Phyre^2

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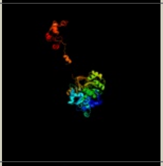
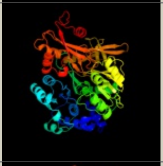
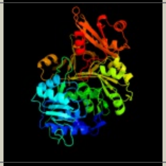
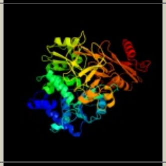
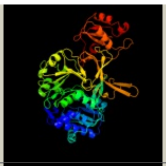
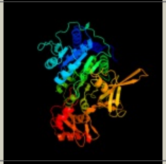
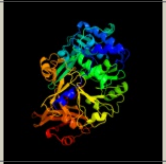
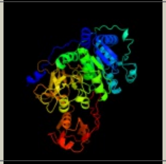
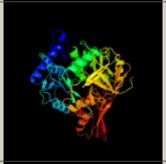
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vsqA_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**surfactin synthetase subunit 3; **PDBTitle:** structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
2	d1pg4a_	Alignment		100.0	18	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
3	d1ry2a_	Alignment		100.0	19	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
4	c3tsyA_	Alignment		100.0	19	**PDB header:**ligase, transferase **Chain:** A: **PDB Molecule:**fusion protein 4-coumarate--coa ligase 1, resveratrol **PDBTitle:** 4-coumaroyl-coa ligase::stilbene synthase fusion protein
5	d3cw9a1	Alignment		100.0	19	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
6	d1mdba_	Alignment		100.0	19	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
7	c3e7wA_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** crystal structure of dlta: implications for the reaction2 mechanism of non-ribosomal peptide synthetase (nrps)3 adenylation domains
8	c3etcB_	Alignment		100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-binding protein; **PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
9	c3ni2A_	Alignment		100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**4-coumarate:coa ligase; **PDBTitle:** crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
10	c3gqwB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fatty acid amp ligase; **PDBTitle:** crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
11	c3kxwA_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b; **PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila

12	c3iteB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sidn siderophore synthetase; **PDBTitle:** the third adenylation domain of the fungal sidn non-2 ribosomal peptide synthetase
13	c3eynB_	Alignment		100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acyl-coenzyme a synthetase acsm2a; **PDBTitle:** crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
14	c2d1tA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**luciferin 4-monooxygenase; **PDBTitle:** crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
15	d1amua_	Alignment		100.0	18	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
16	c2v7bB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
17	c1amuB_	Alignment		100.0	16	**PDB header:**peptide synthetase **Chain:** B: **PDB Molecule:**gramicidin synthetase 1; **PDBTitle:** phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
18	d1v25a_	Alignment		100.0	22	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
19	c3nyrA_	Alignment		100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
20	c3iplB_	Alignment		100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
21	d1lcia_	Alignment	not modelled	100.0	18	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
22	c3g7sA_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
23	c3dhvA_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
24	c3l8cA_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** structure of probable d-alanine--poly(phosphoribitol) ligase2 subunit-1 from streptococcus pyogenes
25	c3o82B_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
26	c3o82A_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
27	c3ivrA_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative long-chain-fatty-acid coa ligase; **PDBTitle:** crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009
						PDB header:ligase

28	c3e53A_	Alignment	not modelled	100.0	22	**Chain:** A: **PDB Molecule:**fatty-acid-coa ligase fadd28; **PDBTitle:** crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis
29	c2y4oA_	Alignment	not modelled	100.0	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak2 in complex with phenylacetyl adenylate
30	c2y27B_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
31	c3qovD_	Alignment	not modelled	100.0	13	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
32	c3hguB_	Alignment	not modelled	100.0	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ehpf; **PDBTitle:** structure of phenazine antibiotic biosynthesis protein
33	c3laxA_	Alignment	not modelled	99.4	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
34	d1iuqa_	Alignment		98.4	14	**Fold:**Glycerol-3-phosphate (1)-acyltransferase **Superfamily:**Glycerol-3-phosphate (1)-acyltransferase **Family:**Glycerol-3-phosphate (1)-acyltransferase
35	d2z67a1	Alignment	not modelled	69.4	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
36	c3ewbX_	Alignment	not modelled	61.0	10	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
37	d1nvma2	Alignment	not modelled	43.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
38	d1ky8a_	Alignment	not modelled	43.2	15	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
39	c1nvmG_	Alignment	not modelled	39.5	10	**PDB header:**lyase/oxidoreductase **Chain:** G: **PDB Molecule:**4-hydroxy-2-oxovalerate aldolase; **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
40	d3bc8a1	Alignment	not modelled	38.8	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
41	c3eegB_	Alignment	not modelled	36.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
42	c2i2xD_	Alignment	not modelled	36.4	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
43	c3bcxA_	Alignment	not modelled	34.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
44	c2ov3A_	Alignment	not modelled	34.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein component of an abc **PDBTitle:** crystal structure of 138-173 znua deletion mutant plus zinc2 bound
45	c2ec5B_	Alignment	not modelled	33.8	19	**PDB header:**toxin **Chain:** B: **PDB Molecule:**dermonecrotic toxin; **PDBTitle:** crystal structures reveal a thiol-protease like catalytic triad in the2 c-terminal region of pasteurella multocida toxin
46	c2o1eB_	Alignment	not modelled	33.6	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ycdh; **PDBTitle:** crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
47	c1bmtB_	Alignment	not modelled	33.1	7	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
48	d1ja1a1	Alignment	not modelled	30.9	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
49	d1hrua_	Alignment	not modelled	30.5	21	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
50	c3ezxA_	Alignment	not modelled	30.5	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1; **PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein
51	c1ydnA_	Alignment	not modelled	28.8	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
52	d1f06a2	Alignment	not modelled	28.3	14	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain

						Family: Dihydrodipicolinate reductase-like
53	d2trcp_	Alignment	not modelled	26.8	50	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Phosducin
54	d1f20a1	Alignment	not modelled	26.1	11	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
55	c2cw6B_	Alignment	not modelled	25.7	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa lyase, mitochondrial; **PDBTitle:** crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
56	c2ps3A_	Alignment	not modelled	24.4	9	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
57	d1pq4a_	Alignment	not modelled	23.2	18	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
58	d1ddga1	Alignment	not modelled	21.7	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
59	d3bula2	Alignment	not modelled	21.1	7	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
60	d2ayia1	Alignment	not modelled	20.8	10	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
61	c2dkjB_	Alignment	not modelled	20.4	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
62	d1jcua_	Alignment	not modelled	19.5	25	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
63	c3bleA_	Alignment	not modelled	18.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
64	c2kkhA_	Alignment	not modelled	18.5	6	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
65	c2ga7A_	Alignment	not modelled	18.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
66	c2ywiA_	Alignment	not modelled	18.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
67	c2jg7G_	Alignment	not modelled	18.1	8	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**antiquitin; **PDBTitle:** crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
68	d1z7wa1	Alignment	not modelled	17.9	13	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
69	c3ivuB_	Alignment	not modelled	17.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
70	c1k98A_	Alignment	not modelled	17.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
71	c1l9xA_	Alignment	not modelled	17.1	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
72	d1l9xa_	Alignment	not modelled	17.1	3	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
73	c2zy3A_	Alignment	not modelled	17.0	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
74	c3hjtB_	Alignment	not modelled	16.8	20	**PDB header:**cell adhesion, transport protein **Chain:** B: **PDB Molecule:**lmb; **PDBTitle:** structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
75	c3cx3A_	Alignment	not modelled	16.5	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
76	c3eqnB_	Alignment	not modelled	16.4	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucan 1,3-beta-glucosidase; **PDBTitle:** crystal structure of beta-1,3-glucanase from phanerochaete2 chrysosporium (lam55a)
77	d2ewca1	Alignment	not modelled	15.9	6	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like

						Family: YjgF/L-PSP
78	d1cpza_	Alignment	not modelled	15.9	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
79	d1h80a_	Alignment	not modelled	15.0	38	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**iota-carrageenase
80	d1dfoa_	Alignment	not modelled	14.9	10	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
81	c3gjzB_	Alignment	not modelled	14.6	18	**PDB header:**immune system **Chain:** B: **PDB Molecule:**microcin immunity protein mccf; **PDBTitle:** crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
82	c3i7tA_	Alignment	not modelled	14.5	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rv2704, a member of highly conserved2 yjgf/yer057c/uk114 family, from mycobacterium tuberculosis
83	c2ogwB_	Alignment	not modelled	14.4	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua **PDBTitle:** structure of abc type zinc transporter from e. coli
84	d1a0rp_	Alignment	not modelled	14.2	50	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Phosducin
85	c2e11B_	Alignment	not modelled	14.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrolase; **PDBTitle:** crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
86	c2iyjA_	Alignment	not modelled	14.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol disulfide interchange protein dsbc; **PDBTitle:** crystal structure of the n-terminal dimer domain of e.coli2 dsbc
87	d1vjoa_	Alignment	not modelled	13.6	7	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
88	c1sfeA_	Alignment	not modelled	13.6	17	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**ada o6-methylguanine-dna methyltransferase; **PDBTitle:** ada o6-methylguanine-dna methyltransferase from escherichia coli
89	c3nnkC_	Alignment	not modelled	13.6	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ureidoglycine-glyoxylate aminotransferase; **PDBTitle:** biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
90	c3mfqB_	Alignment	not modelled	13.4	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
91	c3jurA_	Alignment	not modelled	13.1	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-poly-alpha-d-galacturonosidase; **PDBTitle:** the crystal structure of a hyperthermoactive exopolygalacturonase from2 thermotoga maritima
92	d2ch1a1	Alignment	not modelled	13.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
93	c3b46B_	Alignment	not modelled	13.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase bna3; **PDBTitle:** crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
94	d1kola2	Alignment	not modelled	12.9	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
95	c2l69A_	Alignment	not modelled	12.3	16	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
96	c3hkxA_	Alignment	not modelled	12.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidase; **PDBTitle:** crystal structure analysis of an amidase from nesterenkonia sp.
97	c3kjjL_	Alignment	not modelled	12.0	11	**PDB header:**unknown function **Chain:** L: **PDB Molecule:**nmb1025 protein; **PDBTitle:** crystal structure of nmb1025, a member of yjgf protein family, from2 neisseria meningitidis (hexagonal crystal form)
98	d1li4a2	Alignment	not modelled	11.6	17	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
99	c3d64A_	Alignment	not modelled	11.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei