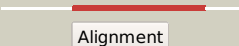



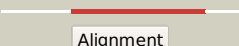





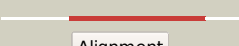












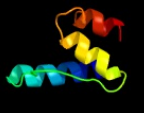
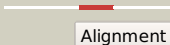
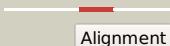
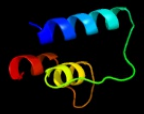





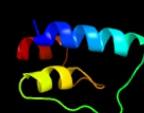




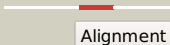
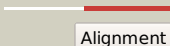
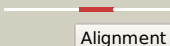

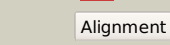



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3091 (-) _3459113_3460804
Date	Thu Aug 8 16:20:27 BST 2019
Unique Job ID	676ba439044964fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4akfA_	 Alignment		100.0	14	PDB header: transferase Chain: A; PDB Molecule: vipd; PDBTitle: crystal structure of vipd from legionella pneumophila
2	c4qmkB_	 Alignment		100.0	17	PDB header: toxin Chain: B; PDB Molecule: type iii secretion system effector protein exou; PDBTitle: crystal structure of type iii effector protein exou (exou)
3	c5fyaA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: patatin-like protein, plpd; PDBTitle: cubic crystal of the native plpd
4	c4akxB_	 Alignment		100.0	18	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
5	c3tu3B_	 Alignment		100.0	17	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
6	c6aunB_	 Alignment		99.9	15	PDB header: hydrolase Chain: B; PDB Molecule: pla2g6, ipla2beta; PDBTitle: calcium-independent phospholipase a2 beta
7	d1oxwa_	 Alignment		99.9	14	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Patatin
8	c5izrC_	 Alignment		98.6	14	PDB header: hydrolase/hydrolase inhibitor Chain: C; PDB Molecule: cytosolic phospholipase a2 delta; PDBTitle: human givd cytosolic phospholipase a2 in complex with methyl gamma-2 linolenyl fluorophosphonate inhibitor and terbium chloride
9	d1cjya2	 Alignment		98.3	18	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Lysophospholipase
10	c1cjb_	 Alignment		97.7	18	PDB header: hydrolase Chain: B; PDB Molecule: protein (cytosolic phospholipase a2); PDBTitle: human cytosolic phospholipase a2
11	d1mlaal	 Alignment		96.1	15	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like

12	c4qbuA_	 Alignment		95.7	20	PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
13	c4ammA_	 Alignment		95.5	20	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
14	c5ydmA_	 Alignment		95.4	24	PDB header: transferase Chain: A: PDB Molecule: pk5; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
15	c4mz0B_	 Alignment		95.4	21	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
16	c4rr5A_	 Alignment		95.3	21	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
17	c2jfkD_	 Alignment		95.3	22	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
18	c3tqeA_	 Alignment		95.2	12	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
19	c3ptwA_	 Alignment		95.2	9	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
20	c3rgiA_	 Alignment		95.2	16	PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
21	c6iyrA_	 Alignment	not modelled	95.1	27	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
22	c3eenA_	 Alignment	not modelled	94.9	13	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl-coa:acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331
23	c5dz7A_	 Alignment	not modelled	94.8	20	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase
24	c3im8A_	 Alignment	not modelled	94.7	12	PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
25	c2qo3A_	 Alignment	not modelled	94.6	20	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
26	c5bp1A_	 Alignment	not modelled	94.5	20	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
27	c3g87A_	 Alignment	not modelled	94.5	16	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
						PDB header: transferase

28	c2cuyA	Alignment	not modelled	94.1	16	Chain: A: PDB Molecule: malonyl coa-[acyl carrier protein] transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8
29	c6iyvA	Alignment	not modelled	94.1	17	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	c5czcA	Alignment	not modelled	93.9	10	PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink
31	c3tzzA	Alignment	not modelled	93.9	10	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
32	c5dz6A	Alignment	not modelled	93.9	9	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks
33	c2g2oA	Alignment	not modelled	93.9	15	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate
34	c2h1yA	Alignment	not modelled	93.8	10	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
35	c6iytA	Alignment	not modelled	93.5	16	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
36	c6c9uA	Alignment	not modelled	93.4	20	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 deoxyerythronolide b synthase in complex with antibody fragment (fab)
37	c3hhdC	Alignment	not modelled	93.2	24	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.
38	c3ezoA	Alignment	not modelled	92.6	15	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
39	d1nm2a1	Alignment	not modelled	92.2	18	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
40	c2cdh9	Alignment	not modelled	91.1	18	PDB header: transferase Chain: 9: PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
41	c2vz8A	Alignment	not modelled	90.9	20	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
42	c2qj3B	Alignment	not modelled	90.9	21	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: mycobacterium tuberculosis fabd
43	c4rl1A	Alignment	not modelled	90.9	14	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
44	c3qatB	Alignment	not modelled	90.3	11	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
45	c6a4tB	Alignment	not modelled	90.1	19	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
46	c6fikA	Alignment	not modelled	87.3	8	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
47	c5ypvA	Alignment	not modelled	87.0	12	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of fabd from acinetobacter baumannii
48	c2vz8B	Alignment	not modelled	86.0	20	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
49	c3l4eA	Alignment	not modelled	84.3	28	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
50	c2c2nA	Alignment	not modelled	83.8	13	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of human mitochondrial malonyltransferase
51	c2hg4A	Alignment	not modelled	82.3	15	PDB header: transferase Chain: A: PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
						Fold: Flavodoxin-like

52	d1fyea_	Alignment	not modelled	81.4	19	Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
53	c3i1aA_	Alignment	not modelled	81.4	21	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from 2 bacillus anthracis
54	c1cr6A_	Alignment	not modelled	79.8	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
55	c1qgeD_	Alignment	not modelled	77.6	32	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
56	c4fleA_	Alignment	not modelled	77.3	14	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
57	c3n5iC_	Alignment	not modelled	76.8	24	PDB header: hydrolase Chain: C: PDB Molecule: beta-peptidyl aminopeptidase; PDBTitle: crystal structure of the precursor (s250a mutant) of the n-terminal2 beta-aminopeptidase bapa
58	c3i28A_	Alignment	not modelled	76.3	21	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
59	c2drhD_	Alignment	not modelled	76.0	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: 361aa long hypothetical d-aminopeptidase; PDBTitle: crystal structure of the ph0078 protein from pyrococcus horikoshii ot3
60	c4qlaB_	Alignment	not modelled	73.3	28	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
61	c5w8pA_	Alignment	not modelled	72.8	21	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
62	c3flaB_	Alignment	not modelled	72.1	34	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
63	c4i19A_	Alignment	not modelled	71.5	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
64	c2qmqa_	Alignment	not modelled	71.5	21	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
65	c3l80A_	Alignment	not modelled	71.2	7	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
66	c2vavL_	Alignment	not modelled	70.5	17	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
67	c3vv1A_	Alignment	not modelled	70.4	17	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
68	c4qloA_	Alignment	not modelled	69.6	21	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from 2 staphylococcus aureus
69	c3en0A_	Alignment	not modelled	69.3	18	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
70	c6n63A_	Alignment	not modelled	68.2	31	PDB header: metal binding protein Chain: A: PDB Molecule: encapsulin cargo protein; PDBTitle: crystal structure of an iron binding protein
71	c2y6vB_	Alignment	not modelled	68.1	17	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
72	c4z8zA_	Alignment	not modelled	68.1	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
73	c6e6uA_	Alignment	not modelled	67.6	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc
74	d2b61a1	Alignment	not modelled	67.4	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
75	c5jkjA_	Alignment	not modelled	67.2	28	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
76	c1t2aC_	Alignment	not modelled	67.1	22	PDB header: structural genomics,lyase Chain: C: PDB Molecule: gdp-mannose 4,6 dehydratase; PDBTitle: crystal structure of human gdp-d-mannose 4,6-dehydratase
						Fold: NAD(P)-binding Rossmann-fold domains

77	d1t2aa_	Alignment	not modelled	67.1	22	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	d1b65a_	Alignment	not modelled	66.8	15	Fold: DmpA/ArgJ-like Superfamily: DmpA/ArgJ-like Family: DmpA-like
79	d2vata1	Alignment	not modelled	66.5	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
80	c4qlaA_	Alignment	not modelled	66.4	28	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
81	c5d6oB_	Alignment	not modelled	66.2	15	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
82	d1n7ha_	Alignment	not modelled	65.6	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
83	c1n7gB_	Alignment	not modelled	65.2	28	PDB header: lyase Chain: B: PDB Molecule: gdp-d-mannose-4,6-dehydratase; PDBTitle: crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
84	c2exxB_	Alignment	not modelled	64.9	38	PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from homo sapiens in complex with nadp
85	c3s3uB_	Alignment	not modelled	64.4	28	PDB header: transferase Chain: B: PDB Molecule: cysteine transferase; PDBTitle: crystal structure of uncleaved thnt t282c
86	c5fydB_	Alignment	not modelled	63.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: structural and biochemical insights into 7beta-2 hydroxysteroid dehydrogenase stereoselectivity
87	d2dsta1	Alignment	not modelled	63.4	7	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: TTHA1544-like
88	c5hw4C_	Alignment	not modelled	63.0	20	PDB header: transferase Chain: C: PDB Molecule: ribosomal rna small subunit methyltransferase i; PDBTitle: crystal structure of escherichia coli 16s rrna methyltransferase rsmi2 in complex with adomet
89	c4b3yB_	Alignment	not modelled	61.7	14	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
90	c3lp5A_	Alignment	not modelled	61.5	24	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
91	c3cdiA_	Alignment	not modelled	61.4	18	PDB header: transferase Chain: A: PDB Molecule: polynucleotide phosphorylase; PDBTitle: crystal structure of e. coli npase
92	c5f4zB_	Alignment	not modelled	61.1	10	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
93	c3im9A_	Alignment	not modelled	59.8	9	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus
94	c4gw3A_	Alignment	not modelled	59.4	24	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
95	d1lspa_	Alignment	not modelled	57.6	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
96	c3ds8A_	Alignment	not modelled	56.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
97	d1a9xa4	Alignment	not modelled	56.2	25	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
98	d2pl5a1	Alignment	not modelled	53.1	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
99	c4k3bA_	Alignment	not modelled	51.8	18	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein assembly factor bama; PDBTitle: the crystal structure of bama from neisseria gonorrhoeae
100	c3kwpA_	Alignment	not modelled	51.5	10	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
101	d1xgka_	Alignment	not modelled	51.1	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
102	c6cl4A_	Alignment	not modelled	50.5	24	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
103	c1na6B_	Alignment	not modelled	49.8	23	PDB header: solute-binding protein Chain: B: PDB Molecule: putative abc transporter;

103	c4pevB	Alignment	not modelled	49.0	23	PDBTitle: crystal structure of abc transporter solute binding protein from2 thermobispora bispora dsm 43833
104	d1vhqa	Alignment	not modelled	49.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
105	d1a9xa3	Alignment	not modelled	49.0	21	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
106	d1ex9a	Alignment	not modelled	48.5	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
107	c1pjaA	Alignment	not modelled	46.0	12	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)
108	d1pjaa	Alignment	not modelled	46.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
109	c3bdvB	Alignment	not modelled	45.6	29	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
110	c3wj7B	Alignment	not modelled	45.4	19	PDB header: oxidoreductase Chain: B; PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2253
111	d1iiba	Alignment	not modelled	44.6	5	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
112	c2rh8A	Alignment	not modelled	44.0	28	PDB header: oxidoreductase Chain: A; PDB Molecule: anthocyanidin reductase; PDBTitle: structure of apo anthocyanidin reductase from vitis vinifera
113	c3wxiB	Alignment	not modelled	43.9	14	PDB header: transferase Chain: B; PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
114	c4lk3A	Alignment	not modelled	43.3	22	PDB header: lyase Chain: A; PDB Molecule: udp-glucuronic acid decarboxylase 1; PDBTitle: crystal structure of human udp-xylose synthase r236a substitution
115	c5df1A	Alignment	not modelled	42.9	22	PDB header: oxidoreductase Chain: A; PDB Molecule: iridoid synthase; PDBTitle: iridoid synthase from catharanthus roseus - ternary complex with nadp+2 and geranic acid
116	c5u9cC	Alignment	not modelled	42.9	22	PDB header: hydrolase,oxidoreductase Chain: C; PDB Molecule: dt dp-4-dehydrohamnose reductase; PDBTitle: 1.9 angstrom resolution crystal structure of dt dp-4-dehydrohamnose2 reductase from yersinia enterocolitica
117	c6aayD	Alignment	not modelled	42.6	16	PDB header: oxidoreductase Chain: D; PDB Molecule: gdp-l-fucose synthetase; PDBTitle: crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
118	c4dyvA	Alignment	not modelled	42.4	31	PDB header: oxidoreductase Chain: A; PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of a short-chain dehydrogenase/reductase sdr from2 xanthobacter autotrophicus py2
119	c5lnkd	Alignment	not modelled	41.2	25	PDB header: oxidoreductase Chain: D; PDB Molecule: PDBTitle: entire ovine respiratory complex i
120	c4yxfB	Alignment	not modelled	40.8	28	PDB header: oxidoreductase Chain: B; PDB Molecule: mups; PDBTitle: mups, a 3-oxoacyl (acp) reductase involved in mupirocin biosynthesis