



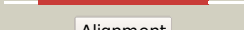

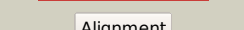
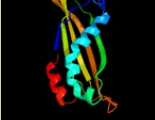
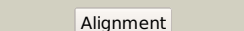




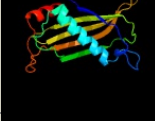
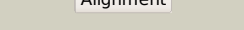

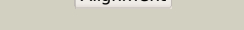

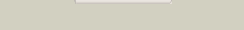

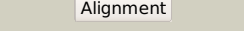









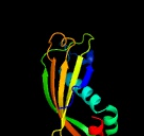


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2475c_(-) _2776985_2777401
Date	Wed Aug 7 12:50:10 BST 2019
Unique Job ID	af87e21ac8dee8f7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2nuja1</a>	 Alignment		100.0	20	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
2	<a href="#">d2oafa1</a>	 Alignment		100.0	17	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
3	<a href="#">c4i4jE_</a>	 Alignment		100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> acp-polyene thioesterase; <b>PDBTitle:</b> the structure of sgce10, the acp-polyene thioesterase involved in c-2 1027 biosynthesis
4	<a href="#">d2oiwa1</a>	 Alignment		100.0	19	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
5	<a href="#">d2o5ua1</a>	 Alignment		100.0	17	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
6	<a href="#">c5eo4A_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> structural and biochemical characterization of the hypothetical2 protein sav2348 from staphylococcus aureus.
7	<a href="#">c3ck1B_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of a putative thioesterase (reut_a2179) from2 ralstonia eutropha jmp134 at 1.74 a resolution
8	<a href="#">c2pzhC_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> hypothetical protein hp_0496; <b>PDBTitle:</b> ybgc thioesterase (hp0496) from helicobacter pylori
9	<a href="#">d2gf6a1</a>	 Alignment		100.0	17	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
10	<a href="#">d2hx5a1</a>	 Alignment		100.0	17	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
11	<a href="#">c5vpjB_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> the crystal structure of a thioesteras from actinomadura2 verrucospora.

12	<a href="#">c2xfiB</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dyne7; <b>PDBTitle:</b> induced-fit and allosteric effects upon polyene binding2 revealed by crystal structures of the dynamycin3 thioesterase
13	<a href="#">d1njka</a>	Alignment		100.0	24	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
14	<a href="#">d2alia1</a>	Alignment		100.0	21	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
15	<a href="#">c2aliaA</a>	Alignment		100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa2801; <b>PDBTitle:</b> structure of protein of unknown function pa2801 from pseudomonas2 aeruginosa, putative thioesterase
16	<a href="#">c2w3xE</a>	Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> cale7; <b>PDBTitle:</b> crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
17	<a href="#">c4k00A</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa hydrolase; <b>PDBTitle:</b> crystal structure of slr0204, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from synechocystis
18	<a href="#">d1lo7a</a>	Alignment		100.0	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
19	<a href="#">c5byuA</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
20	<a href="#">c3r87A</a>	Alignment		100.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of orf6 protein from photobacterium profundum
21	<a href="#">c5v10B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the putative tol-pal system-associated acyl-coa2 thioesterase from pseudomonas aeruginosa pao1
22	<a href="#">d1s5ua</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
23	<a href="#">d2cyea1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
24	<a href="#">d2owna1</a>	Alignment	not modelled	100.0	10	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
25	<a href="#">d1z54a1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
26	<a href="#">d2hja1</a>	Alignment	not modelled	100.0	10	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
27	<a href="#">c5lqID</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxybenzoyl-coa thioesterase; <b>PDBTitle:</b> high resolution crystal structure of the 4-hydroxybenzoyl coenzyme-a2 thioesterase from staphylococcus aureus <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> hypothetical protein aq_1494; <b>PDBTitle:</b> crystal structure of a hypothetical protein(aq1494) from aquifex2 aeolicus
28	<a href="#">c2egiE</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dodecanoyl-[acyl-carrier-protein]
29	<a href="#">c5v04B</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dodecanoyl-[acyl-carrier-protein]

29	<a href="#">c3xv4B</a>	Alignment	not modelled	99.9	19	hydrolase, chloroplastic; <b>PDBTitle:</b> 12:0-acyl thioesterase from umbellularia californica
30	<a href="#">c3hm0C</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> probable thioesterase; <b>PDBTitle:</b> crystal structure of probable thioesterase from bartonella henselae
31	<a href="#">c5wh9C</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> 4-hydroxybenzoyl-coa thioesterase; <b>PDBTitle:</b> structure of bh1999 gentisyl-coenzyme a thioesterase
32	<a href="#">d2essa1</a>	Alignment	not modelled	99.9	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
33	<a href="#">c4gakA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-acyl thioesterase; <b>PDBTitle:</b> crystal structure of acyl-acyl thioesterase from spirosona linguale
34	<a href="#">d2fuja1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
35	<a href="#">c2ownA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative oleoyl-[acyl-carrier protein] thioesterase; <b>PDBTitle:</b> crystal structure of oleoyl thioesterase (putative) (np_784467.1) from2 lactobacillus plantarum at 2.00 a resolution
36	<a href="#">c2essaA</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-acyl thioesterase; <b>PDBTitle:</b> crystal structure of an acyl-acyl thioesterase (np_810988.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution
37	<a href="#">c5byuD</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> crystal structure of unnamed thioesterase ipg2867 from legionella2 pneumophila
38	<a href="#">d2owna2</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
39	<a href="#">d2essa2</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
40	<a href="#">c4zv3B</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of the n- and c-terminal domains of mouse acyl-coa2 thioesterase 7
41	<a href="#">c3d6IA</a>	Alignment	not modelled	99.2	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
42	<a href="#">d1ylia1</a>	Alignment	not modelled	99.1	10	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
43	<a href="#">d1vpma</a>	Alignment	not modelled	99.1	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
44	<a href="#">c4ncpF</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> unknown function <b>Chain:</b> F; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of 4-hbt like thioesterase sav1878 from2 staphylococcus aureus subsp. aureus mu50
45	<a href="#">c4ienB</a>	Alignment	not modelled	99.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative acyl-coa hydrolase; <b>PDBTitle:</b> crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
46	<a href="#">c5dm5E</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> putative acyl-coa thioester hydrolase; <b>PDBTitle:</b> crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
47	<a href="#">c2eisA</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein tthb207; <b>PDBTitle:</b> x-ray structure of acyl-coa hydrolase-like protein, tt1379, from2 thermus thermophilus hb8
48	<a href="#">c2v1oF</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of n-terminal domain of acyl-coa2 thioesterase 7
49	<a href="#">c2qq2C</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> cytosolic acyl coenzyme a thioester hydrolase; <b>PDBTitle:</b> crystal structure of c-terminal domain of human acyl-coa thioesterase2 7
50	<a href="#">d1y7ua1</a>	Alignment	not modelled	98.9	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
51	<a href="#">c3b7kA</a>	Alignment	not modelled	98.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 12; <b>PDBTitle:</b> human acyl-coenzyme a thioesterase 12
52	<a href="#">d2gvha2</a>	Alignment	not modelled	98.6	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
53	<a href="#">c2gvhC</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> agr_I_2016p; <b>PDBTitle:</b> crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
54	<a href="#">d2gvha1</a>	Alignment	not modelled	98.5	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like

55	<a href="#">c3lbeA</a>	Alignment	not modelled	98.1	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.793; <b>PDBTitle:</b> the crystal structure of smu.793 from streptococcus mutans ua159 bound2 to acetyl coa
56	<a href="#">c4i82A</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of hypothetical thioesterase protein sp_1851 from2 streptococcus pneumoniae tigr4
57	<a href="#">c4k02A</a>	Alignment	not modelled	98.0	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa thioesterase; <b>PDBTitle:</b> crystal structure of atdhna1, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from arabidopsis thaliana
58	<a href="#">c5hmcA</a>	Alignment	not modelled	98.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> azi13; <b>PDBTitle:</b> crystal structure of s. sahachiroi azig complexed with 5-methyl2 naphthoic acid
59	<a href="#">d1wluu1</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
60	<a href="#">c4ae7A</a>	Alignment	not modelled	97.8	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase superfamily member 5; <b>PDBTitle:</b> crystal structure of human them5
61	<a href="#">d2h4ua1</a>	Alignment	not modelled	97.8	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
62	<a href="#">d2f0xa1</a>	Alignment	not modelled	97.8	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
63	<a href="#">c4ae8D</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> thioesterase superfamily member 4; <b>PDBTitle:</b> crystal structure of human them4
64	<a href="#">d1ixla</a>	Alignment	not modelled	97.6	7	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
65	<a href="#">d1vh5a</a>	Alignment	not modelled	97.6	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
66	<a href="#">d2cy9a1</a>	Alignment	not modelled	97.6	7	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
67	<a href="#">c3gekA</a>	Alignment	not modelled	97.6	4	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase yhda; <b>PDBTitle:</b> crystal structure of putative thioesterase yhda from lactococcus2 lactis. northeast structural genomics consortium target kr113
68	<a href="#">c3lwgB</a>	Alignment	not modelled	97.6	10	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hp0420 homologue; <b>PDBTitle:</b> crystal structure of hp0420-homologue c46a from helicobacter felis
69	<a href="#">c3s4kA</a>	Alignment	not modelled	97.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase rv1847/mt1895; <b>PDBTitle:</b> structure of a putative esterase rv1847/mt1895 from mycobacterium2 tuberculosis
70	<a href="#">d1q4ua</a>	Alignment	not modelled	97.5	7	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
71	<a href="#">c2pimA</a>	Alignment	not modelled	97.5	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetic acid degradation-related protein; <b>PDBTitle:</b> crystal structure of a putative thioesterase, phenylacetic acid2 degradation-related protein (reut_b4779) from ralstonia eutropha3 jmp134 at 2.20 a resolution
72	<a href="#">c3nzwD</a>	Alignment	not modelled	97.5	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> bh2602 protein; <b>PDBTitle:</b> crystal structure of bh2602 protein from bacillus halodurans with coa,2 northeast structural genomics consortium target bhr199
73	<a href="#">c2qwzB</a>	Alignment	not modelled	97.4	7	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylacetic acid degradation-related protein; <b>PDBTitle:</b> crystal structure of a putative thioesterase (tm1040_1390) from2 silicibacter sp. tm1040 at 2.15 a resolution
74	<a href="#">c4qdbF</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> thioesterase pa1618; <b>PDBTitle:</b> crystal structure of mutant thioesterase pa1618 (q49a) from2 pseudomonas aeruginosa
75	<a href="#">c3e1eE</a>	Alignment	not modelled	97.2	8	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> thioesterase family protein; <b>PDBTitle:</b> crystal structure of a thioesterase family protein from2 silicibacter pomeroyi. northeast structural genomics3 target sir180a
76	<a href="#">d1zkia1</a>	Alignment	not modelled	97.2	7	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
77	<a href="#">d1vh9a</a>	Alignment	not modelled	97.1	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
78	<a href="#">d2hboa1</a>	Alignment	not modelled	97.1	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
79	<a href="#">d1sc0a</a>	Alignment	not modelled	97.1	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
						<b>PDB header:</b> hydrolase

80	<a href="#">c3hduB_</a>	Alignment	not modelled	97.1	11	<b>Chain:</b> B: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of a putative thioesterase (syn_01977) from2 syntrophus aciditrophicus sb at 2.50 a resolution
81	<a href="#">d2ov9a1</a>	Alignment	not modelled	97.1	18	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
82	<a href="#">d2cwza1</a>	Alignment	not modelled	97.1	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> TTHA0967-like
83	<a href="#">d2f41a1</a>	Alignment	not modelled	97.0	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
84	<a href="#">c4m20D_</a>	Alignment	not modelled	97.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of hypothetical protein sav0944 from staphylococcus2 aureus subsp. aureus mu50
85	<a href="#">c2f3xA_</a>	Alignment	not modelled	97.0	10	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor fapr; <b>PDBTitle:</b> crystal structure of fapr (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
86	<a href="#">d2fs2a1</a>	Alignment	not modelled	96.9	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
87	<a href="#">d1t82a_</a>	Alignment	not modelled	96.8	12	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
88	<a href="#">c3f1tB_</a>	Alignment	not modelled	96.7	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein q913c8_pseae; <b>PDBTitle:</b> crystal structure of the q913c8_pseae protein from pseudomonas2 aeruginosa. northeast structural genomics consortium target par319a.
89	<a href="#">c3dkzA_</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase superfamily protein; <b>PDBTitle:</b> crystal structure of the q7w9w5_borpa protein from2 bordetella parapertussis. northeast structural genomics3 consortium target bpr208c.
90	<a href="#">c3kuvB_</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fluoroacetyl coenzyme a thioesterase; <b>PDBTitle:</b> structural basis of the activity and substrate specificity of the2 fluoroacetyl-coa thioesterase flk - t42s mutant in complex with3 acetate.
91	<a href="#">c4a0zA_</a>	Alignment	not modelled	96.6	7	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor fapr; <b>PDBTitle:</b> structure of the global transcription regulator fapr from2 staphylococcus aureus in complex with malonyl-coa
92	<a href="#">d1yoca1</a>	Alignment	not modelled	96.4	13	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
93	<a href="#">c3lmbA_</a>	Alignment	not modelled	96.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum t1s
94	<a href="#">c3e8pA_</a>	Alignment	not modelled	96.1	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the protein q8e9m7 from shewanella oneidensis2 related to thioesterase superfamily. northeast structural genomics3 consortium target sor246.
95	<a href="#">c3bnvD_</a>	Alignment	not modelled	95.9	10	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> cj0977; <b>PDBTitle:</b> crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
96	<a href="#">c4rmmA_</a>	Alignment	not modelled	95.9	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the q7nvp2_chrv0 protein from chromobacterium2 violaceum. northeast structural genomics consortium target cvr191
97	<a href="#">c4rv2A_</a>	Alignment	not modelled	95.7	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0336 protein msmeg_1340/msmei_1302; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-accp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
98	<a href="#">c2prxB_</a>	Alignment	not modelled	95.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> thioesterase superfamily protein; <b>PDBTitle:</b> crystal structure of thioesterase superfamily protein (zp_00837258.1)2 from shewanella loihica pv-4 at 1.65 a resolution
99	<a href="#">c4mzqG_</a>	Alignment	not modelled	95.0	17	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> beta-alanyl-coa:ammonia lyase; <b>PDBTitle:</b> beta-alanyl-coa:ammonia lyase from clostridium propionicum in complex2 with propionyl-coa
100	<a href="#">c5zy8A_</a>	Alignment	not modelled	94.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0336 protein rv0637; <b>PDBTitle:</b> crystal structure of c terminal truncated hadbc (3r-hydroxyacyl-accp2 dehydratase) complex from mycobacterium tuberculosis
101	<a href="#">c3ir3B_</a>	Alignment	not modelled	94.7	8	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-thioester dehydratase 2; <b>PDBTitle:</b> crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
102	<a href="#">c3e29C_</a>	Alignment	not modelled	94.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein q7we92_borbr; <b>PDBTitle:</b> x-ray structure of the protein q7we92_borbr from thioesterase2 superfamily. northeast structural genomics consortium target bor214a.
103	<a href="#">c4hznA_</a>	Alignment	not modelled	94.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional methylmalonyl-coa:accp <b>PDBTitle:</b> the structure of the bifunctional acetyltransferase/decarboxylase lnmk2 from the leinamycin biosynthetic pathway revealing novel activity for3 a double hot dog fold

104	<a href="#">c4ritA_</a>	Alignment	not modelled	94.2	12	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxyacyl-acp dehydratase subunit hada; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin
105	<a href="#">d1sh8a_</a>	Alignment	not modelled	94.2	8	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
106	<a href="#">d2q78a1</a>	Alignment	not modelled	93.7	11	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> TTHA0967-like
107	<a href="#">c3qooA_</a>	Alignment	not modelled	93.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of hot-dog-like taci_0573 protein from2 thermaerovibrio acidaminovorans
108	<a href="#">d1iq6a_</a>	Alignment	not modelled	91.2	14	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
109	<a href="#">c4w7bG_</a>	Alignment	not modelled	90.4	8	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> hydratase chsh1; <b>PDBTitle:</b> crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
110	<a href="#">c5cpgA_</a>	Alignment	not modelled	89.4	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (r)-specific enoyl-coa hydratase; <b>PDBTitle:</b> r-hydratase phaj1 from pseudomonas aeruginosa in the unliganded form
111	<a href="#">c4ffuA_</a>	Alignment	not modelled	89.1	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidase; <b>PDBTitle:</b> crystal structure of putative maoc-like (monoamine oxidase-like)2 protein, similar to nodn from sinorhizo bium meliloti 1021
112	<a href="#">d2b3na1</a>	Alignment	not modelled	88.2	9	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> MaoC-like
113	<a href="#">c4v12A_</a>	Alignment	not modelled	88.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> maoc like domain protein; <b>PDBTitle:</b> crystal structure of the msmeq_6754 dehydratase from mycobacterium2 smegmatis
114	<a href="#">c3exzA_</a>	Alignment	not modelled	86.9	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> maoc-like dehydratase; <b>PDBTitle:</b> crystal structure of the maoc-like dehydratase from rhodospirillum2 rubrum. northeast structural genomics consortium target rrr103a.
115	<a href="#">c4zw0A_</a>	Alignment	not modelled	86.6	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; <b>PDBTitle:</b> crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from candidatus asiaticum
116	<a href="#">c5buyA_</a>	Alignment	not modelled	83.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; <b>PDBTitle:</b> crystal structure of beta-hydroxyacyl-acyl carrier protein dehydratase2 (fabz) from francisella tularensis
117	<a href="#">c2glvA_</a>	Alignment	not modelled	78.5	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxymyristoyl-acyl carrier protein dehydratase; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
118	<a href="#">c4i83A_</a>	Alignment	not modelled	78.2	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-[acyl-carrier-protein] dehydratase fabz; <b>PDBTitle:</b> crystal structure of (3r)-hydroxymyristoyl-acp dehydratase from2 neisseria meningitidis fam18
119	<a href="#">c3khpB_</a>	Alignment	not modelled	77.4	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> maoc family protein; <b>PDBTitle:</b> crystal structure of a possible dehydrogenase from mycobacterium2 tuberculosis at 2.3a resolution
120	<a href="#">c4e3eA_</a>	Alignment	not modelled	75.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> maoc domain protein dehydratase; <b>PDBTitle:</b> crystal structure of putative maoc domain protein dehydratase from2 chloroflexus aurantiacus j-10-fl