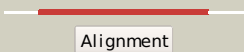

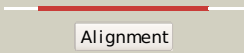






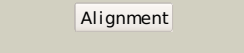




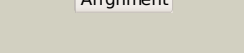

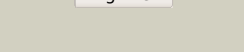



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gyoB_	 Alignment		100.0	100	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: methanethiol-cys 112 inhibition complex of e. coli ketoacyl synthase2 iii (fabh) and coenzyme a
2	c3il3A_	 Alignment		100.0	66	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: structure of haemophilus influenzae fabh
3	c1mjzB_	 Alignment		100.0	38	PDB header: transferase Chain: B: PDB Molecule: beta-ketoacylsynthase iii; PDBTitle: crystal structure of the priming beta-ketosynthase from the2 r1128 polyketide biosynthetic pathway
4	c2qnxA_	 Alignment		100.0	36	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)dithio]-undecanoic acid
5	c1zowB_	 Alignment		100.0	42	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
6	c2ebdB_	 Alignment		100.0	48	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
7	c3h76A_	 Alignment		100.0	40	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
8	c3gwaA_	 Alignment		100.0	32	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
9	c1ub7A_	 Alignment		100.0	41	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.
10	c3il5D_	 Alignment		100.0	40	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
11	c2x3eA_	 Alignment		100.0	40	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

12	c3fk5A_	Alignment		100.0	23	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
13	c1u0mA_	Alignment		100.0	22	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
14	c1ee0A_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: 2-pyrone synthase; PDBTitle: 2-pyrone synthase complexed with acetoacetyl-coa
15	c2f9aA_	Alignment		100.0	20	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
16	c1cmlA_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: protein (chalcone synthase); PDBTitle: chalcone synthase from alfalfa complexed with malonyl-coa
17	c3aleB_	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: os07g0271500 protein; PDBTitle: a type iii polyketide synthase that produces diarylheptanoid
18	c1x9eB_	Alignment		100.0	19	PDB header: lyase Chain: B: PDB Molecule: hmg-coa synthase; PDBTitle: crystal structure of hmg-coa synthase from enterococcus2 faecalis
19	c2h84A_	Alignment		100.0	22	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)
20	c3ledA_	Alignment		100.0	28	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
21	c1xetD_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: D: PDB Molecule: dihydropinosylvin synthase; PDBTitle: crystal structure of stilbene synthase from pinus2 sylvestris, complexed with methylmalonyl coa
22	c3s3lB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: cerj; PDBTitle: crystal structure of cerj from streptomyces tendae
23	c3oitB_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: os07g0271500 protein; PDBTitle: crystal structure of curcuminoid synthase cus from oryza sativa
24	c2v4wB_	Alignment	not modelled	100.0	19	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)
25	d1teda_	Alignment	not modelled	100.0	23	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
26	c3a5qA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: benzalacetone synthase; PDBTitle: benzalacetone synthase from rheum palmatum
27	c1xtB_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxy-3-methylglutaryl-coa synthase; PDBTitle: staphylococcus aureus 3-hydroxy-3-methylglutaryl-coa2 synthase
28	c2p0uB_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: B: PDB Molecule: stilbenecarboxylate synthase 2; PDBTitle: crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2)
						PDB header: transferase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa synthase,

29	c2p8uB_	Alignment	not modelled	100.0	17	cytoplasmic; PDBTitle: crystal structure of human 3-hydroxy-3-methylglutaryl coa synthase i
30	c3ov3A_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: curcumin synthase; PDBTitle: g211f mutant of curcumin synthase 1 from curcuma longa
31	c3e1hA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a type iii polyketide synthase2 pksiiiinc from neurospora crassa
32	c3euoB_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: type iii pentaketide synthase; PDBTitle: crystal structure of a fungal type iii polyketide synthase,2 oras
33	c2d3mA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: pentaketide chromone synthase; PDBTitle: pentaketide chromone synthase complexed with coenzyme a
34	c3lehA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: putative hydroxymethyl glutaryl-coa synthase; PDBTitle: the crystal structure of smu.943c from streptococcus mutans ua159
35	c3tsyA_	Alignment	not modelled	100.0	21	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
36	d1hnja1	Alignment	not modelled	100.0	100	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
37	d1mzja1	Alignment	not modelled	100.0	42	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
38	d1u6ea1	Alignment	not modelled	100.0	40	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
39	d1ub7a1	Alignment	not modelled	100.0	40	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
40	d1xpma1	Alignment	not modelled	100.0	27	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
41	d1bi5a1	Alignment	not modelled	100.0	25	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
42	d1ee0a1	Alignment	not modelled	100.0	27	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
43	d1u0ma1	Alignment	not modelled	100.0	24	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
44	d1u0ua1	Alignment	not modelled	100.0	23	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
45	c2vu2D_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: biosynthetic thiolase from z. ramigera. complex with s-2 pantetheine-11-pivalate.
46	c2iikA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase, peroxisomal; PDBTitle: crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acca1)
47	d1u0va1	Alignment	not modelled	100.0	26	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
48	d1hnja2	Alignment	not modelled	100.0	100	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
49	c3ss6B_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
50	d1ub7a2	Alignment	not modelled	99.9	42	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
51	c2c7yB_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: B: PDB Molecule: 3-ketoacyl-coa thiolase 2; PDBTitle: plant enzyme
52	c1wl5A_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: acetyl-coenzyme a acetyltransferase 2; PDBTitle: human cytosolic acetoacetyl-coa thiolase
53	c2ibyD_	Alignment	not modelled	99.9	19	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
54	c2vz8B_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
						PDB header: transferase Chain: A: PDB Molecule: ervaii erythromycin polyketide synthase

55	c2qo3A_	Alignment	not modelled	99.9	22	modules 3 and 4; PDBTitle: crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerythronolide b synthase
56	c1ulqD_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: D: PDB Molecule: putative acetyl-coa acetyltransferase; PDBTitle: crystal structure of tt0182 from thermus thermophilus hb8
57	c3goaA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase; PDBTitle: crystal structure of the salmonella typhimurium fada 3-2 ketoacyl-coa thiolase
58	c2wuaA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: acetoacetyl coa thiolase; PDBTitle: structure of the peroxisomal 3-ketoacyl-coa thiolase from2 sunflower
59	d1mzja2	Alignment	not modelled	99.9	33	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
60	c1afwB_	Alignment	not modelled	99.9	18	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
61	d1u6ea2	Alignment	not modelled	99.9	31	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
62	c2hg4A_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debbs.
63	c3hhdC_	Alignment	not modelled	99.9	18	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.
64	c1tqyC_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: C: PDB Molecule: beta-ketoacyl synthase/acyl transferase; PDBTitle: the actinorhodin ketosynthase/chain length factor
65	c1j3nB_	Alignment	not modelled	99.9	17	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
66	c3e60A_	Alignment	not modelled	99.9	18	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
67	c2gqdB_	Alignment	not modelled	99.9	16	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
68	c1oxhD_	Alignment	not modelled	99.9	17	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
69	c2ix4B_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: arabidopsis thaliana mitochondrial beta-ketoacyl acp2 synthase hexanoic acid complex
70	d1u0ma2	Alignment	not modelled	99.9	20	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
71	c3o04A_	Alignment	not modelled	99.9	16	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
72	c2d3tC_	Alignment	not modelled	99.9	19	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	c1e5mA_	Alignment	not modelled	99.9	15	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.
74	c2gfvA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: structure of e. coli fabf (kasii) c163q mutant
75	c2iwyB_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: human mitochondrial beta-ketoacyl acp synthase
76	d1u0ua2	Alignment	not modelled	99.9	15	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
77	c2gp6B_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PDBTitle: x-ray crystal structure of mycobacterium tuberculosis beta-2 ketoacyl acyl carrier protein synthase ii (mtkasb)
78	c3lrfA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: beta-ketoacyl synthase; PDBTitle: crystal structure of beta-ketoacyl synthase from brucella2 melitensis
79	c1tqvD_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: D: PDB Molecule: actinorhodin polyketide putative beta-

79	c1qyb_	Alignment	not modelled	99.9	17	ketoacyl synthase 2; PDBTitle: the actinorhodin ketosynthase/chain length factor
80	c2wggA_	Alignment	not modelled	99.9	16	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
81	d1bi5a2	Alignment	not modelled	99.9	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
82	c2buiC_	Alignment	not modelled	99.9	16	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
83	d1ee0a2	Alignment	not modelled	99.9	17	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
84	c3svkB_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of acetyl-coa acetyltransferase from mycobacterium2 avium
85	c2uv9B_	Alignment	not modelled	99.8	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
86	c2uv8C_	Alignment	not modelled	99.8	18	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
87	d1xpm2	Alignment	not modelled	99.8	13	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
88	c2vkzC_	Alignment	not modelled	99.7	18	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
89	d1m3ka1	Alignment	not modelled	99.7	14	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
90	c3lmaC_	Alignment	not modelled	99.6	16	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.
91	d1ulqa1	Alignment	not modelled	99.6	16	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
92	d1afwa1	Alignment	not modelled	99.5	12	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
93	d1wdkc1	Alignment	not modelled	99.4	17	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
94	d2vbaa1	Alignment	not modelled	99.4	15	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
95	d2ix4a1	Alignment	not modelled	99.3	14	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
96	d1ox0a1	Alignment	not modelled	99.3	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
97	d1j3na1	Alignment	not modelled	99.2	20	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
98	d1e5ma1	Alignment	not modelled	99.2	20	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
99	d2gfva1	Alignment	not modelled	99.1	17	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
100	d1tqya1	Alignment	not modelled	98.9	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
101	d1tqyb2	Alignment	not modelled	98.9	16	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
102	d1tqyb1	Alignment	not modelled	98.9	23	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
103	d1tqya2	Alignment	not modelled	98.8	16	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
104	d1afwa2	Alignment	not modelled	98.6	16	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related

105	d1m3ka2	Alignment	not modelled	98.5	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
106	d1ox0a2	Alignment	not modelled	98.4	14	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
107	d1ulqa2	Alignment	not modelled	98.3	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
108	d1wdkc2	Alignment	not modelled	98.3	12	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
109	d1e5ma2	Alignment	not modelled	98.2	15	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
110	d1j3na2	Alignment	not modelled	98.2	12	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
111	d2gfva2	Alignment	not modelled	98.2	19	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
112	d2ix4a2	Alignment	not modelled	97.8	16	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
113	d2vbaa2	Alignment	not modelled	97.0	15	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
114	d1xhoa_	Alignment	not modelled	77.2	13	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
115	c1xhoB_	Alignment	not modelled	77.2	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: chorismate mutase; PDBTitle: chorismate mutase from clostridium thermocellum cth-682
116	c2a6aB_	Alignment	not modelled	74.6	5	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
117	d2a6aa1	Alignment	not modelled	73.1	5	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
118	d1okja1	Alignment	not modelled	72.5	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
119	d1dbfa_	Alignment	not modelled	71.3	12	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
120	c2r2dC_	Alignment	not modelled	70.8	19	PDB header: hydrolase Chain: C: PDB Molecule: zn-dependent hydrolases; PDBTitle: structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens