Phyre^2

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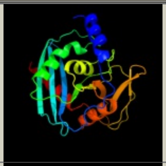
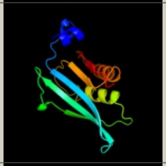
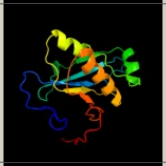
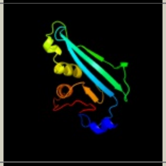
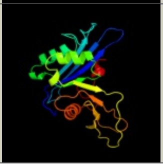
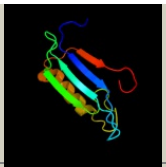
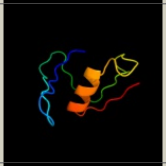
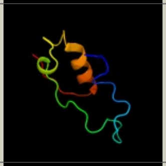
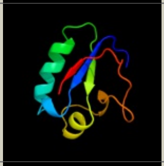
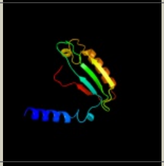
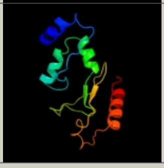
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gocB_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
2	c3ga2A_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624
3	c2w36B_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease v; **PDBTitle:** structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
4	c2qh9B_	Alignment		98.5	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0215 protein af_1433; **PDBTitle:** the crystal structure of a protein of unknown function from2 archaeoglobus fulgidus dsm 4304
5	c2nrzB_	Alignment		97.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation
6	c3c65A_	Alignment		97.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of bacillus stearothermophilus uvrc 5'2 endonuclease domain
7	c2nrrA_	Alignment		96.2	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal rnaseh endonuclase2 domain of uvrc
8	c1u04A_	Alignment		94.4	14	**PDB header:**hydrolase/gene regulation **Chain:** A: **PDB Molecule:**hypothetical protein pf0537; **PDBTitle:** crystal structure of full length argonaute from pyrococcus furiosus
9	c2f8sA_	Alignment		93.2	16	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**argonaute protein; **PDBTitle:** crystal structure of aa-ago with externally-bound sirna
10	d1u04a2	Alignment		85.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain
11	d1yvua2	Alignment		85.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain

12	d3bzka5	Alignment		81.3	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
13	c3taiB_	Alignment		71.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna double-strand break repair protein nura; **PDBTitle:** crystal structure of nura
14	c2zkqb_	Alignment		60.7	27	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
15	c3bchA_	Alignment		58.8	24	**PDB header:**cell adhesion, ribosomal protein **Chain:** A: **PDB Molecule:**40s ribosomal protein sa; **PDBTitle:** crystal structure of the human laminin receptor precursor
16	d1efva2	Alignment		56.4	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
17	c2oceA_	Alignment		54.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
18	c1efpC_	Alignment		49.6	17	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**protein (electron transfer flavoprotein); **PDBTitle:** electron transfer flavoprotein (etf) from paracoccus2 denitrificans
19	c3bbnB_	Alignment		47.0	23	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
20	c2obnA_	Alignment		46.2	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
21	d1efpa2	Alignment	not modelled	45.5	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
22	d1vi6a_	Alignment	not modelled	44.6	29	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
23	c3rggD_	Alignment	not modelled	41.6	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
24	c3cvoA_	Alignment	not modelled	36.8	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase-like protein of unknown function; **PDBTitle:** crystal structure of a methyltransferase-like protein (spo2022) from2 silicibacter pomeroyi dss-3 at 1.80 a resolution
25	d1kcfa2	Alignment	not modelled	35.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Mitochondrial resolvase ydc2 catalytic domain
26	c3izbA_	Alignment	not modelled	35.3	29	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein rps0 (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
27	c2qmoA_	Alignment	not modelled	32.8	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
28	c2etiA	Alignment	not modelled	31.8	57	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease hii;

28	c2etjA_	Alignment	not modelled	31.8	57	**PDBTitle:** crystal structure of ribonuclease hii (ec 3.1.26.4) (rnase hii)2 (tm0915) from thermotoga maritima at 1.74 a resolution
29	d2etja1	Alignment	not modelled	31.8	57	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
30	c1jb0M_	Alignment	not modelled	31.2	50	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**photosystem 1 reaction centre subunit xii; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
31	d1jb0m_	Alignment	not modelled	31.2	50	**Fold:**Single transmembrane helix **Superfamily:**Subunit XII of photosystem I reaction centre, PsaM **Family:**Subunit XII of photosystem I reaction centre, PsaM
32	c3c6aA_	Alignment	not modelled	29.2	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**terminase large subunit; **PDBTitle:** crystal structure of the rb49 gp17 nuclease domain
33	d2uubb1	Alignment	not modelled	29.0	23	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
34	d3clsd2	Alignment	not modelled	28.7	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
35	c1xuzA_	Alignment	not modelled	28.5	24	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
36	c2f1rA_	Alignment	not modelled	26.3	24	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis **PDBTitle:** crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
37	d2gy9b1	Alignment	not modelled	25.2	16	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
38	c1s1hB_	Alignment	not modelled	24.4	30	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
39	d2zdra2	Alignment	not modelled	21.7	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
40	c3iz6A_	Alignment	not modelled	19.8	26	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
41	d2foka4	Alignment	not modelled	19.8	33	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease FokI, C-terminal (catalytic) domain
42	d1io2a_	Alignment	not modelled	19.7	28	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
43	c2xznB_	Alignment	not modelled	16.6	26	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rps0e; **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 2
44	d2g0ta1	Alignment	not modelled	14.6	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
45	c1fokA_	Alignment	not modelled	13.4	26	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (foki restriction endonucleas); **PDBTitle:** structure of restriction endonuclease foki bound to dna
46	c3jvpA_	Alignment	not modelled	13.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
47	d1qcza_	Alignment	not modelled	12.7	19	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
48	c2ivoC_	Alignment	not modelled	12.5	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
49	c1glbG_	Alignment	not modelled	12.3	17	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
50	d2p3ra1	Alignment	not modelled	12.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
51	c3kgkA_	Alignment	not modelled	11.7	31	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**arsenical resistance operon trans-acting repressor arsd; **PDBTitle:** crystal structure of arsd
52	d1o66a_	Alignment	not modelled	11.6	35	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB

53	c2ygkA_	Alignment	not modelled	11.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nura; **PDBTitle:** crystal structure of the nura nuclease from sulfolobus solfataricus
54	c3ktbD_	Alignment	not modelled	10.6	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
55	d1k38a_	Alignment	not modelled	10.0	10	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
56	d1g6sa_	Alignment	not modelled	8.8	11	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
57	d2d0oa2	Alignment	not modelled	8.6	35	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
58	d1k1sa1	Alignment	not modelled	8.6	21	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
59	d2ayia1	Alignment	not modelled	8.4	11	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
60	d1w9ha1	Alignment	not modelled	8.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain
61	c3ezkB_	Alignment	not modelled	8.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna packaging protein gp17; **PDBTitle:** bacteriophage t4 gp17 motor assembly based on crystal2 structures and cryo-em reconstructions
62	c3oirA_	Alignment	not modelled	7.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter sulfate transporter family protein; **PDBTitle:** crystal structure of sulfate transporter family protein from wolinella2 succinogenes
63	c2dcqA_	Alignment	not modelled	7.7	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative protein at4g01050; **PDBTitle:** fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
64	d1o4va_	Alignment	not modelled	7.7	15	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
65	d1pswa_	Alignment	not modelled	7.7	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**ADP-heptose LPS heptosyltransferase II
66	d1nija1	Alignment	not modelled	7.6	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
67	d1gzga_	Alignment	not modelled	7.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
68	d2b7ta1	Alignment	not modelled	7.6	9	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
69	c1zu4A_	Alignment	not modelled	7.4	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
70	c2wcvI_	Alignment	not modelled	7.4	27	**PDB header:**isomerase **Chain:** I: **PDB Molecule:**l-fucose mutarotase; **PDBTitle:** crystal structure of bacterial fucu
71	c3orsD_	Alignment	not modelled	7.3	17	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
72	c3cf4G_	Alignment	not modelled	7.3	21	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
73	c3fmfA_	Alignment	not modelled	7.1	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
74	c2iuwA_	Alignment	not modelled	7.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkylated repair protein alkb homolog 3; **PDBTitle:** crystal structure of human abh3 in complex with iron ion2 and 2-oxoglutarate
75	c3trhI_	Alignment	not modelled	7.0	29	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
76	c3gbtA_	Alignment	not modelled	6.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus

						acidophilus
77	c1u8xX_	Alignment	not modelled	6.8	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**maltose-6'-phosphate glucosidase; **PDBTitle:** crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
78	c2a6aB_	Alignment	not modelled	6.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein tm0874; **PDBTitle:** crystal structure of glycoprotein endopeptidase (tm0874) from2 thermotoga maritima at 2.50 a resolution
79	c2odaB_	Alignment	not modelled	6.5	32	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**hypothetical protein pspto_2114; **PDBTitle:** crystal structure of pspto_2114
80	d1xo1a2	Alignment	not modelled	6.5	31	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
81	c3ezfA_	Alignment	not modelled	6.2	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**para; **PDBTitle:** partition protein
82	d2iuwa1	Alignment	not modelled	6.1	20	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**AlkB-like
83	c3n53B_	Alignment	not modelled	6.0	39	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase; **PDBTitle:** crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
84	d1rf6a_	Alignment	not modelled	6.0	17	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
85	c3iabB_	Alignment	not modelled	5.9	30	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**ribonucleases p/mrp protein subunit pop7; **PDBTitle:** crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
86	d1xmpa_	Alignment	not modelled	5.9	17	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
87	d1jx4a1	Alignment	not modelled	5.9	14	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
88	d1oy0a_	Alignment	not modelled	5.9	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
89	c3odhB_	Alignment	not modelled	5.7	22	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**okrai endonuclease; **PDBTitle:** structure of okrai/dna complex
90	c2d0bA_	Alignment	not modelled	5.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease hiii; **PDBTitle:** crystal structure of bst-rnase hiii in complex with mg2+
91	d1osna_	Alignment	not modelled	5.6	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
92	c1qeyA_	Alignment	not modelled	5.5	28	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (regulatory protein mnt); **PDBTitle:** nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
93	c1qeyD_	Alignment	not modelled	5.5	28	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**protein (regulatory protein mnt); **PDBTitle:** nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
94	c1qeyB_	Alignment	not modelled	5.5	28	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**protein (regulatory protein mnt); **PDBTitle:** nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
95	c1qeyC_	Alignment	not modelled	5.5	28	**PDB header:**gene regulation **Chain:** C: **PDB Molecule:**protein (regulatory protein mnt); **PDBTitle:** nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
96	d1bdoa_	Alignment	not modelled	5.4	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
97	c3g25B_	Alignment	not modelled	5.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
98	d1u11a_	Alignment	not modelled	5.3	15	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
99	c2fw9A_	Alignment	not modelled	5.3	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8