Phyre^2

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Description	P19636
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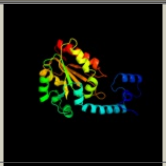
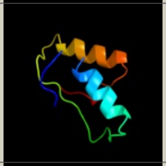
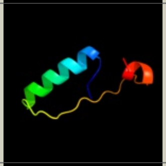
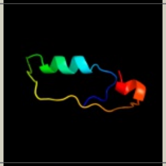
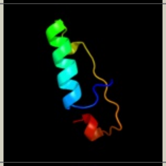
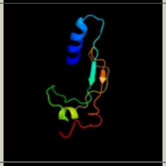
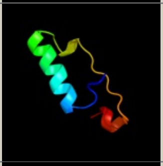
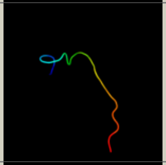
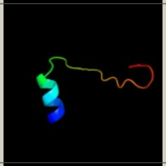
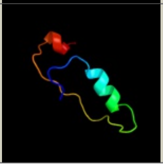
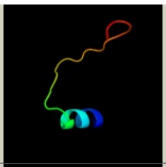
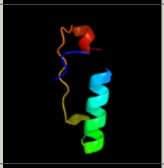
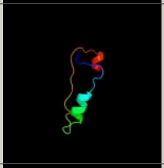
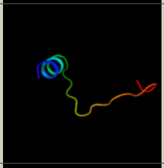
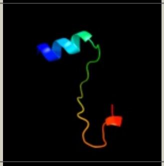
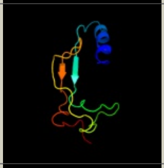
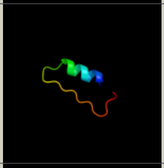
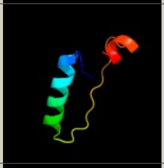
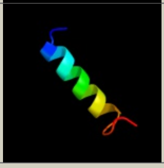
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3absD_	Alignment		100.0	100	**PDB header:**lyase **Chain:** D: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
2	c3anyB_	Alignment		100.0	100	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
3	c2e5cA_	Alignment		75.7	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinamide phosphoribosyltransferase; **PDBTitle:** crystal structure of human nmprtase complexed with 5'-phosphoribosyl-2 1'-pyrophosphate
4	d2f7fa1	Alignment		55.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
5	c2i14B_	Alignment		51.5	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from pyrococcus furiosus
6	d1yira1	Alignment		50.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
7	d1dysa_	Alignment		49.6	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
8	c1yirA_	Alignment		46.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase
9	d2huha1	Alignment		44.4	38	**Fold:**C2 domain-like **Superfamily:**Smr-associated domain-like **Family:**Smr-associated domain
10	d3bgsa1	Alignment		43.7	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
11	d2i14a1	Alignment		43.4	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like

12	d3pnpa_	Alignment		42.0	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
13	c3os4A_	Alignment		41.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
14	d1ytda1	Alignment		36.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
15	c3ggsA_	Alignment		36.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
16	c2p4sA_	Alignment		35.9	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
17	d1qjwa_	Alignment		34.0	22	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
18	c3l0oB_	Alignment		33.8	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
19	c2f7fA_	Alignment		32.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase, putative; **PDBTitle:** crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
20	d1ng6a_	Alignment		31.7	22	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/YqeY domain
21	c1xpuB_	Alignment	not modelled	31.5	38	**PDB header:**transcription/rna **Chain:** B: **PDB Molecule:**rho transcription termination factor; **PDBTitle:** structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
22	c3otbB_	Alignment	not modelled	31.2	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna(his) guanylyltransferase; **PDBTitle:** crystal structure of human trnahis guanylyltransferase (thg1) - dgtp2 complex
23	c2gsoB_	Alignment	not modelled	31.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
24	d2vapa1	Alignment	not modelled	29.4	19	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
25	c1tcvB_	Alignment	not modelled	29.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine-nucleoside phosphorylase; **PDBTitle:** crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
26	d1oc7a_	Alignment	not modelled	27.1	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
27	c3a64A_	Alignment	not modelled	25.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** crystal structure of cccel6c, a glycoside hydrolase family 62 enzyme, from coprinopsis cinerea
						Fold: Rv1873-like

28	d2jeka1	Alignment	not modelled	25.2	23	**Superfamily:**Rv1873-like **Family:**Rv1873-like
29	d1dk0a_	Alignment	not modelled	24.7	25	**Fold:**Heme-binding protein A (HasA) **Superfamily:**Heme-binding protein A (HasA) **Family:**Heme-binding protein A (HasA)
30	d1ofua1	Alignment	not modelled	24.5	17	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
31	c3la8A_	Alignment	not modelled	24.5	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative purine nucleoside phosphorylase; **PDBTitle:** the crystal structure of smu.1229 from streptococcus mutans ua159
32	d1qe5a_	Alignment	not modelled	23.9	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
33	c3ddrC_	Alignment	not modelled	21.7	25	**PDB header:**membrane protein/heme binding protein **Chain:** C: **PDB Molecule:**hemophore hasa; **PDBTitle:** structure of the serratia marcescens hemophore receptor hasr-ile671gly2 mutant in complex with its hemophore hasa and heme
34	d1gdta1	Alignment	not modelled	21.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
35	c2zf8A_	Alignment	not modelled	21.4	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
36	c1ybeA_	Alignment	not modelled	21.2	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase
37	d1vmka_	Alignment	not modelled	20.8	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
38	d1rvxa_	Alignment	not modelled	20.6	26	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
39	c1vlpA_	Alignment	not modelled	19.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a putative nicotinate phosphoribosyltransferase2 (yor209c, npt1) from saccharomyces cerevisiae at 1.75 a resolution
40	c3dmaA_	Alignment	not modelled	19.1	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** crystal structure of an exopolyphosphatase-related protein2 from bacteroides fragilis. northeast structural genomics3 target bfr192
41	c1ytkA_	Alignment	not modelled	19.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase from thermoplasma **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase from2 thermoplasma acidophilum with nicotinate mononucleotide
42	c2rhoB_	Alignment	not modelled	18.8	19	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
43	c1w5fA_	Alignment	not modelled	18.6	17	**PDB header:**cell division **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz, t7 mutated, domain swapped (t. maritima)
44	c3crqA_	Alignment	not modelled	18.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** structure of trna dimethylallyltransferase: rna2 modification through a channel
45	c1b0aA_	Alignment	not modelled	18.3	20	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
46	c3szzA_	Alignment	not modelled	18.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
47	c2p10D_	Alignment	not modelled	17.1	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
48	c2c2pA_	Alignment	not modelled	16.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g/u mismatch-specific dna glycosylase; **PDBTitle:** the crystal structure of mismatch specific uracil-dna2 glycosylase (mug) from deinococcus radiodurans
49	d1rq2a1	Alignment	not modelled	16.6	20	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
50	d2p10a1	Alignment	not modelled	16.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
51	c2vg2C_	Alignment	not modelled	16.1	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
52	d1ybea1	Alignment	not modelled	15.7	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain

53	d1xpua3	Alignment	not modelled	15.5	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
54	d2jdia3	Alignment	not modelled	15.5	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
55	c2vawA_	Alignment	not modelled	15.2	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz pseudomonas aeruginosa gdp
56	c3q3qA_	Alignment	not modelled	15.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
57	d1jlja_	Alignment	not modelled	14.6	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
58	d1ns5a_	Alignment	not modelled	14.6	24	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
59	d1w5fa1	Alignment	not modelled	14.3	17	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
60	d1q6za1	Alignment	not modelled	14.3	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
61	c3khsB_	Alignment	not modelled	14.1	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
62	c2vxyA_	Alignment	not modelled	14.0	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** the structure of ftsz from bacillus subtilis at 1.7a2 resolution
63	c2r6r1_	Alignment	not modelled	13.9	17	**PDB header:**cell cycle **Chain:** 1: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** aquifex aeolicus ftsz
64	c1e9kA_	Alignment	not modelled	13.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp specific phosphodiesterase pde4d5; **PDBTitle:** the structure of the rack1 interaction sites located within2 the unique n-terminal region of the camp-specific3 phosphodiesterase, pde4d5.
65	c1ofuB_	Alignment	not modelled	13.4	20	**PDB header:**bacterial cell division inhibitor **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of sula:ftsz from pseudomonas aeruginosa
66	d1muga_	Alignment	not modelled	13.1	24	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
67	d2jdid3	Alignment	not modelled	13.0	50	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
68	c2d3yA_	Alignment	not modelled	12.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from thermus thermophilus2 hb8
69	c3ikbB_	Alignment	not modelled	12.9	56	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a conserved protein from streptococcus2 mutans ua159.
70	d1fx0a3	Alignment	not modelled	12.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
71	d1yo6a1	Alignment	not modelled	12.8	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
72	d1skye3	Alignment	not modelled	12.1	50	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
73	c3cvjB_	Alignment	not modelled	11.8	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
74	d1fx0b3	Alignment	not modelled	11.8	50	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
75	c2rbaB_	Alignment	not modelled	11.6	24	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**g/t mismatch-specific thymine dna glycosylase; **PDBTitle:** structure of human thymine dna glycosylase bound to abasic and2 undamaged dna
76	c1w59B_	Alignment	not modelled	11.6	23	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
77	c2c2xB_	Alignment	not modelled	11.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
						Fold:P-loop containing nucleoside triphosphate hydrolases

78	d1skyb3	Alignment	not modelled	11.4	8	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
79	c2d07A_	Alignment	not modelled	11.1	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g/t mismatch-specific thymine dna glycosylase; **PDBTitle:** crystal structure of sumo-3-modified thymine-dna glycosylase
80	c3ragA_	Alignment	not modelled	10.5	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
81	d1ecfa1	Alignment	not modelled	10.2	24	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
82	d1d0gr1	Alignment	not modelled	10.1	45	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
83	c2l25A_	Alignment	not modelled	9.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** np_888769.1
84	c3nglA_	Alignment	not modelled	9.8	20	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
85	c3lxqB_	Alignment	not modelled	9.8	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp1736; **PDBTitle:** the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a
86	c3kzvA_	Alignment	not modelled	9.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized oxidoreductase yir035c; **PDBTitle:** the crystal structure of a cytoplasmic protein with unknown function2 from saccharomyces cerevisiae
87	d1fsua_	Alignment	not modelled	9.4	18	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
88	c2q1yB_	Alignment	not modelled	9.4	19	**PDB header:**cell cycle, signaling protein **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
89	c2l6pA_	Alignment	not modelled	9.3	18	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**phac1, phac2 and phad genes; **PDBTitle:** nmr solution structure of the protein np_253742.1
90	c1ecjB_	Alignment	not modelled	8.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
91	d1ei6a_	Alignment	not modelled	8.9	22	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
92	c3fybA_	Alignment	not modelled	8.7	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function (duf1244); **PDBTitle:** crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
93	d1kifa1	Alignment	not modelled	7.8	22	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
94	d1yt3a1	Alignment	not modelled	7.8	12	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains
95	d1g2oa_	Alignment	not modelled	7.8	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
96	c3h87D_	Alignment	not modelled	7.7	25	**PDB header:**toxin/antitoxin **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
97	d1wura1	Alignment	not modelled	7.5	10	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
98	c1wm9D_	Alignment	not modelled	7.5	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase i; **PDBTitle:** structure of gtp cyclohydrolase i from thermus thermophilus hb8
99	d1hdha_	Alignment	not modelled	7.4	31	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase