Phyre^2

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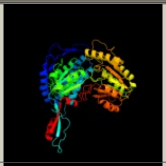
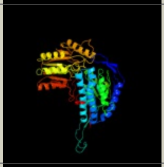
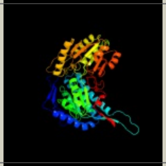
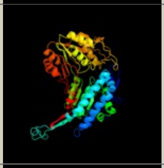
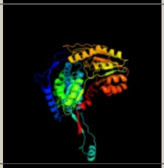
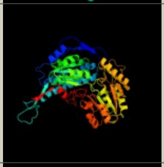
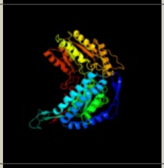
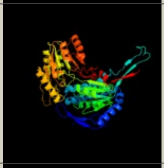
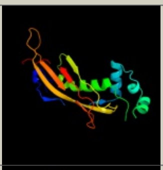
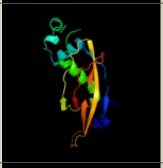
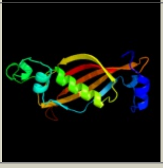
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vroB_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
2	d1uzba_	Alignment		100.0	21	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
3	d1a4sa_	Alignment		100.0	24	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
4	c3ed6B_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
5	c3qanB_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-pyrroline-5-carboxylate dehydrogenase 1; **PDBTitle:** crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
6	c2jg7G_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**antiquitin; **PDBTitle:** crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
7	c3rh9A_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nad(p)(+)); **PDBTitle:** the crystal structure of oxidoreductase from marinobacter aquaeolei
8	d1bxsa_	Alignment		100.0	22	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
9	c3iwkB_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
10	c2d4eB_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-carboxymethyl-2-hydroxymuconate semialdehyde **PDBTitle:** crystal structure of the hpcc from thermus thermophilus hb8
11	d1o9ja_	Alignment		100.0	22	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like

12	c2o2qA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formyltetrahydrofolate dehydrogenase; **PDBTitle:** crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp
13	c2ve5H_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
14	c1t90B_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable methylmalonate-semialdehyde **PDBTitle:** crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
15	d1euha_	Alignment		100.0	21	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
16	c3i44A_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
17	d1o04a_	Alignment		100.0	21	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
18	d1ky8a_	Alignment		100.0	21	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
19	d1wnda_	Alignment		100.0	23	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
20	c3ifgH_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of succinate-semialdehyde dehydrogenase from2 burkholderia pseudomallei, part 1 of 2
21	c3hazA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
22	d1ag8a_	Alignment	not modelled	100.0	22	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
23	c2w8qA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase, **PDBTitle:** the crystal structure of human ssadh in complex with ssa.
24	c3r31A_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
25	c3b4wA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
26	c3k2wD_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
27	c3ek1C_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
28	c3prlD_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadp-dependent glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of nadp-dependent glyceraldehyde-3-phosphate2 dehydrogenase from bacillus halodurans c-125

29	c3ju8B_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinylglutamic semialdehyde dehydrogenase; **PDBTitle:** crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
30	c3jz4C_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
31	c2hg2A_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
32	d1bi9a_	Alignment	not modelled	100.0	22	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
33	c3r64A_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad dependent benzaldehyde dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
34	c3efvC_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative succinate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of a putative succinate-semialdehyde dehydrogenase2 from salmonella typhimurium lt2 with bound nad
35	c3rosA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
36	c3v4cB_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
37	c3pqaA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactaldehyde dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
38	d1ez0a_	Alignment	not modelled	100.0	20	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
39	d1ad3a_	Alignment	not modelled	100.0	19	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
40	c3lnsD_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**benzaldehyde dehydrogenase; **PDBTitle:** benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
41	c3k9dD_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
42	d1o20a_	Alignment	not modelled	100.0	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
43	c3my7A_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase/acetaldehyde dehydrogenase; **PDBTitle:** the crystal structure of the acdh domain of an alcohol dehydrogenase2 from vibrio parahaemolyticus to 2.25a
44	d1vlua_	Alignment	not modelled	100.0	20	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
45	c2h5gA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**delta 1-pyrroline-5-carboxylate synthetase; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate synthetase
46	c1vluB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gamma-glutamyl phosphate reductase; **PDBTitle:** crystal structure of gamma-glutamyl phosphate reductase (yor323c) from2 saccharomyces cerevisiae at 2.40 a resolution
47	c2bi0A_	Alignment		100.0	18	**PDB header:**hypothetical protein **Chain:** A: **PDB Molecule:**hypothetical protein rv0216; **PDBTitle:** rv0216, a conserved hypothetical protein from mycobacterium2 tuberculosis that is essential for bacterial survival3 during infection, has a double hotdogfold
48	d2bi0a1	Alignment		100.0	19	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
49	d2bi0a2	Alignment		100.0	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
50	c3exzA_	Alignment	not modelled	100.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**maoc-like dehydratase; **PDBTitle:** crystal structure of the maoc-like dehydratase from

						rhodospirillum2 rubrum. northeast structural genomics consortium target rrr103a.
51	d1q6wa_	Alignment	not modelled	100.0	37	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
52	d2b3na1	Alignment	not modelled	100.0	26	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
53	d1iq6a_	Alignment	not modelled	99.9	25	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
54	d2c2ia1	Alignment	not modelled	99.9	24	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
55	c3ir3B_	Alignment	not modelled	99.9	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-thioester dehydratase 2; **PDBTitle:** crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
56	d1pn2a2	Alignment	not modelled	99.8	23	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
57	d1s9ca1	Alignment	not modelled	99.8	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
58	c3kh8B_	Alignment	not modelled	99.6	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**maoc-like dehydratase; **PDBTitle:** crystal structure of maoc-like dehydratase from phytophthora capsici
59	c1pn2D_	Alignment	not modelled	99.6	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**peroxisomal hydratase-dehydrogenase-epimerase; **PDBTitle:** crystal structure analysis of the selenomethionine labelled2 2-enoyl-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2
60	c1s9cK_	Alignment	not modelled	99.6	21	**PDB header:**lyase **Chain:** K: **PDB Molecule:**peroxisomal multifunctional enzyme type 2; **PDBTitle:** crystal structure analysis of the 2-enoyl-coa hydratase 22 domain of human peroxisomal multifunctional enzyme type 2
61	c2cdhT_	Alignment	not modelled	99.6	21	**PDB header:**transferase **Chain:** T: **PDB Molecule:**dehydratase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
62	c3khpB_	Alignment	not modelled	99.5	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maoc family protein; **PDBTitle:** crystal structure of a possible dehydrogenase from2 mycobacterium tuberculosis at 2.3a resolution
63	c3omlA_	Alignment	not modelled	99.4	24	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**peroxisomal multifunctional enzyme type 2, cg3415; **PDBTitle:** structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster
64	c2vkzH_	Alignment	not modelled	99.0	17	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
65	c2uvaI_	Alignment	not modelled	99.0	19	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
66	c2f3xA_	Alignment	not modelled	98.2	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**transcription factor fapr; **PDBTitle:** crystal structure of fapr (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
67	d1s9ca2	Alignment	not modelled	97.8	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
68	d1z6ba1	Alignment	not modelled	97.7	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
69	d1pn2a1	Alignment	not modelled	97.5	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
70	c3d6xA_	Alignment	not modelled	97.5	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; **PDBTitle:** crystal structure of campylobacter jejuni fabz
71	d1mkaa_	Alignment	not modelled	97.4	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**beta-Hydroxydecanol thiol ester dehydrase
72	c3gekA_	Alignment	not modelled	97.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioesterase yhda; **PDBTitle:** crystal structure of putative thioesterase yhda from lactococcus2 lactis. northeast structural genomics consortium target kr113
73	c3qooA_	Alignment	not modelled	97.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of hot-dog-like taci_0573 protein from2 thermanaerovibrio acidaminovorans
74	d1u1za_	Alignment	not modelled	97.3	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like

75	d1ixla_	Alignment	not modelled	97.3	27	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
76	c2glvA_	Alignment	not modelled	97.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-acyl carrier protein **PDBTitle:** crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
77	d2cy9a1	Alignment	not modelled	97.0	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
78	c3lwgB_	Alignment	not modelled	97.0	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hp0420 homologue; **PDBTitle:** crystal structure of hp0420-homologue c46a from helicobacter2 felis
79	c2cf2L_	Alignment	not modelled	96.9	19	**PDB header:**transferase **Chain:** L: **PDB Molecule:**fatty acid synthase, dh domain; **PDBTitle:** architecture of mammalian fatty acid synthase
80	c3bnvD_	Alignment	not modelled	96.9	14	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cj0977; **PDBTitle:** crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
81	c3esiD_	Alignment	not modelled	96.8	15	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 erwinia carotovora subsp. atroseptica. northeast3 structural genomics target ewr179
82	d2h4ua1	Alignment	not modelled	96.8	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
83	c3lbeA_	Alignment	not modelled	96.8	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.793; **PDBTitle:** the crystal structure of smu.793 from streptococcus mutans ua159 bound2 to acetyl coa
84	d2cwza1	Alignment	not modelled	96.7	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**TTHA0967-like
85	d2f41a1	Alignment	not modelled	96.6	21	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
86	d2f0xa1	Alignment	not modelled	96.6	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
87	d1ylia1	Alignment	not modelled	96.5	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
88	c2gvhC_	Alignment	not modelled	96.4	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**agr_l_2016p; **PDBTitle:** crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
89	c2eisA_	Alignment	not modelled	96.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein tthb207; **PDBTitle:** x-ray structure of acyl-coa hydrolase-like protein, tt1379, from2 thermus thermophilus hb8
90	d1q4ua_	Alignment	not modelled	96.3	17	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
91	d2fs2a1	Alignment	not modelled	96.2	25	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
92	c2qwzB_	Alignment	not modelled	96.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phenylacetic acid degradation-related protein; **PDBTitle:** crystal structure of a putative thioesterase (tm1040_1390) from2 silicibacter sp. tm1040 at 2.15 a resolution
93	d1y7ua1	Alignment	not modelled	96.0	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
94	d1vh9a_	Alignment	not modelled	96.0	18	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
95	c2pimA_	Alignment	not modelled	95.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phenylacetic acid degradation-related protein; **PDBTitle:** crystal structure of a putative thioesterase, phenylacetic acid2 degradation-related protein (reut_b4779) from ralstonia eutropha3 jmp134 at 2.20 a resolution
96	c3nwzD_	Alignment	not modelled	95.9	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**bh2602 protein; **PDBTitle:** crystal structure of bh2602 protein from bacillus halodurans with coa,2 northeast structural genomics consortium target bhr199
97	d1vh5a_	Alignment	not modelled	95.9	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
98	d2gvha1	Alignment	not modelled	95.9	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
99	d1wlua1	Alignment	not modelled	95.9	22	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
						Fold: Thioesterase/thiol ester dehydrase-isomerase

100	d2gvha2	Alignment	not modelled	95.8	11	**Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
101	d1k75a_	Alignment	not modelled	95.7	13	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
102	c3f1tB_	Alignment	not modelled	95.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein q9i3c8_pseae; **PDBTitle:** crystal structure of the q9i3c8_pseae protein from pseudomonas2 aeruginosa. northeast structural genomics consortium target par319a.
103	c3b7kA_	Alignment	not modelled	95.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 12; **PDBTitle:** human acyl-coenzyme a thioesterase 12
104	c2v1oF_	Alignment	not modelled	95.6	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cytosolic acyl coenzyme a thioester hydrolase; **PDBTitle:** crystal structure of n-terminal domain of acyl-coa2 thioesterase 7
105	d1s5ua_	Alignment	not modelled	95.6	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
106	c3s4kA_	Alignment	not modelled	95.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase rv1847/mt1895; **PDBTitle:** structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
107	d2ov9a1	Alignment	not modelled	95.5	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
108	c2qq2C_	Alignment	not modelled	95.5	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosolic acyl coenzyme a thioester hydrolase; **PDBTitle:** crystal structure of c-terminal domain of human acyl-coa thioesterase2 7
109	c3hduB_	Alignment	not modelled	95.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative thioesterase; **PDBTitle:** crystal structure of a putative thioesterase (syn_01977) from2 syntrophus aciditrophicus sb at 2.50 a resolution
110	d1zkia1	Alignment	not modelled	95.2	10	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
111	d1vpma_	Alignment	not modelled	95.2	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
112	c3ck1B_	Alignment	not modelled	95.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative thioesterase; **PDBTitle:** crystal structure of a putative thioesterase (reut_a2179) from2 ralstonia eutropha jmp134 at 1.74 a resolution
113	c3e8pA_	Alignment	not modelled	95.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the protein q8e9m7 from shewanella2 oneidensis related to thioesterase superfamily. northeast3 structural genomics consortium target sor246.
114	d2hboa1	Alignment	not modelled	94.9	9	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
115	c3e29C_	Alignment	not modelled	94.9	14	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein q7we92_borbr; **PDBTitle:** x-ray structure of the protein q7we92_borbr from thioesterase2 superfamily. northeast structural genomics consortium target bor214a.
116	c3kuvB_	Alignment	not modelled	94.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fluoroacetyl coenzyme a thioesterase; **PDBTitle:** structural basis of the activity and substrate specificity of the2 fluoroacetyl-coa thioesterase flk - t42s mutant in complex with3 acetate.
117	d2fuja1	Alignment	not modelled	94.7	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
118	c3hm0C_	Alignment	not modelled	94.6	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable thioesterase; **PDBTitle:** crystal structure of probable thioesterase from bartonella2 henselae
119	c2prxB_	Alignment	not modelled	94.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**thioesterase superfamily protein; **PDBTitle:** crystal structure of thioesterase superfamily protein (zp_00837258.1)2 from shewanella loihica pv-4 at 1.65 a resolution
120	d1sc0a_	Alignment	not modelled	94.4	16	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like