Phyre2

Email	l.a.kelley@imperial.ac.uk
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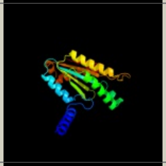
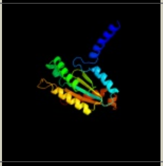
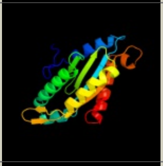
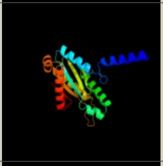
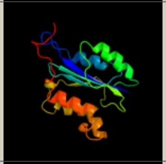
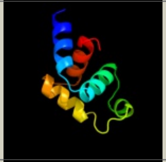
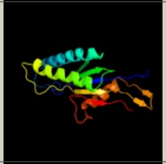
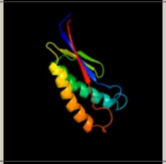
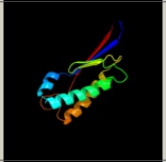
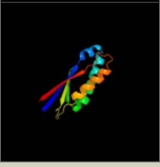
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w25B_	Alignment		100.0	32	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
2	c3ezuA_	Alignment		100.0	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef domain protein; **PDBTitle:** crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
3	c3breA_	Alignment		100.0	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
4	c3i5aA_	Alignment		100.0	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
5	c3hvaA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
6	c3i5cA_	Alignment		100.0	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fusion of general control protein gcn4 and wspr response **PDBTitle:** crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
7	c3ignA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase; **PDBTitle:** crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
8	c3i5bA_	Alignment		100.0	36	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
9	c3iclA_	Alignment		99.9	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**eal/ggdef domain protein; **PDBTitle:** x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
10	d1w25a3	Alignment		99.9	37	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
11	c3mtkA_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase/phosphodiesterase; **PDBTitle:** x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c

12	c3qyyB_	Alignment		99.9	30	**PDB header:**signaling protein/inhibitor **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
13	c3pjwA_	Alignment		99.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
14	c3hvwA_	Alignment		99.9	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc); **PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
15	c3gfzB_	Alignment		99.3	11	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
16	c3p7nB_	Alignment		98.1	6	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
17	c2qv6D_	Alignment		97.2	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
18	c1wc6B_	Alignment		90.8	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
19	d1wc1a_	Alignment		90.7	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
20	d1azsa_	Alignment		89.6	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
21	c1cjkA_	Alignment	not modelled	89.4	14	**PDB header:**lyase/lyase/signaling protein **Chain:** A: **PDB Molecule:**adenylate cyclase, type v; **PDBTitle:** complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
22	d1fx4a_	Alignment	not modelled	89.2	18	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
23	c1y10C_	Alignment	not modelled	89.2	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
24	d1fx2a_	Alignment	not modelled	88.7	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
25	c3et6A_	Alignment	not modelled	88.4	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**soluble guanylyl cyclase beta; **PDBTitle:** the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
26	c3uvjC_	Alignment	not modelled	86.0	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**guanylate cyclase soluble subunit alpha-3; **PDBTitle:** crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
27	c3mr7B_	Alignment	not modelled	84.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, alpha/beta fold **PDBTitle:** crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
						PDB header:lyase

28	c2w01C_	Alignment	not modelled	84.2	12	**Chain:** C: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the guanylyl cyclase cya2
29	c3r5gB_	Alignment	not modelled	82.3	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cyab; **PDBTitle:** crystal structure of the adenylyl cyclase cyab from p. aeruginosa
30	d1vh8a_	Alignment	not modelled	76.6	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
31	c3b6nA_	Alignment	not modelled	76.1	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax
32	c1s97D_	Alignment	not modelled	73.0	15	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
33	c1ybuA_	Alignment	not modelled	72.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipj; **PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
34	c2pmpA_	Alignment	not modelled	72.4	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
35	d1w55a2	Alignment	not modelled	70.5	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
36	d1t0aa_	Alignment	not modelled	70.1	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
37	d1gx1a_	Alignment	not modelled	69.4	12	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
38	d1iv3a_	Alignment	not modelled	68.8	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
39	c2aq4A_	Alignment	not modelled	67.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
40	c3f0gA_	Alignment	not modelled	67.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
41	c1yk9A_	Alignment	not modelled	66.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
42	d1im4a_	Alignment	not modelled	64.1	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
43	c3gqcB_	Alignment	not modelled	61.0	24	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
44	c3re3B_	Alignment	not modelled	57.8	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
45	c1k1qA_	Alignment	not modelled	55.6	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
46	c2wz1B_	Alignment	not modelled	55.3	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**guanylate cyclase soluble subunit beta-1; **PDBTitle:** structure of the catalytic domain of human soluble2 guanylate cyclase 1 beta 3.
47	c1w57A_	Alignment	not modelled	55.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
48	d1jx4a2	Alignment	not modelled	51.0	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
49	c2r8kB_	Alignment	not modelled	50.7	28	**PDB header:**replication, transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase eta; **PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna
50	d1azsb_	Alignment	not modelled	40.5	11	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
51	c1jihA_	Alignment	not modelled	37.8	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
52	c3mr2A_	Alignment	not modelled	32.7	32	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
						PDB header:transferase/dna

53	c2oh2B_	Alignment	not modelled	31.3	21	**Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
54	c1xaxA_	Alignment	not modelled	24.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
55	d1k1sa2	Alignment	not modelled	24.9	16	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
56	d2ox6a1	Alignment	not modelled	20.5	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**YdiL-like
57	c3qkbB_	Alignment	not modelled	20.0	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
58	d1jiha2	Alignment	not modelled	19.5	28	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
59	c1yy3A_	Alignment	not modelled	19.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
60	d2o5aa1	Alignment	not modelled	17.3	10	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
61	d1wdia_	Alignment	not modelled	16.9	18	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
62	c2uzhB_	Alignment	not modelled	15.3	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
63	c1qgeE_	Alignment	not modelled	14.5	16	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
64	c2y1bA_	Alignment	not modelled	14.1	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein, signal; **PDBTitle:** crystal structure of the e. coli outer membrane lipoprotein2 rcsf
65	d2fiqa1	Alignment	not modelled	12.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
66	c2bblA_	Alignment	not modelled	11.0	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome linked protein vpg; **PDBTitle:** nmr structures of the peptide linked to the genome (vpg) of2 poliovirus in a stabilizing solvent
67	c3l7xA_	Alignment	not modelled	10.7	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle **PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159
68	d1xxaa_	Alignment	not modelled	10.7	18	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
69	d2oyra1	Alignment	not modelled	10.6	25	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhiQ-like
70	d2djka1	Alignment	not modelled	9.9	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
71	c2r6zA_	Alignment	not modelled	9.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**upf0341 protein in rsp 3' region; **PDBTitle:** crystal structure of the sam-dependent methyltransferase2 ngo1261 from neisseria gonorrhoeae, northeast structural3 genomics consortium target ngr48
72	c3iyuY_	Alignment	not modelled	9.3	20	**PDB header:**virus **Chain:** Y: **PDB Molecule:**outer capsid protein vp4; **PDBTitle:** atomic model of an infectious rotavirus particle
73	c3onqB_	Alignment	not modelled	9.1	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**regulator of polyketide synthase expression; **PDBTitle:** crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
74	c1iojA_	Alignment	not modelled	9.0	56	**PDB header:**apolipoprotein **Chain:** A: **PDB Molecule:**apoc-i; **PDBTitle:** human apolipoprotein c-i, nmr, 18 structures
75	d2dlxa1	Alignment	not modelled	8.7	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain
76	c3anoA_	Alignment	not modelled	8.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ap-4-a phosphorylase; **PDBTitle:** crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
77	d1ei7a_	Alignment	not modelled	8.5	40	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
						Fold:S-adenosyl-L-methionine-dependent methyltransferases

78	d2pkwa1	Alignment	not modelled	8.5	25	**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhiQ-like
79	d1nhoa_	Alignment	not modelled	8.5	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
80	c3kmlB_	Alignment	not modelled	8.5	36	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**coat protein; **PDBTitle:** circular permutant of the tobacco mosaic virus
81	c3upsA_	Alignment	not modelled	8.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis
82	d1zaka2	Alignment	not modelled	8.3	29	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
83	c3hf3A_	Alignment	not modelled	8.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
84	c2zhoB_	Alignment	not modelled	8.2	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
85	c3imiB_	Alignment	not modelled	8.1	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
86	c2i46A_	Alignment	not modelled	8.1	5	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**adrenocortical dysplasia protein homolog; **PDBTitle:** crystal structure of human tpp1
87	d1vtmp_	Alignment	not modelled	8.0	20	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
88	d1xm5a_	Alignment	not modelled	8.0	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
89	d1fo5a_	Alignment	not modelled	7.9	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
90	d2jnwa1	Alignment	not modelled	7.8	10	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XPF/Rad1/Mus81 nuclease
91	d2id1a1	Alignment	not modelled	7.7	5	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
92	d1h2vc2	Alignment	not modelled	7.7	36	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
93	d1qgva_	Alignment	not modelled	7.6	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
94	c3nj2B_	Alignment	not modelled	7.4	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**duf269-containing protein; **PDBTitle:** crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
95	c2htfA_	Alignment	not modelled	7.4	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain
96	c2qsiB_	Alignment	not modelled	7.3	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
97	c1ps9A_	Alignment	not modelled	7.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
98	c3k30B_	Alignment	not modelled	7.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
99	c2zqeA_	Alignment	not modelled	7.1	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2