Phyre2

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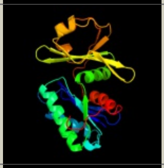
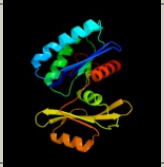
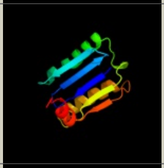
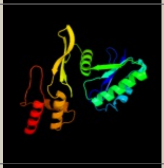
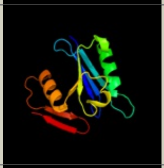
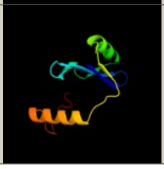
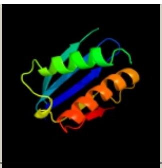
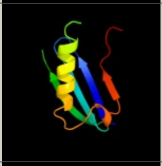
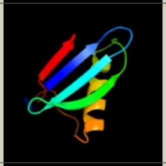
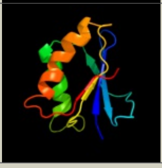
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1okjB_	Alignment		100.0	100	**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"
2	c3r6mD_	Alignment		100.0	55	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**yeaz, resuscitation promoting factor; **PDBTitle:** crystal structure of vibrio parahaemolyticus yeaz
3	c2a6aB_	Alignment		100.0	26	**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
4	d1okja1	Alignment		100.0	100	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
5	d2a6aa1	Alignment		100.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
6	c2ivoC_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
7	c3enoB_	Alignment		99.9	22	**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
8	c3en9B_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
9	d1okja2	Alignment		99.7	100	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
10	d1huxa_	Alignment		97.5	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
11	d2a6aa2	Alignment		97.3	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like

12	d1saza1	Alignment		96.4	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
13	c1sazA_	Alignment		95.8	17	**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
14	d1hjra_	Alignment		94.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**RuvC resolvase
15	c2aa4B_	Alignment		94.0	19	**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
16	d1zc6a1	Alignment		94.0	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
17	c2iikA_	Alignment		93.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-ketoacyl-coa thiolase, peroxisomal; **PDBTitle:** crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)
18	c2wuaA_	Alignment		93.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetoacetyl coa thiolase; **PDBTitle:** structure of the peroxisomal 3-ketoacyl-coa thiolase from2 sunflower
19	c2qm1D_	Alignment		93.5	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
20	d1iv0a_	Alignment		93.5	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
21	d1ulqa1	Alignment	not modelled	93.4	8	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
22	c3goaA_	Alignment	not modelled	92.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-ketoacyl-coa thiolase; **PDBTitle:** crystal structure of the salmonella typhimurium fada 3-2 ketoacyl-coa thiolase
23	d1m3ka1	Alignment	not modelled	92.8	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
24	d1vhxa_	Alignment	not modelled	92.6	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
25	d1nu0a_	Alignment	not modelled	92.2	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
26	c1ulqD_	Alignment	not modelled	91.8	8	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of tt0182 from thermus thermophilus hb8
27	c3gg4B_	Alignment	not modelled	91.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
28	d2a9va1	Alignment	not modelled	91.7	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
29	c2vu2D	Alignment	not modelled	91.4	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coa acetyltransferase;

29	c2vu2D_	Alignment	not modelled	91.4	13	**PDBTitle:** biosynthetic thiolase from z. ramigera. complex with s-2 pantetheine-11-pivalate.
30	c2zf5O_	Alignment	not modelled	91.2	19	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
31	c3hz6A_	Alignment	not modelled	90.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
32	c3ss6B_	Alignment	not modelled	90.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
33	d1wdkc1	Alignment	not modelled	88.7	12	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
34	d1afwa1	Alignment	not modelled	88.6	10	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
35	c2ibyD_	Alignment	not modelled	88.4	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** crystallographic and kinetic studies of human mitochondrial2 acetoacetyl-coa thiolase (t2): the importance of potassium and3 chloride for its structure and function
36	c1z6rC_	Alignment	not modelled	88.4	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
37	c3ezwD_	Alignment	not modelled	88.3	22	**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
38	c1zc6A_	Alignment	not modelled	88.2	18	**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.
39	c2dpnB_	Alignment	not modelled	88.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
40	c2c7yB_	Alignment	not modelled	88.0	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-ketoacyl-coa thiolase 2; **PDBTitle:** plant enzyme
41	c1glbG_	Alignment	not modelled	86.0	22	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
42	c2d3mA_	Alignment	not modelled	85.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pentaketide chromone synthase; **PDBTitle:** pentaketide chromone synthase complexed with coenzyme a
43	c1keeH_	Alignment	not modelled	85.6	19	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
44	d1ka9h_	Alignment	not modelled	85.2	27	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
45	d1a9xb2	Alignment	not modelled	85.2	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
46	c1ee0A_	Alignment	not modelled	85.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-pyrone synthase; **PDBTitle:** 2-pyrone synthase complexed with acetoacetyl-coa
47	c3eo3B_	Alignment	not modelled	85.0	14	**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
48	c3g25B_	Alignment	not modelled	84.9	23	**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.
49	d2p3ra1	Alignment	not modelled	84.9	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
50	c2ap1A_	Alignment	not modelled	84.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
51	c3flcX_	Alignment	not modelled	84.5	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
52	c3tsuA_	Alignment	not modelled	84.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
53	c2d4wA_	Alignment	not modelled	84.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
54	c2h3gX_	Alignment	not modelled	83.6	15	**PDB header:**biosynthetic protein **Chain:** X: **PDB Molecule:**biosynthetic protein; **PDBTitle:** structure of the type iii pantothenate kinase (coax) from

						bacillus2 anthracis
55	d1g99a1	Alignment	not modelled	82.6	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
56	d3eeqa1	Alignment	not modelled	82.4	10	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
57	c1afwB_	Alignment	not modelled	82.3	14	**PDB header:**thiolase **Chain:** B: **PDB Molecule:**3-ketoacetyl-coa thiolase; **PDBTitle:** the 1.8 angstrom crystal structure of the dimeric2 peroxisomal thiolase of saccharomyces cerevisiae
58	d3bzka5	Alignment	not modelled	81.9	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
59	d1u6ea2	Alignment	not modelled	81.8	9	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
60	c3ifrB_	Alignment	not modelled	81.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
61	d1bi5a1	Alignment	not modelled	80.8	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
62	c2qnxA_	Alignment	not modelled	80.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** crystal structure of the complex between the mycobacterium beta-2 ketoacyl-acyl carrier protein synthase iii (fabh) and 11-3 [(decyloxycarbonyl)dithio]-undecanoic acid
63	c2e2pA_	Alignment	not modelled	80.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
64	c3eeqB_	Alignment	not modelled	79.7	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative cobalamin biosynthesis protein g **PDBTitle:** crystal structure of a putative cobalamin biosynthesis2 protein g homolog from sulfolobus solfataricus
65	d1ee0a2	Alignment	not modelled	79.3	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
66	c2w40C_	Alignment	not modelled	79.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
67	d1ub7a2	Alignment	not modelled	79.0	9	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
68	d2ch5a2	Alignment	not modelled	78.7	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
69	c2p0uB_	Alignment	not modelled	78.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**stilbenecarboxylate synthase 2; **PDBTitle:** crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2)
70	c3djcA_	Alignment	not modelled	77.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type iii pantothenate kinase; **PDBTitle:** crystal structure of pantothenate kinase from legionella pneumophila
71	d1mzja2	Alignment	not modelled	77.5	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
72	c2d3tC_	Alignment	not modelled	77.4	12	**PDB header:**lyase, oxidoreductase/transferase **Chain:** C: **PDB Molecule:**3-ketoacyl-coa thiolase; **PDBTitle:** fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
73	c1u0mA_	Alignment	not modelled	77.3	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative polyketide synthase; **PDBTitle:** crystal structure of 1,3,6,8-tetrahydroxynaphthalene synthase (thns)2 from streptomyces coelicolor a3(2): a bacterial type iii polyketide3 synthase (pks) provides insights into enzymatic control of reactive4 polyketide intermediates
74	d1u0ma2	Alignment	not modelled	77.3	9	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
75	c2cgkB_	Alignment	not modelled	76.9	11	**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.
76	d1u0ua2	Alignment	not modelled	76.1	10	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
77	c3i8bA_	Alignment	not modelled	76.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
78	c2ch5D_	Alignment	not modelled	75.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
79	c3aleB_	Alignment	not modelled	75.1	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**os07g0271500 protein; **PDBTitle:** a type iii polyketide synthase that produces diarylheptanoid

80	d1hnja2	Alignment	not modelled	74.3	10	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
81	c1z05A_	Alignment	not modelled	73.2	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.
82	d1k9vf_	Alignment	not modelled	72.9	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
83	c3euoB_	Alignment	not modelled	71.2	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**type iii pentaketide synthase; **PDBTitle:** crystal structure of a fungal type iii polyketide synthase,2 oras
84	d1mzja1	Alignment	not modelled	70.9	12	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
85	d1bi5a2	Alignment	not modelled	70.8	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
86	c3oitB_	Alignment	not modelled	70.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**os07g0271500 protein; **PDBTitle:** crystal structure of curcuminoid synthase cus from oryza sativa
87	c3fk5A_	Alignment	not modelled	70.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-synthase iii; **PDBTitle:** crystal structure of 3-oxoacyl-(acyl carrier protein)2 synthase iii, fabh (xoo4209) from xanthomonas oryzae pv.3 oryzae kacc10331
88	c3il3A_	Alignment	not modelled	69.1	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** structure of haemophilus influenzae fabh
89	d1z6ra2	Alignment	not modelled	69.1	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
90	c2ad5B_	Alignment	not modelled	69.1	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
91	c3il5D_	Alignment	not modelled	69.0	11	**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
92	c1xetD_	Alignment	not modelled	68.6	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dihydropinosylvin synthase; **PDBTitle:** crystal structure of stilbene synthase from pinus2 sylvestris, complexed with methylmalonyl coa
93	c3nvaB_	Alignment	not modelled	68.5	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
94	c1vcnA_	Alignment	not modelled	67.9	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
95	c3ov3A_	Alignment	not modelled	66.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**curcumin synthase; **PDBTitle:** g211f mutant of curcumin synthase 1 from curcuma longa
96	d1z05a3	Alignment	not modelled	66.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
97	c3e1hA_	Alignment	not modelled	65.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a type iii polyketide synthase2 pksiiinc from neurospora crassa
98	c1tqyD_	Alignment	not modelled	65.1	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**actinorhodin polyketide putative beta-ketoacyl synthase 2; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
99	c1cmlA_	Alignment	not modelled	64.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chalcone synthase); **PDBTitle:** chalcone synthase from alfalfa complexed with malonyl-coa
100	c2gyoB_	Alignment	not modelled	64.5	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** methanethiol-cys 112 inhibition complex of e. coli ketoacyl synthase2 iii (fabh) and coenzyme a
101	c1e5mA_	Alignment	not modelled	64.3	18	**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.
102	d3bexa1	Alignment	not modelled	63.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**CoaX-like
103	d1ub7a1	Alignment	not modelled	62.0	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
104	c2h84A_	Alignment	not modelled	61.9	15	**PDB header:**biosynthetic protein, transferase **Chain:** A: **PDB Molecule:**steely1; **PDBTitle:** crystal structure of the c-terminal type iii polyketide synthase (pks2 iii) domain of 'steely1' (a type i/iii pks hybrid from dictyostelium)

105	d2ewsa1	Alignment	not modelled	61.4	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
106	d1u0ua1	Alignment	not modelled	61.3	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
107	d1afwa2	Alignment	not modelled	61.3	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
108	c3gbtA_	Alignment	not modelled	61.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
109	d1wdkc2	Alignment	not modelled	60.9	22	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
110	c2ebdB_	Alignment	not modelled	60.5	9	**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
111	c3uowB_	Alignment	not modelled	60.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
112	c1mzjB_	Alignment	not modelled	60.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**beta-ketoacylsynthase iii; **PDBTitle:** crystal structure of the priming beta-ketosynthase from the2 r1128 polyketide biosynthetic pathway
113	c1jvnB_	Alignment	not modelled	59.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
114	d1qdlb_	Alignment	not modelled	59.0	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
115	c3s3lB_	Alignment	not modelled	58.6	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cerj; **PDBTitle:** crystal structure of cerj from streptomyces tendae
116	c1zowB_	Alignment	not modelled	58.5	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase iii; **PDBTitle:** crystal structure of s. aureus fabh, beta-ketoacyl carrier protein2 synthase iii
117	d1i1qb_	Alignment	not modelled	57.8	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
118	c2w7tA_	Alignment	not modelled	56.7	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative cytidine triphosphate synthase; **PDBTitle:** trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
119	d2aa4a1	Alignment	not modelled	56.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
120	d2ap1a2	Alignment	not modelled	56.7	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK