







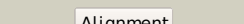

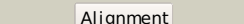

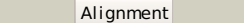

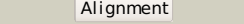

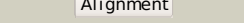

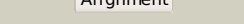

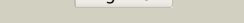



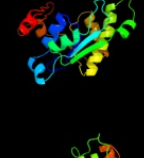

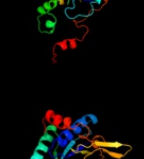



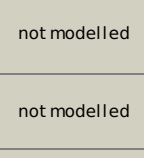


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3a2kB_</a>	 Alignment		100.0	16	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna(ile)-lysidine synthase; <b>PDBTitle:</b> crystal structure of tils complexed with trna
2	<a href="#">c2e21A_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysidine synthase; <b>PDBTitle:</b> crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
3	<a href="#">c1ni5A_</a>	 Alignment		100.0	15	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell cycle protein mesj; <b>PDBTitle:</b> structure of the mesj pp-atpase from escherichia coli
4	<a href="#">d1ni5a1</a>	 Alignment		100.0	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
5	<a href="#">d1wy5a1</a>	 Alignment		100.0	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
6	<a href="#">d2c5sa1</a>	 Alignment		100.0	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
7	<a href="#">c2nz2A_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
8	<a href="#">c1vl2C_</a>	 Alignment		100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
9	<a href="#">c3k32D_</a>	 Alignment		99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein mj0690; <b>PDBTitle:</b> the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
10	<a href="#">c1k97A_</a>	 Alignment		99.9	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
11	<a href="#">c1kh2D_</a>	 Alignment		99.9	22	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> argininosuccinate synthetase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp


12	<a href="#">dlj20a1</a>	Alignment		99.9	25	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
13	<a href="#">dlvl2a1</a>	Alignment		99.9	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
14	<a href="#">dlk92a1</a>	Alignment		99.9	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
15	<a href="#">c2dplA_</a>	Alignment		99.9	18	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit b; <b>PDBTitle:</b> crystal structure of the gmp synthase from pyrococcus horikoshii ot3
16	<a href="#">c2hmaA_</a>	Alignment		99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable trna (5-methylaminomethyl-2-thiouridylate)- <b>PDBTitle:</b> the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
17	<a href="#">c2derA_</a>	Alignment		99.9	19	<b>PDB header:</b> transferase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> trna-specific 2-thiouridylase mnma; <b>PDBTitle:</b> cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
18	<a href="#">c2c5sA_</a>	Alignment		99.9	22	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> probable thiamine biosynthesis protein thii; <b>PDBTitle:</b> crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
19	<a href="#">dl1sura_</a>	Alignment		99.9	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
20	<a href="#">c3p52B_</a>	Alignment		99.9	15	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
21	<a href="#">c3tqiB_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> structure of the gmp synthase (guaa) from coxiella burnetii
22	<a href="#">dlgpmal</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
23	<a href="#">c2o8vA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> paps reductase in a covalent complex with thioredoxin c35a
24	<a href="#">dlvbkal</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
25	<a href="#">dlzuna1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
26	<a href="#">c2goyC_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> adenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
27	<a href="#">dlxnga1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
28	<a href="#">c2ywcC_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp



55	<a href="#">c3ilvA</a>	Alignment	not modelled	97.4	16	<b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
56	<a href="#">c2pfsA</a>	Alignment	not modelled	95.2	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of universal stress protein from nitrosomonas2 europaea
57	<a href="#">c3nbmA</a>	Alignment	not modelled	93.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, lactose-specific iibc components; <b>PDBTitle:</b> the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
58	<a href="#">d1tq8a</a>	Alignment	not modelled	92.7	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
59	<a href="#">c3e15D</a>	Alignment	not modelled	92.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> 6-phosphogluconolactonase from plasmodium vivax
60	<a href="#">d1ne7a</a>	Alignment	not modelled	91.3	11	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> NagB-like
61	<a href="#">c3hgmD</a>	Alignment	not modelled	90.5	24	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> universal stress protein tead; <b>PDBTitle:</b> universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
62	<a href="#">d2z3va1</a>	Alignment	not modelled	90.5	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
63	<a href="#">c3oc6A</a>	Alignment	not modelled	90.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
64	<a href="#">c3n0vD</a>	Alignment	not modelled	90.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
65	<a href="#">d1fsfa</a>	Alignment	not modelled	89.1	11	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> NagB-like
66	<a href="#">c2l2qA</a>	Alignment	not modelled	88.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, cellobiose-specific iib component (cela); <b>PDBTitle:</b> solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
67	<a href="#">d1q77a</a>	Alignment	not modelled	86.7	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
68	<a href="#">c2j0eA</a>	Alignment	not modelled	86.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
69	<a href="#">c3hn6D</a>	Alignment	not modelled	85.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> glucosamine-6-phosphate deaminase; <b>PDBTitle:</b> crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
70	<a href="#">c3o1lB</a>	Alignment	not modelled	85.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
71	<a href="#">c2bkxB</a>	Alignment	not modelled	85.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine-6-phosphate deaminase; <b>PDBTitle:</b> structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
72	<a href="#">d2gm3a1</a>	Alignment	not modelled	84.3	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
73	<a href="#">c3p9xB</a>	Alignment	not modelled	82.2	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
74	<a href="#">c3mt0A</a>	Alignment	not modelled	79.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa1789; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
75	<a href="#">c2o0mA</a>	Alignment	not modelled	78.3	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, sorc family; <b>PDBTitle:</b> the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
76	<a href="#">d2o0ma1</a>	Alignment	not modelled	78.3	13	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
77	<a href="#">c2j37W</a>	Alignment	not modelled	77.6	13	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
78	<a href="#">d1iiba</a>	Alignment	not modelled	77.5	13	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Lactose/Cellobiose specific IIB subunit
79	<a href="#">c3mcfF</a>	Alignment	not modelled	76.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dipicolinate synthase, b chain; <b>PDBTitle:</b> crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.

80	<a href="#">c3lqkA</a>	 Alignment	not modelled	75.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit b; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
81	<a href="#">c3zquA</a>	 Alignment	not modelled	74.9	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> structure of a probable aromatic acid decarboxylase
82	<a href="#">c3louB</a>	 Alignment	not modelled	74.2	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
83	<a href="#">c3icoA</a>	 Alignment	not modelled	74.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphoglucanactonase; <b>PDBTitle:</b> crystal structure of 6-phosphoglucanactonase from2 mycobacterium tuberculosis
84	<a href="#">d1p3y1</a>	 Alignment	not modelled	73.0	11	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
85	<a href="#">d1jmva</a>	 Alignment	not modelled	72.6	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
86	<a href="#">c1y89B</a>	 Alignment	not modelled	72.4	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> devb protein; <b>PDBTitle:</b> crystal structure of devb protein
87	<a href="#">c3loqA</a>	 Alignment	not modelled	72.1	20	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> the crystal structure of a universal stress protein from2 archaeoglobus fulgidus dsm 4304
88	<a href="#">d1meoa</a>	 Alignment	not modelled	72.0	18	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
89	<a href="#">d1rz3a</a>	 Alignment	not modelled	71.4	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
90	<a href="#">d2auna2</a>	 Alignment	not modelled	70.6	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> LD-carboxypeptidase A N-terminal domain-like
91	<a href="#">c3dloC</a>	 Alignment	not modelled	70.3	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> structure of universal stress protein from archaeoglobus fulgidus
92	<a href="#">d1odfa</a>	 Alignment	not modelled	70.2	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
93	<a href="#">c2ejbA</a>	 Alignment	not modelled	69.8	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
94	<a href="#">d1sbza</a>	 Alignment	not modelled	68.9	17	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
95	<a href="#">c3fh0A</a>	 Alignment	not modelled	68.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative universal stress protein kpn_01444; <b>PDBTitle:</b> crystal structure of putative universal stress protein kpn_01444 -2 atpase
96	<a href="#">c2yvka</a>	 Alignment	not modelled	66.6	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylthioribose-1-phosphate isomerase; <b>PDBTitle:</b> crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
97	<a href="#">c2ywrA</a>	 Alignment	not modelled	66.1	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of gar transformylase from aquifex2 aeolicus
98	<a href="#">c3obiC</a>	 Alignment	not modelled	64.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
99	<a href="#">d1liua3</a>	 Alignment	not modelled	62.5	21	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> Pyruvate kinase, C-terminal domain
100	<a href="#">d1ur4a</a>	 Alignment	not modelled	62.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
101	<a href="#">c1zrsB</a>	 Alignment	not modelled	61.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> wild-type ld-carboxypeptidase
102	<a href="#">c3cssA</a>	 Alignment	not modelled	61.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphoglucanactonase; <b>PDBTitle:</b> crystal structure of 6-phosphoglucanactonase from leishmania2 guyanensis



103	<a href="#">d1sq5a_</a>	Alignment		60.8	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
104	<a href="#">c3s3tD_</a>	Alignment	not modelled	60.0	17	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> nucleotide-binding protein, universal stress protein uspa <b>PDBTitle:</b> universal stress protein uspa from lactobacillus plantarum
105	<a href="#">d1ej0a_</a>	Alignment	not modelled	59.9	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> RNA methyltransferase FtsJ
106	<a href="#">c1qzwC_</a>	Alignment	not modelled	57.8	14	<b>PDB header:</b> signaling protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
107	<a href="#">c3lwdA_</a>	Alignment	not modelled	57.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
108	<a href="#">c2px0D_</a>	Alignment	not modelled	55.4	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> flagellar biosynthesis protein flhf; <b>PDBTitle:</b> crystal structure of flhf complexed with gmpnp/mg(2+)
109	<a href="#">c3qjgD_</a>	Alignment	not modelled	55.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> signal recognition protein epid; <b>PDBTitle:</b> epidermin biosynthesis protein epid from staphylococcus aureus
110	<a href="#">c2dumD_</a>	Alignment	not modelled	54.5	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein ph0823; <b>PDBTitle:</b> crystal structure of hypothetical protein, ph0823
111	<a href="#">c3dmdA_</a>	Alignment	not modelled	54.5	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle receptor; <b>PDBTitle:</b> structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
112	<a href="#">d1j8yf2</a>	Alignment	not modelled	54.3	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
113	<a href="#">d2g50a3</a>	Alignment	not modelled	54.1	13	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> Pyruvate kinase, C-terminal domain
114	<a href="#">c1mvlA_</a>	Alignment	not modelled	53.5	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ppc decarboxylase athal3a; <b>PDBTitle:</b> ppc decarboxylase mutant c175s
115	<a href="#">d1mvlA_</a>	Alignment	not modelled	53.5	12	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
116	<a href="#">c3nrbD_</a>	Alignment	not modelled	53.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
117	<a href="#">c3olqA_</a>	Alignment	not modelled	53.1	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein e; <b>PDBTitle:</b> the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
118	<a href="#">d1dv5a_</a>	Alignment	not modelled	52.0	25	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> apo-D-alanyl carrier protein
119	<a href="#">c1pbtA_</a>	Alignment	not modelled	49.7	24	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
120	<a href="#">d1pjqa3</a>	Alignment	not modelled	49.1	42	<b>Fold:</b> Siroheme synthase middle domains-like <b>Superfamily:</b> Siroheme synthase middle domains-like <b>Family:</b> Siroheme synthase middle domains-like