Phyre^2

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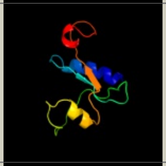
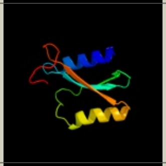
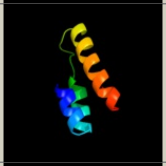
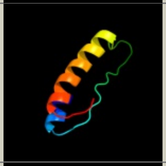
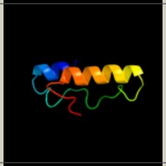
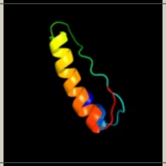
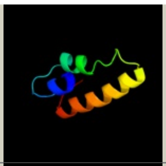
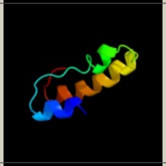
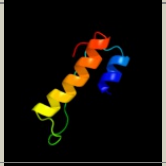
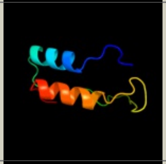
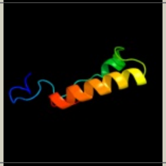
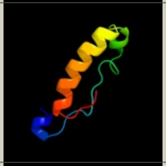
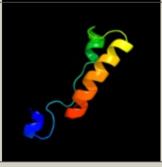
Description	P76362
Date	Thu Jan 5 12:22:22 GMT 2012
Unique Job ID	0cf04155d76fc2e6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qlcC_	Alignment		100.0	39	**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		96.7	21	**Fold:**Cytidine deaminase-like **Superfamily:**JAB1/MPN domain **Family:**JAB1/MPN domain
3	c2kcqA_	Alignment		95.3	15	**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		94.9	18	**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		80.2	11	**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	c3q94B_	Alignment		60.3	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'
7	d1gvfa_	Alignment		58.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
8	c3tdmD_	Alignment		57.0	10	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
9	d2csua1	Alignment		56.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
10	c3c52B_	Alignment		55.4	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
11	c2yciX_	Alignment		54.5	17	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native

12	c3pm6B_	Alignment		54.3	20	**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
13	c2iswB_	Alignment		54.2	20	**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
14	d1rvga_	Alignment		51.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
15	c3jrkG_	Alignment		43.5	19	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
16	d1hl9a2	Alignment		40.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
17	c3elfA_	Alignment		35.3	14	**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
18	c3e49A_	Alignment		34.8	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
19	d1dosa_	Alignment		30.9	2	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
20	c3qm3C_	Alignment		30.8	11	**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
21	d3bzka5	Alignment	not modelled	29.9	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
22	c2xrfA_	Alignment	not modelled	29.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
23	d1je0a_	Alignment	not modelled	29.5	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
24	d1ybfa_	Alignment	not modelled	27.9	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
25	c3stgA_	Alignment	not modelled	26.9	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
26	d2isya2	Alignment	not modelled	26.2	25	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
27	c3lotC_	Alignment	not modelled	22.3	19	**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
28	c3t18D_	Alignment	not modelled	22.0	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.

29	c3zqoK_	Alignment	not modelled	19.9	19	**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)
30	c3c6cA_	Alignment	not modelled	19.2	17	**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
31	c3op1A_	Alignment	not modelled	18.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
32	c3eypB_	Alignment	not modelled	18.2	25	**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
33	d1k9sa_	Alignment	not modelled	18.2	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
34	c3k13A_	Alignment	not modelled	17.8	19	**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
35	d1ywxa1	Alignment	not modelled	17.5	22	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
36	d1rw0a_	Alignment	not modelled	17.3	25	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
37	d1rv9a_	Alignment	not modelled	17.2	19	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
38	c1k97A_	Alignment	not modelled	16.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
39	c2wvsD_	Alignment	not modelled	16.0	28	**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
40	c3gndC_	Alignment	not modelled	16.0	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
41	c3fiuD_	Alignment	not modelled	15.8	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
42	c3av0A_	Alignment	not modelled	15.0	23	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
43	d1xafa_	Alignment	not modelled	15.0	25	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
44	d1ii7a_	Alignment	not modelled	14.7	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
45	c3mo4B_	Alignment	not modelled	14.5	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase; **PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
46	d1xn9a_	Alignment	not modelled	14.3	20	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
47	d1g3wa2	Alignment	not modelled	14.1	25	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
48	d1ka9f_	Alignment	not modelled	13.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
49	d1e0fi_	Alignment	not modelled	13.3	44	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
50	c1e0fI_	Alignment	not modelled	13.3	44	**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
51	d1f6ya_	Alignment	not modelled	13.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
52	c2it0A_	Alignment	not modelled	12.7	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
53	c1e0fJ_	Alignment	not modelled	12.2	44	**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
						PDB header:structural genomics, unknown function

54	c3no5C_	Alignment	not modelled	12.1	19	**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
55	d1xi3a_	Alignment	not modelled	12.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
56	d1w5da1	Alignment	not modelled	11.8	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
57	c3iz5w_	Alignment	not modelled	11.8	42	**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
58	c2y85D_	Alignment	not modelled	11.6	13	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
59	c3eufC_	Alignment	not modelled	11.6	2	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase 1; **PDBTitle:** crystal structure of bau-bound human uridine phosphorylase 1
60	c2j8qB_	Alignment	not modelled	11.3	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.
61	c1jvnB_	Alignment	not modelled	11.3	17	**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
62	c1t3tA_	Alignment	not modelled	10.9	67	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
63	c2x0kB_	Alignment	not modelled	10.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
64	c1e0fK_	Alignment	not modelled	10.4	44	**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
65	d2ex2a1	Alignment	not modelled	10.2	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
66	d1odka_	Alignment	not modelled	10.1	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
67	c3chvA_	Alignment	not modelled	10.1	24	**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
68	d1t3ta4	Alignment	not modelled	10.0	67	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
69	d1h5ya_	Alignment	not modelled	9.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
70	c3e02A_	Alignment	not modelled	9.6	24	**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
71	c2w1oA_	Alignment	not modelled	9.5	33	**PDB header:**translation **Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p2; **PDBTitle:** nmr structure of dimerization domain of human ribosomal2 protein p2
72	c1o98A_	Alignment	not modelled	9.4	16	**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
73	c3izcw_	Alignment	not modelled	9.1	29	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein rpl22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
74	d2qi2a3	Alignment	not modelled	9.1	12	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
75	d1yj5a1	Alignment	not modelled	8.9	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
76	c3a3eB_	Alignment	not modelled	8.8	22	**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)
77	c3f0hA_	Alignment	not modelled	8.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
						PDB header:recombination

78	c3auzA_	Alignment	not modelled	8.6	20	**Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
79	c2y7eA_	Alignment	not modelled	8.4	26	**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)
80	c3izbU_	Alignment	not modelled	8.0	18	**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
81	c3iz6U_	Alignment	not modelled	8.0	45	**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
82	d1s7ia_	Alignment	not modelled	7.9	12	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
83	d1vhwa_	Alignment	not modelled	7.8	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
84	d1dfoa_	Alignment	not modelled	7.7	5	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
85	c2bdqA_	Alignment	not modelled	7.7	23	**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.
86	d1gpma1	Alignment	not modelled	7.6	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
87	c3guzB_	Alignment	not modelled	7.5	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
88	c3pj0D_	Alignment	not modelled	7.2	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**lmo0305 protein; **PDBTitle:** crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution
89	c2deoA_	Alignment	not modelled	7.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**441aa long hypothetical nfed protein; **PDBTitle:** 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
90	c2csuB_	Alignment	not modelled	7.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
91	c3gzaB_	Alignment	not modelled	7.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
92	d1q1ga_	Alignment	not modelled	6.9	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
93	c1nw4C_	Alignment	not modelled	6.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase, putative; **PDBTitle:** crystal structure of plasmodium falciparum purine nucleoside2 phosphorylase in complex with immh and sulfate
94	c2xzmP_	Alignment	not modelled	6.7	32	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**rps24e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
95	c2x5fB_	Alignment	not modelled	6.6	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate_tyrosine_phenylalanine pyridoxal-5' **PDBTitle:** crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase
96	c1hl8B_	Alignment	not modelled	6.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
97	d1x6va2	Alignment	not modelled	6.4	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
98	c2vxoB_	Alignment	not modelled	6.3	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
99	c1z34A_	Alignment	not modelled	6.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine