Phyre2

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Description	P05852
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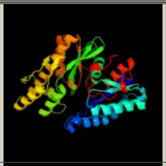
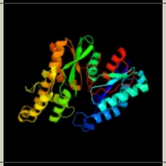
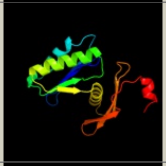
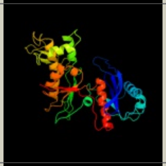
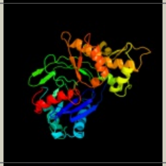
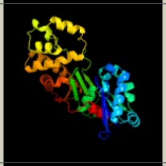
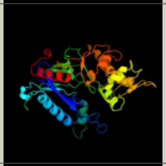
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3en9B_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
2	c2ivoC_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
3	c3enoB_	Alignment		100.0	33	**PDB header:**hydrolase/unknown function **Chain:** B: **PDB Molecule:**putative o-sialoglycoprotein endopeptidase; **PDBTitle:** crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
4	c3tsuA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
5	c1okjB_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protease yeaz; **PDBTitle:** crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
6	d1huxa_	Alignment		99.9	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
7	c3r6mD_	Alignment		99.9	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**yeaz, resuscitation promoting factor; **PDBTitle:** crystal structure of vibrio parahaemolyticus yeaz
8	d1okja1	Alignment		99.8	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
9	c2a6aB_	Alignment		99.8	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein tm0874; **PDBTitle:** crystal structure of glycoprotein endopeptidase (tm0874) from2 thermotoga maritima at 2.50 a resolution
10	d2a6aa1	Alignment		99.7	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
11	d2ewsa1	Alignment		99.7	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like

12	c3h1qB_	Alignment		99.0	14	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
13	c3hz6A_	Alignment		98.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
14	c3ifrB_	Alignment		98.9	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
15	c2zf5O_	Alignment		98.7	18	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
16	c3g25B_	Alignment		98.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
17	c2e2pA_	Alignment		98.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
18	c2cgkB_	Alignment		98.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-rhamnulose kinase; **PDBTitle:** crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
19	c2dpnB_	Alignment		98.6	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
20	c3gbtA_	Alignment		98.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
21	c3eo3B_	Alignment	not modelled	98.6	12	**PDB header:**isomerase, transferase **Chain:** B: **PDB Molecule:**bifunctional udp-n-acetylglucosamine 2-epimerase/n- **PDBTitle:** crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
22	c1sazA_	Alignment	not modelled	98.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable butyrate kinase 2; **PDBTitle:** membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
23	c2ap1A_	Alignment	not modelled	98.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
24	c2aa4B_	Alignment	not modelled	98.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative n-acetylmannosamine kinase; **PDBTitle:** crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
25	c3cqyA_	Alignment	not modelled	98.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
26	c2qm1D_	Alignment	not modelled	98.4	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
27	c2d4wA_	Alignment	not modelled	98.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
						PDB header:transferase

28	c2ch5D_	Alignment	not modelled	98.3	11	**Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
29	c1glbG_	Alignment	not modelled	98.2	14	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
30	c3gg4B_	Alignment	not modelled	98.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
31	c3smpA_	Alignment	not modelled	98.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 1; **PDBTitle:** monoclinic crystal structure of human pantothenate kinase 1 alpha
32	c1zc6A_	Alignment	not modelled	98.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable n-acetylglucosamine kinase; **PDBTitle:** crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
33	c3flcX_	Alignment	not modelled	98.0	20	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
34	d2i7na2	Alignment	not modelled	97.9	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
35	c3qbwA_	Alignment	not modelled	97.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 actetylmuramic acid kinase (anmk) bound to adenosine diphosphate
36	c1z6rC_	Alignment	not modelled	97.9	16	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
37	c1z05A_	Alignment	not modelled	97.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, rok family; **PDBTitle:** crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
38	c2nlxA_	Alignment	not modelled	97.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
39	d2i7pa1	Alignment	not modelled	97.8	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
40	c3ezwD_	Alignment	not modelled	97.8	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
41	c2i7pA_	Alignment	not modelled	97.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
42	d2p3ra2	Alignment	not modelled	97.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
43	c1mwmA_	Alignment	not modelled	97.7	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
44	c2gupA_	Alignment	not modelled	97.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rok family protein; **PDBTitle:** structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
45	c1zbsA_	Alignment	not modelled	97.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg1100; **PDBTitle:** crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
46	c3htvA_	Alignment	not modelled	97.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-allose kinase; **PDBTitle:** crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
47	c2w40C_	Alignment	not modelled	97.4	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
48	c2v7yA_	Alignment	not modelled	97.3	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein dnak; **PDBTitle:** crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
49	d1saza1	Alignment	not modelled	97.3	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
50	c3i8bA_	Alignment	not modelled	97.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
51	c1tuuA_	Alignment	not modelled	97.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase crystallized with atpgs
52	c3r8eA_	Alignment	not modelled	97.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical sugar kinase; **PDBTitle:** crystal structure of a hypothetical sugar kinase (chu_1875) from2 cytophaga hutchinsonii atcc 33406 at 1.65 a resolution
						PDB header:transferase

53	c2iirJ_	Alignment	not modelled	97.2	16	**Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
54	d1r59o2	Alignment	not modelled	97.2	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
55	c2d0oA_	Alignment	not modelled	97.2	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**diol dehydratase-reactivating factor large **PDBTitle:** strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
56	d1jcea2	Alignment	not modelled	97.1	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
57	c3iucC_	Alignment	not modelled	97.1	12	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock 70kda protein 5 (glucose-regulated **PDBTitle:** crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
58	c1zxoB_	Alignment	not modelled	97.0	8	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein q8a1p1; **PDBTitle:** x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
59	c1xupO_	Alignment	not modelled	97.0	22	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
60	c3vgkB_	Alignment	not modelled	97.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
61	d1bupa2	Alignment	not modelled	97.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
62	c2v7zA_	Alignment	not modelled	97.0	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock cognate 71 kda protein; **PDBTitle:** crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
63	c1x3nA_	Alignment	not modelled	96.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
64	d2e8aa2	Alignment	not modelled	96.7	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
65	c2hoeA_	Alignment	not modelled	96.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetylglucosamine kinase; **PDBTitle:** crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
66	d2zgya2	Alignment	not modelled	96.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
67	c3jvpA_	Alignment	not modelled	96.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
68	c1dkgD_	Alignment	not modelled	96.5	22	**PDB header:**complex (hsp24/hsp70) **Chain:** D: **PDB Molecule:**molecular chaperone dnak; **PDBTitle:** crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
69	c1xc3A_	Alignment	not modelled	96.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructokinase; **PDBTitle:** structure of a putative fructokinase from bacillus subtilis
70	d1dkgd2	Alignment	not modelled	96.4	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
71	c1e4gT_	Alignment	not modelled	96.3	9	**PDB header:**bacterial cell division **Chain:** T: **PDB Molecule:**cell division protein ftsa; **PDBTitle:** ftsa (atp-bound form) from thermotoga maritima
72	d2p3ra1	Alignment	not modelled	96.2	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
73	c2khoA_	Alignment	not modelled	95.7	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 70; **PDBTitle:** nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
74	d1zc6a1	Alignment	not modelled	95.6	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
75	c3js6A_	Alignment	not modelled	95.5	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized parm protein; **PDBTitle:** crystal structure of apo psk41 parm protein
76	c3d2fC_	Alignment	not modelled	95.4	15	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70
77	c1woqB_	Alignment	not modelled	95.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inorganic polyphosphate/atp-glucomannokinase; **PDBTitle:** crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
78	d1e4ft2	Alignment	not modelled	94.7	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

						Family: Actin/HSP70
79	d2ch5a2	Alignment	not modelled	94.7	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
80	c1hpmA_	Alignment	not modelled	94.6	20	**PDB header:**hydrolase (acting on acid anhydrides) **Chain:** A: **PDB Molecule:**44k atpase fragment (n-terminal) of 7o kd heat- **PDBTitle:** how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
81	c1jcgA_	Alignment	not modelled	94.5	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
82	d2ch5a1	Alignment	not modelled	94.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
83	d2fsja1	Alignment	not modelled	92.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
84	c3p4iA_	Alignment	not modelled	92.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** crystal structure of acetate kinase from mycobacterium avium
85	c1o1f4_	Alignment	not modelled	92.0	10	**PDB header:**contractile protein **Chain:** 4: **PDB Molecule:**skeletal muscle actin; **PDBTitle:** molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
86	d2gupa2	Alignment	not modelled	91.6	5	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
87	d2ap1a1	Alignment	not modelled	91.6	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
88	d2aa4a2	Alignment	not modelled	91.2	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
89	d1z6ra2	Alignment	not modelled	90.9	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
90	c1tqyD_	Alignment	not modelled	90.7	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**actinorhodin polyketide putative beta-ketoacyl synthase 2; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
91	d1r59o1	Alignment	not modelled	89.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
92	d2hoea2	Alignment	not modelled	88.9	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
93	d1tqyb2	Alignment	not modelled	88.6	22	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
94	d1u6ea2	Alignment	not modelled	88.6	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
95	d1e5ma2	Alignment	not modelled	87.5	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
96	d2hoea3	Alignment	not modelled	87.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
97	d1m3ka1	Alignment	not modelled	86.9	10	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
98	c2iwyB_	Alignment	not modelled	86.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** human mitochondrial beta-ketoacyl acp synthase
99	d1vhxa_	Alignment	not modelled	86.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
100	c1e5mA_	Alignment	not modelled	86.0	21	**PDB header:**condensing enzyme **Chain:** A: **PDB Molecule:**beta ketoacyl acyl carrier protein synthase ii; **PDBTitle:** beta ketoacyl acyl carrier protein synthase ii (kasii) from2 synechocystis sp.
101	c2gqdB_	Alignment	not modelled	85.3	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 2; **PDBTitle:** the crystal structure of b-ketoacyl-acp synthase ii (fabf)2 from staphylococcus aureus
102	c2iikA_	Alignment	not modelled	85.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-ketoacyl-coa thiolase, peroxisomal; **PDBTitle:** crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)
103	c3dwlB_	Alignment	not modelled	85.2	10	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**actin-related protein 3; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
104	d2aa4a1	Alignment	not modelled	85.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

						Family:ROK
105	d1g99a1	Alignment	not modelled	84.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
106	d2gfva2	Alignment	not modelled	84.2	23	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
107	c2gfvA_	Alignment	not modelled	83.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 2; **PDBTitle:** structure of e. coli fabf (kasii) c163q mutant
108	c3o04A_	Alignment	not modelled	83.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-keto-acyl carrier protein synthase ii; **PDBTitle:** crystal structure of the beta-keto-acyl carrier protein synthase ii2 (lmo2201) from listeria monocytogenes
109	d1j3na2	Alignment	not modelled	83.0	17	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
110	c1oxhD_	Alignment	not modelled	82.8	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**beta ketoacyl-acyl carrier protein synthase; **PDBTitle:** the crystal structure of beta-ketoacyl-[acyl carrier2 protein] synthase ii from streptococcus pneumoniae,3 triclinic form
111	d1z05a3	Alignment	not modelled	82.7	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
112	c3e60A_	Alignment	not modelled	82.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase ii; **PDBTitle:** crystal structure of 3-oxoacyl-(acyl carrier protein)2 synthase ii from bartonella henselae
113	c2ychA_	Alignment	not modelled	82.3	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
114	c1tqyC_	Alignment	not modelled	81.6	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**beta-ketoacyl synthase/acyl transferase; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
115	d1ox0a2	Alignment	not modelled	81.5	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
116	d1ub7a2	Alignment	not modelled	81.5	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
117	c2gp6B_	Alignment	not modelled	81.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 2; **PDBTitle:** x-ray crystal structure of mycobacterium tuberculosis beta-2 ketoacyl acyl carrier protein synthase ii (mtkasb)
118	d1xc3a2	Alignment	not modelled	81.0	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
119	c2wggA_	Alignment	not modelled	80.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 1; **PDBTitle:** crystal structure of mycobacterium tuberculosis c171q kasa2 variant with bound tlm
120	d2ix4a2	Alignment	not modelled	80.8	23	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related