

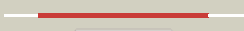






















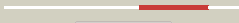



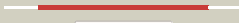

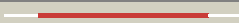



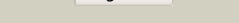


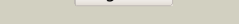
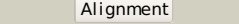
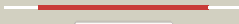


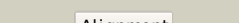



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d3tC_	 Alignment		100.0	64	PDB header: lyase, oxidoreductase/transferase Chain: C: PDB Molecule: 3-ketoacyl-coa thiolase; PDBTitle: fatty acid beta-oxidation multienzyme complex from <i>Pseudomonas fragi</i> , form v
2	c1ulqD_	 Alignment		100.0	48	PDB header: transferase Chain: D: PDB Molecule: putative acetyl-coa acetyltransferase; PDBTitle: crystal structure of tt0182 from <i>Thermus thermophilus</i> hb8
3	c3goaA_	 Alignment		100.0	90	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase; PDBTitle: crystal structure of the <i>Salmonella typhimurium</i> fadA 3-2 ketoacyl-coa thiolase
4	c3ss6B_	 Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of the <i>Bacillus anthracis</i> acetyl-coa2 acetyltransferase
5	c2vu2D_	 Alignment		100.0	43	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: biosynthetic thiolase from <i>Z. ramigera</i> . complex with s-2 pantetheine-11-pivalate.
6	c2wuaA_	 Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: acetoacetyl coa thiolase; PDBTitle: structure of the peroxisomal 3-ketoacyl-coa thiolase from <i>Sunflower</i>
7	c1afwB_	 Alignment		100.0	39	PDB header: thiolase Chain: B: PDB Molecule: 3-ketoacetyl-coa thiolase; PDBTitle: the 1.8 angstrom crystal structure of the dimeric <i>C2</i> peroxisomal thiolase of <i>Saccharomyces cerevisiae</i>
8	c2ibyD_	 Alignment		100.0	33	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystallographic and kinetic studies of human mitochondrial <i>2</i> acetoacetyl-coa thiolase (<i>t2</i>): the importance of potassium and <i>3</i> chloride for its structure and function
9	c2c7yB_	 Alignment		100.0	44	PDB header: transferase Chain: B: PDB Molecule: 3-ketoacyl-coa thiolase 2; PDBTitle: plant enzyme
10	c2iikA_	 Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase, peroxisomal; PDBTitle: crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (<i>acaa1</i>)
11	c1wl5A_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: acetyl-coenzyme a acetyltransferase 2; PDBTitle: human cytosolic acetoacetyl-coa thiolase

12	c3svkB_	Alignment		100.0	37	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of acetyl-coa acetyltransferase from mycobacterium2 avium
13	d1wdkc1	Alignment		100.0	62	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
14	d1m3ka1	Alignment		100.0	38	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	d1ulqa1	Alignment		100.0	41	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
17	d1wdkc2	Alignment		100.0	69	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
18	d1ulqa2	Alignment		100.0	62	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
19	d1m3ka2	Alignment		100.0	52	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
20	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
21	c2gfvA_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: structure of e. coli fabf (kasii) c163q mutant
22	c1oxhD_	Alignment	not modelled	100.0	29	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
23	c1e5mA_	Alignment	not modelled	100.0	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.
24	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
25	c2ix4B_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: arabidopsis thaliana mitochondrial beta-ketoacyl acp2 synthase hexanoic acid complex
26	c2gqdB_	Alignment	not modelled	100.0	26	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
27	c3e60A_	Alignment	not modelled	100.0	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

28	c2gp6B	 Alignment	not modelled	100.0	23	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)
29	c2qo3A	 Alignment	not modelled	100.0	20	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
30	c2buiC	 Alignment	not modelled	100.0	19	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
31	d1afwa2	 Alignment	not modelled	100.0	50	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
32	c2iwyB	 Alignment	not modelled	100.0	28	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: human mitochondrial beta-ketoacyl acp synthase
33	c3lrfA	 Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of beta-ketoacyl synthase from brucella2 melitensis
34	c3o04A	 Alignment	not modelled	100.0	27	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
35	c2vz8B	 Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
36	c2wggA	 Alignment	not modelled	100.0	25	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	c1tqyD	 Alignment	not modelled	100.0	24	PDB header: transferase Chain: D: PDB Molecule: actinorhodin polyketide putative beta-ketoacyl synthase 2; PDBTitle: the actinorhodin ketosynthase/chain length factor
38	c2hg4A	 Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
39	c3hhdC	 Alignment	not modelled	100.0	20	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	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
41	c2uv9B	 Alignment	not modelled	100.0	23	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
42	c2vkzC	 Alignment	not modelled	100.0	23	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
43	c3ledA	 Alignment	not modelled	99.9	12	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
44	c3fk5A	 Alignment	not modelled	99.9	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
45	c2ebdB	 Alignment	not modelled	99.9	26	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
46	c2qnxA	 Alignment	not modelled	99.9	24	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 [(decyloxy carbonyl)diithio]-undecanoic acid
47	c1ee0A	 Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: 2-pyrone synthase; PDBTitle: 2-pyrone synthase complexed with acetoacetyl-coa
48	c3gwaA	 Alignment	not modelled	99.9	16	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
49	c2p0uB	 Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: stilbenecarboxylate synthase 2; PDBTitle: crystal structure of marchanti a polymorpha stilbenecarboxylate2 synthase 2 (stcs2)
50	c1mzjB	 Alignment	not modelled	99.9	19	PDB header: transferase Chain: B: PDB Molecule: beta-ketoacylsynthase iii; PDBTitle: crystal structure of the priming beta-ketosynthase from

					the2 r1128 polyketide biosynthetic pathway
51	c1xetD_	Alignment	not modelled	99.9	15 PDB header: transferase Chain: D: PDB Molecule: dihydropinosylvin synthase; PDBTitle: crystal structure of stilbene synthase from pinus2 sylvestris, complexed with methylmalonyl coa
52	c3ov3A_	Alignment	not modelled	99.9	14 PDB header: transferase Chain: A: PDB Molecule: curcumin synthase; PDBTitle: g211f mutant of curcumin synthase 1 from curcuma longa
53	c1zowB_	Alignment	not modelled	99.9	25 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
54	c3a5qA_	Alignment	not modelled	99.9	13 PDB header: transferase Chain: A: PDB Molecule: benzalacetone synthase; PDBTitle: benzalacetone synthase from rheum palmatum
55	c1cmlA_	Alignment	not modelled	99.9	14 PDB header: transferase Chain: A: PDB Molecule: protein (chalcone synthase); PDBTitle: chalcone synthase from alfalfa complexed with malonyl-coa
56	c2gyoB_	Alignment	not modelled	99.9	17 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
57	c3il3A_	Alignment	not modelled	99.9	14 PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: structure of haemophilus influenzae fabh
58	c2d3mA_	Alignment	not modelled	99.9	14 PDB header: transferase Chain: A: PDB Molecule: pentaketide chromone synthase; PDBTitle: pentaketide chromone synthase complexed with coenzyme a
59	d1teda_	Alignment	not modelled	99.9	20 Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
60	c1u0mA_	Alignment	not modelled	99.9	15 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
61	c3h76A_	Alignment	not modelled	99.9	20 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
62	c3s3lB_	Alignment	not modelled	99.9	24 PDB header: transferase Chain: B: PDB Molecule: cerj; PDBTitle: crystal structure of cerj from streptomyces tendae
63	c1ub7A_	Alignment	not modelled	99.9	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.
64	c3oitB_	Alignment	not modelled	99.9	18 PDB header: transferase Chain: B: PDB Molecule: os07g0271500 protein; PDBTitle: crystal structure of curcuminoid synthase cus from oryza sativa
65	c2x3eA_	Alignment	not modelled	99.9	18 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
66	c3il5D_	Alignment	not modelled	99.9	25 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
67	c3tsyA_	Alignment	not modelled	99.9	18 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
68	c2h84A_	Alignment	not modelled	99.8	18 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)
69	c3aleB_	Alignment	not modelled	99.8	17 PDB header: transferase Chain: B: PDB Molecule: os07g0271500 protein; PDBTitle: a type iii polyketide synthase that produces diarylheptanoid
70	d2vbaa1	Alignment	not modelled	99.8	22 Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
71	d1tqyb2	Alignment	not modelled	99.8	19 Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
72	d1tqya2	Alignment	not modelled	99.8	18 Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
73	d2ix4a1	Alignment	not modelled	99.8	24 Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
74	d1j3na1	Alignment	not modelled	99.8	27 Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related

75	d1ox0a1	Alignment	not modelled	99.8	33	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
76	c3euoB_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: B: PDB Molecule: type iii pentaketide synthase; PDBTitle: crystal structure of a fungal type iii polyketide synthase,2 oras
77	c3e1hA_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a type iii polyketide synthase2 pksiiiinc from neurospora crassa
78	d1e5ma1	Alignment	not modelled	99.7	27	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
79	d2gfva1	Alignment	not modelled	99.7	30	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
80	c2f9aA_	Alignment	not modelled	99.7	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
81	c3leha_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: A: PDB Molecule: putative hydroxymethylglutaryl-coa synthase; PDBTitle: the crystal structure of smu.943c from streptococcus mutans ua159
82	c2v4wB_	Alignment	not modelled	99.6	17	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)
83	c1x9eB_	Alignment	not modelled	99.6	19	PDB header: lyase Chain: B: PDB Molecule: hmg-coa synthase; PDBTitle: crystal structure of hmg-coa synthase from enterococcus2 faecalis
84	c2p8uB_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa synthase, cytoplasmic; PDBTitle: crystal structure of human 3-hydroxy-3-methylglutaryl coa synthase i
85	c1xtB_	Alignment	not modelled	99.6	18	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxy-3-methylglutaryl-coa synthase; PDBTitle: staphylococcus aureus 3-hydroxy-3-methylglutaryl-coa2 synthase
86	d1mzja1	Alignment	not modelled	99.5	15	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
87	d1u6ea1	Alignment	not modelled	99.4	21	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
88	d1hnja1	Alignment	not modelled	99.4	16	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
89	d2gfva2	Alignment	not modelled	99.4	21	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
90	d1bi5a1	Alignment	not modelled	99.4	9	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
91	d1tqya1	Alignment	not modelled	99.3	24	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
92	d1ox0a2	Alignment	not modelled	99.3	19	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
93	d1ee0a1	Alignment	not modelled	99.3	10	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
94	d1e5ma2	Alignment	not modelled	99.3	22	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
95	d1j3na2	Alignment	not modelled	99.3	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
96	d1ub7a1	Alignment	not modelled	99.3	19	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
97	d1u0ma1	Alignment	not modelled	99.3	12	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
98	d1u0ua1	Alignment	not modelled	99.3	15	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
99	d2ix4a2	Alignment	not modelled	99.3	23	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
100	d1u0va1	Alignment	not modelled	99.3	12	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
						PDB header: membrane protein Chain: C: PDB Molecule: stage v sporulation protein ad (spovad);

101	c3lmaC	Alignment	not modelled	99.2	19	PDBTitle: crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
102	d1tqyb1	Alignment	not modelled	99.0	14	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
103	d1xpma1	Alignment	not modelled	98.9	10	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
104	d2vbaa2	Alignment	not modelled	98.9	17	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
105	d1mzja2	Alignment	not modelled	98.6	20	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
106	d1hnja2	Alignment	not modelled	98.5	14	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
107	d1u6ea2	Alignment	not modelled	98.4	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
108	d1u0ma2	Alignment	not modelled	98.3	12	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
109	d1ub7a2	Alignment	not modelled	98.3	21	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
110	d1u0ua2	Alignment	not modelled	98.1	11	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
111	d1bi5a2	Alignment	not modelled	97.9	12	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
112	d1ee0a2	Alignment	not modelled	97.9	14	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
113	d1xpma2	Alignment	not modelled	92.2	15	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
114	c1okjB	Alignment	not modelled	90.9	13	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	d2a6aa1	Alignment	not modelled	90.5	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
116	d1okja1	Alignment	not modelled	89.2	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
117	c2a6aB	Alignment	not modelled	89.0	15	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
118	c3r6mD	Alignment	not modelled	85.9	15	PDB header: hydrolase Chain: D: PDB Molecule: yeaz, resuscitation promoting factor; PDBTitle: crystal structure of vibrio parahaemolyticus yeaz
119	c3enoB	Alignment	not modelled	66.8	15	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
120	c2ivoC	Alignment	not modelled	51.1	20	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein