Phyre2

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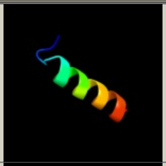
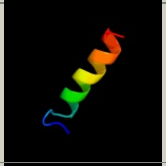
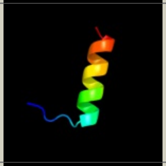
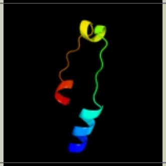
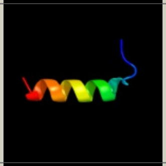
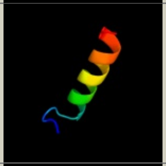
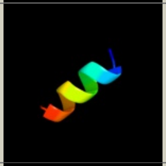
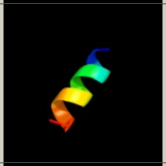
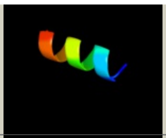
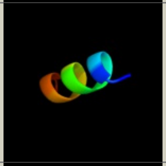
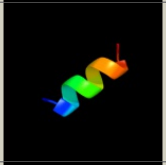
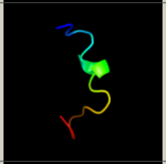
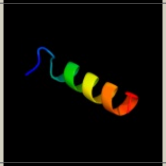
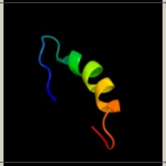
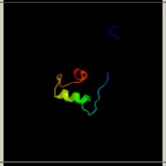
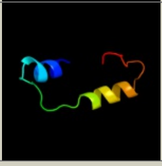
Description	P64476
Date	Thu Jan 5 12:08:44 GMT 2012
Unique Job ID	c0739c190bdb1230

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qx0A_	Alignment		28.5	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**7,8-dihydro-6-hydroxymethylpterin- **PDBTitle:** crystal structure of yersinia pestis hppk (ternary complex)
2	d1f9ya_	Alignment		28.1	25	**Fold:**Ferredoxin-like **Superfamily:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK **Family:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
3	d1cbka_	Alignment		24.3	35	**Fold:**Ferredoxin-like **Superfamily:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK **Family:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
4	c2qdmA_	Alignment		18.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type 7; **PDBTitle:** crystal structure of the heptp catalytic domain c270s/d236a/q314a2 mutant
5	c3mcnA_	Alignment		17.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-amino-4-hydroxy-6-hydroxymethyldihydropteridine **PDBTitle:** crystal structure of the 6-hyroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis
6	c1onvB_	Alignment		13.9	55	**PDB header:**transcription **Chain:** B: **PDB Molecule:**serine phosphatase fcp1a; **PDBTitle:** nmr structure of a complex containing the tfiif subunit2 rap74 and the rnap ii ctd phosphatase fcp1
7	c2cg8B_	Alignment		12.1	25	**PDB header:**lyase/transferase **Chain:** B: **PDB Molecule:**dihydroneopterin aldolase 6-hydroxymethyl-7,8- **PDBTitle:** the bifunctional dihydroneopterin aldolase 6-hydroxymethyl-2 7,8-dihydropterin synthase from streptococcus pneumoniae
8	c1kddC_	Alignment		8.9	50	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
9	c1kddF_	Alignment		8.7	50	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
10	c1kddA_	Alignment		8.7	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
11	c3igmA_	Alignment		8.6	27	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pf14_0633 protein; **PDBTitle:** a 2.2a crystal structure of the ap2 domain of pf14_0633 from p.2 falciparum, bound as a domain-swapped dimer to its cognate dna

12	c1kd9F_	Alignment		8.5	50	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16l; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
13	c1kd9A_	Alignment		8.5	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16l; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
14	c1kd9C_	Alignment		8.5	50	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16l; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
15	c3kf8D_	Alignment		8.2	33	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**protein ten1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
16	c2bmbA_	Alignment		7.7	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**folic acid synthesis protein fol1; **PDBTitle:** x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
17	c2v4xA_	Alignment		6.8	50	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein p27; **PDBTitle:** crystal structure of jaagsiekte sheep retrovirus capsid n-2 terminal domain
18	d2pa2a1	Alignment		6.7	31	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L10e
19	d1b8ia_	Alignment		6.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
20	c3pn1A_	Alignment		5.9	33	**PDB header:**ligase/ligase inhibitor **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
21	c2kgfA_	Alignment	not modelled	5.7	38	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein p27; **PDBTitle:** n-terminal domain of capsid protein from the mason-pfizer2 monkey virus
22	d1d1da2	Alignment	not modelled	5.5	50	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
23	c1zuoA_	Alignment	not modelled	5.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**hypothetical protein loc92912; **PDBTitle:** structure of human ubiquitin-conjugating enzyme (ubci)2 involved in embryo attachment and implantation
24	d1zuoa1	Alignment	not modelled	5.5	17	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
25	c2q97T_	Alignment	not modelled	5.3	53	**PDB header:**structural protein/cell invasion **Chain:** T: **PDB Molecule:**toxofilin; **PDBTitle:** complex of mammalian actin with toxofilin from toxoplasma gondii
26	d1em9a_	Alignment	not modelled	5.2	50	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
27	d1b04a_	Alignment	not modelled	5.2	22	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
28	c1xdtT_	Alignment	not modelled	5.2	33	**PDB header:**complex (toxin/growth factor) **Chain:** T: **PDB Molecule:**diphtheria toxin; **PDBTitle:** complex of diphtheria toxin and heparin-binding epidermal growth2 factor
29	d1ta8a_	Alignment	not modelled	5.1	36	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase

30	c1kd8F_	Alignment	not modelled	5.0	42	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**gcn4 acid base heterodimer acid-d12ia16v; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l