Phyre^2

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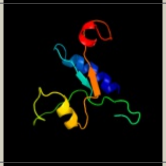
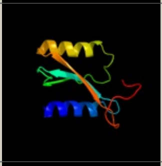
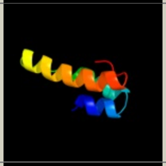
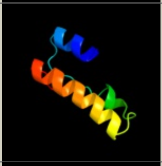
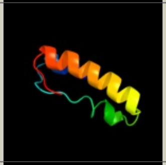
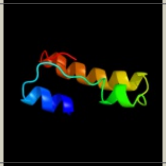
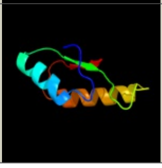
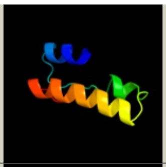
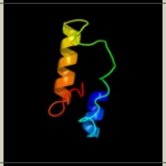
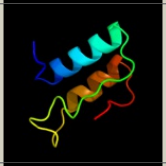
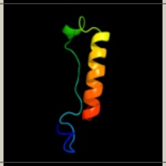
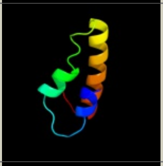
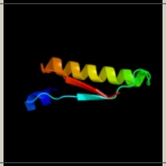
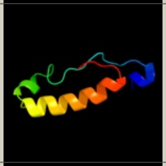
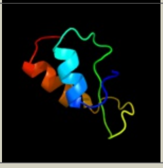
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qlcC_	Alignment		100.0	37	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein radc homolog; **PDBTitle:** the crystal structure of dna repair protein radc from chlorobium2 tepidum tls
2	d1oi0a_	Alignment		96.9	19	**Fold:**Cytidine deaminase-like **Superfamily:**JAB1/MPN domain **Family:**JAB1/MPN domain
3	c2kcqA_	Alignment		95.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mov34/mpn/pad-1 family; **PDBTitle:** solution structure of protein sru_2040 from salinibacter2 ruber (strain dsm 13855) . northeast structural genomics3 consortium target srr106
4	c2kksA_	Alignment		95.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein dsy2949 from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr27
5	c2w6rA_	Alignment		84.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**imidazole glycerol phosphate synthase subunit **PDBTitle:** crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
6	c3tdmD_	Alignment		70.5	10	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
7	c3q94B_	Alignment		68.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
8	d1gvfa_	Alignment		66.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
9	c3c52B_	Alignment		62.6	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
10	c2iswB_	Alignment		61.8	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
11	c2yciX_	Alignment		60.9	18	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native

12	d1rvga_	Alignment		58.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
13	d2csua1	Alignment		51.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
14	c3e49A_	Alignment		50.6	25	**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
15	c3elfA_	Alignment		45.4	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
16	c3pm6B_	Alignment		43.2	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
17	c3jrkG_	Alignment		41.2	23	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
18	c3qm3C_	Alignment		38.9	9	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
19	d1dosa_	Alignment		38.5	5	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
20	c3lotC_	Alignment		32.0	23	**PDB header:**structure genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
21	d1hl9a2	Alignment	not modelled	31.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
22	c3c6cA_	Alignment	not modelled	30.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
23	d1oxja2	Alignment	not modelled	28.6	8	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**PHAT domain
24	c3e02A_	Alignment	not modelled	24.7	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849; **PDBTitle:** crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
25	d1je0a_	Alignment	not modelled	24.3	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
26	c3stgA_	Alignment	not modelled	24.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
27	c3k13A_	Alignment	not modelled	23.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3

						bacteroides thetaiotaomicron
28	c2xrfA_	Alignment	not modelled	22.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
29	d1ybfa_	Alignment	not modelled	22.1	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
30	d1o98a1	Alignment	not modelled	20.7	18	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
31	c1jvnB_	Alignment	not modelled	20.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hisHF; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
32	c3t18D_	Alignment	not modelled	20.4	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
33	d2isya2	Alignment	not modelled	20.4	25	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
34	c3op1A_	Alignment	not modelled	20.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
35	d1f6ya_	Alignment	not modelled	17.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
36	d1kfta_	Alignment	not modelled	17.1	14	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
37	c1kftA_	Alignment	not modelled	17.1	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
38	d1ywxa1	Alignment	not modelled	15.6	22	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
39	c1k97A_	Alignment	not modelled	15.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
40	d1ka9f_	Alignment	not modelled	14.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
41	d3bzka5	Alignment	not modelled	14.7	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
42	d1h5ya_	Alignment	not modelled	14.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
43	c2y85D_	Alignment	not modelled	13.3	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
44	d1k9sa_	Alignment	not modelled	13.3	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
45	c2y7eA_	Alignment	not modelled	13.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
46	c3chvA_	Alignment	not modelled	12.8	16	**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
47	c3no5C_	Alignment	not modelled	12.7	13	**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
48	c3gndC_	Alignment	not modelled	12.5	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
49	c2bdqA_	Alignment	not modelled	12.5	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
50	d1xn9a_	Alignment	not modelled	12.2	20	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
51	d1cuka2	Alignment	not modelled	12.2	9	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain

52	d1e0fi_	Alignment	not modelled	12.1	56	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
53	c1e0fl_	Alignment	not modelled	12.1	56	**PDB header:**coagulation/crystal structure/heparin-b **Chain:** I: **PDB Molecule:**haemadin; **PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor
54	c3av0A_	Alignment	not modelled	11.6	25	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
55	d2i1qa1	Alignment	not modelled	10.9	4	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
56	c1e0fJ_	Alignment	not modelled	10.9	56	**PDB header:**coagulation/crystal structure/heparin-b **Chain:** J: **PDB Molecule:**haemadin; **PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor
57	c2csdB_	Alignment	not modelled	10.8	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
58	d1yj5a1	Alignment	not modelled	10.7	9	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
59	d1ii7a_	Alignment	not modelled	10.6	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
60	d2a1jb1	Alignment	not modelled	9.7	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
61	d1xi3a_	Alignment	not modelled	9.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
62	c1o98A_	Alignment	not modelled	9.6	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
63	d1g3wa2	Alignment	not modelled	9.5	25	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
64	d1ixra1	Alignment	not modelled	9.5	5	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
65	c3eypB_	Alignment	not modelled	9.5	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
66	c1t3tA_	Alignment	not modelled	9.4	67	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
67	c2wvsD_	Alignment	not modelled	9.4	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
68	d1w5da1	Alignment	not modelled	9.2	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
69	c3iz5w_	Alignment	not modelled	9.2	50	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
70	c1hjpA_	Alignment	not modelled	9.1	19	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
71	c1e0fK_	Alignment	not modelled	9.0	56	**PDB header:**coagulation/crystal structure/heparin-b **Chain:** K: **PDB Molecule:**haemadin; **PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor
72	d1x2ia1	Alignment	not modelled	8.9	8	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
73	c2j8qB_	Alignment	not modelled	8.9	19	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 5; **PDBTitle:** crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
74	c2x0kB_	Alignment	not modelled	8.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
75	d1bvsa2	Alignment	not modelled	8.9	5	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
76	d1t3ta4	Alignment	not modelled	8.9	67	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
77	d2ex2a1	Alignment	not modelled	8.2	22	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like

78	c3auzA_	Alignment	not modelled	7.9	22	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
79	d1szpa1	Alignment	not modelled	7.9	4	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
80	d1szpb1	Alignment	not modelled	7.9	0	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
81	d2qi2a3	Alignment	not modelled	7.7	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
82	d1rv9a_	Alignment	not modelled	7.6	16	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
83	c3zqoK_	Alignment	not modelled	7.5	15	**PDB header:**dna-binding protein **Chain:** K: **PDB Molecule:**terminase small subunit; **PDBTitle:** crystal structure of the small terminase oligomerization2 core domain from a spp1-like bacteriophage (crystal form 3)
84	d1x6va2	Alignment	not modelled	7.3	27	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
85	c2h5xA_	Alignment	not modelled	7.2	5	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
86	c2it0A_	Alignment	not modelled	7.1	25	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
87	c3a3eB_	Alignment	not modelled	7.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**penicillin-binding protein 4; **PDBTitle:** crystal structure of penicillin binding protein 4 (dacb)2 from haemophilus influenzae, complexed with novel beta-3 lactam (cmv)
88	d1rw0a_	Alignment	not modelled	7.1	26	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
89	c2w1oA_	Alignment	not modelled	7.1	33	**PDB header:**translation **Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p2; **PDBTitle:** nmr structure of dimerization domain of human ribosomal2 protein p2
90	c3f0hA_	Alignment	not modelled	6.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
91	d1wmhb_	Alignment	not modelled	6.8	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
92	d1pzna1	Alignment	not modelled	6.8	4	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
93	c3izbU_	Alignment	not modelled	6.8	9	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**40s ribosomal protein s24; **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
94	d1nmpa_	Alignment	not modelled	6.7	16	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
95	c3iz6U_	Alignment	not modelled	6.7	36	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**40s ribosomal protein s24 (s24e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
96	c3eufC_	Alignment	not modelled	6.7	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase 1; **PDBTitle:** crystal structure of bau-bound human uridine phosphorylase 1
97	c1oxjA_	Alignment	not modelled	6.6	8	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein smaug; **PDBTitle:** crystal structure of the smaug rna binding domain
98	d1dfoa_	Alignment	not modelled	6.4	5	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
99	d3etja2	Alignment	not modelled	6.4	28	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like