Phyre^2

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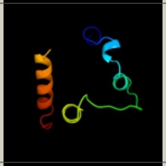
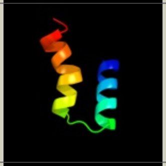
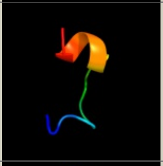
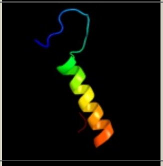
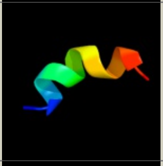
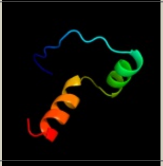
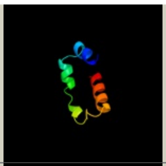
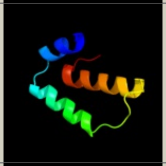
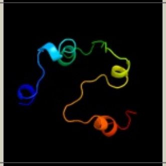
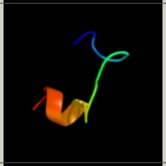
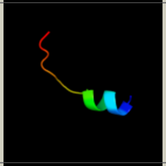
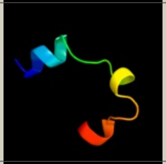
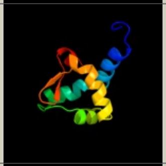
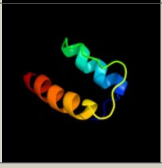
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3knyA_	Alignment		53.1	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt_3535; **PDBTitle:** crystal structure of a two domain protein with unknown function2 (bt_3535) from bacteroides thetaiotaomicron vpi-5482 at 2.60 a3 resolution
2	c1pbyA_	Alignment		48.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda **PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
3	d1qmga1	Alignment		45.0	20	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)
4	c2v79B_	Alignment		29.4	12	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
5	d1khba1	Alignment		27.5	31	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
6	c2vn2B_	Alignment		24.5	14	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
7	c2qeyA_	Alignment		23.8	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxykinase, cytosolic [gtp]; **PDBTitle:** rat cytosolic pepck in complex with gtp
8	c2f5uA_	Alignment		20.6	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**virion protein ul25; **PDBTitle:** structural characterization of the ul25 dna packaging2 protein from herpes simplex virus type 1
9	c2jrdA_	Alignment		20.6	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** influenza hemagglutinin fusion domain mutant f9a
10	d1bdta_	Alignment		19.1	27	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
11	c2zciD_	Alignment		18.5	38	**PDB header:**signaling protein, lyase **Chain:** D: **PDB Molecule:**phosphoenolpyruvate carboxykinase [gtp]; **PDBTitle:** structure of a gtp-dependent bacterial pep-carboxykinase2 from corynebacterium glutamicum

12	d1t07a_	Alignment		17.2	20	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
13	d1xs8a_	Alignment		16.1	17	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
14	c1jmxA_	Alignment		15.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amine dehydrogenase; **PDBTitle:** crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida
15	d1seda_	Alignment		15.9	17	**Fold:**Hypothetical protein YhaI **Superfamily:**Hypothetical protein YhaI **Family:**Hypothetical protein YhaI
16	c2fahB_	Alignment		13.2	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate carboxykinase; **PDBTitle:** the structure of mitochondrial pepck, complex with mn and gdp
17	c3bdrA_	Alignment		12.6	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ycf58 protein; **PDBTitle:** crystal structure of fatty acid-binding protein-like ycf582 from thermosynecoccus elongatus. northeast structural3 genomics consortium target ter13.
18	d1pbya1	Alignment		12.5	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
19	c1tw3A_	Alignment		12.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carminomycin 4-o-methyltransferase; **PDBTitle:** crystal structure of carminomycin-4-o-methyltransferase2 (dnrk) in complex with s-adenosyl-l-homocystein (sah) and3 4-methoxy-e-rhodomycin t (m-et)
20	d1gjja2	Alignment		11.3	17	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
21	d6paxa1	Alignment	not modelled	11.2	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
22	c1iboA_	Alignment	not modelled	10.5	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin ha2 chain peptide; **PDBTitle:** nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 7.4
23	c1ibnA_	Alignment	not modelled	10.5	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin ha2 chain peptide; **PDBTitle:** nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 5
24	d1z5ga1	Alignment	not modelled	10.2	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Class B acid phosphatase, AphA
25	d1zbsa2	Alignment	not modelled	9.5	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
26	c3chxG_	Alignment	not modelled	9.3	23	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**pmoc; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
27	c2kxaA_	Alignment	not modelled	9.1	23	**PDB header:**viral protein, immune system **Chain:** A: **PDB Molecule:**haemagglutinin ha2 chain peptide; **PDBTitle:** the hemagglutinin fusion peptide (h1 subtype) at ph 7.4
28	c1gjjA_	Alignment	not modelled	9.1	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lap2; **PDBTitle:** n-terminal constant region of the nuclear envelope protein2 lap2
						Fold: Ribbon-helix-helix

29	d1b28a_	Alignment	not modelled	8.8	29	**Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
30	d1h9fa_	Alignment	not modelled	8.2	30	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
31	d1k78a1	Alignment	not modelled	7.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
32	d1iuqa_	Alignment	not modelled	7.7	17	**Fold:**Glycerol-3-phosphate (1)-acyltransferase **Superfamily:**Glycerol-3-phosphate (1)-acyltransferase **Family:**Glycerol-3-phosphate (1)-acyltransferase
33	c1yewC_	Alignment	not modelled	7.0	15	**PDB header:**oxidoreductase, membrane protein **Chain:** C: **PDB Molecule:**particulate methane monooxygenase subunit c2; **PDBTitle:** crystal structure of particulate methane monooxygenase
34	c2pjwH_	Alignment	not modelled	6.8	16	**PDB header:**endocytosis/exocytosis **Chain:** H: **PDB Molecule:**uncharacterized protein yhl002w; **PDBTitle:** the vps27/hse1 complex is a gat domain-based scaffold for2 ubiquitin-dependent sorting
35	c2k1oA_	Alignment	not modelled	6.7	41	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative; **PDBTitle:** nmr structure of helicobacter pylori jhp0511 (hp0564).
36	c2pfcA_	Alignment	not modelled	6.6	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv0098/mt0107; **PDBTitle:** structure of mycobacterium tuberculosis rv0098
37	c1xopA_	Alignment	not modelled	6.4	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** nmr structure of g1v mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
38	c1xooA_	Alignment	not modelled	6.3	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** nmr structure of g1s mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
39	c3bhwA_	Alignment	not modelled	6.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from magnetospirillum2 magneticum
40	d1fi6a_	Alignment	not modelled	5.9	24	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
41	d1c07a_	Alignment	not modelled	5.7	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
42	c2bn5A_	Alignment	not modelled	5.6	25	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**psi; **PDBTitle:** p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
43	c2ia2D_	Alignment	not modelled	5.5	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
44	d2o9aa1	Alignment	not modelled	5.4	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
45	d1cmca_	Alignment	not modelled	5.4	50	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Met repressor, MetJ (MetR)