Phyre^2

Email	l.a.kelley@imperial.ac.uk
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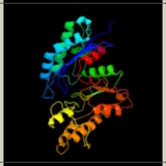
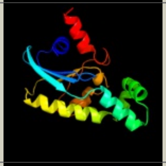
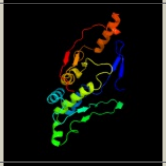
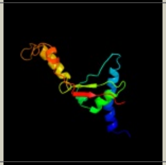
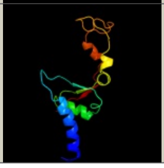
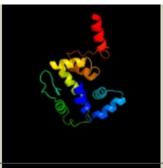
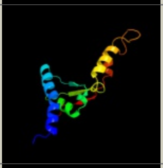
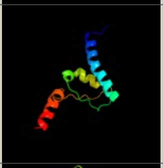
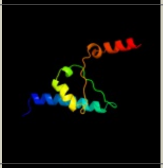
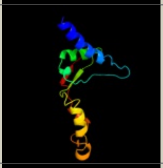
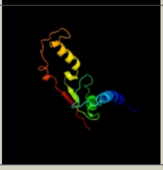
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cqyA_	Alignment		100.0	48	**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
2	c3qbwA_	Alignment		100.0	49	**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
3	c3enoB_	Alignment		99.2	21	**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	c2ivoC_	Alignment		98.2	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
5	d1huxa_	Alignment		98.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
6	c3h1qB_	Alignment		97.9	17	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
7	c3i8bA_	Alignment		97.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
8	c3en9B_	Alignment		97.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
9	d2p3ra2	Alignment		97.4	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
10	c1glbG_	Alignment		97.4	23	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
11	c3gbtA_	Alignment		97.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus

12	c3gg4B_	Alignment		97.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
13	c3hz6A_	Alignment		97.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
14	c3flcX_	Alignment		97.1	22	**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
15	c3ezwD_	Alignment		97.1	25	**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
16	d1e4ft2	Alignment		97.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
17	c3ifrB_	Alignment		97.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
18	c2zf5O_	Alignment		97.0	20	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
19	c2d4wA_	Alignment		96.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
20	d1r59o2	Alignment		96.9	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
21	c2cgkB_	Alignment	not modelled	96.8	19	**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.
22	c2nlxA_	Alignment	not modelled	96.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
23	c1mwmA_	Alignment	not modelled	96.8	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
24	c2dpnB_	Alignment	not modelled	96.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
25	c1xupO_	Alignment	not modelled	96.5	22	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
26	c3g25B_	Alignment	not modelled	96.5	18	**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.
27	c3jvpA_	Alignment	not modelled	96.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
28	c3h6eB_	Alignment	not modelled	96.2	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
						Fold: Ribonuclease H-like motif

29	d2e8aa2	Alignment	not modelled	96.2	22	**Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
30	c2w40C_	Alignment	not modelled	96.0	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
31	d1jcea2	Alignment	not modelled	95.9	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
32	c2v7zA_	Alignment	not modelled	95.9	19	**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
33	d1bupa2	Alignment	not modelled	95.9	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
34	c1hpmA_	Alignment	not modelled	95.4	19	**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
35	c1e4gT_	Alignment	not modelled	94.9	16	**PDB header:**bacterial cell division **Chain:** T: **PDB Molecule:**cell division protein ftsa; **PDBTitle:** ftsa (atp-bound form) from thermotoga maritima
36	c3iucC_	Alignment	not modelled	94.6	19	**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
37	c1dkgD_	Alignment	not modelled	93.9	21	**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
38	d2i7na2	Alignment	not modelled	93.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
39	d2zgya2	Alignment	not modelled	93.7	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
40	c1jcgA_	Alignment	not modelled	93.6	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
41	c2d0oA_	Alignment	not modelled	93.4	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**diol dehydratase-reactivating factor large **PDBTitle:** strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
42	d2i7pa1	Alignment	not modelled	93.3	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
43	d2ewsa1	Alignment	not modelled	92.7	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
44	c3smpA_	Alignment	not modelled	92.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 1; **PDBTitle:** monoclinic crystal structure of human pantothenate kinase 1 alpha
45	c2ychA_	Alignment	not modelled	91.8	22	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
46	d1dkgd2	Alignment	not modelled	91.8	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
47	c2v7yA_	Alignment	not modelled	91.6	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
48	c3d2fC_	Alignment	not modelled	91.1	18	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70
49	c3js6A_	Alignment	not modelled	91.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized parm protein; **PDBTitle:** crystal structure of apo psk41 parm protein
50	c3tsuA_	Alignment	not modelled	90.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
51	c1sazA_	Alignment	not modelled	89.2	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
52	c2fsnB_	Alignment	not modelled	86.2	20	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**hypothetical protein ta0583; **PDBTitle:** crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
53	c1z05A_	Alignment	not modelled	86.2	15	**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.
54	c2khoA_	Alignment	not modelled	85.2	22	**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
55	c2gupA_	Alignment	not modelled	82.8	15	**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
56	d2fsja1	Alignment	not modelled	82.5	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
57	c2i7pA_	Alignment	not modelled	82.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
58	d1saza2	Alignment	not modelled	81.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
59	c1z6rC_	Alignment	not modelled	80.1	10	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
60	d1t6ca2	Alignment	not modelled	79.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
61	c2qm1D_	Alignment	not modelled	78.8	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
62	c1qr6A_	Alignment	not modelled	77.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme 2; **PDBTitle:** human mitochondrial nad(p)-dependent malic enzyme
63	c2e2pA_	Alignment	not modelled	76.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
64	c3euoB_	Alignment	not modelled	72.4	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**type iii pentaketide synthase; **PDBTitle:** crystal structure of a fungal type iii polyketide synthase,2 oras
65	c2gqdB_	Alignment	not modelled	72.3	21	**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
66	d2gfva2	Alignment	not modelled	71.6	28	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
67	d2p3ra1	Alignment	not modelled	71.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
68	c3aleB_	Alignment	not modelled	70.6	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**os07g0271500 protein; **PDBTitle:** a type iii polyketide synthase that produces diarylheptanoid
69	d1j3na2	Alignment	not modelled	70.3	28	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
70	d1e5ma2	Alignment	not modelled	70.1	28	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
71	c1tqyC_	Alignment	not modelled	70.0	34	**PDB header:**transferase **Chain:** C: **PDB Molecule:**beta-ketoacyl synthase/acyl transferase; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
72	d1ox0a2	Alignment	not modelled	69.1	24	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
73	c2wggA_	Alignment	not modelled	68.7	28	**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
74	c2ebdB_	Alignment	not modelled	68.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase iii2 from aquifex aeolicus vf5
75	c2gfvA_	Alignment	not modelled	68.4	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 2; **PDBTitle:** structure of e. coli fabf (kasii) c163q mutant
76	d2ix4a2	Alignment	not modelled	67.6	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
77	c1o1f4_	Alignment	not modelled	67.3	14	**PDB header:**contractile protein **Chain:** 4: **PDB Molecule:**skeletal muscle actin; **PDBTitle:** molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
78	c3p4iA_	Alignment	not modelled	66.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** crystal structure of acetate kinase from mycobacterium avium
79	c2gp6B_	Alignment	not modelled	66.7	21	**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)
						PDB header:transferase

80	c3e1hA_	Alignment	not modelled	66.5	17	**Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a type iii polyketide synthase2 pksiiinc from neurospora crassa
81	c1e5mA_	Alignment	not modelled	65.8	28	**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.
82	c1oxhD_	Alignment	not modelled	64.4	24	**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
83	c2iwyB_	Alignment	not modelled	64.1	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** human mitochondrial beta-ketoacyl acp synthase
84	d1afwa2	Alignment	not modelled	63.1	28	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
85	c2d3mA_	Alignment	not modelled	62.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pentaketide chromone synthase; **PDBTitle:** pentaketide chromone synthase complexed with coenzyme a
86	c2ix4B_	Alignment	not modelled	62.4	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** arabidopsis thaliana mitochondrial beta-ketoacyl acp2 synthase hexanoic acid complex
87	d1tqya2	Alignment	not modelled	62.3	34	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
88	c3hhdC_	Alignment	not modelled	61.6	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.
89	d1u6ea2	Alignment	not modelled	61.6	9	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
90	c1j3nB_	Alignment	not modelled	61.4	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) synthase ii; **PDBTitle:** crystal structure of 3-oxoacyl-(acyl-carrier protein)2 synthase ii from thermus thermophilus hb8
91	c2f9aA_	Alignment	not modelled	61.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-hydroxy-3-methylglutaryl coenzyme a synthase 1; **PDBTitle:** hmg-coa synthase from brassica juncea in complex with f-244
92	c1tqyD_	Alignment	not modelled	61.1	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**actinorhodin polyketide putative beta-ketoacyl synthase 2; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
93	c3mdqA_	Alignment	not modelled	61.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
94	d1tqyb2	Alignment	not modelled	60.1	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
95	c1ub7A_	Alignment	not modelled	59.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] synthase; **PDBTitle:** the crystal analysis of beta-keroacyl-[acyl carrier protein] synthase2 iii (fabh)from thermus thermophilus.
96	c2p0uB_	Alignment	not modelled	59.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**stilbenecarboxylate synthase 2; **PDBTitle:** crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2)
97	c3e60A_	Alignment	not modelled	58.6	24	**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
98	c3o04A_	Alignment	not modelled	58.6	24	**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
99	c2p9lA_	Alignment	not modelled	58.1	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin-like protein 3; **PDBTitle:** crystal structure of bovine arp2/3 complex
100	d1m3ka2	Alignment	not modelled	57.8	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
101	c1tuuA_	Alignment	not modelled	57.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase crystallized with atpgs
102	c2qo3A_	Alignment	not modelled	56.4	24	**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
103	c3eo3B_	Alignment	not modelled	55.4	13	**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
104	d1nvra_	Alignment	not modelled	51.3	18	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like)

						Family: Protein kinases, catalytic subunit
105	d1wdkc2	Alignment	not modelled	50.8	29	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
106	d1bi5a1	Alignment	not modelled	50.4	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
107	d1nm1a2	Alignment	not modelled	49.8	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
108	c1vl6C_	Alignment	not modelled	49.7	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate oxidoreductase; **PDBTitle:** crystal structure of nad-dependent malic enzyme (tm0542) from2 thermotoga maritima at 2.61 a resolution
109	d1ulqa2	Alignment	not modelled	49.0	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
110	d1k8ka2	Alignment	not modelled	48.8	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
111	d1mzja2	Alignment	not modelled	48.0	26	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
112	d2aizp1	Alignment	not modelled	47.0	27	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
113	c3il5D_	Alignment	not modelled	46.8	27	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** structure of e. faecalis fabh in complex with 2-({4-bromo-3-2 [(diethylamino)sulfonyl]benzoyl}amino)benzoic acid
114	d1ub7a2	Alignment	not modelled	46.0	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
115	c2zf8A_	Alignment	not modelled	45.6	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
116	c2ap1A_	Alignment	not modelled	45.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
117	d2hmva1	Alignment	not modelled	44.8	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
118	d1u0ma1	Alignment	not modelled	44.4	17	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
119	d2fxua2	Alignment	not modelled	44.2	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
120	d1ub7a1	Alignment	not modelled	44.1	23	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like