







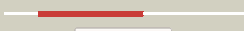













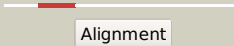
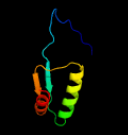
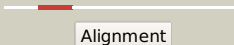

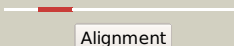

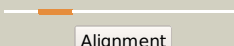

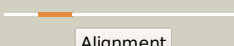

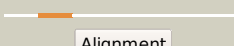

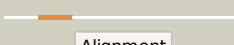





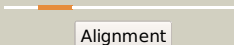
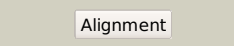
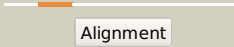
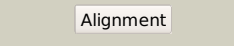
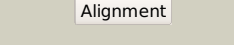
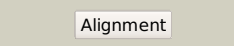
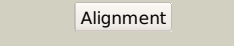
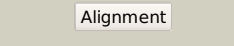


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1063c_(-)_1185746_1186828
Date	Wed Jul 31 22:05:13 BST 2019
Unique Job ID	e8451cd76b5ec53a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fyaA_	 Alignment		100.0	38	PDB header: hydrolase Chain: A: PDB Molecule: patatin-like protein, plpd; PDBTitle: cubic crystal of the native plpd
2	c4akfA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: vipd; PDBTitle: crystal structure of vipd from legionella pneumophila
3	c4qmkB_	 Alignment		100.0	26	PDB header: toxin Chain: B: PDB Molecule: type iii secretion system effector protein exou; PDBTitle: crystal structure of type iii effector protein exou (exou)
4	c3tu3B_	 Alignment		100.0	27	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
5	c4akxB_	 Alignment		100.0	24	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
6	d1oxwa_	 Alignment		100.0	17	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Patatin
7	c6aunB_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: pla2g6, ipla2beta; PDBTitle: calcium-independent phospholipase a2 beta
8	d1cya2	 Alignment		99.4	21	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Lysophospholipase
9	c5izrC_	 Alignment		99.1	22	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
10	c1cjb_	 Alignment		98.2	29	PDB header: hydrolase Chain: B: PDB Molecule: protein (cytosolic phospholipase a2); PDBTitle: human cytosolic phospholipase a2
11	c4rr5A_	 Alignment		92.6	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

12	c4mz0B_	 Alignment		91.8	20	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
13	d1mlaa1	 Alignment		90.0	24	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
14	c5ydmA_	 Alignment		90.0	22	PDB header: transferase Chain: A: PDB Molecule: pks; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
15	c6a4tB_	 Alignment		89.6	21	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
16	c4ammA_	 Alignment		89.2	26	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
17	c6iytA_	 Alignment		89.1	11	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
18	c3im8A_	 Alignment		88.9	26	PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
19	c3ptwA_	 Alignment		88.8	22	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	c2jfkD_	 Alignment		88.2	35	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
21	c6iyrA_	 Alignment	not modelled	87.5	19	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	c3rgiA_	 Alignment	not modelled	87.5	20	PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
23	c4qbuA_	 Alignment	not modelled	86.9	23	PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
24	c3l4eA_	 Alignment	not modelled	86.9	19	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
25	c5bp1A_	 Alignment	not modelled	86.0	26	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
26	c5dz6A_	 Alignment	not modelled	85.8	18	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks
27	c4r11A_	 Alignment	not modelled	85.0	18	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
28	c2qo3A_	 Alignment	not modelled	84.9	18	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

29	c5dz7A	Alignment	not modelled	84.9	20	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase
30	c2cuyA	Alignment	not modelled	84.5	29	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
31	c3tqeA	Alignment	not modelled	84.4	24	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
32	c6iy0A	Alignment	not modelled	84.4	18	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
33	c3tzzA	Alignment	not modelled	84.1	24	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
34	c3g87A	Alignment	not modelled	83.4	18	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
35	c2h1yA	Alignment	not modelled	82.3	20	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
36	c3eenA	Alignment	not modelled	81.8	29	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
37	c3hhdC	Alignment	not modelled	80.6	35	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	c6c9uA	Alignment	not modelled	80.0	18	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)
39	c2hg4A	Alignment	not modelled	79.8	17	PDB header: transferase Chain: A: PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
40	d1fyea	Alignment	not modelled	79.7	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
41	c5czcA	Alignment	not modelled	78.7	12	PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink
42	c3gatB	Alignment	not modelled	78.2	24	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
43	c3en0A	Alignment	not modelled	76.5	23	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
44	d1nm2a1	Alignment	not modelled	76.1	28	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
45	c2g20A	Alignment	not modelled	75.6	27	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate
46	c3ezoA	Alignment	not modelled	74.1	26	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
47	c3iliA	Alignment	not modelled	71.5	17	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
48	c2cdh9	Alignment	not modelled	70.6	28	PDB header: transferase Chain: 9: PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
49	c5ypvA	Alignment	not modelled	70.2	26	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of fabd from acinetobacter baumannii
50	c2qj3B	Alignment	not modelled	68.6	26	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: mycobacterium tuberculosis fabd
51	c6fikA	Alignment	not modelled	65.1	12	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 PDB header: structural genomics, unknown function

52	c2drhD_	Alignment	not modelled	64.3	24	Chain: D: PDB Molecule: 361aa long hypothetical d-aminopeptidase; PDBTitle: crystal structure of the ph0078 protein from pyrococcus horikoshii ot3
53	c5jkjA_	Alignment	not modelled	62.2	23	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
54	c3im9A_	Alignment	not modelled	61.7	14	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus
55	c2vz8A_	Alignment	not modelled	60.4	30	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
56	c4nbqB_	Alignment	not modelled	60.4	24	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of the polynucleotide phosphorylase (cbu_0852) from coxiella2 burnetii
57	c4fleA_	Alignment	not modelled	57.5	20	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
58	c3n5iC_	Alignment	not modelled	56.7	17	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
59	c5n2pA_	Alignment	not modelled	56.7	31	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
60	d2vata1	Alignment	not modelled	56.4	30	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
61	c3s3uB_	Alignment	not modelled	55.6	26	PDB header: transferase Chain: B: PDB Molecule: cysteine transferase; PDBTitle: crystal structure of uncleaved thnt t282c
62	c4z8zA_	Alignment	not modelled	55.6	9	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
63	d2b61a1	Alignment	not modelled	55.2	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
64	c4qloA_	Alignment	not modelled	54.6	21	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
65	c5w8pA_	Alignment	not modelled	54.0	28	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
66	c1cr6A_	Alignment	not modelled	52.7	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
67	c2vz8B_	Alignment	not modelled	51.9	31	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
68	c5d6oB_	Alignment	not modelled	51.1	28	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
69	c1e3hA_	Alignment	not modelled	49.7	18	PDB header: polyribonucleotide transferase Chain: A: PDB Molecule: guanosine pentaphosphate synthetase; PDBTitle: semet derivative of streptomyces antibioticus pnpase/gpsi enzyme
70	c2c2nA_	Alignment	not modelled	48.2	26	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of human mitochondrial malonyltransferase
71	d2pl5a1	Alignment	not modelled	48.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
72	c1fcbA_	Alignment	not modelled	47.9	15	PDB header: oxidoreductase (ch-oh(d)-cytochrome(a)) Chain: A: PDB Molecule: flavocytochrome b2; PDBTitle: molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
73	c4uzjB_	Alignment	not modelled	46.9	31	PDB header: hydrolase Chain: B: PDB Molecule: notum; PDBTitle: structure of the wnt deacylase notum from drosophila -2 crystal form i - 2.4a
74	c3u1kB_	Alignment	not modelled	46.2	27	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase 1, mitochondrial; PDBTitle: crystal structure of human pnpase
75	c3vvlA_	Alignment	not modelled	45.5	21	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
76	c3cdiA_	Alignment	not modelled	45.2	30	PDB header: transferase Chain: A: PDB Molecule: polynucleotide phosphorylase; PDBTitle: crystal structure of e. coli pnpase
77	c3flaB_	Alignment	not modelled	45.1	31	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1 PDB header: hydrolase

78	c3l80A	Alignment	not modelled	44.3	7	Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
79	c5xexC	Alignment	not modelled	44.1	30	PDB header: transferase Chain: C: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of s.aureus pnpase catalytic domain
80	c6dvhF	Alignment	not modelled	43.8	19	PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant
81	c5yjiE	Alignment	not modelled	43.7	30	PDB header: cytosolic protein Chain: E: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of pnpase from staphylococcus epidermidis
82	c3lp5A	Alignment	not modelled	43.1	17	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcf51
83	c4aimA	Alignment	not modelled	42.2	23	PDB header: transferase/peptide Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rna e2 recognition peptide
84	d1qopa	Alignment	not modelled	41.8	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
85	c2x0dA	Alignment	not modelled	41.4	16	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
86	d1b65a	Alignment	not modelled	41.3	16	Fold: DmpA/Argj-like Superfamily: DmpA/Argj-like Family: DmpA-like
87	c1e3pA	Alignment	not modelled	41.1	23	PDB header: polyribonucleotide transferase Chain: A: PDB Molecule: guanosine pentaphosphate synthetase; PDBTitle: tungstate derivative of streptomyces antibioticus pnpase/2 gpsi enzyme
88	c2qmQa	Alignment	not modelled	41.0	17	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
89	c2a7nA	Alignment	not modelled	40.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
90	d2dsta1	Alignment	not modelled	40.8	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: TTHA1544-like
91	c3i28A	Alignment	not modelled	39.6	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
92	c4am3A	Alignment	not modelled	39.3	21	PDB header: transferase/rna Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rna
93	c4uzqA	Alignment	not modelled	39.3	28	PDB header: hydrolase Chain: A: PDB Molecule: protein notum homolog; PDBTitle: structure of the wnt deacylase notum in complex with 2 o-palmitoleoyl serine - crystal form ix - 1.5a
94	c2y6vB	Alignment	not modelled	39.0	28	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
95	c2vavL	Alignment	not modelled	38.4	20	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
96	c5uzwD	Alignment	not modelled	37.2	17	PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
97	c1qgeD	Alignment	not modelled	37.1	31	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
98	c3kwpA	Alignment	not modelled	37.0	13	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
99	c6d6kB	Alignment	not modelled	36.1	24	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of polyribonucleotide nucleotidyltransferase from2 acinetobacter baumannii
100	c5uw7B	Alignment	not modelled	35.1	17	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
101	c3ezwD	Alignment	not modelled	34.6	13	PDB header: transferase Chain: D: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
102	c3ds8A	Alignment	not modelled	34.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crystal structure of the gene lin2722 products from listeria2 innocua
103	d1vcfa1	Alianment	not modelled	33.9	31	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases

						Family: FMN-linked oxidoreductases
104	d1p4ca_	Alignment	not modelled	32.8	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
105	c5ya2A_	Alignment	not modelled	32.4	17	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
106	c4aidC_	Alignment	not modelled	31.8	21	PDB header: transferase/peptide Chain: C: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rnae e2 recognition peptide
107	c4gw3A_	Alignment	not modelled	30.8	30	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
108	c3l3bA_	Alignment	not modelled	30.1	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
109	d1ispa_	Alignment	not modelled	30.0	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
110	c4x2rA_	Alignment	not modelled	29.1	28	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis
111	d1kbia1	Alignment	not modelled	29.1	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
112	c4e1jA_	Alignment	not modelled	28.9	16	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
113	c5hw4C_	Alignment	not modelled	28.7	24	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
114	d1dqza_	Alignment	not modelled	28.2	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
115	c1kbiB_	Alignment	not modelled	28.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
116	c1yr2A_	Alignment	not modelled	28.0	18	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
117	d1lepa_	Alignment	not modelled	27.6	26	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
118	c3tdnB_	Alignment	not modelled	27.5	21	PDB header: de novo protein Chain: B: PDB Molecule: f1r symmetric alpha-beta tim barrel; PDBTitle: computationally designed two-fold symmetric tim-barrel protein, f1r
119	c5h3bA_	Alignment	not modelled	27.1	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
120	c2e77B_	Alignment	not modelled	26.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex