Phyre2

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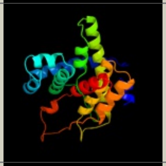
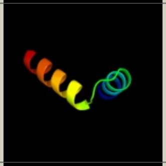
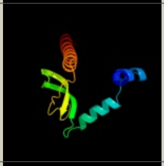
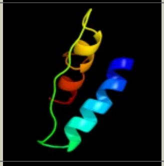
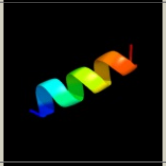
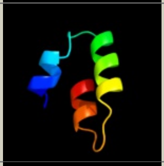
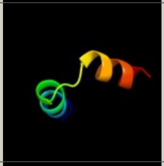
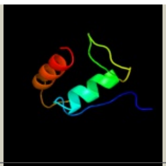
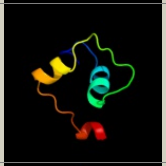
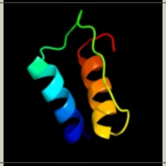
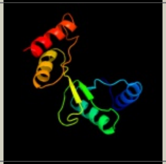
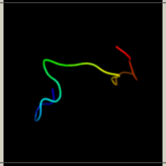
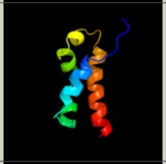
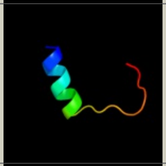
Description	P42626
Date	Thu Jan 5 12:01:57 GMT 2012
Unique Job ID	707af8fcb89e9c7b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hp0A_	Alignment		98.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ids-epimerase; **PDBTitle:** crystal structure of iminodisuccinate epimerase
2	d1szqa_	Alignment		98.0	14	**Fold:**2-methylcitrate dehydratase PrpD **Superfamily:**2-methylcitrate dehydratase PrpD **Family:**2-methylcitrate dehydratase PrpD
3	c3u4gA_	Alignment		56.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**namn:dmb phosphoribosyltransferase; **PDBTitle:** the structure of cobt from pyrococcus horikoshii
4	c3nepX_	Alignment		53.0	18	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
5	d1v59a2	Alignment		47.3	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
6	c2o2jA_	Alignment		38.7	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** mycobacterium tuberculosis tryptophan synthase beta chain2 dimer (apoform)
7	c2klzA_	Alignment		28.3	57	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ataxin-3; **PDBTitle:** solution structure of the tandem uim domain of ataxin-3 complexed with2 ubiquitin
8	c1x1qA_	Alignment		23.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
9	d1o58a_	Alignment		20.3	23	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
10	c3l0zC_	Alignment		19.5	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative nicotinate-nucleotide-dimethylbenzimidazole **PDBTitle:** crystal structure of a putative nicotinate-nucleotide-2 dimethylbenzimidazole phosphoribosyltransferase from3 methanocaldococcus jannaschii dsm 2661
11	d2hsga1	Alignment		18.8	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator

12	c1m75B_	Alignment		18.5	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa
13	d1efaa1	Alignment		16.7	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
14	d1e3ja2	Alignment		15.6	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
15	c3e49A_	Alignment		15.0	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849 with a tim barrel fold; **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bxe_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
16	d1v71a1	Alignment		14.8	19	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
17	c2hldH_	Alignment		14.3	25	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**atp synthase delta chain, mitochondrial; **PDBTitle:** crystal structure of yeast mitochondrial f1-atpase
18	d1wfza_	Alignment		13.7	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
19	d1r4qa_	Alignment		12.2	5	**Fold:**Ribosome inactivating proteins (RIP) **Superfamily:**Ribosome inactivating proteins (RIP) **Family:**Shiga toxin, A-chain
20	d1fcja_	Alignment		12.2	27	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
21	d1nvmb1	Alignment	not modelled	12.1	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
22	c3doaA_	Alignment	not modelled	11.6	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibrinogen binding protein; **PDBTitle:** the crystal structure of the fibrinogen binding protein from2 staphylococcus aureus
23	c3rfuC_	Alignment	not modelled	11.2	13	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
24	c3co7C_	Alignment	not modelled	10.9	29	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
25	d1j0aa_	Alignment	not modelled	10.7	18	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
26	c3a58A_	Alignment	not modelled	10.6	20	**PDB header:**protein transport/exocytosis **Chain:** A: **PDB Molecule:**exocyst complex component sec3; **PDBTitle:** crystal structure of sec3p - rho1p complex from2 saccharomyces cerevisiae
27	d3bpya1	Alignment	not modelled	10.6	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
28	c3g73A_	Alignment	not modelled	10.6	29	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**forkhead box protein m1; **PDBTitle:** structure of the foxm1 dna binding

29	d1kq8a_	Alignment	not modelled	10.5	43	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
30	c1kq8A_	Alignment	not modelled	10.5	43	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 3 forkhead homolog 1; **PDBTitle:** solution structure of winged helix protein hfh-1
31	d2dx7a1	Alignment	not modelled	10.5	23	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
32	d1tyza_	Alignment	not modelled	10.5	11	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
33	c3c1zA_	Alignment	not modelled	10.4	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna integrity scanning protein disa; **PDBTitle:** structure of the ligand-free form of a bacterial dna damage2 sensor protein
34	d1vela1	Alignment	not modelled	10.2	26	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
35	d2ldxa1	Alignment	not modelled	10.2	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
36	d2bjca1	Alignment	not modelled	10.2	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
37	d1j6ua3	Alignment	not modelled	10.0	20	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
38	d2a07f1	Alignment	not modelled	10.0	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
39	d2hfha_	Alignment	not modelled	9.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
40	c1e17A_	Alignment	not modelled	9.7	36	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
41	d1ijwc_	Alignment	not modelled	9.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
42	d1kn1b_	Alignment	not modelled	9.4	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
43	d1pgja2	Alignment	not modelled	9.2	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
44	c3imoC_	Alignment	not modelled	9.1	33	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass14
45	d2vnud2	Alignment	not modelled	8.9	44	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	d1wkva1	Alignment	not modelled	8.8	11	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
47	c2okvC_	Alignment	not modelled	8.7	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable d-tyrosyl-trna(tyr) deacylase 1; **PDBTitle:** c-myc dna unwinding element binding protein
48	d1dxla2	Alignment	not modelled	8.7	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
49	d1k1xa3	Alignment	not modelled	8.7	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**4-alpha-glucanotransferase, N-terminal domain
50	c3mogA_	Alignment	not modelled	8.6	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxybutyryl-coa dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
51	c3sqgF_	Alignment	not modelled	8.6	26	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methyl-coenzyme m reductase, gamma subunit; **PDBTitle:** crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats
52	d2bhsa1	Alignment	not modelled	8.4	28	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes

53	d1hcra_	Alignment	not modelled	8.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
54	d1b74a2	Alignment	not modelled	8.3	19	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
55	d2f1ka2	Alignment	not modelled	8.2	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
56	c3dt5A_	Alignment	not modelled	8.1	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0924; **PDBTitle:** c_terminal domain of protein of unknown function af_0924 from2 archaeoglobus fulgidus.
57	d1j7ga_	Alignment	not modelled	8.1	19	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
58	d1f2da_	Alignment	not modelled	7.9	14	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
59	d2gv8a2	Alignment	not modelled	7.9	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
60	d1qpza1	Alignment	not modelled	7.7	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
61	c2yqfA_	Alignment	not modelled	7.7	35	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** solution structure of the death domain of ankyrin-1
62	c3kg4A_	Alignment	not modelled	7.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from mannheimia2 succiniciproducens
63	d1gv4a2	Alignment	not modelled	7.5	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
64	c2pqmA_	Alignment	not modelled	7.4	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
65	c1nvmB_	Alignment	not modelled	7.4	24	**PDB header:**lyase/oxidoreductase **Chain:** B: **PDB Molecule:**acetaldehyde dehydrogenase (acylating); **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
66	d1iioa_	Alignment	not modelled	7.3	28	**Fold:**EF Hand-like **Superfamily:**Hypothetical protein MTH865 **Family:**Hypothetical protein MTH865
67	d2c6ya1	Alignment	not modelled	7.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
68	c2zskA_	Alignment	not modelled	7.1	100	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
69	c1i7mD_	Alignment	not modelled	7.1	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**s-adenosylmethionine decarboxylase beta chain; **PDBTitle:** human s-adenosylmethionine decarboxylase with covalently bound2 pyruvoyl group and complexed with 4-amidinoindan-1-one-2'-3 amidinohydrazone
70	c3j08A_	Alignment	not modelled	7.0	13	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
71	c2vmlA_	Alignment	not modelled	7.0	20	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycocyanin alpha chain; **PDBTitle:** the monoclinic structure of phycocyanin from gloeobacter2 violaceus
72	d1dlja2	Alignment	not modelled	6.9	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
73	d1jsca3	Alignment	not modelled	6.9	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
74	c1dliA_	Alignment	not modelled	6.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
75	d1d5va_	Alignment	not modelled	6.9	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
76	c2jfzB_	Alignment	not modelled	6.8	80	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
77	c1p8cD_	Alignment	not modelled	6.7	28	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima

78	c3d3kD_	Alignment	not modelled	6.6	14	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
79	d7mdha1	Alignment	not modelled	6.4	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
80	c2pwzG_	Alignment	not modelled	6.4	22	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of the apo form of e.coli malate dehydrogenase
81	c2q2kA_	Alignment	not modelled	6.4	24	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of nucleic-acid binding protein
82	d1dd3a1	Alignment	not modelled	6.3	12	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
83	c2kdtA_	Alignment	not modelled	6.2	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**neuroendocrine convertase 1; **PDBTitle:** pc1/3 dcsg sorting domain structure in dpc
84	d1allb_	Alignment	not modelled	6.2	19	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
85	c1o7dA_	Alignment	not modelled	6.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
86	c3m9hB_	Alignment	not modelled	6.1	44	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa
87	d1poia_	Alignment	not modelled	6.0	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
88	d2nmla1	Alignment	not modelled	6.0	8	**Fold:**ERH-like **Superfamily:**ERH-like **Family:**ERH-like
89	d3bvua3	Alignment	not modelled	6.0	12	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**alpha-mannosidase
90	d1v8za1	Alignment	not modelled	6.0	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
91	d1neka1	Alignment	not modelled	6.0	9	**Fold:**Spectrin repeat-like **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
92	c3jvfC_	Alignment	not modelled	6.0	44	**PDB header:**signaling protein / cytokine **Chain:** C: **PDB Molecule:**interleukin-17 receptor a; **PDBTitle:** crystal structure of an interleukin-17 receptor complex
93	c2jnhA_	Alignment	not modelled	5.9	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
94	c1p5jA_	Alignment	not modelled	5.9	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-serine dehydratase; **PDBTitle:** crystal structure analysis of human serine dehydratase
95	d1p5ja_	Alignment	not modelled	5.9	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
96	d1ez4a1	Alignment	not modelled	5.9	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
97	c2jfnA_	Alignment	not modelled	5.9	80	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
98	c1b74A_	Alignment	not modelled	5.8	80	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
99	c3a3jA_	Alignment	not modelled	5.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pbp5; **PDBTitle:** crystal structures of penicillin binding protein 5 from2 haemophilus influenzae