

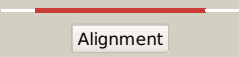

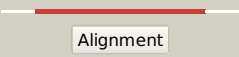

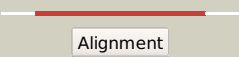

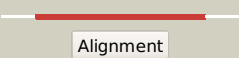

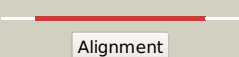

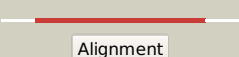







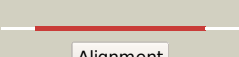



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0809_(purM)_903728_904822
Date	Fri Jul 26 01:50:39 BST 2019
Unique Job ID	06e6c4877f1d8ff5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3m84A_	 Alignment		100.0	32	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis
2	c3mdoB_	 Alignment		100.0	24	PDB header: ligase Chain: B: PDB Molecule: putative phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: crystal structure of a putative phosphoribosylformylglycinamide2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution
3	c1cliD_	 Alignment		100.0	45	PDB header: ligase Chain: D: PDB Molecule: protein (phosphoribosyl-aminoimidazole synthetase); PDBTitle: x-ray crystal structure of aminoimidazole ribonucleotide synthetase2 (purm), from the e. coli purine biosynthetic pathway, at 2.5 a3 resolution
4	c3kizA_	 Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: crystal structure of putative phosphoribosylformylglycinamide cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
5	c2z01A_	 Alignment		100.0	45	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: crystal structure of phosphoribosylaminoimidazole synthetase from2 geobacillus kaustophilus
6	c5vk4B_	 Alignment		100.0	41	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: crystal structure of a phosphoribosylformylglycinamide cyclo-ligase2 from neisseria gonorrhoeae bound to amppnp and magnesium
7	c2btuB_	 Alignment		100.0	46	PDB header: synthase Chain: B: PDB Molecule: phosphoribosyl-aminoimidazole synthetase; PDBTitle: crystal structure of phosphoribosylformylglycinamide cyclo-ligase2 from bacillus anthracis at 2.3a resolution.
8	c2v9yA_	 Alignment		100.0	45	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: human aminoimidazole ribonucleotide synthetase
9	c5avmE_	 Alignment		100.0	45	PDB header: ligase Chain: E: PDB Molecule: phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: crystal structures of 5-aminoimidazole ribonucleotide (air)2 synthetase, purm, from thermus thermophilus
10	c3fd5B_	 Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase 1; PDBTitle: crystal structure of human selenophosphate synthetase 12 complex with ampcp
11	c3mcqA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: thiamine-monophosphate kinase; PDBTitle: crystal structure of thiamine-monophosphate kinase (mfla_0573) from2 methylobacillus flagellatus kt at 1.91 a resolution

12	c3u0oA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: selenide, water dikinase; PDBTitle: the crystal structure of selenophosphate synthetase from e. coli
13	c3c9uB_	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: thiamine monophosphate kinase; PDBTitle: aathil complexed with adp and tpp
14	c2zauB_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase; PDBTitle: crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
15	c3vysC_	Alignment		100.0	17	PDB header: metal binding protein/transferase Chain: C: PDB Molecule: hydrogenase expression/formation protein hype; PDBTitle: crystal structure of the hypc-hypd-hype complex (form i)
16	c2rb9D_	Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hype protein; PDBTitle: crystal structure of e.coli hype
17	c2zodB_	Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase; PDBTitle: crystal structure of selenophosphate synthetase from aquifex aeolicus
18	c5cm7A_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: thiamine-monophosphate kinase; PDBTitle: structure of thiamine-monophosphate kinase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp) and thiamine3 diphosphate (tpp)
19	c2z1tA_	Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: hydrogenase expression/formation protein hype; PDBTitle: crystal structure of hydrogenase maturation protein hype
20	c2yxzA_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: thiamin-monophosphate kinase; PDBTitle: crystal structure of tt0281 from thermus thermophilus hb8
21	c3vtiD_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: D: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of hype-hypf complex
22	c1vqvB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: thiamine monophosphate kinase; PDBTitle: crystal structure of thiamine monophosphate kinase (thil)2 from aquifex aeolicus
23	c2z1eA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: hydrogenase expression/formation protein hype; PDBTitle: crystal structure of hype from thermococcus kodakaraensis (outward2 form)
24	c3ac6A_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase 2; PDBTitle: crystal structure of purl from thermus thermophilus
25	c2hs0A_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase ii; PDBTitle: t. maritima purl complexed with atp
26	d1clia1	Alignment	not modelled	100.0	52	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
27	c5l16A_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: putative selenophosphate synthetase; PDBTitle: crystal structure of n-terminus truncated selenophosphate synthetase2 from leishmania major
28	c3d54I_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: I: PDB Molecule: phosphoribosylformylglycinamide synthase ii; PDBTitle: structure of purlqs from thermotoga maritima

29	d1clib1	Alignment	not modelled	100.0	52	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
30	d1clia2	Alignment	not modelled	100.0	39	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
31	c1t3tA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
32	d3c9ua1	Alignment	not modelled	99.9	19	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
33	d2zoda2	Alignment	not modelled	99.9	15	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
34	d2zaua1	Alignment	not modelled	99.9	19	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
35	d2z1ea2	Alignment	not modelled	99.9	16	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
36	d3c9ua2	Alignment	not modelled	99.9	18	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
37	d2z1ea1	Alignment	not modelled	99.9	20	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
38	d2zoda1	Alignment	not modelled	99.9	19	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
39	d1vk3a2	Alignment	not modelled	99.9	17	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
40	d1vk3a1	Alignment	not modelled	99.8	26	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
41	d1vk3a3	Alignment	not modelled	99.8	22	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
42	d1t3ta6	Alignment	not modelled	99.7	13	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
43	d1t3ta7	Alignment	not modelled	99.6	18	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
44	d1t3ta4	Alignment	not modelled	99.2	19	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
45	d1t3ta5	Alignment	not modelled	98.2	12	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
46	d1to3a_	Alignment	not modelled	81.8	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
47	d3dhxa1	Alignment	not modelled	76.6	32	Fold: Ferredoxin-like Superfamily: ACT-like Family: NIL domain-like
48	c5kdmD_	Alignment	not modelled	74.2	13	PDB header: chaperone / dna binding protein Chain: D: PDB Molecule: major tegument protein; PDBTitle: crystal structure of ebv tegument protein bnr1 in complex with2 histone chaperone daxx and histones h3.3-h4
49	c3dzvB_	Alignment	not modelled	66.7	16	PDB header: transferase Chain: B: PDB Molecule: 4-methyl-5-(beta-hydroxyethyl)thiazole kinase; PDBTitle: crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole kinase2 (np_816404.1) from enterococcus faecalis v583 at 2.57 a resolution
50	c5cgaC_	Alignment	not modelled	58.5	27	PDB header: transferase Chain: C: PDB Molecule: hydroxyethylthiazole kinase; PDBTitle: structure of hydroxyethylthiazole kinase thim from staphylococcus2 aureus in complex with substrate analog 2-(1,3,5-trimethyl-1h-3 pyrazole-4-yl)ethanol
51	d1q3oa_	Alignment	not modelled	54.6	15	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
52	d2qrra1	Alignment	not modelled	50.3	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: NIL domain-like
53	c3l4fD_	Alignment	not modelled	48.5	15	PDB header: signaling protein/protein binding Chain: D: PDB Molecule: sh3 and multiple ankyrin repeat domains protein 1; PDBTitle: crystal structure of betapix coiled-coil domain and shank pdz complex
54	c2q6tB_	Alignment	not modelled	47.2	22	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
						PDB header: protein binding Chain: D: PDB Molecule: sorting nexin-27;

55	c3qglD_	Alignment	not modelled	40.5	12	PDBTitle: crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of gir3
56	c3jrkG_	Alignment	not modelled	38.9	15	PDB header: lyase Chain: G; PDB Molecule: tagatose 1,6-diphosphate aldolase 2; PDBTitle: a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
57	d1v8aa_	Alignment	not modelled	37.4	20	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
58	c5f67A_	Alignment	not modelled	36.2	20	PDB header: protein binding Chain: A; PDB Molecule: inactivation-no-after-potential d protein; PDBTitle: an exquisitely specific pdz/target recognition revealed by the2 structure of inad pdz3 in complex with trp channel tail
59	d1jyea_	Alignment	not modelled	35.2	26	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
60	c1jyeA_	Alignment	not modelled	35.2	26	PDB header: transcription Chain: A; PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
61	c4a1fB_	Alignment	not modelled	34.7	8	PDB header: hydrolase Chain: B; PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
62	c2xkxB_	Alignment	not modelled	34.2	18	PDB header: structural protein Chain: B; PDB Molecule: disks large homolog 4; PDBTitle: single particle analysis of psd-95 in negative stain
63	c1vjqB_	Alignment	not modelled	33.6	22	PDB header: structural genomics, de novo protein Chain: B; PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
64	d1n55a_	Alignment	not modelled	32.1	25	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
65	c3qstA_	Alignment	not modelled	32.0	24	PDB header: isomerase Chain: A; PDB Molecule: triosephosphate isomerase, putative; PDBTitle: crystal structure of trichomonas vaginalis triosephosphate isomerase2 tvag_096350 gene (val-45 variant)
66	d2csua1	Alignment	not modelled	31.8	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
67	c6hyhA_	Alignment	not modelled	31.5	20	PDB header: sugar binding protein Chain: A; PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucofuranose
68	c3shwA_	Alignment	not modelled	31.4	18	PDB header: cell adhesion Chain: A; PDB Molecule: tight junction protein zo-1; PDBTitle: crystal structure of zo-1 pdz3-sh3-guk supramodule complex with2 connexin-45 peptide
69	c3d8uA_	Alignment	not modelled	30.8	12	PDB header: transcription regulator Chain: A; PDB Molecule: purr transcriptional regulator; PDBTitle: the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
70	d1trea_	Alignment	not modelled	30.2	27	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
71	c4ohqB_	Alignment	not modelled	30.2	20	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase, chloroplastic; PDBTitle: crystal structure of chloroplast triose phosphate isomerase from2 arabidopsis thaliana
72	c5uprA_	Alignment	not modelled	29.8	20	PDB header: isomerase Chain: A; PDB Molecule: triosephosphate isomerase; PDBTitle: x-ray structure of a putative triosephosphate isomerase from2 toxoplasma gondii me49
73	d2btma_	Alignment	not modelled	29.2	25	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
74	c4nmnA_	Alignment	not modelled	29.1	9	PDB header: replication Chain: A; PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
75	c4y8fA_	Alignment	not modelled	29.0	22	PDB header: isomerase Chain: A; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from clostridium2 perfringens
76	c3bgwD_	Alignment	not modelled	28.0	7	PDB header: replication Chain: D; PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
77	c2vk2A_	Alignment	not modelled	27.1	12	PDB header: transport protein Chain: A; PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
78	c3rotA_	Alignment	not modelled	27.0	10	PDB header: transport protein Chain: A; PDB Molecule: abc sugar transporter, periplasmic sugar binding protein; PDBTitle: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
79	d1kv5a_	Alignment	not modelled	27.0	25	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
80	c4y9aB_	Alignment	not modelled	26.1	22	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from

						streptomyces2 coelicolor PDB header: transferase Chain: A: PDB Molecule: loganic acid o-methyltransferase; PDBTitle: loganic acid o-methyltransferase complexed with sah and loganic acid
81	c6c8rA_	Alignment	not modelled	25.7	18	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
82	c4zc0A_	Alignment	not modelled	25.4	7	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
83	d2f0aa1	Alignment	not modelled	25.3	16	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
84	d1m6ja_	Alignment	not modelled	25.0	20	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
85	c5jxfA_	Alignment	not modelled	24.8	25	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
86	d1suxa_	Alignment	not modelled	24.6	24	PDB header: transferase Chain: C: PDB Molecule: xanthosine methyltransferase; PDBTitle: the structure of xanthosine methyltransferase
87	c2eg5C_	Alignment	not modelled	24.5	32	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Salicylic acid carboxyl methyltransferase (SAMT)
88	d1m6ex_	Alignment	not modelled	23.8	20	PDB header: transport protein Chain: A: PDB Molecule: possible sugar abc superfamily atp binding cassette PDBTitle: crystal structure of periplasmic abc transporter solute binding2 protein a7jw62 from manheimia haemolytica phl213, target efi-511105,3 in complex with myo-inositol
89	c4rxmA_	Alignment	not modelled	23.7	6	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from deinococcus2 radiodurans
90	c4y90B_	Alignment	not modelled	23.5	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
91	d1wfga_	Alignment	not modelled	22.9	20	PDB header: isomerase Chain: D: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from francisella2 tularensis subsp. tularensis schu s4
92	c5ujwD_	Alignment	not modelled	22.5	17	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein cgl0159; PDBTitle: crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
93	c3fokH_	Alignment	not modelled	22.2	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
94	d1o5xa_	Alignment	not modelled	22.1	27	PDB header: transport protein Chain: D: PDB Molecule: abc sugar (ribose) transporter, periplasmic substrate- PDBTitle: crystal structure of abc sugar transporter subunit from rhodobacter2 sphaeroides 2.4.1
95	c3l49D_	Alignment	not modelled	22.0	9	PDB header: transport protein Chain: D: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of 5-methylthioribose transporter solute binding2 protein tlet_1677 from thermotoga lettingae tmo target efi-511109 in3 complex with 5-methylthioribose
96	c4ry8D_	Alignment	not modelled	21.9	15	PDB header: protein binding Chain: A: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf1; PDBTitle: structural characterization of the extended pdz1 domain from nherf1
97	c2m0tA_	Alignment	not modelled	21.6	15	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
98	c3gndC_	Alignment	not modelled	21.5	15	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: the periplasmic binding protein component of the arabinose abc2 transporter from shewanella sp. ana-3 bound to alpha and beta-l-3 arabinofuranose
99	c5ocpA_	Alignment	not modelled	21.5	6	PDB header: solute-binding protein Chain: A: PDB Molecule: putative periplasmic binding protein with substrate ribose; PDBTitle: crystal structure of a putative periplasmic solute binding protein2 (ipr025997) from ochrobactrum anthropi atcc49188 (oant_2843, target3 efi-511085)
100	c5braA_	Alignment	not modelled	21.3	10	PDB header: dna binding protein Chain: B: PDB Molecule: recombination and repair protein; PDBTitle: crystal structure of a dimeric form of the uvx4 recombinase core2 domain from enterobacteria phage t4
101	c3io5B_	Alignment	not modelled	21.3	6	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of leptospira interrogans triosephosphate isomerase2 (litim)
102	c4x22A_	Alignment	not modelled	21.2	24	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from gemmata2 obscuriglobus
103	c4y96B_	Alignment	not modelled	21.1	22	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, nucleotide

104	c5hsgA_	Alignment	not modelled	21.1	12	binding/atpase PDBTitle: crystal structure of an abc transporter solute binding protein from2 klebsiella pneumoniae (kpn_01730, target efi-511059), apo open3 structure
105	c2vyeA_	Alignment	not modelled	21.0	9	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnc-ssdna complex
106	c1yyaA_	Alignment	not modelled	20.7	25	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
107	d1pcaa1	Alignment	not modelled	20.7	12	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
108	c4kzkA_	Alignment	not modelled	20.6	6	PDB header: sugar binding protein Chain: A: PDB Molecule: l-arabinose abc transporter, periplasmic l-arabinose- PDBTitle: the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis
109	d1o6xa_	Alignment	not modelled	20.6	8	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
110	c4g1kB_	Alignment	not modelled	20.5	24	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from burkholderia2 thailandensis
111	c3e61A_	Alignment	not modelled	20.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional repressor of ribose operon; PDBTitle: crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
112	c3jy6B_	Alignment	not modelled	20.4	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI transcriptional regulator from lactobacillus2 brevis
113	c3krsB_	Alignment	not modelled	20.3	24	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution