Phyre^2

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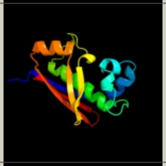
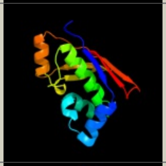
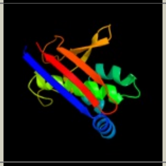
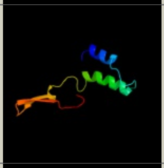
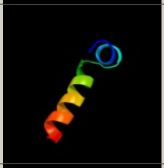
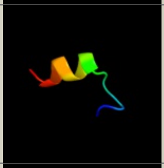
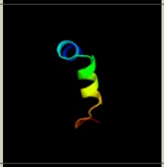
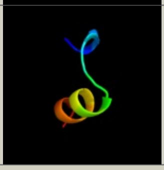
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h88A_	Alignment		100.0	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** crystal structure of 4'-phosphopantetheinyl transferase acps from2 vibrio cholerae o1 biovar eltor
2	c2jbzA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** crystal structure of the streptomyces coelicolor holo-2 [acyl-carrier-protein] synthase (acps) in complex with3 coenzyme a at 1.6 a
3	c2qg8A_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein synthase py06285; **PDBTitle:** plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
4	d1ftha_	Alignment		100.0	35	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**Holo-(acyl carrier protein) synthase ACPS
5	c3ne9B_	Alignment		100.0	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphopantethiene protein transferase, ppt1p; **PDBTitle:** mycobacterium tuberculosis acyl carrier protein synthase adopts two2 different structural conformations: ph driven conformational changes3 of acps enzyme
6	c3hqjA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** structure-function analysis of mycobacterium tuberculosis2 acyl carrier protein synthase (acps).
7	d1f7la_	Alignment		100.0	43	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**Holo-(acyl carrier protein) synthase ACPS
8	c2wasA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** structure of the fungal type i fas ppt domain
9	c3hykB_	Alignment		100.0	41	**PDB header:**transferase **Chain:** B: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** 2.31 angstrom resolution crystal structure of a holo-(acyl-carrier-2 protein) synthase from bacillus anthracis str. ames in complex with3 coa (3',5'-adp)
10	c3f09B_	Alignment		100.0	42	**PDB header:**transferase **Chain:** B: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** 1.82 angstrom resolution crystal structure of holo-(acyl-carrier-2 protein) synthase (acps) from staphylococcus aureus
11	d1qr0a2	Alignment		99.7	22	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**4'-Phosphopantetheinyl transferase SFP

12	c1qr0A_	Alignment		99.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4'-phosphopantetheinyl transferase sfp; **PDBTitle:** crystal structure of the 4'-phosphopantetheinyl transferase sfp-2 coenzyme a complex
13	c2cg5A_	Alignment		99.5	16	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**l-aminoadipate-semialdehyde dehydrogenase- **PDBTitle:** structure of aminoadipate-semialdehyde dehydrogenase-2 phosphopantetheinyl transferase in complex with cytosolic3 acyl carrier protein and coenzyme a
14	d1qr0a1	Alignment		98.3	14	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**4'-Phosphopantetheinyl transferase SFP
15	c2im5C_	Alignment		29.0	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of nicotinate phosphoribosyltransferase2 from porphyromonas gingivalis
16	c3frwF_	Alignment		17.6	15	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
17	c2z0rA_	Alignment		15.6	46	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0547; **PDBTitle:** crystal structure of hypothetical protein ttha0547
18	c2knjA_	Alignment		15.3	0	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**microplusin preprotein; **PDBTitle:** nmr structure of microplusin a antimicrobial peptide from2 rhipicephalus (boophilus) microplus
19	c3korD_	Alignment		12.9	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor; **PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
20	d1p65a_	Alignment		12.1	13	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Arterivirus nucleocapsid protein
21	c1p65A_	Alignment	not modelled	12.1	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleocapsid protein; **PDBTitle:** crystal structure of the nucleocapsid protein of porcine reproductive2 and respiratory syndrome virus (prrsv)
22	c1bh1A_	Alignment	not modelled	10.8	25	**PDB header:**toxin **Chain:** A: **PDB Molecule:**melittin; **PDBTitle:** structural studies of d-pro melittin, nmr, 20 structures
23	d2ae8a2	Alignment	not modelled	10.0	38	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
24	c1f93F_	Alignment	not modelled	9.5	56	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
25	d1f93f_	Alignment	not modelled	9.5	56	**Fold:**Dimerisation interlock **Superfamily:**Dimerization cofactor of HNF-1 alpha **Family:**Dimerization cofactor of HNF-1 alpha
26	c1g39D_	Alignment	not modelled	8.9	56	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** wild-type hnf-1alpha dimerization domain
27	c1g39B_	Alignment	not modelled	8.9	56	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** wild-type hnf-1alpha dimerization domain
28	c2gypA_	Alignment	not modelled	8.8	50	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** diabetes mellitus due to a frustrated schellman motif in hnf-1a
29	c2gypB_	Alignment	not modelled	8.8	50	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha;

29	c2gypB_	Alignment	not modelled	8.8	50	**PDBTitle:** diabetes mellitus due to a frustrated schellman motif in hnf-1a
30	c1g2yA_	Alignment	not modelled	8.7	56	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hnf-1alpha dimerization domain, with selenomethionine2 substitued at leu 12
31	d1g2ya_	Alignment	not modelled	8.7	56	**Fold:**Dimerisation interlock **Superfamily:**Dimerization cofactor of HNF-1 alpha **Family:**Dimerization cofactor of HNF-1 alpha
32	c1g2zB_	Alignment	not modelled	8.6	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** dimerization domain of hnf-1alpha with a leu 13 selenomethionine2 substitution
33	c1f93E_	Alignment	not modelled	8.6	56	**PDB header:**transcription **Chain:** E: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
34	c1jb6A_	Alignment	not modelled	8.6	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of dimerization domain (1-33) of hnf-1alpha
35	d1g2za_	Alignment	not modelled	8.5	50	**Fold:**Dimerisation interlock **Superfamily:**Dimerization cofactor of HNF-1 alpha **Family:**Dimerization cofactor of HNF-1 alpha
36	c1g2zA_	Alignment	not modelled	8.5	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** dimerization domain of hnf-1alpha with a leu 13 selenomethionine2 substitution
37	d2fr2a1	Alignment	not modelled	8.1	19	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Rv2717c-like
38	c2mltA_	Alignment	not modelled	8.0	25	**PDB header:**toxin (hemolytic polypeptide) **Chain:** A: **PDB Molecule:**melittin; **PDBTitle:** melittin
39	d2i6ha1	Alignment	not modelled	7.7	15	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Atu0120-like
40	c2i6hA_	Alignment	not modelled	7.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0120; **PDBTitle:** structure of protein of unknown function atu0120 from agrobacterium2 tumefaciens
41	d2f1da2	Alignment	not modelled	7.6	63	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
42	c2mltB_	Alignment	not modelled	7.5	25	**PDB header:**toxin (hemolytic polypeptide) **Chain:** B: **PDB Molecule:**melittin; **PDBTitle:** melittin
43	d1rhya2	Alignment	not modelled	6.7	50	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
44	c3qrxB_	Alignment	not modelled	6.6	25	**PDB header:**metal binding protein/toxin **Chain:** B: **PDB Molecule:**melittin; **PDBTitle:** chlamydomonas reinhardtii centrin bound to melittin
45	d1trra_	Alignment	not modelled	6.5	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
46	d1jhga_	Alignment	not modelled	6.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
47	d1vlpa1	Alignment	not modelled	5.9	14	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
48	d1qasa3	Alignment	not modelled	5.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
49	c3me5A_	Alignment	not modelled	5.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytosine-specific methyltransferase; **PDBTitle:** crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 301