


























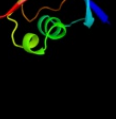


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1vj7B_</a>	 Alignment		100.0	50	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional rela/spot; <b>PDBTitle:</b> crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
2	<a href="#">d1vj7a1</a>	 Alignment		100.0	55	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
3	<a href="#">c3nr1A_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hd domain-containing protein 3; <b>PDBTitle:</b> a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
4	<a href="#">d1vj7a2</a>	 Alignment		100.0	45	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> RelA/SpoT domain
5	<a href="#">c3nqwB_</a>	 Alignment		100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cg11900; <b>PDBTitle:</b> a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
6	<a href="#">d2be3a1</a>	 Alignment		100.0	24	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> RelA/SpoT domain
7	<a href="#">c3l9dA_</a>	 Alignment		99.9	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative gtp pyrophosphokinase; <b>PDBTitle:</b> the crystal structure of smu.1046c from streptococcus mutans ua159
8	<a href="#">c2kmmA_</a>	 Alignment		99.9	46	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> guanosine-3',5'-bis(diphosphate) 3'- <b>PDBTitle:</b> solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
9	<a href="#">c3hvvB_</a>	 Alignment		99.9	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
10	<a href="#">c2ekiA_</a>	 Alignment		99.8	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> developmentally-regulated gtp-binding protein 1; <b>PDBTitle:</b> solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
11	<a href="#">d1tkea1</a>	 Alignment		99.7	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain

12	<a href="#">d1wxqa2</a>	Alignment		99.7	27	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
13	<a href="#">d1nyra2</a>	Alignment		99.6	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
14	<a href="#">c3ibwA_</a>	Alignment		99.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp pyrophosphokinase; <b>PDBTitle:</b> crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
15	<a href="#">c1wwtA_</a>	Alignment		99.4	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> solution structure of the tgs domain from human threonyl-2 trna synthetase
16	<a href="#">d1u8sa2</a>	Alignment		98.6	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Glycine cleavage system transcriptional repressor
17	<a href="#">c1tkeA_</a>	Alignment		98.5	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
18	<a href="#">c2dwqB_</a>	Alignment		98.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> thermus thermophilus ychf gtp-binding protein
19	<a href="#">c2ohfA_</a>	Alignment		98.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein 9; <b>PDBTitle:</b> crystal structure of human ola1 in complex with amppcp
20	<a href="#">c1wxqA_</a>	Alignment		98.2	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
21	<a href="#">d1sc6a3</a>	Alignment	not modelled	98.1	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
22	<a href="#">c1jalA_</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yachf protein; <b>PDBTitle:</b> yachf protein (hi0393)
23	<a href="#">c1ni3A_</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> yachf gtp-binding protein; <b>PDBTitle:</b> structure of the schizosaccharomyces pombe yachf gtpase
24	<a href="#">c1u8sB_</a>	Alignment		97.9	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> glycine cleavage system transcriptional <b>PDBTitle:</b> crystal structure of putative glycine cleavage system2 transcriptional repressor
25	<a href="#">d2f1fa1</a>	Alignment	not modelled	97.9	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
26	<a href="#">d1ygya3</a>	Alignment	not modelled	97.8	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
27	<a href="#">d2pc6a2</a>	Alignment	not modelled	97.8	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
						<b>Fold:</b> Ferredoxin-like

28	<a href="#">d2fgca2</a>	Alignment	not modelled	97.8	18	<b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
29	<a href="#">c1qf6A</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
30	<a href="#">c2pc6C</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> probable acetolactate synthase isozyme iii (small subunit); <b>PDBTitle:</b> crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
31	<a href="#">c1nyqA</a>	Alignment	not modelled	97.7	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase 1; <b>PDBTitle:</b> structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
32	<a href="#">c2fgcA</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase, small subunit; <b>PDBTitle:</b> crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
33	<a href="#">c2f1fA</a>	Alignment	not modelled	97.5	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase isozyme iii small subunit; <b>PDBTitle:</b> crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
34	<a href="#">d1zpva1</a>	Alignment	not modelled	97.4	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> SP0238-like
35	<a href="#">c2nyiB</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> unknown protein; <b>PDBTitle:</b> crystal structure of an unknown protein from galdieria2 sulphuraria
36	<a href="#">c1y7pB</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein af1403; <b>PDBTitle:</b> 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
37	<a href="#">d1u8sa1</a>	Alignment	not modelled	97.2	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Glycine cleavage system transcriptional repressor
38	<a href="#">c3n0vD</a>	Alignment	not modelled	96.8	5	<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
39	<a href="#">c1ybaC</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> the active form of phosphoglycerate dehydrogenase
40	<a href="#">c3k5pA</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
41	<a href="#">c3nrbD</a>	Alignment	not modelled	96.3	6	<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
42	<a href="#">c1ygyA</a>	Alignment	not modelled	96.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
43	<a href="#">d1phza1</a>	Alignment	not modelled	96.1	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phenylalanine metabolism regulatory domain
44	<a href="#">c2qmxB</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> prephenate dehydratase; <b>PDBTitle:</b> the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
45	<a href="#">c3o1lB</a>	Alignment	not modelled	96.0	10	<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
46	<a href="#">d2f06a2</a>	Alignment	not modelled	95.9	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> BT0572-like
47	<a href="#">c3mwbA</a>	Alignment	not modelled	95.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydratase; <b>PDBTitle:</b> the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aureescens to 2.0a
48	<a href="#">d1zud21</a>	Alignment	not modelled	95.5	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
49	<a href="#">c1rwuA</a>	Alignment	not modelled	95.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0250 protein ybed; <b>PDBTitle:</b> solution structure of conserved protein ybed from e. coli
50	<a href="#">d1rwua</a>	Alignment	not modelled	95.5	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> YbeD/HP0495-like <b>Family:</b> YbeD-like
51	<a href="#">d2qmwA2</a>	Alignment	not modelled	95.5	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phenylalanine metabolism regulatory domain
52	<a href="#">d2qgsa1</a>	Alignment	not modelled	95.4	19	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
						<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase;

53	<a href="#">c3louB_</a>	Alignment	not modelled	95.4	9	<b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
54	<a href="#">c3luyA_</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable chorismate mutase; <b>PDBTitle:</b> putative chorismate mutase from bifidobacterium adolescentis
55	<a href="#">c2f06B_</a>	Alignment	not modelled	95.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of protein bt0572 from bacteroides thetaiotaomicron
56	<a href="#">c3obiC_</a>	Alignment	not modelled	94.8	9	<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
57	<a href="#">c3mtjA_</a>	Alignment	not modelled	94.5	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
58	<a href="#">d2f06a1</a>	Alignment	not modelled	94.5	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> BT0572-like
59	<a href="#">c2qmwA_</a>	Alignment	not modelled	94.4	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydratase; <b>PDBTitle:</b> the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
60	<a href="#">d2hj1a1</a>	Alignment	not modelled	93.6	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> HI0395-like
61	<a href="#">c2hj1A_</a>	Alignment	not modelled	93.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
62	<a href="#">c3cwiA_</a>	Alignment	not modelled	93.6	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine-biosynthesis protein thi3; <b>PDBTitle:</b> crystal structure of thiamine biosynthesis protein (thi3)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
63	<a href="#">d1tygb_</a>	Alignment	not modelled	93.3	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
64	<a href="#">c2phmA_</a>	Alignment	not modelled	93.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (phenylalanine-4-hydroxylase); <b>PDBTitle:</b> structure of phenylalanine hydroxylase dephosphorylated
65	<a href="#">c1tdjA_</a>	Alignment	not modelled	92.3	11	<b>PDB header:</b> allostery <b>Chain:</b> A: <b>PDB Molecule:</b> biosynthetic threonine deaminase; <b>PDBTitle:</b> threonine deaminase (biosynthetic) from e. coli
66	<a href="#">d1vjka_</a>	Alignment	not modelled	91.5	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
67	<a href="#">c1tygG_</a>	Alignment	not modelled	91.4	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> G: <b>PDB Molecule:</b> yjbs; <b>PDBTitle:</b> structure of the thiazole synthase/this complex
68	<a href="#">c2kl0A_</a>	Alignment	not modelled	90.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiamin biosynthesis thi3; <b>PDBTitle:</b> solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
69	<a href="#">c2qieB_</a>	Alignment	not modelled	90.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin synthase small subunit; <b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex2 with precursor z
70	<a href="#">d3djb1</a>	Alignment	not modelled	90.8	20	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
71	<a href="#">d2cu3a1</a>	Alignment	not modelled	90.7	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
72	<a href="#">c3po0A_</a>	Alignment	not modelled	90.6	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> small archaeal modifier protein 1; <b>PDBTitle:</b> crystal structure of samp1 from haloferax volcanii
73	<a href="#">c2dqbB_</a>	Alignment	not modelled	90.4	34	<b>PDB header:</b> hydrolase, dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> deoxyguanosinetriphosphate triphosphohydrolase, putative; <b>PDBTitle:</b> crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
74	<a href="#">c3ccgA_</a>	Alignment	not modelled	89.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hd superfamily hydrolase; <b>PDBTitle:</b> crystal structure of predicted hd superfamily hydrolase involved in2 nad metabolism (np_347894.1) from clostridium acetobutylicum at 1.503 a resolution
75	<a href="#">d1dm9a_</a>	Alignment	not modelled	88.9	12	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Heat shock protein 15 kD
76	<a href="#">c1dm9A_</a>	Alignment	not modelled	88.9	12	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 15.5 kd protein in mrca-pcka <b>PDBTitle:</b> heat shock protein 15 kd
77	<a href="#">d1y7pa2</a>	Alignment	not modelled	87.8	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> AF1403 N-terminal domain-like
						<b>Fold:</b> Ferredoxin-like

78	<a href="#">d2joqa1</a>	Alignment	not modelled	87.7	13	<b>Superfamily:</b> YbeD/HP0495-like <b>Family:</b> HP0495-like
79	<a href="#">c2ogiA</a>	Alignment	not modelled	87.3	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sag1661; <b>PDBTitle:</b> crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
80	<a href="#">d1jala2</a>	Alignment	not modelled	85.9	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
81	<a href="#">c2k6pA</a>	Alignment	not modelled	84.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hp_1423; <b>PDBTitle:</b> solution structure of hypothetical protein, hp1423
82	<a href="#">c3mzoA</a>	Alignment	not modelled	83.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lin2634 protein; <b>PDBTitle:</b> crystal structure of a hd-domain phosphohydrolase (lin2634) from2 listeria innocua at 1.98 a resolution
83	<a href="#">c2dtjA</a>	Alignment	not modelled	82.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
84	<a href="#">c3gqsB</a>	Alignment	not modelled	82.1	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate cyclase-like protein; <b>PDBTitle:</b> crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
85	<a href="#">d1ni3a2</a>	Alignment	not modelled	81.9	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
86	<a href="#">d1fm0d</a>	Alignment	not modelled	81.6	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
87	<a href="#">d1rwsa</a>	Alignment	not modelled	81.0	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
88	<a href="#">c3p96A</a>	Alignment	not modelled	80.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase serb; <b>PDBTitle:</b> crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
89	<a href="#">c2o08B</a>	Alignment	not modelled	79.8	34	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bh1327 protein; <b>PDBTitle:</b> crystal structure of a putative hd superfamily hydrolase (bh1327) from2 bacillus halodurans at 1.90 a resolution
90	<a href="#">c3l76B</a>	Alignment	not modelled	79.5	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> crystal structure of aspartate kinase from synechocystis
91	<a href="#">c3fm8A</a>	Alignment	not modelled	78.6	13	<b>PDB header:</b> transport protein/hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif13b; <b>PDBTitle:</b> crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
92	<a href="#">d3b57a1</a>	Alignment	not modelled	78.0	17	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
93	<a href="#">c3mgjA</a>	Alignment	not modelled	77.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj1480; <b>PDBTitle:</b> crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.
94	<a href="#">d2piea1</a>	Alignment	not modelled	76.8	14	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
95	<a href="#">d2paqa1</a>	Alignment	not modelled	76.7	27	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
96	<a href="#">d2gz4a1</a>	Alignment	not modelled	76.6	25	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
97	<a href="#">d1c06a</a>	Alignment	not modelled	75.7	27	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
98	<a href="#">c2g1eA</a>	Alignment	not modelled	75.2	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0895; <b>PDBTitle:</b> solution structure of ta0895
99	<a href="#">d2pjqa1</a>	Alignment	not modelled	74.1	26	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
100	<a href="#">c2eh0A</a>	Alignment	not modelled	73.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif1b; <b>PDBTitle:</b> solution structure of the fha domain from human kinesin-2 like protein kif1b
101	<a href="#">c3bbnD</a>	Alignment	not modelled	73.6	14	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s4; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
102	<a href="#">c2bs2E</a>	Alignment	not modelled	73.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> quinol-fumarate reductase iron-sulfur subunit b; <b>PDBTitle:</b> quinol:fumarate reductase from wolinetlla succinogenes
103	<a href="#">d2g1la1</a>	Alignment	not modelled	72.7	17	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
104	<a href="#">c2jsxA</a>	Alignment	not modelled	72.3	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> protein napd; <b>PDBTitle:</b> solution structure of the e. coli tat proofreading2

						chaperone protein napd
105	<a href="#">d2uubd1</a>	Alignment	not modelled	72.0	14	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
106	<a href="#">d2fug33</a>	Alignment	not modelled	71.0	28	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
107	<a href="#">d2heka1</a>	Alignment	not modelled	70.2	31	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
108	<a href="#">c2cqzA_</a>	Alignment	not modelled	69.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 177aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of ph0347 protein from pyrococcus horikoshii ot3
109	<a href="#">d1p9ka_</a>	Alignment	not modelled	69.3	29	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> YbcJ-like
110	<a href="#">d1xo3a_</a>	Alignment	not modelled	69.1	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> C9orf74 homolog
111	<a href="#">c2jqlA_</a>	Alignment	not modelled	68.4	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dna damage response protein kinase dun1; <b>PDBTitle:</b> nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
112	<a href="#">c3dwmA_</a>	Alignment	not modelled	67.5	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 9.5 kda culture filtrate antigen cfp10a; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cyso, an antigen
113	<a href="#">d2gy9d1</a>	Alignment	not modelled	67.3	18	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
114	<a href="#">c3dh3C_</a>	Alignment	not modelled	67.2	9	<b>PDB header:</b> isomerase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase f; <b>PDBTitle:</b> crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
115	<a href="#">d1yjma1</a>	Alignment	not modelled	67.0	22	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
116	<a href="#">d1gxca_</a>	Alignment	not modelled	66.9	17	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
117	<a href="#">c1gxcA_</a>	Alignment	not modelled	66.9	17	<b>PDB header:</b> phosphoprotein-binding domain <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase chk2; <b>PDBTitle:</b> fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
118	<a href="#">d1vioa2</a>	Alignment	not modelled	66.8	5	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Pseudouridine synthase RsaA N-terminal domain
119	<a href="#">c2re1A_</a>	Alignment	not modelled	66.2	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartokinase, alpha and beta subunits; <b>PDBTitle:</b> crystal structure of aspartokinase alpha and beta subunits
120	<a href="#">c2o6iA_</a>	Alignment	not modelled	66.1	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hd domain protein; <b>PDBTitle:</b> structure of an enterococcus faecalis hd domain phosphohydrolase