Phyre^2

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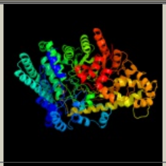
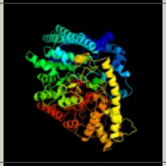
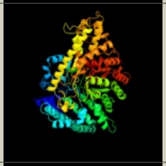
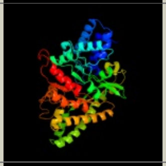
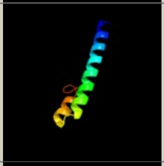
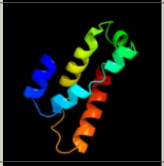
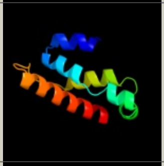
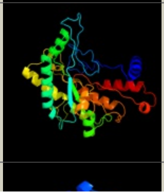
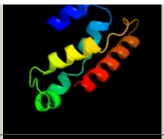
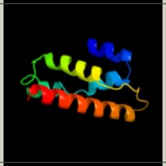
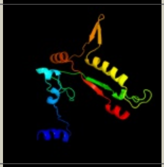
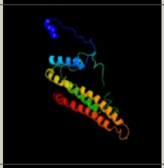
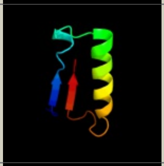
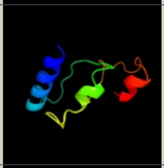
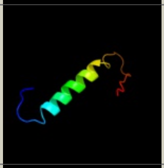
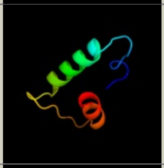
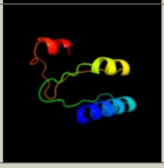
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r9da_	Alignment		100.0	42	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
2	c2y8nC_	Alignment		100.0	28	**PDB header:**lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate decarboxylase large subunit; **PDBTitle:** crystal structure of glycyl radical enzyme
3	c2f3oB_	Alignment		100.0	38	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
4	d1h16a_	Alignment		100.0	24	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
5	d1qhma_	Alignment		100.0	21	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
6	d1hk8a_	Alignment		99.4	17	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
7	c1hk8A_	Alignment		99.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
8	d1qkra_	Alignment		85.3	24	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
9	d1r0ka1	Alignment		84.4	27	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
10	d1q0qa1	Alignment		83.0	17	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
11	d1rlra2	Alignment		73.7	14	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**R1 subunit of ribonucleotide reductase, C-terminal domain

12	c1r0lD_	Alignment		65.5	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
13	c2eghA_	Alignment		61.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
14	c1xjeA_	Alignment		55.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleotide reductase, b12-dependent; **PDBTitle:** structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dttp-gdp complex
15	c1tt9B_	Alignment		53.2	11	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**formimidoyltransferase-cyclodeaminase **PDBTitle:** structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
16	c3gr1A_	Alignment		51.8	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
17	c2d2rA_	Alignment		50.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
18	d1u5tb1	Alignment		45.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
19	d1dq3a4	Alignment		43.1	14	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
20	d1ueha_	Alignment		42.6	9	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
21	d2gykb1	Alignment	not modelled	41.9	12	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
22	d1jvaa3	Alignment	not modelled	41.8	11	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
23	c2jcyA_	Alignment	not modelled	39.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
24	c1jp3A_	Alignment	not modelled	39.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of e.coli undecaprenyl pyrophosphate synthase
25	c1k5hB_	Alignment	not modelled	37.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose-5-phosphate reductoisomerase
26	c1rh1A_	Alignment	not modelled	33.3	11	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**colicin b; **PDBTitle:** crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution
27	d1st6a7	Alignment	not modelled	32.3	8	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
28	c3au9A_	Alignment	not modelled	31.9	14	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase

29	c2vg2C_	Alignment	not modelled	29.3	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
30	c3odeA_	Alignment	not modelled	26.4	18	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** human parp-1 zinc finger 2 (zn2) bound to dna
31	c1v9xA_	Alignment	not modelled	25.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase; **PDBTitle:** solution structure of the first zn-finger domain of2 poly(adp-ribose) polymerase-1
32	d1fi3a_	Alignment	not modelled	25.6	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
33	c2f40A_	Alignment	not modelled	25.4	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf1455; **PDBTitle:** structure of a novel protein from backbone-centered nmr data and nmr-2 assisted structure prediction
34	d1f75a_	Alignment	not modelled	23.4	16	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
35	d1nh2a2	Alignment	not modelled	22.7	29	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
36	c3gr0D_	Alignment	not modelled	22.6	12	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**protein prgh; **PDBTitle:** periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
37	c3thgA_	Alignment	not modelled	22.5	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase activase 1, **PDBTitle:** crystal structure of the creosote rubisco activase c-domain
38	c3ajfA_	Alignment	not modelled	21.6	27	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structural insigths into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus
39	c2dmjA_	Alignment	not modelled	21.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase family, member 1; **PDBTitle:** solution structure of the first zf-parp domain of human2 poly(adp-ribose)polymerase-1
40	d1mp9a1	Alignment	not modelled	21.5	29	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
41	d1nh2a1	Alignment	not modelled	21.4	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
42	d1l1la_	Alignment	not modelled	21.3	19	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**B12-dependent (class II) ribonucleotide reductase
43	d1qnaa2	Alignment	not modelled	21.2	29	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
44	d1aisa1	Alignment	not modelled	20.9	18	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
45	d1vioa2	Alignment	not modelled	20.9	12	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
46	d1rlfa_	Alignment	not modelled	20.3	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
47	d1aisa2	Alignment	not modelled	20.0	29	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
48	d1pugb_	Alignment	not modelled	19.6	26	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
49	d1qnaa1	Alignment	not modelled	19.5	21	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
50	d1v5ra1	Alignment	not modelled	18.9	44	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GAS2 domain-like **Family:**GAS2 domain
51	d2i15a1	Alignment	not modelled	18.7	30	**Fold:**MG296-like **Superfamily:**MG296-like **Family:**MG296-like
52	c1fuiB_	Alignment	not modelled	18.6	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
53	c2cvuA_	Alignment	not modelled	18.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large chain **PDBTitle:** structures of yeast ribonucleotide reductase i
54	d1mp9a2	Alignment	not modelled	18.2	29	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
55	c3hnfA_	Alignment	not modelled	17.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large subunit;

						PDBTitle: crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
56	c3mf2B_	Alignment	not modelled	17.5	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**bll0957 protein; **PDBTitle:** crystal structure of class ii aars homologue (bll0957) complexed with2 amp
57	d351ca_	Alignment	not modelled	17.3	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
58	d2g39a2	Alignment	not modelled	17.2	23	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
59	d1cdwa1	Alignment	not modelled	17.0	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
60	c3inpA_	Alignment	not modelled	17.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
61	d1lfda_	Alignment	not modelled	16.7	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
62	d2bm3a1	Alignment	not modelled	16.2	29	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
63	c3kh0A_	Alignment	not modelled	16.2	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ral guanine nucleotide dissociation stimulator; **PDBTitle:** crystal structure of the ras-association (ra) domain of2 ralgds
64	d1tyja1	Alignment	not modelled	15.6	29	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
65	d1uj8a1	Alignment	not modelled	15.5	24	**Fold:**Another 3-helical bundle **Superfamily:**IscX-like **Family:**IscX-like
66	c2b59A_	Alignment	not modelled	15.5	29	**PDB header:**hydrolase/structural protein **Chain:** A: **PDB Molecule:**cog1196: chromosome segregation atpases; **PDBTitle:** the type ii cohesin dockerin complex
67	c2cs2A_	Alignment	not modelled	15.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of the second zn-finger domain of2 poly(adp-ribose) polymerase-1
68	c3hp7A_	Alignment	not modelled	15.3	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
69	d1cdwa2	Alignment	not modelled	15.1	21	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
70	c3rmrA_	Alignment	not modelled	15.0	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**avirulence protein; **PDBTitle:** crystal structure of hyaloperonospora arabidopsidis atr1 effector2 domain
71	c2jobA_	Alignment	not modelled	15.0	15	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
72	c3ugsB_	Alignment	not modelled	14.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
73	d1ynra1	Alignment	not modelled	14.9	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
74	d1rypi_	Alignment	not modelled	14.8	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
75	c3ol0C_	Alignment	not modelled	14.6	17	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
76	d2rgfa_	Alignment	not modelled	14.5	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
77	c3fnkA_	Alignment	not modelled	14.5	36	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** crystal structure of the second type ii cohesin module from2 the cellulosomal adaptor scaa scaffoldin of acetivibrio3 cellulolyticus
78	c3ghpA_	Alignment	not modelled	14.4	36	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** structure of the second type ii cohesin module from the2 adaptor scaa scaffoldin of acetivibrio cellulolyticus3 (including long c-terminal linker)
79	d1q5qh_	Alignment	not modelled	14.0	6	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
						PDB header:hydrolase

80	c3oryA_	Alignment	not modelled	14.0	19	**Chain:** A: **PDB Molecule:**flap endonuclease 1; **PDBTitle:** crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
81	d1lghb_	Alignment	not modelled	14.0	5	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
82	c2wghA_	Alignment	not modelled	14.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large **PDBTitle:** human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
83	c2vpmB_	Alignment	not modelled	13.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
84	d1irxa1	Alignment	not modelled	13.9	14	**Fold:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Superfamily:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Family:**C-terminal domain of class I lysyl-tRNA synthetase
85	d1yuaa2	Alignment	not modelled	13.8	56	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
86	d1zv9a1	Alignment	not modelled	13.5	50	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
87	d1twda_	Alignment	not modelled	13.5	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
88	d1nj1a3	Alignment	not modelled	13.5	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
89	c2qguA_	Alignment	not modelled	13.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
90	c3nzwH_	Alignment	not modelled	13.0	19	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** H: **PDB Molecule:**proteasome component pup1; **PDBTitle:** crystal structure of the yeast 20s proteasome in complex with 2b
91	d1xppa_	Alignment	not modelled	12.9	10	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RBP11/RpoL
92	c2kwvA_	Alignment	not modelled	12.6	36	**PDB header:**protein binding/signaling protein **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution structure of ubm1 of murine polymerase iota in complex with2 ubiquitin
93	c3eagA_	Alignment	not modelled	12.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- **PDBTitle:** the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
94	d1i36a1	Alignment	not modelled	12.5	16	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Conserved hypothetical protein MTH1747
95	c3a14B_	Alignment	not modelled	12.1	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
96	d1w7pd1	Alignment	not modelled	12.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
97	d1zsqa2	Alignment	not modelled	12.0	18	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Myotubularin-like phosphatases
98	d1seda_	Alignment	not modelled	12.0	9	**Fold:**Hypothetical protein YhaI **Superfamily:**Hypothetical protein YhaI **Family:**Hypothetical protein YhaI
99	c2hx6A_	Alignment	not modelled	11.9	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb