignment		15.1	8	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
16	d1v92a_	Alignment		11.4	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
17	c2nrjA_	Alignment		11.1	16	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hbl b protein; **PDBTitle:** crystal structure of hemolysin binding component from2 bacillus cereus
18	d1y2oa1	Alignment		10.8	16	**Fold:**BAR/IMD domain-like **Superfamily:**BAR/IMD domain-like **Family:**IMD domain
19	c2g8yB_	Alignment		9.8	46	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate/l-lactate dehydrogenases; **PDBTitle:** the structure of a putative malate/lactate dehydrogenase from e. coli.
20	d2e9xa1	Alignment		8.9	17	**Fold:**GINS helical bundle-like **Superfamily:**GINS helical bundle-like **Family:**PSF1 N-terminal domain-like
21	d1d4ua1	Alignment	not modelled	8.8	12	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA repair factor XPA DNA- and RPA-binding domain, C-terminal subdomain
22	c3pcsB_	Alignment	not modelled	8.4	29	**PDB header:**protein transport/transferase **Chain:** B: **PDB Molecule:**espg; **PDBTitle:** structure of espg-pak2 autoinhibitory ialpha3 helix complex
23	d2fbqa2	Alignment	not modelled	8.0	20	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
24	c1z56B_	Alignment	not modelled	7.8	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ligase interacting factor 1; **PDBTitle:** co-crystal structure of lif1p-lig4p
25	c3oqlB_	Alignment	not modelled	7.5	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tena homolog; **PDBTitle:** crystal structure of a tena homolog (pspto1738) from pseudomonas2 syringae pv. tomato str. dc3000 at 2.54 a resolution
26	d2nvna1	Alignment	not modelled	7.4	29	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
27	d1x2ma1	Alignment	not modelled	7.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
28	d1brwa1	Alignment	not modelled	7.2	11	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain

29	c3r89A_	Alignment	not modelled	7.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548
30	c3dkaA_	Alignment	not modelled	6.8	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**dinb-like protein; **PDBTitle:** crystal structure of a dinb-like protein (yjoa, bsu12410) from2 bacillus subtilis at 2.30 a resolution
31	d2it9a1	Alignment	not modelled	6.8	11	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
32	c2e19A_	Alignment	not modelled	6.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor 8; **PDBTitle:** solution structure of the homeobox domain from human nil-2-2 a zinc finger protein, transcription factor 8
33	c3m9hB_	Alignment	not modelled	6.6	28	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa
34	d1v8ga1	Alignment	not modelled	6.0	10	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
35	c1xawA_	Alignment	not modelled	6.0	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** crystal structure of the cytoplasmic distal c-terminal2 domain of occludin
36	c2q9qC_	Alignment	not modelled	5.9	17	**PDB header:**replication **Chain:** C: **PDB Molecule:**dna replication complex gins protein psf1; **PDBTitle:** the crystal structure of full length human gins complex
37	c3e5aB_	Alignment	not modelled	5.9	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**targeting protein for xklp2; **PDBTitle:** crystal structure of aurora a in complex with vx-680 and tpx2
38	d1z3xa2	Alignment	not modelled	5.9	18	**Fold:**GUN4-like **Superfamily:**GUN4-like **Family:**GUN4-like
39	d1oaia_	Alignment	not modelled	5.7	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
40	c2da7A_	Alignment	not modelled	5.7	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc finger homeobox protein 1b; **PDBTitle:** solution structure of the homeobox domain of zinc finger2 homeobox protein 1b (smad interacting protein 1)
41	c1a92B_	Alignment	not modelled	5.5	31	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**delta antigen; **PDBTitle:** oligomerization domain of hepatitis delta antigen
42	d2vo1a1	Alignment	not modelled	5.5	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
43	d1u9pa1	Alignment	not modelled	5.5	29	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
44	c2w45A_	Alignment	not modelled	5.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline exonuclease; **PDBTitle:** epstein-barr virus alkaline nuclease
45	d2p0ma1	Alignment	not modelled	5.4	12	**Fold:**Lipoxigenase **Superfamily:**Lipoxigenase **Family:**Animal lipoxigenases
46	c2dmpA_	Alignment	not modelled	5.3	30	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 2; **PDBTitle:** solution structure of the third homeobox domain of zinc2 fingers and homeoboxes protein 2
47	d1ydha_	Alignment	not modelled	5.1	10	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
48	d1upka_	Alignment	not modelled	5.1	14	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Mo25 protein