



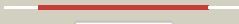









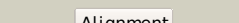

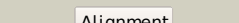



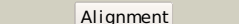







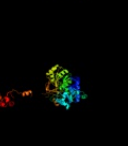



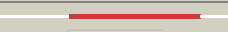
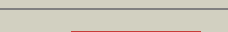
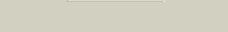
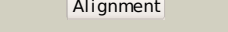



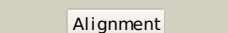
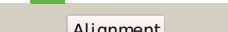
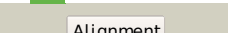
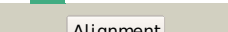
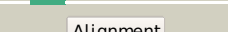
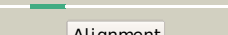
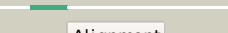



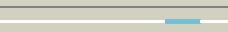




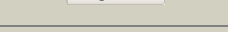
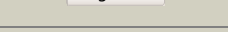


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlpg4a_</a>	 Alignment		100.0	21	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
2	<a href="#">dlmdba_</a>	 Alignment		100.0	24	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
3	<a href="#">dlry2a_</a>	 Alignment		100.0	23	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
4	<a href="#">c2vsqA_</a>	 Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
5	<a href="#">c3e7wA_</a>	 Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 1; <b>PDBTitle:</b> crystal structure of dltA: implications for the reaction2 mechanism of non-ribosomal peptide synthetase (nrps)3 adenylation domains
6	<a href="#">d3cw9a1</a>	 Alignment		100.0	26	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
7	<a href="#">c3eynB_</a>	 Alignment		100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coenzyme a synthetase acsm2a; <b>PDBTitle:</b> crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
8	<a href="#">c3ni2A_</a>	 Alignment		100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-coumarate:coa ligase; <b>PDBTitle:</b> crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
9	<a href="#">c3etcB_</a>	 Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> amp-binding protein; <b>PDBTitle:</b> 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
10	<a href="#">c2d1tA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> luciferin 4-monooxygenase; <b>PDBTitle:</b> crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
11	<a href="#">dlamua_</a>	 Alignment		100.0	20	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like

12	<a href="#">c2v7bB_</a>	Alignment		100.0	26 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoate-coenzyme a ligase; <b>PDBTitle:</b> crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
13	<a href="#">c1amuB_</a>	Alignment		100.0	20 <b>PDB header:</b> peptide synthetase <b>Chain:</b> B: <b>PDB Molecule:</b> gramicidin synthetase 1; <b>PDBTitle:</b> phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
14	<a href="#">c3gqwB_</a>	Alignment		100.0	22 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid amp ligase; <b>PDBTitle:</b> crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
15	<a href="#">c3dhvA_</a>	Alignment		100.0	19 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-poly(phosphoribitol) ligase; <b>PDBTitle:</b> crystal structure of dltA protein in complex with d-alanine2 adenylate
16	<a href="#">d1lclA_</a>	Alignment		100.0	26 <b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
17	<a href="#">c3kxwA_</a>	Alignment		100.0	22 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> saframycin mx1 synthetase b; <b>PDBTitle:</b> the crystal structure of fatty acid amp ligase from legionella2 pneumophila
18	<a href="#">c3tsyA_</a>	Alignment		100.0	24 <b>PDB header:</b> ligase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein 4-coumarate--coa ligase 1, resveratrol <b>PDBTitle:</b> 4-coumaroyl-coa ligase::stilbene synthase fusion protein
19	<a href="#">c3iteB_</a>	Alignment		100.0	20 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> sidn siderophore synthetase; <b>PDBTitle:</b> the third adenylation domain of the fungal sidn non-2 ribosomal peptide synthetase
20	<a href="#">d1v25a_</a>	Alignment		100.0	25 <b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
21	<a href="#">c3l8cA_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 1; <b>PDBTitle:</b> structure of probable d-alanine--poly(phosphoribitol) ligase2 subunit-1 from streptococcus pyogenes
22	<a href="#">c3iplB_</a>	Alignment	not modelled	100.0	24 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
23	<a href="#">c3nyrA_</a>	Alignment	not modelled	100.0	26 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl-coa ligase; <b>PDBTitle:</b> malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
24	<a href="#">c3g7sA_</a>	Alignment	not modelled	100.0	28 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> long-chain-fatty-acid--coa ligase (fadd-1); <b>PDBTitle:</b> crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
25	<a href="#">c3o82B_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide arylation enzyme; <b>PDBTitle:</b> structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
26	<a href="#">c3o82A_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide arylation enzyme; <b>PDBTitle:</b> structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
27	<a href="#">c3ivrA_</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> putative long-chain-fatty-acid coa ligase; <b>PDBTitle:</b> crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009

28	<a href="#">c3e53A_</a>	 <div>Alignment</div>	not modelled	100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty-acid-coa ligase fadd28; <b>PDBTitle:</b> crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis
29	<a href="#">c2y4oA_</a>	 <div>Alignment</div>	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of paak2 in complex with phenylacetyl adenylate
30	<a href="#">c3qovD_</a>	 <div>Alignment</div>	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
31	<a href="#">c2y27B_</a>	 <div>Alignment</div>	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
32	<a href="#">c3laxA_</a>	 <div>Alignment</div>	not modelled	99.5	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
33	<a href="#">c3hguB_</a>	 <div>Alignment</div>	not modelled	99.4	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> ehpf; <b>PDBTitle:</b> structure of phenazine antibiotic biosynthesis protein
34	<a href="#">d2aya1a1</a>	 <div>Alignment</div>	not modelled	86.2	20	<b>Fold:</b> Thermophilic metalloprotease-like <b>Superfamily:</b> Thermophilic metalloprotease-like <b>Family:</b> Thermophilic metalloprotease (M29)
35	<a href="#">d1f06a2</a>	 <div>Alignment</div>	not modelled	53.2	31	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
36	<a href="#">d1pl8a2</a>	 <div>Alignment</div>	not modelled	52.1	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
37	<a href="#">d1p0fa2</a>	 <div>Alignment</div>	not modelled	50.6	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
38	<a href="#">d1d1ta2</a>	 <div>Alignment</div>	not modelled	48.9	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
39	<a href="#">d1e3ia2</a>	 <div>Alignment</div>	not modelled	47.5	5	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
40	<a href="#">d1zjca1</a>	 <div>Alignment</div>	not modelled	44.7	18	<b>Fold:</b> Thermophilic metalloprotease-like <b>Superfamily:</b> Thermophilic metalloprotease-like <b>Family:</b> Thermophilic metalloprotease (M29)
41	<a href="#">d2jhf2</a>	 <div>Alignment</div>	not modelled	44.5	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
42	<a href="#">c2ywiA_</a>	 <div>Alignment</div>	not modelled	42.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
43	<a href="#">d1ykfa2</a>	 <div>Alignment</div>	not modelled	39.4	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
44	<a href="#">d1e3ja2</a>	 <div>Alignment</div>	not modelled	36.7	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
45	<a href="#">c1vs3B_</a>	 <div>Alignment</div>	not modelled	34.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> trna pseudouridine synthase a; <b>PDBTitle:</b> crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
46	<a href="#">d1piwa2</a>	 <div>Alignment</div>	not modelled	33.3	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
47	<a href="#">d1u3wa2</a>	 <div>Alignment</div>	not modelled	33.3	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
48	<a href="#">c3smaD_</a>	 <div>Alignment</div>	not modelled	32.9	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> frbf; <b>PDBTitle:</b> a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
49	<a href="#">d1l9xa_</a>	 <div>Alignment</div>	not modelled	32.9	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
50	<a href="#">c1l9xA_</a>	 <div>Alignment</div>	not modelled	32.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> structure of gamma-glutamyl hydrolase
51	<a href="#">d1cdoa2</a>	 <div>Alignment</div>	not modelled	32.1	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
52	<a href="#">d2fzwa2</a>	 <div>Alignment</div>	not modelled	31.0	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding

54	<a href="#">dlj7ja_</a>	Alignment	not modelled	27.7	7	<b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
55	<a href="#">dlilga2</a>	Alignment	not modelled	25.5	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
56	<a href="#">dlg9sa_</a>	Alignment	not modelled	24.9	9	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
57	<a href="#">c3ippA_</a>	Alignment	not modelled	23.4	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase ynj <sub>e</sub> ; <b>PDBTitle:</b> crystal structure of sulfur-free ynj <sub>e</sub>
58	<a href="#">dlja1a1</a>	Alignment	not modelled	23.1	31	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
59	<a href="#">cluarA_</a>	Alignment	not modelled	22.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese; <b>PDBTitle:</b> crystal structure of rhodanese from thermus thermophilus hb8
60	<a href="#">c3bcxA_</a>	Alignment	not modelled	22.4	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- <b>PDBTitle:</b> e1 dehydrase
61	<a href="#">c3ewbX_</a>	Alignment	not modelled	22.0	9	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
62	<a href="#">c3isIA_</a>	Alignment	not modelled	21.8	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine catabolism protein pucg; <b>PDBTitle:</b> crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
63	<a href="#">clc4kA_</a>	Alignment	not modelled	21.5	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (ornithine decarboxylase); <b>PDBTitle:</b> ornithine decarboxylase mutant (gly121tyr)
64	<a href="#">dlf20a1</a>	Alignment	not modelled	21.3	22	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
65	<a href="#">dlz7wa1</a>	Alignment	not modelled	20.8	11	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
66	<a href="#">d2ch1a1</a>	Alignment	not modelled	20.6	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
67	<a href="#">c2jwB_</a>	Alignment	not modelled	20.6	5	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein tol <sub>r</sub> ; <b>PDBTitle:</b> solution structure of periplasmic domain of tol <sub>r</sub> from h.2 influenzae with saxes data
68	<a href="#">d2nyga1</a>	Alignment	not modelled	20.5	27	<b>Fold:</b> TTHA0583/YokD-like <b>Superfamily:</b> TTHA0583/YokD-like <b>Family:</b> Aminoglycoside 3-N-acetyltransferase-like
69	<a href="#">dliz0a2</a>	Alignment	not modelled	20.4	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
70	<a href="#">c2cw6B_</a>	Alignment	not modelled	19.8	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase, mitochondrial; <b>PDBTitle:</b> crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
71	<a href="#">dl1luA2</a>	Alignment	not modelled	19.3	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
72	<a href="#">c3e4fB_</a>	Alignment	not modelled	18.2	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside n3-acetyltransferase; <b>PDBTitle:</b> crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
73	<a href="#">c2pfuA_</a>	Alignment	not modelled	17.5	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> biopolymer transport exbd protein; <b>PDBTitle:</b> nmr strcture determination of the periplasmic domain of exbd from2 e.coli
74	<a href="#">c3eegB_</a>	Alignment	not modelled	17.3	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
75	<a href="#">c3hjtB_</a>	Alignment	not modelled	16.9	13	<b>PDB header:</b> cell adhesion, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lmb; <b>PDBTitle:</b> structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
76	<a href="#">c2zy3A_</a>	Alignment	not modelled	16.8	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase
77	<a href="#">clydnA_</a>	Alignment	not modelled	16.6	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target l <sub>r</sub> 35.
78	<a href="#">dlkola2</a>	Alignment	not modelled	16.6	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
79	<a href="#">dlvj0a2</a>	Alignment	not modelled	16.1	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains

					<b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
80	<a href="#">dls6ua_</a>	Alignment	not modelled	15.9	23 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
81	<a href="#">d1jqba2</a>	Alignment	not modelled	15.6	10 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
82	<a href="#">c2vycA_</a>	Alignment	not modelled	15.3	25 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> biodegradative arginine decarboxylase; <b>PDBTitle:</b> crystal structure of acid induced arginine decarboxylase2 from e. coli
83	<a href="#">c2ofhX_</a>	Alignment	not modelled	15.3	21 <b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
84	<a href="#">d1jvba2</a>	Alignment	not modelled	14.9	7 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
85	<a href="#">c1y3kA_</a>	Alignment	not modelled	14.8	21 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the apo form of the fifth domain of2 menkes protein
86	<a href="#">d2vqa1</a>	Alignment	not modelled	14.7	17 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> F112-like
87	<a href="#">c2vqa_</a>	Alignment	not modelled	14.7	17 <b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 13.2 kda protein; <b>PDBTitle:</b> structure of a dna binding winged-helix protein, f-112,2 from sulfolobus spindle-shaped virus 1.
88	<a href="#">d2okga1</a>	Alignment	not modelled	14.4	8 <b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
89	<a href="#">c2zbcH_</a>	Alignment	not modelled	14.1	20 <b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 83aa long hypothetical transcriptional regulator asnc; <b>PDBTitle:</b> crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
90	<a href="#">d1udxa3</a>	Alignment	not modelled	14.0	23 <b>Fold:</b> Obg GTP-binding protein C-terminal domain <b>Superfamily:</b> Obg GTP-binding protein C-terminal domain <b>Family:</b> Obg GTP-binding protein C-terminal domain
91	<a href="#">d1ddga1</a>	Alignment	not modelled	13.8	21 <b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
92	<a href="#">d1pn0a3</a>	Alignment	not modelled	13.8	13 <b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> PHBH-like
93	<a href="#">c2ps3A_</a>	Alignment	not modelled	13.6	13 <b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> high-affinity zinc uptake system protein znua; <b>PDBTitle:</b> structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
94	<a href="#">d2cg4a2</a>	Alignment	not modelled	13.4	11 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
95	<a href="#">c3bleA_</a>	Alignment	not modelled	13.2	8 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citramalate synthase from leptospira interrogans; <b>PDBTitle:</b> crystal structure of the catalytic domain of licms in2 complexed with malonate
96	<a href="#">c2l66B_</a>	Alignment	not modelled	13.1	27 <b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, abrb family; <b>PDBTitle:</b> the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
97	<a href="#">c3olhA_</a>	Alignment	not modelled	13.0	8 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> human 3-mercaptopyruvate sulfurtransferase
98	<a href="#">c2ga7A_</a>	Alignment	not modelled	12.8	22 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
99	<a href="#">c3g23A_</a>	Alignment	not modelled	12.5	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ld-carboxypeptidase a; <b>PDBTitle:</b> crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution