Phyre2

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Description	P30177
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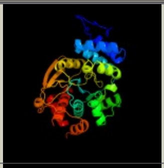
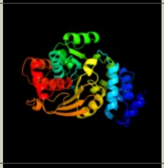
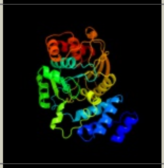
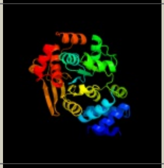
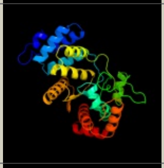
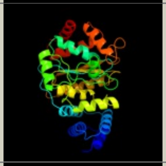
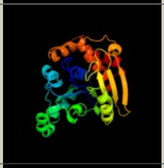
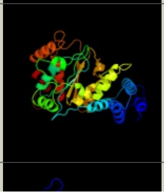
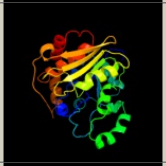
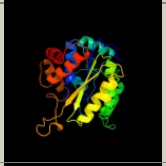
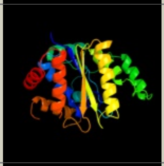
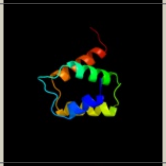
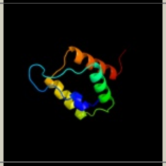
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1v8gB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
2	c1o17A_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
3	c1khdD_	Alignment		100.0	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)
4	c2bpqB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
5	c1vquB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
6	c3h5qA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
7	c1brwB_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
8	d1o17a2	Alignment		100.0	19	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
9	d2elca2	Alignment		100.0	21	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
10	c2j0fC_	Alignment		100.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
11	c2dsjA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8

12	c1otpA_	Alignment		100.0	13	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
13	d1khda2	Alignment		100.0	18	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
14	d1uoua2	Alignment		100.0	16	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
15	d1brwa2	Alignment		100.0	12	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
16	d2tpta2	Alignment		100.0	13	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
17	d1o17a1	Alignment		99.7	37	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
18	d1khda1	Alignment		99.6	20	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
19	d1brwa1	Alignment		99.6	21	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
20	d2tpta1	Alignment		99.6	13	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
21	d1v8ga1	Alignment	not modelled	99.5	25	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
22	d1uoua1	Alignment	not modelled	99.5	23	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
23	d2elca1	Alignment	not modelled	99.1	27	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
24	d1vkma_	Alignment	not modelled	90.5	18	**Fold:**Indigoidine synthase A-like **Superfamily:**Indigoidine synthase A-like **Family:**Indigoidine synthase A-like
25	d1tuea_	Alignment	not modelled	72.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
26	d1svma_	Alignment	not modelled	71.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
27	d1kfia1	Alignment	not modelled	69.0	12	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
28	c2kycA	Alignment	not modelled	68.6	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis

28	c2kvcA_	Alignment	not modelled	68.6	15	protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
29	d1p88a_	Alignment	not modelled	68.5	17	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
30	c2o0zA_	Alignment	not modelled	66.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** mycobacterium tuberculosis epsp synthase in complex with2 product (eps)
31	d2gc6a2	Alignment	not modelled	64.6	12	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
32	c2lkyA_	Alignment	not modelled	61.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
33	c2px0D_	Alignment	not modelled	60.6	14	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
34	c3n2aA_	Alignment	not modelled	51.2	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**bifunctional folylpolyglutamate synthase/dihydrofolate **PDBTitle:** crystal structure of bifunctional folylpolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
35	c2yvqA_	Alignment	not modelled	50.8	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
36	c3chgB_	Alignment	not modelled	47.8	21	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**glycine betaine-binding protein; **PDBTitle:** the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
37	c2gc6A_	Alignment	not modelled	47.2	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase; **PDBTitle:** s73a mutant of l. casei fpgs
38	c1kfiA_	Alignment	not modelled	46.8	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoglucomutase 1; **PDBTitle:** crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
39	d3pmga1	Alignment	not modelled	46.7	10	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
40	d1j9ia_	Alignment	not modelled	45.6	11	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
41	c2cnwF_	Alignment	not modelled	45.2	17	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
42	d1rf6a_	Alignment	not modelled	44.9	16	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
43	c1w96B_	Alignment	not modelled	43.1	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
44	c3k2gA_	Alignment	not modelled	42.2	11	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
45	c1r71B_	Alignment	not modelled	41.5	13	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna
46	d2jwda1	Alignment	not modelled	39.6	11	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
47	c2pqdA_	Alignment	not modelled	39.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** a100g cp4 epsps liganded with (r)-difluoromethyl tetrahedral reaction2 intermediate analog
48	d1ukza_	Alignment	not modelled	38.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
49	c3rmtB_	Alignment	not modelled	37.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase 1; **PDBTitle:** crystal structure of putative 5-enolpyruvoylshikimate-3-phosphate2 synthase from bacillus halodurans c-125
50	d1ejda_	Alignment	not modelled	37.5	11	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
51	d1tz9a_	Alignment	not modelled	36.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
52	d1r71a_	Alignment	not modelled	36.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like

						Family: KorB DNA-binding domain-like
53	c2qguA_	Alignment	not modelled	36.2	2	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
54	c3r38A_	Alignment	not modelled	35.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; **PDBTitle:** 2.23 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase (mura) from listeria monocytogenes egd-e
55	c2oz5A_	Alignment	not modelled	35.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phosphotyrosine protein phosphatase ptpb; **PDBTitle:** crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
56	c3jvpA_	Alignment	not modelled	34.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
57	c1w78A_	Alignment	not modelled	34.4	18	**PDB header:**synthase **Chain:** A: **PDB Molecule:**folc bifunctional protein; **PDBTitle:** e.coli folc in complex with dhpp and adp
58	c3ewbX_	Alignment	not modelled	34.4	9	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
59	c3eegB_	Alignment	not modelled	34.2	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
60	c3bg3B_	Alignment	not modelled	34.1	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase, mitochondrial; **PDBTitle:** crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
61	c1nsfA_	Alignment	not modelled	33.9	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
62	d1a0pa2	Alignment	not modelled	32.8	23	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
63	d1uaea_	Alignment	not modelled	32.3	10	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
64	c1rr2A_	Alignment	not modelled	30.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
65	c2yhsA_	Alignment	not modelled	30.7	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
66	d1g6sa_	Alignment	not modelled	30.6	18	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
67	d1ywfa1	Alignment	not modelled	29.9	15	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Mycobacterial PtpB-like
68	c2ip4A_	Alignment	not modelled	29.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
69	c3dnfB_	Alignment	not modelled	29.3	10	**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
70	c2vosA_	Alignment	not modelled	28.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase protein folc; **PDBTitle:** mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
71	c2iy3A_	Alignment	not modelled	27.6	15	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
72	d1b8za_	Alignment	not modelled	26.9	10	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
73	d1wb9a2	Alignment	not modelled	26.6	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
74	c3ol4B_	Alignment	not modelled	26.5	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
75	c2j37W_	Alignment	not modelled	26.4	13	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
76	d1o5za2	Alignment	not modelled	25.9	21	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase

77	c3bdkB_	Alignment	not modelled	25.6	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
78	c3kc2A_	Alignment	not modelled	25.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w; **PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
79	c2dmxA_	Alignment	not modelled	25.0	8	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 8; **PDBTitle:** solution structure of the j domain of dnaj homolog2 subfamily b member 8
80	d2jdid1	Alignment	not modelled	24.9	12	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
81	d1ak2a1	Alignment	not modelled	24.2	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
82	d1ewqa2	Alignment	not modelled	24.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
83	c2hjwA_	Alignment	not modelled	24.1	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2
84	d2afhe1	Alignment	not modelled	23.5	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
85	d1fc2c_	Alignment	not modelled	23.5	14	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
86	c3eihB_	Alignment	not modelled	23.3	14	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of s.cerevisiae vps4 in the presence of atpgammas
87	c3ff5B_	Alignment	not modelled	23.0	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 14; **PDBTitle:** crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
88	c1wbdA_	Alignment	not modelled	22.9	20	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of e. coli dna mismatch repair enzyme2 muts, e38q mutant, in complex with a g.t mismatch
89	d1mula_	Alignment	not modelled	22.8	20	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
90	d1sr9a2	Alignment	not modelled	22.6	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
91	c2dn9A_	Alignment	not modelled	22.6	5	**PDB header:**apoptosis, chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3; **PDBTitle:** solution structure of j-domain from the dnaj homolog, human2 tid1 protein
92	d1g5ta_	Alignment	not modelled	22.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
93	c2w40C_	Alignment	not modelled	22.0	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
94	c3roiA_	Alignment	not modelled	21.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** 2.20 angstrom resolution structure of 3-phosphoshikimate 1-2 carboxyvinyltransferase (aroa) from coxiella burnetii
95	c2iz1C_	Alignment	not modelled	21.9	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data
96	d1tlha_	Alignment	not modelled	21.8	28	**Fold:**Anti-sigma factor AsiA **Superfamily:**Anti-sigma factor AsiA **Family:**Anti-sigma factor AsiA
97	c3endA_	Alignment	not modelled	21.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase **PDBTitle:** crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
98	d1rqba2	Alignment	not modelled	21.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
99	d1g64b_	Alignment	not modelled	21.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
100	d1iura_	Alignment	not modelled	21.1	9	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein

101	c2yztA_	Alignment	not modelled	21.0	21	ttha1756; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
102	c1djyB_	Alignment	not modelled	20.9	15	**PDB header:**lipid degradation **Chain:** B: **PDB Molecule:**phosphoinositide-specific phospholipase c, **PDBTitle:** phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate
103	d1gvnb_	Alignment	not modelled	20.5	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Plasmid maintenance system epsilon/zeta, toxin zeta subunit
104	c1o5zA_	Alignment	not modelled	20.3	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase/dihydrofolate synthase; **PDBTitle:** crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution