Phyre^2

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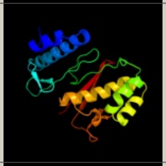
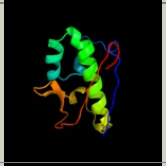
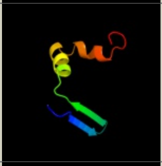
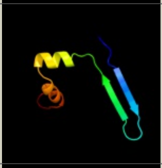
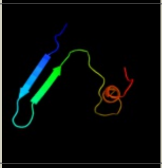
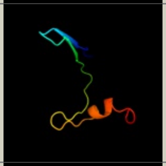
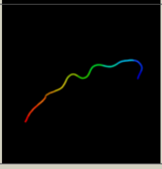
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qr0A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4'-phosphopantetheinyl transferase sfp; **PDBTitle:** crystal structure of the 4'-phosphopantetheinyl transferase sfp-2 coenzyme a complex
2	c2cg5A_	Alignment		100.0	14	**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
3	d1qr0a2	Alignment		99.8	19	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**4'-Phosphopantetheinyl transferase SFP
4	c2wasA_	Alignment		99.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** structure of the fungal type i fas ppt domain
5	c3h88A_	Alignment		99.4	22	**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
6	c3hykB_	Alignment		99.4	21	**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)
7	d1ftha_	Alignment		99.4	24	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**Holo-(acyl carrier protein) synthase ACPS
8	c2jbzA_	Alignment		99.4	18	**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
9	d1f7la_	Alignment		99.3	22	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**Holo-(acyl carrier protein) synthase ACPS
10	c3ne9B_	Alignment		99.3	19	**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
11	d1qr0a1	Alignment		99.3	12	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**4'-Phosphopantetheinyl transferase SFP

12	c3f09B_	Alignment		99.3	24	**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
13	c2qg8A_	Alignment		99.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein synthase py06285; **PDBTitle:** plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
14	c3hqjA_	Alignment		98.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** structure-function analysis of mycobacterium tuberculosis2 acyl carrier protein synthase (acps).
15	c2ch4A_	Alignment		41.9	22	**PDB header:**transferase/chemotaxis **Chain:** A: **PDB Molecule:**chemotaxis protein chea; **PDBTitle:** complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
16	c1y8oA_	Alignment		36.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
17	c2q8fA_	Alignment		29.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
18	c3d2rB_	Alignment		23.5	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; **PDBTitle:** crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
19	c2bu8A_	Alignment		21.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase kinase isoenzyme 2; **PDBTitle:** crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands
20	d1hq0a_	Alignment		16.1	25	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**Type 1 cytotoxic necrotizing factor, catalytic domain
21	d1xhna1	Alignment	not modelled	8.2	22	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
22	d1pv0a_	Alignment	not modelled	6.3	47	**Fold:**Long alpha-hairpin **Superfamily:**Sporulation inhibitor Sda **Family:**Sporulation inhibitor Sda
23	c3pmiC_	Alignment	not modelled	6.3	33	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**pwwp domain-containing protein mum1; **PDBTitle:** pwwp domain of human mutated melanoma-associated antigen 1
24	d1jmxa3	Alignment	not modelled	6.0	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
25	d1i58a_	Alignment	not modelled	5.9	15	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
26	d2f1da2	Alignment	not modelled	5.9	50	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
27	d2ae8a2	Alignment	not modelled	5.6	50	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
28	c1wnmA_	Alignment	not modelled	5.5	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fibroin-modulator binding-protein-1; **PDBTitle:** nmr structure of fmbp-1 tandem repeat 2 in 30%(v/v) tfe2 solution

29	d1pbya3	Alignment	not modelled	5.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5