










# Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4qvhA_</a>	Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, 4'-phosphopantetheinyl <b>PDBTitle:</b> crystal structure of the essential mycobacterium tuberculosis2 phosphopantetheinyl transferase pptt, solved as a fusion protein with3 maltose binding protein
2	<a href="#">c1qr0A_</a>	Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4'-phosphopantetheinyl transferase sfp; <b>PDBTitle:</b> crystal structure of the 4'-phosphopantetheinyl transferase sfp-2 coenzyme a complex
3	<a href="#">c2cg5A_</a>	Alignment		99.9	15	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aminoadipate-semialdehyde dehydrogenase- <b>PDBTitle:</b> structure of aminoadipate-semialdehyde dehydrogenase-2 phosphopantetheinyl transferase in complex with cytosolic acyl3 carrier protein and coenzyme a
4	<a href="#">d1qr0a2</a>	Alignment		99.5	14	<b>Fold:</b> 4'-phosphopantetheinyl transferase <b>Superfamily:</b> 4'-phosphopantetheinyl transferase <b>Family:</b> 4'-Phosphopantetheinyl transferase SFP
5	<a href="#">c3h88A_</a>	Alignment		99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> crystal structure of 4'-phosphopantetheinyl transferase acps from2 vibrio cholerae o1 biovar eltor
6	<a href="#">c3hykB_</a>	Alignment		99.4	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> 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	<a href="#">c5xumA_</a>	Alignment		99.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> crystal structure of thermotoga maritima holo-[acyl-carrier-protein]2 synthase (acps)
8	<a href="#">d1f7la_</a>	Alignment		99.4	17	<b>Fold:</b> 4'-phosphopantetheinyl transferase <b>Superfamily:</b> 4'-phosphopantetheinyl transferase <b>Family:</b> Holo-(acyl carrier protein) synthase ACPS
9	<a href="#">c5vbxB_</a>	Alignment		99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> crystal structure of holo-[acyl-carrier-protein] synthase (acps) from2 escherichia coli
10	<a href="#">c5xukA_</a>	Alignment		99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> crystal structure of helicobacter pylori holo-[acyl-carrier-protein]2 synthase (acps) in complex with coenzyme a
11	<a href="#">c2wasA_</a>	Alignment		99.3	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> structure of the fungal type i fas ppt domain

12	<a href="#">c5cmoB_</a>	Alignment		99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> crystal structure of holo-[acyl-carrier-protein] synthase (acps) from2 neisseria meningitidis
13	<a href="#">c2jbzA_</a>	Alignment		99.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> crystal structure of the streptomyces coelicolor holo-2 [acyl-carrier-protein] synthase (acps) in complex with3 coenzyme a at 1.6 a
14	<a href="#">d1ftha_</a>	Alignment		99.2	21	<b>Fold:</b> 4'-phosphopantetheinyl transferase <b>Superfamily:</b> 4'-phosphopantetheinyl transferase <b>Family:</b> Holo-(acyl carrier protein) synthase ACPS
15	<a href="#">c3ne9B_</a>	Alignment		99.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantetheine protein transferase, ppt1p; <b>PDBTitle:</b> chronobacterium ammoiniagenes apo-acps strucutre
16	<a href="#">d1qr0a1</a>	Alignment		99.1	13	<b>Fold:</b> 4'-phosphopantetheinyl transferase <b>Superfamily:</b> 4'-phosphopantetheinyl transferase <b>Family:</b> 4'-Phosphopantetheinyl transferase SFP
17	<a href="#">c2qg8A_</a>	Alignment		99.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein synthase py06285; <b>PDBTitle:</b> plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
18	<a href="#">c3f09B_</a>	Alignment		98.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> 1.82 angstrom resolution crystal structure of holo-(acyl-carrier-2 protein) synthase (acps) from staphylococcus aureus
19	<a href="#">c3hqjA_</a>	Alignment		98.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> structure-function analysis of mycobacterium tuberculosis2 acyl carrier protein synthase (acps).
20	<a href="#">c3hmjB_</a>	Alignment		95.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> saccharomyces cerevisiae fas type i
21	<a href="#">c5xyiZ_</a>	Alignment	not modelled	16.3	33	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
22	<a href="#">c2kwvA_</a>	Alignment	not modelled	15.1	30	<b>PDB header:</b> protein binding/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iota; <b>PDBTitle:</b> solution structure of ubm1 of murine polymerase iota in complex with2 ubiquitin
23	<a href="#">c3mwdA_</a>	Alignment	not modelled	13.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> truncated human atp-citrate lyase with citrate bound
24	<a href="#">d2f1da2</a>	Alignment	not modelled	10.7	26	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
25	<a href="#">d2ae8a2</a>	Alignment	not modelled	10.6	31	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
26	<a href="#">c5lw6A_</a>	Alignment	not modelled	9.6	20	<b>PDB header:</b> adp-ribose binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ddb_g0293866; <b>PDBTitle:</b> crystal structure of a se-met substituted dictyostelium discoideum2 adp-ribose binding macrodomain (residues 342-563) of ddb_g0293866
27	<a href="#">d1rhya2</a>	Alignment	not modelled	9.6	23	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
28	<a href="#">c2ch4A_</a>	Alignment	not modelled	9.5	26	<b>PDB header:</b> transferase/chemotaxis <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein chea; <b>PDBTitle:</b> complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew <b>PDB header:</b> de novo protein

29	<a href="#">c6g6dC_</a>	Alignment	not modelled	7.9	29	<b>Chain:</b> C; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
30	<a href="#">c6g6dB_</a>	Alignment	not modelled	7.9	29	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
31	<a href="#">c6g6dA_</a>	Alignment	not modelled	7.9	29	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
32	<a href="#">c6g68N_</a>	Alignment	not modelled	7.4	29	<b>PDB header:</b> de novo protein <b>Chain:</b> N; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
33	<a href="#">c6g68G_</a>	Alignment	not modelled	7.4	29	<b>PDB header:</b> de novo protein <b>Chain:</b> G; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
34	<a href="#">c6g68L_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> L; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
35	<a href="#">c6g68A_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
36	<a href="#">c6g68Q_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> Q; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
37	<a href="#">c6g68H_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> H; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
38	<a href="#">c6g68K_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> K; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
39	<a href="#">c6g68E_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> E; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
40	<a href="#">c6g68B_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
41	<a href="#">c6g68P_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> P; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
42	<a href="#">c6g68D_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> D; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
43	<a href="#">c6g68C_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
44	<a href="#">c6g68M_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> M; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
45	<a href="#">c6g68R_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> R; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
46	<a href="#">c6g68O_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> O; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
47	<a href="#">c6g68I_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> I; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
48	<a href="#">c6g68J_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> J; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
49	<a href="#">c6g68F_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> cc-type2-ll-sg; <b>PDBTitle:</b> crystal structure of a parallel six-helix coiled coil cc-type2-ll-sg
50	<a href="#">c2f1dP_</a>	Alignment	not modelled	6.7	26	<b>PDB header:</b> lyase <b>Chain:</b> P; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase 1; <b>PDBTitle:</b> x-ray structure of imidazoleglycerol-phosphate dehydratase
51	<a href="#">c2ae8C_</a>	Alignment	not modelled	6.6	31	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
52	<a href="#">c5dnIA_</a>	Alignment	not modelled	6.5	23	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> crystal structure of igpd from pyrococcus furiosus in complex with2 (s)-c348
53	<a href="#">c4lomA_</a>	Alignment	not modelled	6.1	26	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis hisb in complex with2 its substrate
54	<a href="#">c4wlpB_</a>	Alignment	not modelled	6.1	11	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> nuclear factor related to kappa-b-binding protein;

						<b>PDBTitle:</b> crystal structure of uch37-nfrkb inhibited deubiquitylating complex
55	<a href="#">c1rhyB_</a>	Alignment	not modelled	6.1	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> imidazole glycerol phosphate dehydratase; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate dehydratase
56	<a href="#">c6ncsB_</a>	Alignment	not modelled	6.1	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylneuraminic acid (sialic acid) synthetase; <b>PDBTitle:</b> crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
57	<a href="#">c2yvqA_</a>	Alignment	not modelled	6.0	43	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
58	<a href="#">c6fwhH_</a>	Alignment	not modelled	5.9	23	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> acanthamoeba igpd in complex with r-c348 to 1.7a resolution
59	<a href="#">c6eizB_</a>	Alignment	not modelled	5.7	43	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2 with farnesol bound2 in the channel.
60	<a href="#">c4pn9A_</a>	Alignment	not modelled	5.7	43	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2
61	<a href="#">c4pn9B_</a>	Alignment	not modelled	5.7	43	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2
62	<a href="#">c6eizF_</a>	Alignment	not modelled	5.7	43	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2 with farnesol bound2 in the channel.
63	<a href="#">c4pn9F_</a>	Alignment	not modelled	5.7	43	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2
64	<a href="#">c6eizC_</a>	Alignment	not modelled	5.6	43	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2 with farnesol bound2 in the channel.
65	<a href="#">c4pn9D_</a>	Alignment	not modelled	5.6	43	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2
66	<a href="#">c4pn9C_</a>	Alignment	not modelled	5.6	43	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2
67	<a href="#">c6eizD_</a>	Alignment	not modelled	5.6	43	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2 with farnesol bound2 in the channel.
68	<a href="#">c4pn9E_</a>	Alignment	not modelled	5.6	43	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2
69	<a href="#">c6eizA_</a>	Alignment	not modelled	5.6	43	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc-hex2; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex2 with farnesol bound2 in the channel.