Phyre^2

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Description	Q7DFV4
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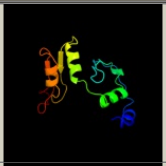
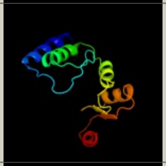
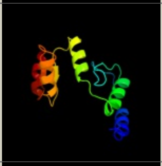
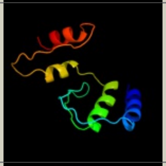
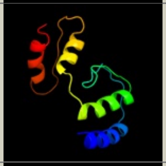
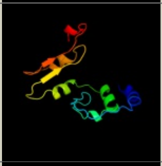
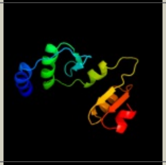
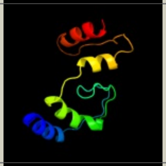
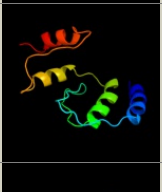
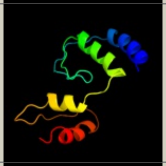
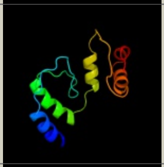
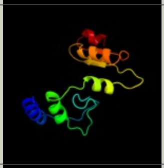
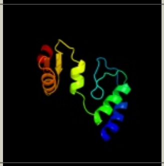
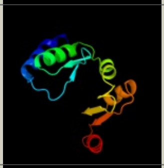
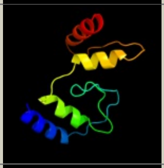
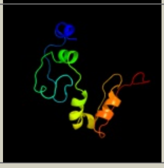
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qo3A_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**eryaii erythromycin polyketide synthase modules 3 and 4; **PDBTitle:** crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthronolide b synthase
2	c3eenA_	Alignment		99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acp transacylase; **PDBTitle:** crystal structure of malonyl-coa:acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331
3	d1nm2a1	Alignment		99.9	14	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like
4	c2qj3B_	Alignment		99.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** mycobacterium tuberculosis fabd
5	c3im9A_	Alignment		99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of mcat from staphylococcus aureus
6	c3ezoA_	Alignment		99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein s-2 malonyltransferase from burkholderia pseudomallei 1710b
7	d1mlaa1	Alignment		99.9	21	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like
8	c2hg4A_	Alignment		99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-deoxyerythronolide b synthase; **PDBTitle:** structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
9	c2cuyA_	Alignment		99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-[acyl carrier protein] transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8
10	c3rgiA_	Alignment		99.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**disd protein; **PDBTitle:** trans-acting transferase from disorazole synthase
11	c2cdh9_	Alignment		99.9	16	**PDB header:**transferase **Chain:** 9: **PDB Molecule:**acetyl transferase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.

12	c3qatB_	Alignment		99.9	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
13	c2g2oA_	Alignment		99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** structure of e.coli fabd complexed with sulfate
14	c2c2nA_	Alignment		99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** structure of human mitochondrial malonyltransferase
15	c3ptwA_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
16	c3tqeA_	Alignment		99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl-coa-[acyl-carrier-protein] transacylase; **PDBTitle:** structure of the malonyl coa-acyl carrier protein transacylase (fabd)2 from coxiella burnetii
17	c2h1yA_	Alignment		99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coenzyme a-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl-coa:acyl carrier protein transacylase2 (mcat) from helicobacter pylori
18	c3im8A_	Alignment		99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl acyl carrier protein transacylase; **PDBTitle:** crystal structure of mcat from streptococcus pneumoniae
19	c3g87A_	Alignment		99.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
20	c2jfkD_	Alignment		99.8	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the mat domain of human fas with malonyl-coa
21	c3hhdC_	Alignment	not modelled	99.8	17	**PDB header:**transferase, hydrolase **Chain:** C: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the human fatty acid synthase ks-mat didomain2 as a framework for inhibitor design.
22	c2vz8B_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase; **PDBTitle:** crystal structure of mammalian fatty acid synthase
23	c2uv9B_	Alignment	not modelled	99.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase alpha subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
24	c2uv8C_	Alignment	not modelled	98.7	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**fatty acid synthase subunit alpha (fas2); **PDBTitle:** crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
25	c2vkzC_	Alignment	not modelled	98.7	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**fatty acid synthase subunit alpha; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
26	c2vkzH_	Alignment	not modelled	97.8	15	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
27	c2uvaI_	Alignment	not modelled	97.4	14	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400

28	c2xznC_	Alignment	not modelled	68.4	10	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**kh domain containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
29	c2zkqc_	Alignment	not modelled	67.1	9	**PDB header:**ribosomal protein/rna **Chain:** C: **PDB Molecule:**rna expansion segment es4; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
30	c1s1hC_	Alignment	not modelled	59.7	5	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**40s ribosomal protein s3; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
31	c3izbB_	Alignment	not modelled	53.4	5	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein rps3 (s3p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
32	c3iraA_	Alignment	not modelled	52.2	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
33	c3ea0B_	Alignment	not modelled	38.3	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase, para family; **PDBTitle:** crystal structure of para family atpase from chlorobium tepidum tls
34	c3fhkF_	Alignment	not modelled	23.8	27	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**upf0403 protein yphp; **PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
35	c1x0uB_	Alignment	not modelled	13.7	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical methylmalonyl-coa decarboxylase alpha subunit; **PDBTitle:** crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfolobus tokodaii
36	c3u9rB_	Alignment	not modelled	12.8	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**methylcrotonyl-coa carboxylase, beta-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc), beta subunit
37	c2p4gA_	Alignment	not modelled	11.3	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a pyrimidine reductase-like protein (dip1392)2 from corynebacterium diphtheriae nctc at 2.30 a resolution
38	d2qalc2	Alignment	not modelled	9.7	13	**Fold:**Ribosomal protein S3 C-terminal domain **Superfamily:**Ribosomal protein S3 C-terminal domain **Family:**Ribosomal protein S3 C-terminal domain
39	c1hnwC_	Alignment	not modelled	9.6	9	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**30s ribosomal protein s3; **PDBTitle:** structure of the thermus thermophilus 30s ribosomal subunit2 in complex with tetracycline
40	c1pnxC_	Alignment	not modelled	9.6	9	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**30s ribosomal protein s3; **PDBTitle:** crystal structure of the wild type ribosome from e. coli,2 30s subunit of 70s ribosome. this file, 1pnx, contains3 only molecules of the 30s ribosomal subunit. the 50s4 subunit is in the pdb file 1pny.
41	d2uubc2	Alignment	not modelled	8.7	0	**Fold:**Ribosomal protein S3 C-terminal domain **Superfamily:**Ribosomal protein S3 C-terminal domain **Family:**Ribosomal protein S3 C-terminal domain
42	c3n6rF_	Alignment	not modelled	8.7	10	**PDB header:**ligase **Chain:** F: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
43	d1szaa_	Alignment	not modelled	8.2	13	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**RPR domain (SMART 00582)
44	d1oc4a2	Alignment	not modelled	7.3	10	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
45	d1h05a_	Alignment	not modelled	7.3	46	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
46	d1xb4a2	Alignment	not modelled	6.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
47	c3uzuA_	Alignment	not modelled	6.7	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase a; **PDBTitle:** the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
48	c2gy9C_	Alignment	not modelled	6.6	13	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**30s ribosomal subunit protein s3; **PDBTitle:** structure of the 30s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and3 protein components into cryo-em map emd-1056
49	c2qbfC_	Alignment	not modelled	6.6	13	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**30s ribosomal protein s3; **PDBTitle:** crystal structure of the bacterial ribosome from escherichia2 coli in complex with ribosome recycling factor (rrf). this3 file contains the 30s subunit of the second 70s ribosome.4 the entire crystal structure contains two 70s ribosomes and5 is described in remark 400.
						Fold:LDH C-terminal domain-like

50	d1ez4a2	Alignment	not modelled	6.6	13	**Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
51	d1zkda1	Alignment	not modelled	6.4	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**RPA4359-like
52	c1c4kA_	Alignment	not modelled	6.3	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (ornithine decarboxylase); **PDBTitle:** ornithine decarboxylase mutant (gly121tyr)
53	c1i4wA_	Alignment	not modelled	6.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mitochondrial replication protein mtf1; **PDBTitle:** the crystal structure of the transcription factor sc-mttfb2 offers intriguing insights into mitochondrial transcription
54	d1i4wa_	Alignment	not modelled	6.2	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
55	c3n8kG_	Alignment	not modelled	6.1	44	**PDB header:**lyase **Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
56	c2vycA_	Alignment	not modelled	5.8	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biodegradative arginine decarboxylase; **PDBTitle:** crystal structure of acid induced arginine decarboxylase2 from e. coli
57	c2d5nB_	Alignment	not modelled	5.6	9	**PDB header:**hydrolase, oxidoreductase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
58	c3fteA_	Alignment	not modelled	5.6	12	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** crystal structure of a. aeolicus ksga in complex with rna
59	d1o6za2	Alignment	not modelled	5.5	17	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
60	c3d9oB_	Alignment	not modelled	5.5	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rna-binding protein 16; **PDBTitle:** snapshots of the rna processing factor scaf8 bound to different2 phosphorylated forms of the carboxy-terminal domain of rna-polymerase3 ii
61	c2uygF_	Alignment	not modelled	5.4	29	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallogaphic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
62	d2c4va1	Alignment	not modelled	5.4	29	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
63	c2xigA_	Alignment	not modelled	5.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites