Phyre2

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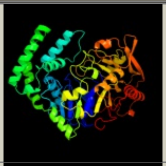
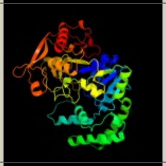
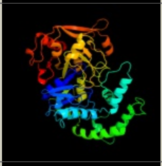
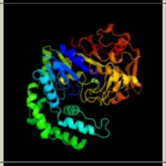
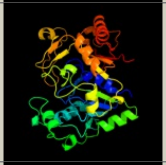
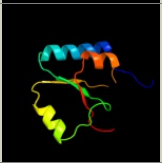
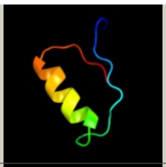
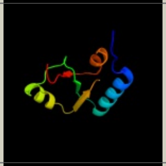
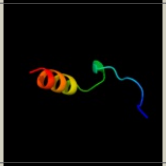
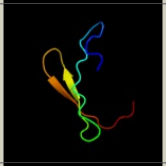
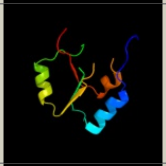
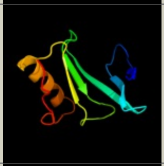
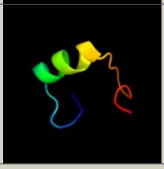
Description	P0A7D4
Date	Wed Jan 25 15:20:17 GMT 2012
Unique Job ID	1ca10b64ca10bd75

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qf5a_	Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
2	d1dj2a_	Alignment		100.0	44	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
3	d1dj3a_	Alignment		100.0	44	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
4	d1iwea_	Alignment		100.0	43	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
5	c1iweB_	Alignment		100.0	43	**PDB header:**ligase **Chain:** B: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** imp complex of the recombinant mouse-muscle2 adenylosuccinate synthetase
6	d1p9ba_	Alignment		100.0	40	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
7	c3ue9A_	Alignment		100.0	61	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of adenylosuccinate synthetase (ampsase) (pura) from2 burkholderia thailandensis
8	c3r7tA_	Alignment		100.0	47	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of adenylosuccinate synthetase from campylobacter2 jejuni
9	c2d7uA_	Alignment		100.0	43	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of hypothetical adenylosuccinate synthetase, ph04382 from pyrococcus horikoshii ot3
10	d1a0ia1	Alignment		88.4	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
11	d1p9pa_	Alignment		57.7	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD

12	c3fwzA_	Alignment		54.0	27	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein ybal; **PDBTitle:** crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
13	d1uala_	Alignment		54.0	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
14	d2jfga1	Alignment		53.2	21	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
15	c3knuD_	Alignment		52.3	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
16	c1zgxA_	Alignment		49.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**guanyl-specific ribonuclease sa; **PDBTitle:** crystal structure of ribonuclease mutant
17	d2f09a1	Alignment		44.9	10	**Fold:**Streptavidin-like **Superfamily:**YdhA-like **Family:**YdhA-like
18	c3ky7A_	Alignment		43.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
19	d1qwda_	Alignment		39.7	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
20	d1gm5a2	Alignment		35.5	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
21	c3iefA_	Alignment	not modelled	34.3	25	**PDB header:**transferase, rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs.
22	c2ixaA_	Alignment	not modelled	34.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
23	c2qioA_	Alignment	not modelled	32.3	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
24	d1jsca3	Alignment	not modelled	30.9	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
25	c1k1qA_	Alignment	not modelled	28.4	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
26	c3dnfB_	Alignment	not modelled	26.3	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
27	c3quvB_	Alignment	not modelled	26.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
28	d1lt7a_	Alignment	not modelled	24.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase

29	c2xf4A_	Alignment	not modelled	24.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydroxyacylglutathione hydrolase; **PDBTitle:** crystal structure of salmonella enterica serovar2 typhimurium ycbl
30	c3opyE_	Alignment	not modelled	24.3	12	**PDB header:**transferase **Chain:** E: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
31	d1k1ga_	Alignment	not modelled	23.4	29	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
32	d1g7oa1	Alignment	not modelled	22.3	14	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
33	d1e6ca_	Alignment	not modelled	22.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
34	c2nm0B_	Alignment	not modelled	21.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 3-oxacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2)
35	c1kyqC_	Alignment	not modelled	21.5	17	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
36	d1hywa_	Alignment	not modelled	20.0	41	**Fold:**gpW/XkdW-like **Superfamily:**Head-to-tail joining protein W, gpW **Family:**Head-to-tail joining protein W, gpW
37	c2inrA_	Alignment	not modelled	19.6	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
38	d1lnia_	Alignment	not modelled	18.8	25	**Fold:**Microbial ribonucleases **Superfamily:**Microbial ribonucleases **Family:**Bacterial ribonucleases
39	c3p19A_	Alignment	not modelled	18.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative blue fluorescent protein; **PDBTitle:** improved nadph-dependent blue fluorescent protein
40	c2z2vA_	Alignment	not modelled	18.6	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
41	c2cfcB_	Alignment	not modelled	18.3	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-(r)-hydroxypropyl-com dehydrogenase; **PDBTitle:** structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
42	c3db2C_	Alignment	not modelled	18.0	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative nadph-dependent oxidoreductase; **PDBTitle:** crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
43	c2gr2A_	Alignment	not modelled	18.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase, bpha4 (oxidized form)
44	c2wfbA_	Alignment	not modelled	17.7	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein orp; **PDBTitle:** high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
45	d1d7ya1	Alignment	not modelled	17.7	42	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
46	d1oy5a_	Alignment	not modelled	17.6	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
47	c1oy5B_	Alignment	not modelled	17.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
48	c1yfsB_	Alignment	not modelled	17.5	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
49	d2i1qa1	Alignment	not modelled	17.4	15	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
50	c3ktsA_	Alignment	not modelled	17.4	14	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein; **PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
51	d1k1sa2	Alignment	not modelled	17.0	16	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
52	d1qyia_	Alignment	not modelled	16.9	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
53	d1qnaa1	Alignment	not modelled	16.7	12	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
						Fold:TBP-like

54	d1nh2a1	Alignment	not modelled	16.5	11	**Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
55	d1jx4a2	Alignment	not modelled	16.3	18	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
56	c2zzfA_	Alignment	not modelled	16.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of alanyl-trna synthetase without2 oligomerization domain
57	c3f6zB_	Alignment	not modelled	15.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pseudomonas aeruginosa mlic in complex2 with hen egg white lysozyme
58	d1q44a_	Alignment	not modelled	15.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
59	c1ujlA_	Alignment	not modelled	15.6	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h **PDBTitle:** solution structure of the herg k+ channel s5-p2 extracellular linker
60	c3dtyA_	Alignment	not modelled	15.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
61	d1fi4a2	Alignment	not modelled	15.1	56	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate 5-diphosphate decarboxylase
62	d1y6ia1	Alignment	not modelled	15.0	78	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**GUN4-associated domain
63	d1cora_	Alignment	not modelled	14.8	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
64	d2bl5a1	Alignment	not modelled	14.7	29	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
65	d1cdwa1	Alignment	not modelled	14.6	12	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
66	d1uuqa_	Alignment	not modelled	14.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
67	c1uz4A_	Alignment	not modelled	14.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**man5a; **PDBTitle:** common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 intineraries for glucoside and mannoside hydrolysis
68	d1pzna1	Alignment	not modelled	13.9	21	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
69	c2hivA_	Alignment	not modelled	13.6	42	**PDB header:**ligase **Chain:** A: **PDB Molecule:**thermostable dna ligase; **PDBTitle:** atp-dependent dna ligase from s. solfataricus
70	d2bcqa2	Alignment	not modelled	13.6	25	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
71	c2v7sA_	Alignment	not modelled	13.5	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable conserved lipoprotein lppa; **PDBTitle:** crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
72	c1t3nB_	Alignment	not modelled	13.4	22	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**polymerase (dna directed) iota; **PDBTitle:** structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
73	d1t6ca1	Alignment	not modelled	13.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
74	d1id1a_	Alignment	not modelled	13.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
75	d1jmsa3	Alignment	not modelled	13.1	38	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
76	d1znwa1	Alignment	not modelled	12.8	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
77	c3c5yD_	Alignment	not modelled	12.6	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
78	d1qsga_	Alignment	not modelled	12.6	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
79	c2y0nD_	Alignment	not modelled	12.6	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**male-specific lethal 3 homolog; **PDBTitle:** crystal structure of the complex between dosage2 compensation factors msl1 and msl3
						Fold: Putative anticodon-binding domain of alanyl-tRNA synthetase

80	d1riqa1	Alignment	not modelled	12.4	13	(AlaRS) **Superfamily:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Family:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
81	c3hi0B_	Alignment	not modelled	12.3	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative exopolyphosphatase; **PDBTitle:** crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
82	d1zeta2	Alignment	not modelled	12.1	22	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
83	d1t94a2	Alignment	not modelled	12.0	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
84	d1x9na2	Alignment	not modelled	11.9	32	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
85	d2a3ra1	Alignment	not modelled	11.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
86	c1u9iA_	Alignment	not modelled	11.6	12	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
87	c1s97D_	Alignment	not modelled	11.5	14	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
88	c2ovfA_	Alignment	not modelled	11.4	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stal; **PDBTitle:** crystal structure of stal-pap complex
89	d1a0rp_	Alignment	not modelled	11.4	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Phosducin
90	c3o38D_	Alignment	not modelled	11.2	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
91	c1ylmA_	Alignment	not modelled	11.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu32300; **PDBTitle:** structure of cytosolic protein of unknown function yute2 from bacillus subtilis
92	d2fmpa2	Alignment	not modelled	11.0	38	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
93	d1fuea_	Alignment	not modelled	10.9	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
94	d2vana1	Alignment	not modelled	10.9	38	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
95	d2ppqa1	Alignment	not modelled	10.8	14	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
96	c3he8A_	Alignment	not modelled	10.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
97	c1fi4A_	Alignment	not modelled	10.5	56	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mevalonate 5-diphosphate decarboxylase; **PDBTitle:** the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
98	c3nbxX_	Alignment	not modelled	10.5	21	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
99	c2fllA_	Alignment	not modelled	10.5	22	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp