Phyre2

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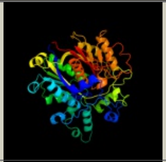
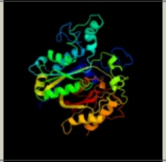
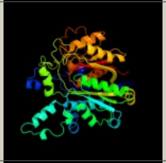
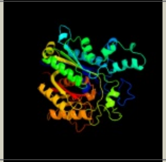
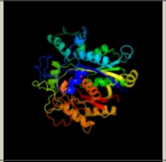
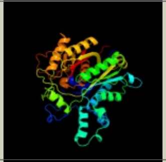
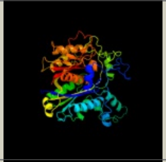
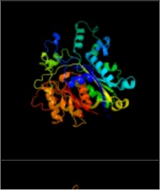
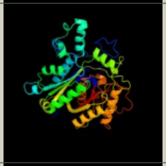
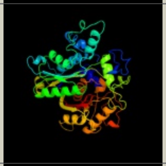
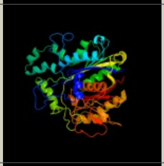
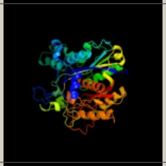
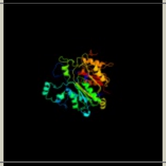
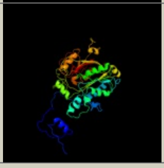
Description	P0A953
Date	Thu Jan 5 11:09:24 GMT 2012
Unique Job ID	15d52f907c3ad5cc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2buiC_	Alignment		100.0	100	**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
2	c2vz8B_	Alignment		100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase; **PDBTitle:** crystal structure of mammalian fatty acid synthase
3	c3lrfA_	Alignment		100.0	61	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-ketoacyl synthase; **PDBTitle:** crystal structure of beta-ketoacyl synthase from brucella2 melitensis
4	c2gqdB_	Alignment		100.0	39	**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
5	c1e5mA_	Alignment		100.0	35	**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.
6	c1tqyC_	Alignment		100.0	31	**PDB header:**transferase **Chain:** C: **PDB Molecule:**beta-ketoacyl synthase/acyl transferase; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
7	c1oxhD_	Alignment		100.0	36	**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
8	c3o04A_	Alignment		100.0	40	**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
9	c3e60A_	Alignment		100.0	39	**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
10	c2gp6B_	Alignment		100.0	32	**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)
11	c2iwyB_	Alignment		100.0	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** human mitochondrial beta-ketoacyl acp synthase

12	c1j3nB_	Alignment		100.0	38	**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
13	c2qo3A_	Alignment		100.0	23	**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
14	c2gfvA_	Alignment		100.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 2; **PDBTitle:** structure of e. coli fabf (kasii) c163q mutant
15	c1tqyD_	Alignment		100.0	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**actinorhodin polyketide putative beta-ketoacyl synthase 2; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
16	c3hhdC_	Alignment		100.0	24	**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.
17	c2ix4B_	Alignment		100.0	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** arabidopsis thaliana mitochondrial beta-ketoacyl acp2 synthase hexanoic acid complex
18	c2wggA_	Alignment		100.0	32	**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
19	c2hg4A_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-deoxyerythronolide b synthase; **PDBTitle:** structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
20	c2uv9B_	Alignment		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
21	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
22	c2uv8C_	Alignment	not modelled	100.0	24	**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
23	d2vbaa1	Alignment	not modelled	100.0	100	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
24	d1j3na1	Alignment	not modelled	100.0	36	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
25	d1e5ma1	Alignment	not modelled	100.0	34	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
26	d1ox0a1	Alignment	not modelled	100.0	35	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
27	d2ix4a1	Alignment	not modelled	100.0	33	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
28	d2gfva1	Alignment	not modelled	100.0	35	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
29	d1tqya2	Alignment	not modelled	100.0	39	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related

30	d1tqyb2	Alignment	not modelled	100.0	26	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
31	d2vbaa2	Alignment	not modelled	100.0	100	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
32	d1tqya1	Alignment	not modelled	100.0	24	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
33	d1e5ma2	Alignment	not modelled	100.0	38	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
34	d1ox0a2	Alignment	not modelled	100.0	37	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
35	d1tqyb1	Alignment	not modelled	100.0	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
36	d2gfva2	Alignment	not modelled	100.0	42	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
37	d1j3na2	Alignment	not modelled	100.0	44	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
38	d2ix4a2	Alignment	not modelled	100.0	44	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
39	c2ibyD_	Alignment	not modelled	100.0	21	**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
40	c3ledA_	Alignment	not modelled	100.0	14	**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
41	c2wuaA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetoacetyl coa thiolase; **PDBTitle:** structure of the peroxisomal 3-ketoacyl-coa thiolase from2 sunflower
42	c2c7yB_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-ketoacyl-coa thiolase 2; **PDBTitle:** plant enzyme
43	c2d3tC_	Alignment	not modelled	100.0	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
44	c3ss6B_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
45	c1afwB_	Alignment	not modelled	100.0	17	**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
46	c2vu2D_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** biosynthetic thiolase from z. ramigera. complex with s-2 pantetheine-11-pivalate.
47	c2iikA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-ketoacyl-coa thiolase, peroxisomal; **PDBTitle:** crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)
48	c3goaA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-ketoacyl-coa thiolase; **PDBTitle:** crystal structure of the salmonella typhimurium fada 3-2 ketoacyl-coa thiolase
49	c2d3mA_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pentaketide chromone synthase; **PDBTitle:** pentaketide chromone synthase complexed with coenzyme a
50	c1ulqD_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of tt0182 from thermus thermophilus hb8
51	c1wl5A_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyl-coenzyme a acetyltransferase 2; **PDBTitle:** human cytosolic acetoacetyl-coa thiolase
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	c3fk5A_	Alignment	not modelled	99.9	15	**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
54	c2p0uB_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**stilbenecarboxylate synthase 2; **PDBTitle:** crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2)
55	c1zowB_	Alignment	not modelled	99.9	19	**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
56	d1teda_	Alignment	not modelled	99.9	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
57	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
58	c3a5qA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**benzalacetone synthase; **PDBTitle:** benzalacetone synthase from rheum palmatum
59	c2ebdB_	Alignment	not modelled	99.9	19	**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
60	c1ee0A_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-pyrone synthase; **PDBTitle:** 2-pyrone synthase complexed with acetoacetyl-coa
61	c3svkB_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of acetyl-coa acetyltransferase from mycobacterium2 avium
62	c2qnxA_	Alignment	not modelled	99.9	16	**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	c2x3eA_	Alignment	not modelled	99.9	16	**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
64	c3il3A_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** structure of haemophilus influenzae fabh
65	c2gyoB_	Alignment	not modelled	99.9	16	**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
66	c3gwaA_	Alignment	not modelled	99.9	14	**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
67	c3oitB_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**os07g0271500 protein; **PDBTitle:** crystal structure of curcuminoid synthase cus from oryza sativa
68	c1mzjB_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**beta-ketoacylsynthase iii; **PDBTitle:** crystal structure of the priming beta-ketosynthase from the2 r1128 polyketide biosynthetic pathway
69	c3h76A_	Alignment	not modelled	99.8	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
70	c1cmlA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chalcone synthase); **PDBTitle:** chalcone synthase from alfalfa complexed with malonyl-coa
71	c1ub7A_	Alignment	not modelled	99.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] synthase; **PDBTitle:** the crystal analysis of beta-keroacyl-[acyl carrier protein] synthase2 iii (fabh)from thermus thermophilus.
72	c3aleB_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**os07g0271500 protein; **PDBTitle:** a type iii polyketide synthase that produces diarylheptanoid
73	c3s3lB_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cerj; **PDBTitle:** crystal structure of cerj from streptomyces tendae
74	c3il5D_	Alignment	not modelled	99.8	16	**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
75	c2h84A_	Alignment	not modelled	99.7	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)
76	c1u0mA_	Alignment	not modelled	99.6	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
77	d1mzja1	Alignment	not modelled	99.6	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
78	d1u6ea1	Alignment	not modelled	99.6	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
						Fold: Thiolase-like

79	d1u0ua1	Alignment	not modelled	99.5	16	**Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
80	c3e1hA_	Alignment	not modelled	99.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a type iii polyketide synthase2 pksiiinc from neurospora crassa
81	c3euoB_	Alignment	not modelled	99.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**type iii pentaketide synthase; **PDBTitle:** crystal structure of a fungal type iii polyketide synthase,2 oras
82	c2f9aA_	Alignment	not modelled	99.4	16	**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
83	d1ee0a1	Alignment	not modelled	99.4	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
84	d1wdkc1	Alignment	not modelled	99.4	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
85	d1u0va1	Alignment	not modelled	99.4	12	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
86	c2p8uB_	Alignment	not modelled	99.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa synthase, cytoplasmic; **PDBTitle:** crystal structure of human 3-hydroxy-3-methylglutaryl coa synthase i
87	c2v4wB_	Alignment	not modelled	99.4	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)
88	d1afwa2	Alignment	not modelled	99.3	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
89	d1hnja1	Alignment	not modelled	99.3	17	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
90	c1x9eB_	Alignment	not modelled	99.3	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hmg-coa synthase; **PDBTitle:** crystal structure of hmg-coa synthase from enterococcus2 faecalis
91	c3tsyA_	Alignment	not modelled	99.2	15	**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
92	c3lehA_	Alignment	not modelled	99.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative hydroxymethylglutaryl-coa synthase; **PDBTitle:** the crystal structure of smu.943c from streptococcus mutans ua159
93	d1ub7a1	Alignment	not modelled	99.2	23	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
94	d1ulqa1	Alignment	not modelled	99.1	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
95	c1txtB_	Alignment	not modelled	99.1	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxy-3-methylglutaryl-coa synthase; **PDBTitle:** staphylococcus aureus 3-hydroxy-3-methylglutaryl-coa2 synthase
96	d1m3ka1	Alignment	not modelled	99.1	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
97	d1bi5a1	Alignment	not modelled	99.1	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
98	d1wdkc2	Alignment	not modelled	98.8	17	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
99	d1u0ma1	Alignment	not modelled	98.7	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
100	d1xpma1	Alignment	not modelled	98.7	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
101	d1afwa1	Alignment	not modelled	98.7	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
102	d1ulqa2	Alignment	not modelled	98.6	15	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
103	d1m3ka2	Alignment	not modelled	98.6	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
104	d1mzja2	Alignment	not modelled	96.3	21	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
						Fold: Thiolase-like

105	d1hnja2	Alignment	not modelled	96.0	21	**Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
106	d1ub7a2	Alignment	not modelled	95.5	22	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
107	d1u0ma2	Alignment	not modelled	95.4	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
108	d1u6ea2	Alignment	not modelled	95.2	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
109	c3lmaC_	Alignment	not modelled	92.6	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.
110	d1u0ua2	Alignment	not modelled	74.3	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
111	d1ee0a2	Alignment	not modelled	71.9	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
112	d1a2za_	Alignment	not modelled	63.6	27	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
113	d1bi5a2	Alignment	not modelled	40.6	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
114	c3gpiA_	Alignment	not modelled	35.0	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
115	c3rfxB_	Alignment	not modelled	32.1	63	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uronate dehydrogenase; **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
116	c3dhnA_	Alignment	not modelled	31.2	38	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
117	c3kd9B_	Alignment	not modelled	29.0	50	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
118	d1bxka_	Alignment	not modelled	27.5	50	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
119	d1oc2a_	Alignment	not modelled	27.1	38	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
120	c2q1wC_	Alignment	not modelled	26.7	63	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+