Phyre^2

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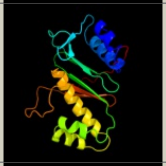
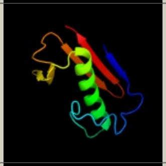
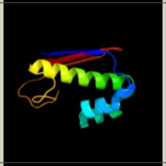
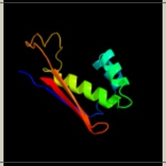
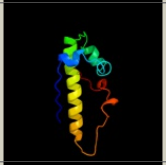
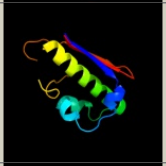
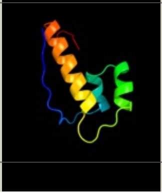
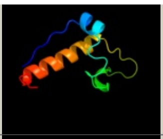
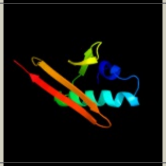
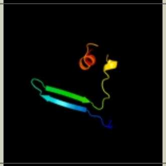
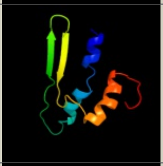
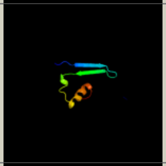
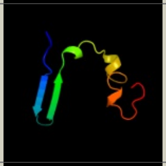
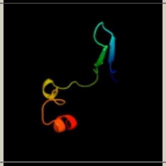
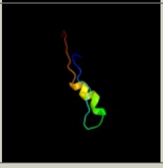
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qr0A_	Alignment		100.0	28	**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	22	**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	27	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**4'-Phosphopantetheinyl transferase SFP
4	d1qr0a1	Alignment		99.6	23	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**4'-Phosphopantetheinyl transferase SFP
5	c3hykB_	Alignment		99.4	17	**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)
6	c2wasA_	Alignment		99.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** structure of the fungal type i fas ppt domain
7	d1f7la_	Alignment		99.4	19	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**Holo-(acyl carrier protein) synthase ACPS
8	d1ftha_	Alignment		99.3	24	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**Holo-(acyl carrier protein) synthase ACPS
9	c3ne9B_	Alignment		99.2	18	**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
10	c3f09B_	Alignment		99.2	18	**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	c3h88A_	Alignment		99.1	25	**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

12	c2jbzA_	Alignment		98.9	22	**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
13	c2qg8A_	Alignment		98.6	23	**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		97.8	28	**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		61.3	31	**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	c2bu8A_	Alignment		46.8	20	**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
17	c2q8fA_	Alignment		44.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; **PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1
18	c1y8oA_	Alignment		44.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; **PDBTitle:** crystal structure of the pdk3-l2 complex
19	c3d2rB_	Alignment		39.9	21	**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
20	c3k8aA_	Alignment		33.5	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative primosomal replication protein; **PDBTitle:** neisseria gonorrhoeae prib
21	c3en2A_	Alignment	not modelled	23.6	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable primosomal replication protein n; **PDBTitle:** three-dimensional structure of the protein prib from2 ralstonia solanacearum at the resolution 2.3a. northeast3 structural genomics consortium target rsr213c.
22	d1txya_	Alignment	not modelled	19.5	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
23	c3fhwB_	Alignment	not modelled	18.2	24	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**primosomal replication protein n; **PDBTitle:** crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
24	d1v1qa_	Alignment	not modelled	14.4	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
25	d1i58a_	Alignment	not modelled	13.0	20	**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	c2z0rA_	Alignment	not modelled	12.3	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0547; **PDBTitle:** crystal structure of hypothetical protein ttha0547
27	d1pfoa_	Alignment	not modelled	11.4	34	**Fold:**Perfringolysin **Superfamily:**Perfringolysin **Family:**Perfringolysin
28	c1pfoA_	Alignment	not modelled	11.4	34	**PDB header:**toxin **Chain:** A: **PDB Molecule:**perfringolysin o;

						PDBTitle: perfringolysin o
29	c2j8pA_	Alignment	not modelled	8.8	31	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 64 kda subunit; **PDBTitle:** nmr structure of c-terminal domain of human cstf-64
30	d1s6la1	Alignment	not modelled	7.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
31	d1y8oa2	Alignment	not modelled	7.8	17	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain
32	d1knxa1	Alignment	not modelled	7.7	12	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
33	d2a13a1	Alignment	not modelled	7.0	24	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Rv2717c-like
34	c1zy7A_	Alignment	not modelled	6.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-specific adenosine deaminase b1, isoform **PDBTitle:** crystal structure of the catalytic domain of an adenosine2 deaminase that acts on rna (hadar2) bound to inositol3 hexakisphosphate (ihp)
35	d2yt9a1	Alignment	not modelled	5.7	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
36	d1zq1a1	Alignment	not modelled	5.4	35	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
37	c2knjA_	Alignment	not modelled	5.2	14	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**microplusin preprotein; **PDBTitle:** nmr structure of microplusin a antimicrobial peptide from2 rhipicephalus (boophilus) microplus