Phyre2

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Description	P05847
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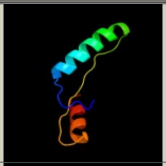
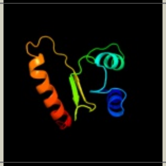
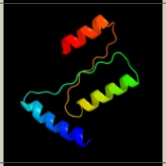
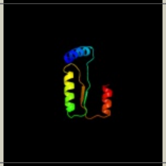
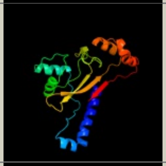
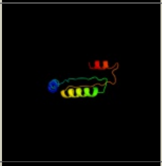
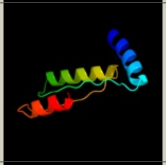
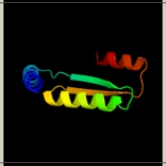
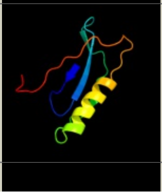
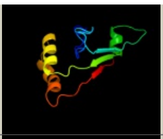
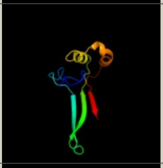
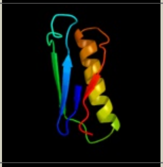
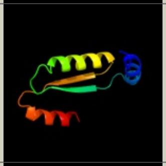
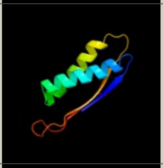
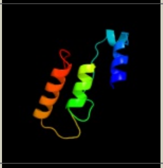
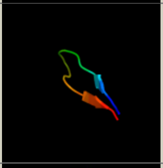
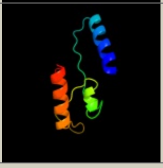
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qv6D_	Alignment		92.7	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
2	d1n0ua3	Alignment		72.9	14	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
3	d1edza2	Alignment		55.0	17	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
4	c3p2oA_	Alignment		51.6	14	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
5	c3p2oB_	Alignment		46.4	14	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
6	c1n9wA_	Alignment		44.6	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2; **PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
7	c1wydB_	Alignment		43.6	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
8	d1a4ia2	Alignment		42.6	11	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
9	c2c2xB_	Alignment		42.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
10	c3l07B_	Alignment		41.7	17	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
11	c3mcpA_	Alignment		41.5	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution

12	c1x55A_	Alignment		40.2	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase; **PDBTitle:** crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
13	d1n9wa2	Alignment		37.4	20	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
14	d2ap1a2	Alignment		36.1	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
15	c1edzA_	Alignment		32.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate dehydrogenase; **PDBTitle:** structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae
16	c1b8aB_	Alignment		32.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
17	c2jfsA_	Alignment		30.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ser-thr phosphatase mspp; **PDBTitle:** crystal structure of the ppm ser-thr phosphatase mspp from2 mycobacterium smegmatis in complex with cacodylate
18	d1hl2a_	Alignment		29.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
19	d1ei5a2	Alignment		27.0	31	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
20	c3chvA_	Alignment		26.3	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**prokaryotic domain of unknown function (duf849) with a tim **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
21	c2j0eA_	Alignment	not modelled	25.2	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
22	d1lfba_	Alignment	not modelled	24.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
23	c3dz1A_	Alignment	not modelled	23.9	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
24	c1a4iB_	Alignment	not modelled	23.6	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
25	d1gkub1	Alignment	not modelled	23.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
26	c1pbtA_	Alignment	not modelled	23.0	25	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
27	d1js3a_	Alignment	not modelled	22.1	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
28	c3orsD_	Alignment	not modelled	21.0	14	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
						Fold: Plant proteinase inhibitors

29	d1fyba1	Alignment	not modelled	20.5	32	**Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
30	d1tiha_	Alignment	not modelled	19.0	32	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
31	c2k4mA_	Alignment	not modelled	18.6	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0146 protein mth_1000; **PDBTitle:** solution nmr structure of m. thermoautotrophicum protein2 mth_1000, northeast structural genomics consortium target3 tr8
32	d1pjua1	Alignment	not modelled	18.5	14	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
33	d4sgbi_	Alignment	not modelled	18.3	29	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
34	d1j2pa_	Alignment	not modelled	17.9	13	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
35	c3trhI_	Alignment	not modelled	17.7	16	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
36	d1ce3a_	Alignment	not modelled	17.3	33	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
37	d1yqea1	Alignment	not modelled	17.2	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
38	d1c0aa3	Alignment	not modelled	16.9	19	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
39	d2oz4a1	Alignment	not modelled	16.6	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C2 set domains
40	c3c00B_	Alignment	not modelled	16.4	11	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**escu; **PDBTitle:** crystal structural of the mutated g247t escu/spas c-terminal domain
41	c2dzaA_	Alignment	not modelled	16.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
42	c3cssA_	Alignment	not modelled	15.8	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis
43	c3fiuD_	Alignment	not modelled	15.8	18	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
44	c3gv1A_	Alignment	not modelled	15.8	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
45	c2jlhA_	Alignment	not modelled	15.7	8	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
46	c4a5oB_	Alignment	not modelled	15.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
47	d1u11a_	Alignment	not modelled	15.1	9	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
48	d1j6xa_	Alignment	not modelled	14.9	8	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
49	d2g39a2	Alignment	not modelled	14.8	9	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
50	d1xmpa_	Alignment	not modelled	14.8	12	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
51	c3hhdC_	Alignment	not modelled	14.5	13	**PDB header:**transferase, hydrolase **Chain:** C: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the human fatty acid synthase ks-mat didomain2 as a framework for inhibitor design.
52	c3fp5A_	Alignment	not modelled	14.5	14	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coa binding protein; **PDBTitle:** crystal structure of acbp from moniliophthora perniciosa
53	c2fw9A_	Alignment	not modelled	14.3	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
						PDB header:hydrolase

54	c3icoA_	Alignment	not modelled	14.1	30	**Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from2 mycobacterium tuberculosis
55	c3c8lB_	Alignment	not modelled	14.0	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ftsz-like protein of unknown function; **PDBTitle:** crystal structure of a ftsz-like protein of unknown function2 (npun_r1471) from nostoc punctiforme pcc 73102 at 1.22 a resolution
56	c1y89B_	Alignment	not modelled	13.9	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**devb protein; **PDBTitle:** crystal structure of devb protein
57	c3i7fA_	Alignment	not modelled	13.8	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
58	d1b0aa2	Alignment	not modelled	13.7	20	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
59	d1bbua2	Alignment	not modelled	13.6	35	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
60	c3kz4A_	Alignment	not modelled	13.4	15	**PDB header:**virus **Chain:** A: **PDB Molecule:**inner capsid protein vp2; **PDBTitle:** crystal structure of the rotavirus double layered particle
61	c3gzuB_	Alignment	not modelled	12.9	15	**PDB header:**virus **Chain:** B: **PDB Molecule:**inner capsid protein vp2; **PDBTitle:** vp7 recoated rotavirus dlp
62	c2oxcA_	Alignment	not modelled	12.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx20; **PDBTitle:** human dead-box rna helicase ddx20, dead domain in complex2 with adp
63	c2oqjF_	Alignment	not modelled	12.8	71	**PDB header:**immune system **Chain:** F: **PDB Molecule:**peptide 2g12.1 (acppshvldmrsgtclaaegk); **PDBTitle:** crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
64	c3no5C_	Alignment	not modelled	12.7	23	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
65	c3gykC_	Alignment	not modelled	12.5	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**27kda outer membrane protein; **PDBTitle:** the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3
66	c2imeA_	Alignment	not modelled	12.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-hydroxychromene-2-carboxylate isomerase; **PDBTitle:** 2-hydroxychromene-2-carboxylate isomerase: a kappa class glutathione-2 s-transferase from pseudomonas putida
67	d1l0wa3	Alignment	not modelled	12.0	15	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
68	d1w3ia_	Alignment	not modelled	11.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
69	c4a26B_	Alignment	not modelled	11.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
70	c2oqjL_	Alignment	not modelled	11.7	71	**PDB header:**immune system **Chain:** L: **PDB Molecule:**peptide 2g12.1 (acppshvldmrsgtclaaegk); **PDBTitle:** crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
71	c2oqjI_	Alignment	not modelled	11.7	71	**PDB header:**immune system **Chain:** I: **PDB Molecule:**peptide 2g12.1 (acppshvldmrsgtclaaegk); **PDBTitle:** crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
72	c2oqjC_	Alignment	not modelled	11.6	71	**PDB header:**immune system **Chain:** C: **PDB Molecule:**peptide 2g12.1 (acppshvldmrsgtclaaegk); **PDBTitle:** crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
73	c2k5jB_	Alignment	not modelled	11.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
74	c3n2xB_	Alignment	not modelled	11.4	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
75	d1ze3h1	Alignment	not modelled	11.2	7	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
76	d1oyvi_	Alignment	not modelled	11.2	14	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
77	c3t7yB_	Alignment	not modelled	11.1	7	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
78	d1rq2a2	Alignment	not modelled	11.0	28	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like

						Family: Tubulin, C-terminal domain
79	d1xkya1	Alignment	not modelled	10.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
80	d1y74a1	Alignment	not modelled	10.7	15	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
81	c1fybA_	Alignment	not modelled	10.7	33	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**proteinase inhibitor; **PDBTitle:** solution structure of c1-t1, a two-domain proteinase2 inhibitor derived from the circular precursor protein na-3 propi from nicotiana alata
82	d1z6ma1	Alignment	not modelled	10.6	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
83	d1nnha_	Alignment	not modelled	10.6	25	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
84	c3fluD_	Alignment	not modelled	10.5	26	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
85	d1u6za3	Alignment	not modelled	10.5	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
86	d1eova2	Alignment	not modelled	10.3	30	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
87	c3aq3A_	Alignment	not modelled	10.3	11	**PDB header:**toxin **Chain:** A: **PDB Molecule:**6b protein; **PDBTitle:** molecular insights into plant cell proliferation disturbance by2 agrobacterium protein 6b
88	c3c01H_	Alignment	not modelled	10.3	11	**PDB header:**membrane protein, protein transport **Chain:** H: **PDB Molecule:**surface presentation of antigens protein spas; **PDBTitle:** crystal structural of native spas c-terminal domain
89	c3dpiA_	Alignment	not modelled	10.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei
90	c3r6aB_	Alignment	not modelled	9.9	16	**PDB header:**isomerase, lyase **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein (hypothetical protein2 mm_3218) from methanosarcina mazei.
91	d2zdra2	Alignment	not modelled	9.8	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
92	c3eb2A_	Alignment	not modelled	9.5	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
93	c3qw4B_	Alignment	not modelled	9.4	22	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
94	d2f6ua1	Alignment	not modelled	9.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
95	c2xgtB_	Alignment	not modelled	9.3	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
96	c3pr3B_	Alignment	not modelled	9.2	30	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
97	d1rypb_	Alignment	not modelled	9.2	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
98	c2vt1B_	Alignment	not modelled	9.1	9	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**surface presentation of antigens protein spas; **PDBTitle:** crystal structure of the cytoplasmic domain of spa40, the2 specificity switch for the shigella flexneri type iii3 secretion system
99	c2kl0A_	Alignment	not modelled	8.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325