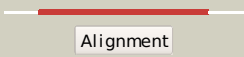
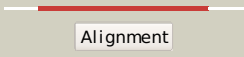
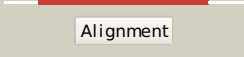
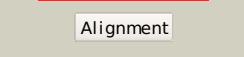
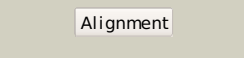
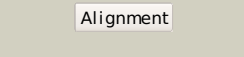
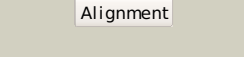
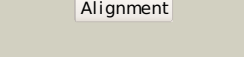
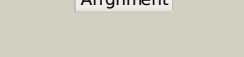
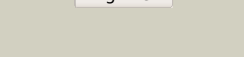
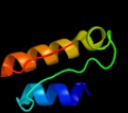
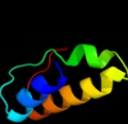


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlb93a_	 Alignment		100.0	100	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
2	dlvmda_	 Alignment		100.0	54	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
3	dlwo8a1	 Alignment		100.0	45	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
4	dla9xa2	 Alignment		100.0	15	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
5	c2yvqA_	 Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase; PDBTitle: crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
6	c1m6vE_	 Alignment		99.9	14	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
7	dlzcza1	 Alignment		98.9	19	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
8	dlpkxa1	 Alignment		98.9	22	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
9	dlg8ma1	 Alignment		98.7	21	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
10	clzczaA_	 Alignment		98.4	19	PDB header: transferase/hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
11	c4a1oB_	 Alignment		98.3	19	PDB header: transferase-hydrolase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.

12	c1thzA_	Alignment		97.6	28	PDB header: transferase, hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
13	d1ytlal	Alignment		87.1	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: ACDE2-like
14	c2o48X_	Alignment		83.3	14	PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase
15	c3ec7C_	Alignment		80.3	15	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
16	d2a0ua1	Alignment		80.2	16	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
17	d1t0kb_	Alignment		76.7	18	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
18	c3cpaB_	Alignment		76.2	18	PDB header: ribosomal protein Chain: B: PDB Molecule: 50s ribosomal protein l30e; PDBTitle: crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
19	d1w41a1	Alignment		75.9	16	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
20	d2bo1a1	Alignment		72.8	16	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
21	c4a1dG_	Alignment	not modelled	72.2	15	PDB header: ribosome Chain: G: PDB Molecule: rpl30; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
22	c2i7pA_	Alignment	not modelled	71.0	14	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase 3; PDBTitle: crystal structure of human pank3 in complex with accoa
23	c3q2kB_	Alignment	not modelled	70.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaa
24	c2vpnB_	Alignment	not modelled	70.9	10	PDB header: transport Chain: B: PDB Molecule: periplasmic substrate binding protein; PDBTitle: high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
25	c3ng3A_	Alignment	not modelled	69.1	16	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
26	d1t9ka_	Alignment	not modelled	68.8	23	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
27	d1n7ka_	Alignment	not modelled	68.5	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
28	c2a5aA_	Alignment	not modelled	68.3	11	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator;

28	c2q3A	Alignment	not modelled	68.3	11	PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum PDB header: transport protein
29	c3fxbB	Alignment	not modelled	66.7	10	Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
30	c2zkr6	Alignment	not modelled	64.4	20	PDB header: ribosomal protein/rna Chain: 6: PDB Molecule: 60s ribosomal protein l30e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
31	c3nklA	Alignment	not modelled	63.2	12	PDB header: oxidoreductase/lyase Chain: A: PDB Molecule: udp-d-quinovosamine 4-dehydrogenase; PDBTitle: crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
32	c2pfzA	Alignment	not modelled	61.8	4	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
33	c2lhwA	Alignment	not modelled	61.4	14	PDB header: rna binding protein Chain: A: PDB Molecule: h/aca ribonucleoprotein complex subunit 2; PDBTitle: solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
34	d1t5oa	Alignment	not modelled	59.3	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
35	d2ctza1	Alignment	not modelled	58.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
36	c1evjC	Alignment	not modelled	58.8	13	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
37	c2pfyA	Alignment	not modelled	57.8	12	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
38	c2jlhA	Alignment	not modelled	57.7	11	PDB header: protein transport Chain: A: PDB Molecule: yop proteins translocation protein u; PDBTitle: crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
39	c3on1A	Alignment	not modelled	56.1	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2414 protein; PDBTitle: the structure of a protein with unknown function from bacillus2 halodurans c
40	c2yvkA	Alignment	not modelled	56.0	19	PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
41	c1zh8B	Alignment	not modelled	55.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
42	c3r6uA	Alignment	not modelled	55.7	19	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis
43	c3pppA	Alignment	not modelled	55.5	19	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline-binding protein; PDBTitle: structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
44	c3t7yB	Alignment	not modelled	53.1	16	PDB header: protein transport Chain: B: PDB Molecule: yop proteins translocation protein u; PDBTitle: structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
45	c3o3nB	Alignment	not modelled	52.9	18	PDB header: lyase Chain: B: PDB Molecule: beta-subunit 2-hydroxyacyl-coa dehydratase; PDBTitle: (r)-2-hydroxysocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxysocaproyl-coa
46	c3btuD	Alignment	not modelled	52.5	15	PDB header: transcription Chain: D: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
47	c1ofgF	Alignment	not modelled	50.9	16	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
48	c1h6dL	Alignment	not modelled	50.9	16	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose PDBTitle: oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
49	c2cb1A	Alignment	not modelled	49.8	22	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
50	c2f5xC	Alignment	not modelled	49.8	19	PDB header: transport protein Chain: C: PDB Molecule: bugd; PDBTitle: structure of periplasmic binding protein bugd
51	c3v5nA	Alignment	not modelled	49.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti
52	d3bzra1	Alignment	not modelled	48.8	18	Fold: EscU C-terminal domain-like Superfamily: EscU C-terminal domain-like Family: EscU C-terminal domain-like

53	c3bzaA	Alignment	not modelled	48.8	18	PDB header: membrane protein, protein transport Chain: A: PDB Molecule: escu; PDBTitle: crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
54	c3c01H	Alignment	not modelled	48.3	16	PDB header: membrane protein, protein transport Chain: H: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structural of native spas c-terminal domain
55	c2zzxD	Alignment	not modelled	48.3	17	PDB header: transport protein Chain: D: PDB Molecule: abc transporter, solute-binding protein; PDBTitle: crystal structure of a periplasmic substrate binding protein in2 complex with lactate
56	d2nvwa1	Alignment	not modelled	47.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
57	c2vt1B	Alignment	not modelled	47.6	18	PDB header: membrane protein Chain: B: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structure of the cytoplasmic domain of spa40, the2 specificity switch for the shigella flexneri type iii3 secretion system
58	c3c00B	Alignment	not modelled	47.3	18	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: escu; PDBTitle: crystal structural of the mutated g247t escu/spas c-terminal domain
59	d1rlga	Alignment	not modelled	45.7	18	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
60	c2xznU	Alignment	not modelled	45.2	12	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein l7ae containing protein; 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
61	d1jx7a	Alignment	not modelled	44.3	20	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
62	c3b50A	Alignment	not modelled	43.9	15	PDB header: transport protein Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
63	c3o3nA	Alignment	not modelled	43.7	18	PDB header: lyase Chain: A: PDB Molecule: alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
64	c2hpgB	Alignment	not modelled	41.9	15	PDB header: ligand binding protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding PDBTitle: the crystal structure of a thermophilic trap periplasmic2 binding protein
65	d1su7a	Alignment	not modelled	41.9	16	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Carbon monoxide dehydrogenase
66	c2hzkB	Alignment	not modelled	39.1	20	PDB header: ligand binding, transport protein Chain: B: PDB Molecule: trap-t family sorbitol/mannitol transporter, periplasmic PDBTitle: crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
67	c1toaA	Alignment	not modelled	37.7	22	PDB header: binding protein Chain: A: PDB Molecule: protein (periplasmic binding protein troa); PDBTitle: periplasmic zinc binding protein troa from treponema pallidum
68	d1toaa	Alignment	not modelled	37.7	22	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
69	c1ibjC	Alignment	not modelled	37.2	18	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
70	d1libja	Alignment	not modelled	37.2	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
71	c3e6gA	Alignment	not modelled	36.9	15	PDB header: lyase Chain: A: PDB Molecule: cystathionine gamma-lyase-like protein; PDBTitle: crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae
72	c2dvzA	Alignment	not modelled	36.7	19	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of a periplasmic transporter
73	c3g13B	Alignment	not modelled	36.4	22	PDB header: recombination Chain: B: PDB Molecule: putative conjugative transposon recombinase; PDBTitle: crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
74	c2pjuD	Alignment	not modelled	36.2	9	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
75	d1rxwa2	Alignment	not modelled	35.5	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
						PDB header: lyase Chain: D: PDB Molecule: methionine gamma-lyase;

76	c3aemD_	Alignment	not modelled	35.4	12	PDBTitle: reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
77	d1y4ia1	Alignment	not modelled	34.8	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
78	c3ce8A_	Alignment	not modelled	34.5	16	PDB header: unknown function Chain: A: PDB Molecule: putative pii-like nitrogen regulatory protein; PDBTitle: crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
79	c3ngjC_	Alignment	not modelled	33.4	17	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
80	d1vqof1	Alignment	not modelled	32.9	20	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
81	d2aifa1	Alignment	not modelled	32.7	14	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
82	c3ndnC_	Alignment	not modelled	32.1	27	PDB header: lyase Chain: C: PDB Molecule: o-succinylhomoserine sulfhydrylase; PDBTitle: crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
83	d1v77a_	Alignment	not modelled	31.7	18	Fold: 7-stranded beta/alpha barrel Superfamily: PHP domain-like Family: RNase P subunit p30
84	c3mc6C_	Alignment	not modelled	31.6	16	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
85	c3o85A_	Alignment	not modelled	31.3	16	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosomal protein l7ae; PDBTitle: giardia lamblia 15.5kd rna binding protein
86	c3moiA_	Alignment	not modelled	29.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
87	d2czwa1	Alignment	not modelled	29.6	24	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
88	d1gc0a_	Alignment	not modelled	29.2	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
89	d1qgna_	Alignment	not modelled	29.1	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
90	d1mc8a2	Alignment	not modelled	28.9	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
91	d2bwna1	Alignment	not modelled	28.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
92	c3jpyA_	Alignment	not modelled	27.9	14	PDB header: transport protein Chain: A: PDB Molecule: glutamate [nmda] receptor subunit epsilon-2; PDBTitle: crystal structure of the zinc-bound amino terminal domain of the nmda2 receptor subunit nr2b
93	d1ul1x2	Alignment	not modelled	27.7	27	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
94	c3h14A_	Alignment	not modelled	27.5	19	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
95	c3ezsB_	Alignment	not modelled	27.3	8	PDB header: transferase Chain: B: PDB Molecule: aminotransferase aspb; PDBTitle: crystal structure of aminotransferase aspb (np_207418.1) from2 helicobacter pylori 26695 at 2.19 a resolution
96	d2ozba1	Alignment	not modelled	26.9	16	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
97	c2nvwB_	Alignment	not modelled	25.7	15	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal sctucture of transcriptional regulator gal80p from2 kluyveromyces lactis
98	d1p1xa_	Alignment	not modelled	25.4	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	d1fc4a_	Alignment	not modelled	25.4	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
100	d1b43a2	Alignment	not modelled	25.2	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
101	c1o94D_	Alignment	not modelled	24.9	14	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein

102	d2fc3a1	Alignment	not modelled	24.8	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
103	d1ydw1	Alignment	not modelled	24.1	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
104	c3h5oB	Alignment	not modelled	24.1	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
105	c3ftqA	Alignment	not modelled	24.0	18	PDB header: cell cycle Chain: A: PDB Molecule: septin-2; PDBTitle: crystal structure of septin 2 in complex with gppnhp and2 mg2+
106	c2hdyA	Alignment	not modelled	23.7	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
107	c3gyyC	Alignment	not modelled	23.4	10	PDB header: transport protein Chain: C: PDB Molecule: periplasmic substrate binding protein; PDBTitle: the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
108	d1a77a2	Alignment	not modelled	23.2	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
109	c1yl7F	Alignment	not modelled	23.1	25	PDB header: oxidoreductase Chain: F: PDB Molecule: dihydropicolinate reductase; PDBTitle: the crystal structure of mycobacterium tuberculosis2 dihydropicolinate reductase (rv2773c) in complex with nadh (crystal3 form c)
110	c2zkrf	Alignment	not modelled	23.0	26	PDB header: ribosomal protein/rna Chain: F: PDB Molecule: rna expansion segment es7 part iii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
111	c3nysA	Alignment	not modelled	22.9	14	PDB header: transferase Chain: A: PDB Molecule: aminotransferase wbpe; PDBTitle: x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution
112	c1a77A	Alignment	not modelled	22.1	21	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
113	d2alea1	Alignment	not modelled	22.1	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
114	c3mfqB	Alignment	not modelled	21.9	15	PDB header: metal binding protein Chain: B: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
115	c3ceaA	Alignment	not modelled	21.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
116	c3g0tA	Alignment	not modelled	21.5	19	PDB header: transferase Chain: A: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution
117	c3f9tB	Alignment	not modelled	21.0	15	PDB header: lyase Chain: B: PDB Molecule: l-tyrosine decarboxylase mfna; PDBTitle: crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
118	c1b43A	Alignment	not modelled	20.5	18	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
119	c3o66A	Alignment	not modelled	20.4	14	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter; PDBTitle: crystal structure of glycine betaine/carnitine/choline abc transporter
120	c2p0oA	Alignment	not modelled	20.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf871; PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function