

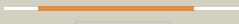
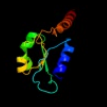


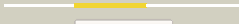

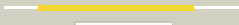

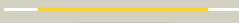





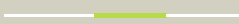

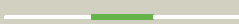



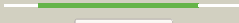

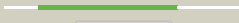

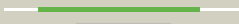






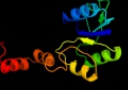








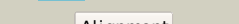


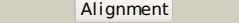
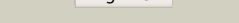



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1o4wa_</a>	 Alignment		87.4	17	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
2	<a href="#">d2gx8a1</a>	 Alignment		86.9	14	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
3	<a href="#">c2dzdB_</a>	 Alignment		85.3	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
4	<a href="#">c3ix7A_</a>	 Alignment		78.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ttha0540; <b>PDBTitle:</b> crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
5	<a href="#">c2gx8B_</a>	 Alignment		78.2	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> nif3-related protein; <b>PDBTitle:</b> the crystal stucture of bacillus cereus protein related to nif3
6	<a href="#">c2vpqA_</a>	 Alignment		73.3	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
7	<a href="#">c3ouzA_</a>	 Alignment		70.2	9	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase-adi complex from campylobacter2 jejuni
8	<a href="#">c1js1Z_</a>	 Alignment		64.8	17	<b>PDB header:</b> transferase <b>Chain:</b> Z: <b>PDB Molecule:</b> transcarbamylase; <b>PDBTitle:</b> crystal structure of a new transcarbamylase from the2 anaerobic bacterium bacteroides fragilis at 2.0 a3 resolution
9	<a href="#">d1cmwa2</a>	 Alignment		61.8	30	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
10	<a href="#">c3i8oA_</a>	 Alignment		56.8	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kh domain-containing protein mj1533; <b>PDBTitle:</b> a domain of a functionally unknown protein from2 methanocaldococcus jannaschii dsm 2661.
11	<a href="#">d1js1x2</a>	 Alignment		55.8	19	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase

12	<a href="#">c2nydB_</a>		Alignment		55.3	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0135 protein sa1388; <b>PDBTitle:</b> crystal structure of staphylococcus aureus hypothetical protein sa1388
13	<a href="#">c3ic5A_</a>		Alignment		53.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
14	<a href="#">c2z04A_</a>		Alignment		51.7	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase atpase <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
15	<a href="#">c2xznU_</a>		Alignment		51.1	12	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> ribosomal protein l7ae containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
16	<a href="#">c3ti8D_</a>		Alignment		47.4	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> aminotransferase class i and ii; <b>PDBTitle:</b> crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
17	<a href="#">c1gsoA_</a>		Alignment		47.0	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glycinamide ribonucleotide synthetase); <b>PDBTitle:</b> glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
18	<a href="#">c3k5iB_</a>		Alignment		45.4	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyl-aminoimidazole carboxylase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimidazole ribonucleotide
19	<a href="#">c1ulzA_</a>		Alignment		44.7	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase n-terminal domain; <b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
20	<a href="#">c1cmwA_</a>		Alignment		40.7	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase i); <b>PDBTitle:</b> crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
21	<a href="#">c3fwnB_</a>		Alignment	not modelled	40.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
22	<a href="#">d2ozba1</a>		Alignment	not modelled	38.6	25	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
23	<a href="#">d2czwa1</a>		Alignment	not modelled	37.7	22	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
24	<a href="#">c3o85A_</a>		Alignment	not modelled	37.1	31	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein l7ae; <b>PDBTitle:</b> giardia lamblia 15.5kd rna binding protein
25	<a href="#">c2lbwA_</a>		Alignment	not modelled	36.7	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 2; <b>PDBTitle:</b> solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
26	<a href="#">d1xata_</a>		Alignment	not modelled	35.9	20	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
27	<a href="#">d2alea1</a>		Alignment	not modelled	35.7	23	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
28	<a href="#">d2fywa1</a>		Alignment	not modelled	34.8	15	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like

29	<a href="#">d1pffa_</a>	Alignment	not modelled	34.4	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
30	<a href="#">d1gc0a_</a>	Alignment	not modelled	34.0	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
31	<a href="#">c3k6gA_</a>	Alignment	not modelled	33.5	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> telomeric repeat-binding factor 2-interacting protein 1; <b>PDBTitle:</b> crystal structure of rap1 and trf2 complex
32	<a href="#">d1yloa1</a>	Alignment	not modelled	33.1	22	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Amino peptidase/glucanase lid domain <b>Family:</b> Amino peptidase/glucanase lid domain
33	<a href="#">c1z2iA_</a>	Alignment	not modelled	33.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
34	<a href="#">c2ph5A_</a>	Alignment	not modelled	31.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
35	<a href="#">d1vqof1</a>	Alignment	not modelled	30.8	22	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
36	<a href="#">c3etjB_</a>	Alignment	not modelled	30.7	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase atpase <b>PDBTitle:</b> crystal structure e. coli purk in complex with mg, adp, and2 pi
37	<a href="#">c3fhaD_</a>	Alignment	not modelled	30.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase; <b>PDBTitle:</b> structure of endo-beta-n-acetylglucosaminidase a
38	<a href="#">c1wqaB_</a>	Alignment	not modelled	28.9	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phospho-sugar mutase; <b>PDBTitle:</b> crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucosylmutase complexed with mg2+
39	<a href="#">d2aifa1</a>	Alignment	not modelled	28.9	31	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
40	<a href="#">d1ozha1</a>	Alignment	not modelled	28.5	21	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
41	<a href="#">c2v4oB_</a>	Alignment	not modelled	28.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> multifunctional protein sur e; <b>PDBTitle:</b> crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
42	<a href="#">c3c04A_</a>	Alignment	not modelled	28.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomannomutase/phosphoglucosylmutase; <b>PDBTitle:</b> structure of the p368g mutant of pmm/pgm from p. aeruginosa
43	<a href="#">d1jj2f_</a>	Alignment	not modelled	27.6	22	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
44	<a href="#">c2hwwC_</a>	Alignment	not modelled	27.3	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> telomerase-binding protein est1a; <b>PDBTitle:</b> structure of pin domain of human smg6
45	<a href="#">c3i0pA_</a>	Alignment	not modelled	26.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of malate dehydrogenase from entamoeba histolytica
46	<a href="#">c2g8yB_</a>	Alignment	not modelled	26.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate/l-lactate dehydrogenases; <b>PDBTitle:</b> the structure of a putative malate/lactate dehydrogenase from e. coli.
47	<a href="#">c3on1A_</a>	Alignment	not modelled	25.0	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2414 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from bacillus2 halodurans c
48	<a href="#">c3eevC_</a>	Alignment	not modelled	24.5	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
49	<a href="#">d1cs1a_</a>	Alignment	not modelled	24.4	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
50	<a href="#">d1qgna_</a>	Alignment	not modelled	24.4	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
51	<a href="#">c1i41J_</a>	Alignment	not modelled	23.7	23	<b>PDB header:</b> lyase <b>Chain:</b> J: <b>PDB Molecule:</b> cystathionine gamma-synthase; <b>PDBTitle:</b> cystathionine gamma-synthase in complex with the inhibitor2 appa
52	<a href="#">c3b8hA_</a>	Alignment	not modelled	23.5	27	<b>PDB header:</b> biosynthetic protein/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 2; <b>PDBTitle:</b> structure of the eef2-exoa(e546a)-nad+ complex
53	<a href="#">d1cl1a_</a>	Alignment	not modelled	23.2	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
54	<a href="#">d1xbia1</a>	Alignment	not modelled	23.2	22	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins

55	<a href="#">d2awia1</a>	Alignment	not modelled	23.2	36	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> PrgX N-terminal domain-like
56	<a href="#">d1vhea1</a>	Alignment	not modelled	22.8	12	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Aminopeptidase/glucanase lid domain <b>Family:</b> Aminopeptidase/glucanase lid domain
57	<a href="#">d2fc3a1</a>	Alignment	not modelled	22.6	15	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
58	<a href="#">d2pgda1</a>	Alignment	not modelled	22.2	21	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
59	<a href="#">c1pggA</a>	Alignment	not modelled	21.9	21	<b>PDB header:</b> oxidoreductase (choh(d)-nadp+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
60	<a href="#">d1vlva2</a>	Alignment	not modelled	21.8	21	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
61	<a href="#">c3ri6A</a>	Alignment	not modelled	21.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-acetylhomoserine sulfhydrylase; <b>PDBTitle:</b> a novel mechanism of sulfur transfer catalyzed by o-acetylhomoserine2 sulfhydrylase in methionine biosynthetic pathway of wolfinella3 succinogenes
62	<a href="#">c3bg5C</a>	Alignment	not modelled	20.8	21	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate2 carboxylase
63	<a href="#">c3uvzB</a>	Alignment	not modelled	20.1	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
64	<a href="#">c2vt1B</a>	Alignment	not modelled	20.1	8	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> surface presentation of antigens protein spas; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of spa40, the2 specificity switch for the shigella flexneri type iii3 secretion system
65	<a href="#">c2iz1C</a>	Alignment	not modelled	19.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> 6pdh complexed with pex inhibitor synchrotron data
66	<a href="#">c1vbiA</a>	Alignment	not modelled	19.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> type 2 malate/lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
67	<a href="#">c1g7tA</a>	Alignment	not modelled	19.9	18	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if2/eif5b; <b>PDBTitle:</b> x-ray structure of translation initiation factor if2/eif5b2 complexed with gdpnp
68	<a href="#">c3c01H</a>	Alignment	not modelled	19.8	14	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> H: <b>PDB Molecule:</b> surface presentation of antigens protein spas; <b>PDBTitle:</b> crystal structural of native spas c-terminal domain
69	<a href="#">d1e5ea</a>	Alignment	not modelled	19.8	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
70	<a href="#">c3c00B</a>	Alignment	not modelled	19.7	29	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> escu; <b>PDBTitle:</b> crystal structural of the mutated g247t escu/spas c-terminal domain
71	<a href="#">d1xrha</a>	Alignment	not modelled	19.7	14	<b>Fold:</b> L-sulfolactate dehydrogenase-like <b>Superfamily:</b> L-sulfolactate dehydrogenase-like <b>Family:</b> L-sulfolactate dehydrogenase-like
72	<a href="#">d3bzra1</a>	Alignment	not modelled	19.6	29	<b>Fold:</b> EscU C-terminal domain-like <b>Superfamily:</b> EscU C-terminal domain-like <b>Family:</b> EscU C-terminal domain-like
73	<a href="#">c3bzrA</a>	Alignment	not modelled	19.6	29	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> escu; <b>PDBTitle:</b> crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
74	<a href="#">c1zq2A</a>	Alignment	not modelled	19.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
75	<a href="#">d1xo1a2</a>	Alignment	not modelled	19.3	15	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
76	<a href="#">c3t7yB</a>	Alignment	not modelled	19.0	21	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> yop proteins translocation protein u; <b>PDBTitle:</b> structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
77	<a href="#">d2fbka1</a>	Alignment	not modelled	19.0	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
78	<a href="#">c1e5IA</a>	Alignment	not modelled	18.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
79	<a href="#">d1iwpq</a>	Alignment	not modelled	18.6	31	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Diol dehydratase, gamma subunit <b>Family:</b> Diol dehydratase, gamma subunit

80	<a href="#">d2etha1</a>	Alignment	not modelled	18.6	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
81	<a href="#">c2axqA</a>	Alignment	not modelled	18.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
82	<a href="#">d1vfga2</a>	Alignment	not modelled	18.1	19	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
83	<a href="#">c3g8cB</a>	Alignment	not modelled	17.9	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
84	<a href="#">c2h5eB</a>	Alignment	not modelled	17.7	15	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> peptide chain release factor rf-3; <b>PDBTitle:</b> crystal structure of e.coli polypeptide release factor rf3
85	<a href="#">d1y4ia1</a>	Alignment	not modelled	17.6	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
86	<a href="#">d1rfma</a>	Alignment	not modelled	17.6	17	<b>Fold:</b> L-sulfolactate dehydrogenase-like <b>Superfamily:</b> L-sulfolactate dehydrogenase-like <b>Family:</b> L-sulfolactate dehydrogenase-like
87	<a href="#">d2fvga1</a>	Alignment	not modelled	17.6	30	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Aminopeptidase/glucanase lid domain <b>Family:</b> Aminopeptidase/glucanase lid domain
88	<a href="#">c1wtjB</a>	Alignment	not modelled	17.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ureidoglycolate dehydrogenase; <b>PDBTitle:</b> crystal structure of delta1-piperidine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
89	<a href="#">c1v9nA</a>	Alignment	not modelled	16.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structure of malate dehydrogenase from pyrococcus horikoshii ot3
90	<a href="#">c3c2qA</a>	Alignment	not modelled	16.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2
91	<a href="#">d1nmpa</a>	Alignment	not modelled	16.7	16	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
92	<a href="#">c3rq1A</a>	Alignment	not modelled	16.6	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase class i and ii; <b>PDBTitle:</b> crystal structure of aminotransferase class i and ii from veillonella2 parvula
93	<a href="#">c3tr5C</a>	Alignment	not modelled	16.5	15	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
94	<a href="#">d1n0ua2</a>	Alignment	not modelled	16.3	33	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
95	<a href="#">c3ndnC</a>	Alignment	not modelled	15.8	20	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> o-succinylhomoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
96	<a href="#">c1tuoA</a>	Alignment	not modelled	15.8	8	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphomannomutase; <b>PDBTitle:</b> crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
97	<a href="#">d1rlga</a>	Alignment	not modelled	15.8	14	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
98	<a href="#">c3ecoB</a>	Alignment	not modelled	15.6	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mepr; <b>PDBTitle:</b> crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
99	<a href="#">c2dr1A</a>	Alignment	not modelled	15.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 386aa long hypothetical serine aminotransferase; <b>PDBTitle:</b> crystal structure of the ph1308 protein from pyrococcus horikoshii ot3