Phyre2

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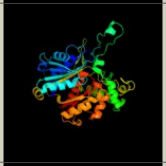
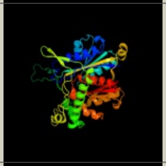
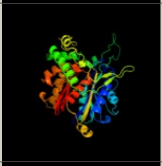
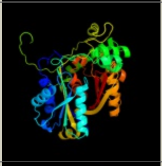
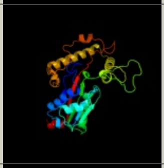
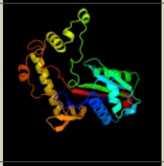
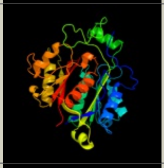
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ss6B_	Alignment		100.0	47	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
2	c2vu2D_	Alignment		100.0	55	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** biosynthetic thiolase from z. ramigera. complex with s-2 pantetheine-11-pivalate.
3	c1ulqD_	Alignment		100.0	47	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of tt0182 from thermus thermophilus hb8
4	c2ibyD_	Alignment		100.0	44	**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
5	c1wl5A_	Alignment		100.0	48	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyl-coenzyme a acetyltransferase 2; **PDBTitle:** human cytosolic acetoacetyl-coa thiolase
6	c2d3tC_	Alignment		100.0	43	**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
7	c1afwB_	Alignment		100.0	37	**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
8	c2wuaA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetoacetyl coa thiolase; **PDBTitle:** structure of the peroxisomal 3-ketoacyl-coa thiolase from2 sunflower
9	c2c7yB_	Alignment		100.0	41	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-ketoacyl-coa thiolase 2; **PDBTitle:** plant enzyme
10	c2iikA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-ketoacyl-coa thiolase, peroxisomal; **PDBTitle:** crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)
11	c3goaA_	Alignment		100.0	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-ketoacyl-coa thiolase; **PDBTitle:** crystal structure of the salmonella typhimurium fada 3-2 ketoacyl-coa thiolase

12	c3svkB_	Alignment		100.0	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of acetyl-coa acetyltransferase from mycobacterium2 avium
13	d1m3ka1	Alignment		100.0	50	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
14	d1ulqa1	Alignment		100.0	42	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
15	d1afwa1	Alignment		100.0	34	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
16	d1wdkc1	Alignment		100.0	38	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
17	c1oxhD_	Alignment		100.0	21	**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
18	c1e5mA_	Alignment		100.0	22	**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.
19	c1j3nB_	Alignment		100.0	24	**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
20	d1m3ka2	Alignment		100.0	63	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
21	c1tqyC_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**beta-ketoacyl synthase/acyl transferase; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
22	c2gqdB_	Alignment	not modelled	100.0	22	**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
23	d1ulqa2	Alignment	not modelled	100.0	58	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
24	c2vz8B_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase; **PDBTitle:** crystal structure of mammalian fatty acid synthase
25	c2gfvA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 2; **PDBTitle:** structure of e. coli fabf (kasii) c163q mutant
26	c3e60A_	Alignment	not modelled	100.0	25	**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
27	c2qo3A_	Alignment	not modelled	100.0	27	**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
28	d1wdkc2	Alignment	not modelled	100.0	53	**Fold:**Thiolase-like **Superfamily:**Thiolase-like

						Family: Thiolase-related
29	c2buiC_	Alignment	not modelled	100.0	22	**PDB header:**synthase **Chain:** C: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase i; **PDBTitle:** e.coli beta-ketoacyl (acyl carrier protein) synthase i in2 complex with octanoic acid, 120k
30	c2ix4B_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** arabidopsis thaliana mitochondrial beta-ketoacyl acp2 synthase hexanoic acid complex
31	d1afwa2	Alignment	not modelled	100.0	45	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
32	c3lrfA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-ketoacyl synthase; **PDBTitle:** crystal structure of beta-ketoacyl synthase from brucella2 melitensis
33	c2iwyB_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** human mitochondrial beta-ketoacyl acp synthase
34	c2gp6B_	Alignment	not modelled	100.0	25	**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)
35	c3o04A_	Alignment	not modelled	100.0	22	**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
36	c2wggA_	Alignment	not modelled	100.0	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
37	c2hg4A_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-deoxyerythronolide b synthase; **PDBTitle:** structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
38	c3fk5A_	Alignment	not modelled	100.0	17	**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
39	c3hhdC_	Alignment	not modelled	100.0	22	**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.
40	c2ebdB_	Alignment	not modelled	100.0	25	**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
41	c1tqyD_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**actinorhodin polyketide putative beta-ketoacyl synthase 2; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
42	c1mzjB_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**beta-ketoacylsynthase iii; **PDBTitle:** crystal structure of the priming beta-ketosynthase from the2 r1128 polyketide biosynthetic pathway
43	c3gwaA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier-protein) synthase iii; **PDBTitle:** 1.6 angstrom crystal structure of 3-oxoacyl-(acyl-carrier-protein)2 synthase iii
44	c2qnxA_	Alignment	not modelled	100.0	23	**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
45	c1ee0A_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-pyrone synthase; **PDBTitle:** 2-pyrone synthase complexed with acetoacetyl-coa
46	c3ledA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-acyl carrier protein synthase iii; **PDBTitle:** crystal structure of 3-oxoacyl-(acyl carrier protein) synthase iii2 from rhodopseudomonas palustris cga009
47	c2p0uB_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**stilbenecarboxylate synthase 2; **PDBTitle:** crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2)
48	c1xetD_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dihydropinosylvin synthase; **PDBTitle:** crystal structure of stilbene synthase from pinus2 sylvestris, complexed with methylmalonyl coa
49	c3il3A_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** structure of haemophilus influenzae fabh
50	c3ov3A_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**curcumin synthase; **PDBTitle:** g211f mutant of curcumin synthase 1 from curcuma longa
51	c1cmlA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chalcone synthase); **PDBTitle:** chalcone synthase from alfalfa complexed with malonyl-coa

52	c1zowB_	Alignment	not modelled	100.0	22	**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
53	c1u0mA_	Alignment	not modelled	100.0	19	**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
54	c2gyoB_	Alignment	not modelled	100.0	22	**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
55	c2vkzC_	Alignment	not modelled	100.0	22	**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
56	c2d3mA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pentaketide chromone synthase; **PDBTitle:** pentaketide chromone synthase complexed with coenzyme a
57	c2uv8C_	Alignment	not modelled	100.0	23	**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
58	c3a5qA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**benzalacetone synthase; **PDBTitle:** benzalacetone synthase from rheum palmatum
59	c3h76A_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pqs biosynthetic enzyme; **PDBTitle:** crystal structure of pqsd, a key enzyme in pseudomonas2 aeruginosa quinolone signal biosynthesis pathway
60	c2uv9B_	Alignment	not modelled	100.0	19	**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
61	d1teda_	Alignment	not modelled	100.0	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
62	c1ub7A_	Alignment	not modelled	100.0	27	**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.
63	c3oitB_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**os07g0271500 protein; **PDBTitle:** crystal structure of curcuminoid synthase cus from oryza sativa
64	c3il5D_	Alignment	not modelled	99.9	24	**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
65	c3tsyA_	Alignment	not modelled	99.9	19	**PDB header:**ligase, transferase **Chain:** A: **PDB Molecule:**fusion protein 4-coumarate--coa ligase 1, resveratrol **PDBTitle:** 4-coumaroyl-coa ligase::stilbene synthase fusion protein
66	c3s3lB_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cerj; **PDBTitle:** crystal structure of cerj from streptomyces tendae
67	c3aleB_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**os07g0271500 protein; **PDBTitle:** a type iii polyketide synthase that produces diarylheptanoid
68	c2x3eA_	Alignment	not modelled	99.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** crystal structure of 3-oxoacyl-(acyl carrier protein)2 synthase iii, fabh from pseudomonas aeruginosa pao1
69	c2h84A_	Alignment	not modelled	99.9	14	**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)
70	c3euoB_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**type iii pentaketide synthase; **PDBTitle:** crystal structure of a fungal type iii polyketide synthase,2 oras
71	c3e1hA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a type iii polyketide synthase2 pksiiinc from neurospora crassa
72	c2f9aA_	Alignment	not modelled	99.9	13	**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
73	c2v4wB_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa synthase, **PDBTitle:** crystal structure of human mitochondrial 3-hydroxy-3-2 methylglutaryl-coenzyme a synthase 2 (hmgcs2)
74	c2p8uB_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa synthase, cytoplasmic; **PDBTitle:** crystal structure of human 3-hydroxy-3-methylglutaryl

						coa synthase i
75	c3lehA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative hydroxymethylglutaryl-coa synthase; **PDBTitle:** the crystal structure of smu.943c from streptococcus mutans ua159
76	c1x9eB_	Alignment	not modelled	99.8	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hmg-coa synthase; **PDBTitle:** crystal structure of hmg-coa synthase from enterococcus2 faecalis
77	c1txtB_	Alignment	not modelled	99.8	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxy-3-methylglutaryl-coa synthase; **PDBTitle:** staphylococcus aureus 3-hydroxy-3-methylglutaryl-coa2 synthase
78	d2vbaa1	Alignment	not modelled	99.8	26	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
79	d1j3na1	Alignment	not modelled	99.8	26	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
80	d1tqyb2	Alignment	not modelled	99.8	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
81	d1tqya2	Alignment	not modelled	99.8	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
82	d2ix4a1	Alignment	not modelled	99.8	26	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
83	d1ox0a1	Alignment	not modelled	99.8	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
84	d1e5ma1	Alignment	not modelled	99.7	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
85	d2gfva1	Alignment	not modelled	99.7	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
86	d1mzja1	Alignment	not modelled	99.6	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
87	d1hnja1	Alignment	not modelled	99.6	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
88	d1u6ea1	Alignment	not modelled	99.6	22	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
89	d1bi5a1	Alignment	not modelled	99.6	17	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
90	d1ub7a1	Alignment	not modelled	99.5	25	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
91	d1ee0a1	Alignment	not modelled	99.5	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
92	d1ox0a2	Alignment	not modelled	99.5	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
93	d1u0ua1	Alignment	not modelled	99.5	17	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
94	d1u0ma1	Alignment	not modelled	99.5	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
95	d1u0va1	Alignment	not modelled	99.4	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
96	d1e5ma2	Alignment	not modelled	99.4	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
97	d1xpma1	Alignment	not modelled	99.4	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
98	d2gfva2	Alignment	not modelled	99.3	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
99	d1j3na2	Alignment	not modelled	99.2	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
100	d1mzja2	Alignment	not modelled	99.2	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
101	d1tqyb1	Alignment	not modelled	99.2	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related

102	d1tqya1	Alignment	not modelled	99.1	22	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
103	d1u6ea2	Alignment	not modelled	99.1	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
104	c3lmaC_	Alignment	not modelled	99.1	19	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**stage v sporulation protein ad (spovad); **PDBTitle:** crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
105	d1hnja2	Alignment	not modelled	99.1	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
106	d1ub7a2	Alignment	not modelled	99.1	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
107	d2ix4a2	Alignment	not modelled	99.1	23	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
108	d1u0ma2	Alignment	not modelled	99.0	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
109	d1u0ua2	Alignment	not modelled	98.8	11	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
110	d2vbaa2	Alignment	not modelled	98.8	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
111	d1ee0a2	Alignment	not modelled	98.7	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
112	d1bi5a2	Alignment	not modelled	98.7	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
113	d1xpma2	Alignment	not modelled	97.1	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
114	c1okjB_	Alignment	not modelled	93.0	16	**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"
115	c2a6aB_	Alignment	not modelled	90.7	19	**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
116	d2a6aa1	Alignment	not modelled	90.2	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
117	c3r6mD_	Alignment	not modelled	88.9	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**yeaz, resuscitation promoting factor; **PDBTitle:** crystal structure of vibrio parahaemolyticus yeaz
118	d1okja1	Alignment	not modelled	87.9	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
119	c2ivoC_	Alignment	not modelled	85.4	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
120	d2w6ka1	Alignment	not modelled	85.4	22	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like