










Phyre2

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Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4akfA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: vipd; PDBTitle: crystal structure of vipd from legionella pneumophila
2	c5fyaA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: patatin-like protein, plpd; PDBTitle: cubic crystal of the native plpd
3	c4qmkB_	 Alignment		100.0	28	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	30	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	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
6	d1oxwa_	 Alignment		100.0	18	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Patatin
7	c6aunB_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: pla2g6, ipla2beta; PDBTitle: calcium-independent phospholipase a2 beta
8	d1cjya2	 Alignment		99.3	20	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Lysophospholipase
9	c5izrC_	 Alignment		99.0	13	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		98.4	24	PDB header: hydrolase Chain: B: PDB Molecule: protein (cytosolic phospholipase a2); PDBTitle: human cytosolic phospholipase a2
11	c5ydmA_	 Alignment		90.6	22	PDB header: transferase Chain: A: PDB Molecule: pk5; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl

12	c6iytA_	Alignment		90.3	22	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
13	d1mlaa1	Alignment		90.3	19	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
14	c3rgiA_	Alignment		89.8	12	PDB header: transferase Chain: A; PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
15	c4rr5A_	Alignment		89.6	23	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
16	c4ammA_	Alignment		89.4	18	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	c3im8A_	Alignment		89.0	24	PDB header: transferase Chain: A; PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
18	c2jfkD_	Alignment		88.8	20	PDB header: transferase Chain: D; PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
19	c4qbuA_	Alignment		88.6	18	PDB header: transferase Chain: A; PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
20	c5dz7A_	Alignment		88.3	14	PDB header: transferase Chain: A; PDB Molecule: polyketide biosynthesis protein pkse; PDBTitle: structural basis of acyl transfer in a trans-at polyketide synthase
21	c6iyrA_	Alignment	not modelled	88.3	24	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	c5dz6A_	Alignment	not modelled	87.7	15	PDB header: transferase Chain: A; PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks
23	c6a4tB_	Alignment	not modelled	87.3	20	PDB header: hydrolase Chain: B; PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
24	c3ptwA_	Alignment	not modelled	87.2	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 clostridium perfringens atcc 13124
25	c3g87A_	Alignment	not modelled	85.5	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
26	c3tzzA_	Alignment	not modelled	85.4	14	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	c2cuyA_	Alignment	not modelled	84.0	21	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
28	c5bp1A_	Alignment	not modelled	83.3	22	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
29	c3tqeA_	Alignment	not modelled	83.3	20	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
30	c3eenA_	Alignment	not modelled	83.1	18	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
31	c2qo3A_	Alignment	not modelled	82.9	24	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
32	d1nm2a1	Alignment	not modelled	82.6	23	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
33	c4r11A_	Alignment	not modelled	80.9	15	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
34	c4mz0B_	Alignment	not modelled	80.4	23	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
35	c3l4eA_	Alignment	not modelled	80.1	22	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
36	c2cdh9_	Alignment	not modelled	77.7	22	PDB header: transferase Chain: 9: PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
37	c6c9uA_	Alignment	not modelled	77.4	24	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)
38	c2hg4A_	Alignment	not modelled	76.8	24	PDB header: transferase Chain: A: PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
39	c2h1yA_	Alignment	not modelled	75.9	11	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
40	c5czcA_	Alignment	not modelled	75.3	17	PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink
41	c6iyoA_	Alignment	not modelled	73.1	22	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
42	c3qatB_	Alignment	not modelled	71.8	18	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	c6aqyD_	Alignment	not modelled	71.6	19	PDB header: oxidoreductase Chain: D: PDB Molecule: gdp-l-fucose synthetase; PDBTitle: crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
44	c3hhdC_	Alignment	not modelled	71.3	20	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.
45	d1fyea_	Alignment	not modelled	70.6	28	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
46	c3en0A_	Alignment	not modelled	70.2	25	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
47	c2g2oA_	Alignment	not modelled	69.9	20	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate
48	c3ezoA_	Alignment	not modelled	58.7	19	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
49	c5ypvA_	Alignment	not modelled	58.2	19	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	58.0	29	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: mycobacterium tuberculosis fabd
51	c4nbqB_	Alignment	not modelled	57.6	33	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of the polynucleotide phosphorylase (cbu_0852)

						from coxiella2 burnetii
52	c4uzjB_	Alignment	not modelled	57.5	31	PDB header: hydrolase Chain: B: PDB Molecule: notum; PDBTitle: structure of the wnt deacylase notum from drosophila -2 crystal form i - 2.4a
53	c3im9A_	Alignment	not modelled	56.5	12	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus
54	c2drhD_	Alignment	not modelled	56.1	10	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
55	c4uzqA_	Alignment	not modelled	55.9	31	PDB header: hydrolase Chain: A: PDB Molecule: protein notum homolog; PDBTitle: structure of the wnt deacylase notum in complex with2 o-palmitoleoyl serine - crystal form ix - 1.5a
56	d2cdqa2	Alignment	not modelled	55.8	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
57	d1hdoa_	Alignment	not modelled	53.1	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
58	c3i1iA_	Alignment	not modelled	52.0	34	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
59	d2j0wa2	Alignment	not modelled	50.9	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
60	c5jkjA_	Alignment	not modelled	50.9	30	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
61	c1e3hA_	Alignment	not modelled	50.7	24	PDB header: polyribonucleotide transferase Chain: A: PDB Molecule: guanosine pentaphosphate synthetase; PDBTitle: semet derivative of streptomyces antibioticus pnpase/gpsi enzyme
62	c6fikA_	Alignment	not modelled	50.0	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
63	c3n5iC_	Alignment	not modelled	49.3	14	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
64	c2iyaB_	Alignment	not modelled	47.6	18	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
65	c3u1kB_	Alignment	not modelled	45.7	30	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase 1, mitochondrial; PDBTitle: crystal structure of human pnpase
66	c3cdiA_	Alignment	not modelled	44.1	36	PDB header: transferase Chain: A: PDB Molecule: polynucleotide phosphorylase; PDBTitle: crystal structure of e. coli pnpase
67	d2hmfa3	Alignment	not modelled	42.7	26	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
68	c5xexC_	Alignment	not modelled	42.5	33	PDB header: transferase Chain: C: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of s.aureus pnpase catalytic domain
69	c5yjiE_	Alignment	not modelled	40.6	33	PDB header: cytosolic protein Chain: E: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of pnpase from staphylococcus epidermidis
70	c6e6uA_	Alignment	not modelled	40.4	31	PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc
71	c4aimA_	Alignment	not modelled	40.4	29	PDB header: transferase/peptide Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rnase e2 recognition peptide
72	c1e3pA_	Alignment	not modelled	40.0	26	PDB header: polyribonucleotide transferase Chain: A: PDB Molecule: guanosine pentaphosphate synthetase; PDBTitle: tungstate derivative of streptomyces antibioticus pnpase/2 gpsi enzyme
73	c4am3A_	Alignment	not modelled	39.1	27	PDB header: transferase/rna Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rna
74	c4fleA_	Alignment	not modelled	38.5	13	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
75	c4z8zA_	Alignment	not modelled	37.2	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
76	d1b65a_	Alignment	not modelled	35.8	16	Fold: DmpA/Argj-like Superfamily: DmpA/Argj-like Family: DmpA-like
77	c2hunB_	Alignment	not modelled	35.5	15	PDB header: lyase Chain: B: PDB Molecule: 336aa long hypothetical dtdp-glucose 4,6-dehydratase;

						PDBTitle: crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
78	c4qloA	Alignment	not modelled	35.3	25	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
79	c2vz8A	Alignment	not modelled	35.1	18	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
80	c2q1uA	Alignment	not modelled	34.6	24	PDB header: sugar binding protein Chain: A: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
81	c5d6oB	Alignment	not modelled	34.4	24	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
82	d1p3y1	Alignment	not modelled	34.1	8	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
83	c5w8pA	Alignment	not modelled	33.6	38	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
84	d2b61a1	Alignment	not modelled	33.4	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
85	c3lu1C	Alignment	not modelled	32.7	14	PDB header: isomerase Chain: C: PDB Molecule: wbgu; PDBTitle: crystal structure analysis of wbgu: a udp-galnac 4-epimerase
86	c4aidC	Alignment	not modelled	30.9	27	PDB header: transferase/peptide Chain: C: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rnae e2 recognition peptide
87	c3sxpD	Alignment	not modelled	30.7	15	PDB header: isomerase Chain: D: PDB Molecule: adp-l-glycero-d-mannoheptose-6-epimerase; PDBTitle: crystal structure of helicobacter pylori adp-l-glycero-d-manno-2 heptose-6-epimerase (rfad, hp0859)
88	c3sjrB	Alignment	not modelled	30.5	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknown function protein cv_1783 from2 chromobacterium violaceum atcc 12472
89	c2c2nA	Alignment	not modelled	30.4	20	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of human mitochondrial malonyltransferase
90	c4j0dB	Alignment	not modelled	29.6	20	PDB header: hydrolase Chain: B: PDB Molecule: tannase; PDBTitle: tannin acyl hydrolase from lactobacillus plantarum (cadmium)
91	d1r88a	Alignment	not modelled	28.4	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
92	c3ezwD	Alignment	not modelled	27.9	24	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
93	c3kwpA	Alignment	not modelled	27.9	17	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
94	c3flaB	Alignment	not modelled	27.6	31	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
95	d1uh5a	Alignment	not modelled	27.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
96	d1wdea	Alignment	not modelled	27.3	16	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
97	d1vhqa	Alignment	not modelled	26.9	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfp1
98	c3wxiB	Alignment	not modelled	26.5	18	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
99	c3krnB	Alignment	not modelled	26.5	27	PDB header: hydrolase Chain: B: PDB Molecule: protein c14a4.5, confirmed by transcript evidence; PDBTitle: crystal structure of c. elegans cell-death-related nuclease 5(crn-5)
100	d1dqza	Alignment	not modelled	26.5	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
101	d2pl5a1	Alignment	not modelled	26.4	30	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
102	c2nrb	Alignment	not modelled	26.4	21	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1;

102	c2pr2B_	Alignment	not modelled	20.4	41	PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed with omp PDB header: transferase
103	c3vv1A_	Alignment	not modelled	25.9	25	Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
104	d1e6ua_	Alignment	not modelled	25.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	c5hw4C_	Alignment	not modelled	25.6	21	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
106	c6d6kB_	Alignment	not modelled	25.0	33	PDB header: transferase Chain: B; PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of polyribonucleotide nucleotidyltransferase from2 acinetobacter baumannii
107	d1t2aa_	Alignment	not modelled	24.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
108	c1t2aC_	Alignment	not modelled	24.7	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
109	d2a35a1	Alignment	not modelled	24.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
110	d2vata1	Alignment	not modelled	24.4	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
111	c3s3uB_	Alignment	not modelled	23.8	27	PDB header: transferase Chain: B; PDB Molecule: cysteine transferase; PDBTitle: crystal structure of uncleaved thnt t282c
112	c3enkB_	Alignment	not modelled	23.4	29	PDB header: isomerase Chain: B; PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from burkholderia2 pseudomallei
113	c1cr6A_	Alignment	not modelled	23.2	17	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
114	c3l80A_	Alignment	not modelled	22.9	10	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
115	c2vz8B_	Alignment	not modelled	22.7	18	PDB header: transferase Chain: B; PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
116	c3l3bA_	Alignment	not modelled	20.7	21	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
117	d2i7pa1	Alignment	not modelled	20.6	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like