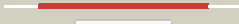



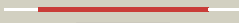




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2243_(fabD)_2516795_2517703
Date	Mon Aug 5 13:25:38 BST 2019
Unique Job ID	38d626d7d76f5607

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qj3B_	 Alignment		100.0	100	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: mycobacterium tuberculosis fabd
2	c2cdh9_	 Alignment		100.0	53	PDB header: transferase Chain: 9: PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
3	c3ezoA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein s-malonyltransferase from2 burkholderia pseudomallei 1710b
4	c3eenA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acp transacylase; PDBTitle: crystal structure of malonyl-coa:acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331
5	c2cuyA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-[acyl carrier protein] transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8
6	c4rr5A_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase
7	c3ptwA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
8	c3qatB_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
9	c2g2oA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate
10	c3im9A_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus
11	c2h1yA_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: malonyl coenzyme a-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl-coa:acyl carrier protein transacylase2 (mcat) from helicobacter pylori

12	c3tqeA_	Alignment		100.0	27	PDB header: transferase Chain: A; PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: structure of the malonyl coa-acyl carrier protein transacylase (fabd)2 from coxiella burnetii
13	c6fikA_	Alignment		100.0	20	PDB header: biosynthetic protein Chain: A; PDB Molecule: polyketide synthase; PDBTitle: acp2 crosslinked to the ks of the loading/condensing region of the2 ctb1 pks
14	c5ypvA_	Alignment		100.0	30	PDB header: transferase Chain: A; PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of fabd from acinetobacter baumannii
15	c3im8A_	Alignment		100.0	30	PDB header: transferase Chain: A; PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
16	c3rgiA_	Alignment		100.0	28	PDB header: transferase Chain: A; PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
17	c4rl1A_	Alignment		100.0	20	PDB header: transferase Chain: A; PDB Molecule: type i polyketide synthase aves 1; PDBTitle: structural and functional analysis of a loading acyltransferase from2 the avermectin modular polyketide synthase
18	c5bp1A_	Alignment		100.0	25	PDB header: transferase Chain: A; PDB Molecule: mycocerosic acid synthase; PDBTitle: condensing di-domain (ks-at) of a mycocerosic acid synthase-like (mas-2 like) pks
19	c2qo3A_	Alignment		100.0	26	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
20	c6c9uA_	Alignment		100.0	26	PDB header: transferase/immune system Chain: A; PDB Molecule: 6-deoxyerythronolide-b synthase erya2, modules 3 and 4; PDBTitle: crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthronolide b synthase in complex with antibody fragment (fab)
21	c2c2nA_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A; PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of human mitochondrial malonyltransferase
22	c5dz6A_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A; PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks
23	c5dz7A_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A; PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase
24	c3g87A_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A; PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
25	c6iytA_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A; PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from second module 142 of salinomycin polyketide synthase
26	c3tzzA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A; PDB Molecule: polyketide synthase pks13; PDBTitle: crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a
27	c2hg4A_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: A; PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
28	c3hhdC_	Alignment	not modelled	100.0	22	PDB header: transferase, hydrolase Chain: C; PDB Molecule: fatty acid synthase; PDBTitle: structure of the human fatty acid synthase ks-mat

					didomain as a2 framework for inhibitor design.
29	c6iyoA_	Alignment	not modelled	100.0	31 PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from the second module2 of the salinomycin polyketide synthase
30	c6iyrA_	Alignment	not modelled	100.0	26 PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from module 8 of the2 salinomycin polyketide synthase
31	c2jfkD_	Alignment	not modelled	100.0	21 PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
32	c5czcA_	Alignment	not modelled	100.0	18 PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink
33	c5ydmA_	Alignment	not modelled	100.0	24 PDB header: transferase Chain: A: PDB Molecule: pk5; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
34	c2vz8A_	Alignment	not modelled	100.0	20 PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
35	c4qbuA_	Alignment	not modelled	100.0	22 PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
36	d1nm2a1	Alignment	not modelled	100.0	58 Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
37	c2vz8B_	Alignment	not modelled	100.0	21 PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
38	d1mlaa1	Alignment	not modelled	100.0	36 Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
39	c4ammA_	Alignment	not modelled	100.0	32 PDB header: transferase Chain: A: PDB Molecule: dyne8; PDBTitle: crystal structure of the acyltransferase domain of the2 iterative polyketide synthase in enediyne biosynthesis3 reveals the molecular basis of substrate specificity
40	c4mz0B_	Alignment	not modelled	100.0	29 PDB header: transferase Chain: B: PDB Molecule: curl; PDBTitle: structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase
41	c4b3yB_	Alignment	not modelled	100.0	20 PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
42	c2vkzH_	Alignment	not modelled	100.0	23 PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
43	c4ro5A_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: sat domain from cazm; PDBTitle: crystal structure of the sat domain from the non-reducing fungal2 polyketide synthase cazm
44	c2uva1_	Alignment	not modelled	100.0	24 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
45	c2pffH_	Alignment	not modelled	100.0	23 PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structural insights of yeast fatty acid synthase
46	c2pffB_	Alignment	not modelled	100.0	23 PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structural insights of yeast fatty acid synthase
47	c2pffE_	Alignment	not modelled	100.0	23 PDB header: transferase Chain: E: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structural insights of yeast fatty acid synthase
48	c4oqiA_	Alignment	not modelled	99.3	14 PDB header: hydrolase Chain: A: PDB Molecule: pk5; PDBTitle: streptomycetes albus ja3453 oxazolomycin ketosynthase domain ozmq ks1
49	d1mlaa2	Alignment	not modelled	98.9	34 Fold: Ferredoxin-like Superfamily: Probable ACP-binding domain of malonyl-CoA ACP transacylase Family: Probable ACP-binding domain of malonyl-CoA ACP transacylase
50	d1nm2a2	Alignment	not modelled	98.9	52 Fold: Ferredoxin-like Superfamily: Probable ACP-binding domain of malonyl-CoA ACP transacylase Family: Probable ACP-binding domain of malonyl-CoA ACP transacylase
51	c2uv9B_	Alignment	not modelled	98.5	35 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
52	c2vkzC_	Alignment	not modelled	98.3	33 PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid

						synthase type i2 multienzyme complex
53	c2uv8C_	Alignment	not modelled	98.3	33	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
54	c3hmjB_	Alignment	not modelled	98.3	33	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: saccharomyces cerevisiae fas type i
55	c4z37A_	Alignment	not modelled	94.3	20	PDB header: transferase Chain: A: PDB Molecule: putative mixed polyketide synthase/non-ribosomal peptide PDBTitle: structure of the ketosynthase of module 2 of c0zgq5 (trans-at pks)2 from brevibacillus brevis
56	c4wkyB_	Alignment	not modelled	93.5	25	PDB header: transferase Chain: B: PDB Molecule: beta-ketoacyl synthase; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2
57	c5erbB_	Alignment	not modelled	82.5	24	PDB header: transferase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: ketosynthase from module 5 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42
58	c3iraA_	Alignment	not modelled	73.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
59	c3i1iA_	Alignment	not modelled	61.5	23	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
60	d1uxoa_	Alignment	not modelled	60.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
61	c4gw3A_	Alignment	not modelled	60.7	31	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
62	c5d6oB_	Alignment	not modelled	60.7	19	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylerter hydrolase from2 corynebacterium glutamicum
63	c3qmwD_	Alignment	not modelled	60.6	18	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
64	c3lcrA_	Alignment	not modelled	59.5	30	PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthhetic pathway
65	d1lppb2	Alignment	not modelled	59.4	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
66	c2qmqa_	Alignment	not modelled	57.8	12	PDB header: signaling protein Chain: A: PDB Molecule: protein ndrg2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
67	c1cr6A_	Alignment	not modelled	57.6	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
68	c4qmkB_	Alignment	not modelled	57.4	27	PDB header: toxin Chain: B: PDB Molecule: type iii secretion system effector protein exou; PDBTitle: crystal structure of type iii effector protein exou (exou)
69	c2vavL_	Alignment	not modelled	56.9	24	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
70	c3ds8A_	Alignment	not modelled	56.6	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
71	c6e6uA_	Alignment	not modelled	55.9	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc
72	c3tu3B_	Alignment	not modelled	55.3	28	PDB header: toxin/toxin chaperone Chain: B: PDB Molecule: exou; PDBTitle: 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
73	c2qs9A_	Alignment	not modelled	53.9	26	PDB header: structural protein Chain: A: PDB Molecule: retinoblastoma-binding protein 9; PDBTitle: crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978
74	d1mo2a_	Alignment	not modelled	53.8	35	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
75	c1mo2A_	Alignment	not modelled	53.8	35	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase (debs te), ph2 8.5
76	d1ex9a_	Alignment	not modelled	53.3	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
77	c2q0xA_	Alignment	not modelled	52.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function

78	c3i28A_	Alignment	not modelled	51.9	21	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
79	c6cl4A_	Alignment	not modelled	51.5	25	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
80	c3bdvB_	Alignment	not modelled	51.0	42	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein duf1234; PDBTitle: crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
81	c3lp5A_	Alignment	not modelled	50.5	19	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
82	d1bu8a2	Alignment	not modelled	50.4	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
83	d2h7xa1	Alignment	not modelled	49.9	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
84	c4z8zA_	Alignment	not modelled	49.7	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
85	d1rp1a2	Alignment	not modelled	48.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
86	c2y6vB_	Alignment	not modelled	48.2	37	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
87	d1gpla2	Alignment	not modelled	47.4	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
88	c5fyaA_	Alignment	not modelled	47.3	17	PDB header: hydrolase Chain: A: PDB Molecule: patatin-like protein, plpd; PDBTitle: cubic crystal of the native plpd
89	c5hdfB_	Alignment	not modelled	47.1	18	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
90	d1xkta_	Alignment	not modelled	47.1	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
91	c4akxB_	Alignment	not modelled	46.7	27	PDB header: transport protein Chain: B: PDB Molecule: exou; PDBTitle: structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
92	c3fleB_	Alignment	not modelled	44.1	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
93	c5w8pA_	Alignment	not modelled	44.1	22	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
94	c4qnnC_	Alignment	not modelled	44.0	16	PDB header: hydrolase Chain: C: PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom
95	c4akfA_	Alignment	not modelled	44.0	24	PDB header: transferase Chain: A: PDB Molecule: vipd; PDBTitle: crystal structure of vipd from legionella pneumophila
96	c4xjvA_	Alignment	not modelled	43.5	33	PDB header: hydrolase Chain: A: PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2
97	c2h7xA_	Alignment	not modelled	43.2	24	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
98	c4f3nA_	Alignment	not modelled	43.1	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized acr, cog1565 superfamily; PDBTitle: high resolution native crystal structure of an uncharacterized acr,2 cog1565 superfamily protein from burkholderia thailandensis, solved3 by iodide ion sad
99	c2cbgA_	Alignment	not modelled	42.9	13	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
100	d2b61a1	Alignment	not modelled	42.8	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
101	c4fleA_	Alignment	not modelled	42.6	29	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of the esterase yqia (ye3661) from yersinia2 enterocolitica, northeast structural genomics consortium target yer85
102	c1qgeD_	Alignment	not modelled	42.2	22	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
						PDB header: hydrolase

103	c5jkiA_	Alignment	not modelled	41.3	24	Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
104	c5h3bA_	Alignment	not modelled	40.8	18	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein hi_1552; PDBTitle: crystal structure of semet-biog from haemophilus influenzae at 1.492 angstroms resolution
105	c4qloA_	Alignment	not modelled	39.6	18	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
106	d1k8qa_	Alignment	not modelled	39.1	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
107	d1hpla2	Alignment	not modelled	38.9	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
108	d1jmkc_	Alignment	not modelled	38.3	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
109	c1pjaA_	Alignment	not modelled	37.1	16	PDB header: hydrolase Chain: A: PDB Molecule: palmitoyl-protein thioesterase 2 precursor; PDBTitle: the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
110	d1pjaa_	Alignment	not modelled	37.1	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
111	d1hlga_	Alignment	not modelled	36.3	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
112	d1i4wa_	Alignment	not modelled	36.3	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
113	c1i4wA_	Alignment	not modelled	36.3	15	PDB header: transcription Chain: A: PDB Molecule: mitochondrial replication protein mtf1; PDBTitle: the crystal structure of the transcription factor sc-mttfb2 offers intriguing insights into mitochondrial transcription
114	d4lipd_	Alignment	not modelled	36.1	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
115	c3l80A_	Alignment	not modelled	35.9	19	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
116	c4eziA_	Alignment	not modelled	35.4	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution
117	d1tiba_	Alignment	not modelled	35.1	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
118	c6gupB_	Alignment	not modelled	34.8	11	PDB header: hydrolase Chain: B: PDB Molecule: siderophore biosynthesis lipase/esterase, putative; PDBTitle: siderophore hydrolase estb from aspergillus fumigatus
119	c5g59A_	Alignment	not modelled	34.2	11	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
120	c3d59B_	Alignment	not modelled	33.2	31	PDB header: hydrolase Chain: B: PDB Molecule: platelet-activating factor acetylhydrolase; PDBTitle: crystal structure of human plasma platelet activating factor2 acetylhydrolase