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 Description RVBD2977c\_(thiL)\_3332797\_3333798  
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3c9uB_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiamine monophosphate kinase; <b>PDBTitle:</b> aathil complexed with adp and tpp
2	<a href="#">c1vqvB_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiamine monophosphate kinase; <b>PDBTitle:</b> crystal structure of thiamine monophosphate kinase (thiL)2 from aquifex aeolicus
3	<a href="#">c5cm7A_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine-monophosphate kinase; <b>PDBTitle:</b> structure of thiamine-monophosphate kinase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp) and thiamine3 diphosphate (tpp)
4	<a href="#">c2yxzA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin-monophosphate kinase; <b>PDBTitle:</b> crystal structure of tt0281 from thermus thermophilus hb8
5	<a href="#">c5vk4B_</a>	 Alignment		100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of a phosphoribosylformylglycinamide cyclo-ligase2 from neisseria gonorrhoeae bound to amppnp and magnesium
6	<a href="#">c3mcqA_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine-monophosphate kinase; <b>PDBTitle:</b> crystal structure of thiamine-monophosphate kinase (mfla_0573) from2 methylobacillus flagellatus kt at 1.91 a resolution
7	<a href="#">c2btuB_</a>	 Alignment		100.0	16	<b>PDB header:</b> synthase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyl-aminoimidazole synthetase; <b>PDBTitle:</b> crystal structure of phosphoribosylformylglycinamide cyclo-ligase2 from bacillus anthracis at 2.3a resolution.
8	<a href="#">c1cliD_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (phosphoribosyl-aminoimidazole synthetase); <b>PDBTitle:</b> x-ray crystal structure of aminoimidazole ribonucleotide synthetase2 (purm), from the e. coli purine biosynthetic pathway, at 2.5 a3 resolution
9	<a href="#">c3vtiD_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of hype-hypf complex
10	<a href="#">c2rb9D_</a>	 Alignment		100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hype protein; <b>PDBTitle:</b> crystal structure of e.coli hype
11	<a href="#">c2z1tA_</a>	 Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase expression/formation protein hype; <b>PDBTitle:</b> crystal structure of hydrogenase maturation protein hype

12	<a href="#">c3fd5B_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase 1; <b>PDBTitle:</b> crystal structure of human selenophosphate synthetase 12 complex with ampcp
13	<a href="#">c3vysC_</a>	Alignment		100.0	23	<b>PDB header:</b> metal binding protein/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> hydrogenase expression/formation protein htype; <b>PDBTitle:</b> crystal structure of the hypc-hypd-hype complex (form i)
14	<a href="#">c3u0aA_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> selenide, water dikinase; <b>PDBTitle:</b> the crystal structure of selenophosphate synthetase from e. coli
15	<a href="#">c2zodB_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase; <b>PDBTitle:</b> crystal structure of selenophosphate synthetase from aquifex aeolicus
16	<a href="#">c2zauB_</a>	Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> selenide, water dikinase; <b>PDBTitle:</b> crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
17	<a href="#">c2z01A_</a>	Alignment		100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole synthetase from2 geobacillus kaustophilus
18	<a href="#">c3m84A_</a>	Alignment		100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis
19	<a href="#">c2z1eA_</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase expression/formation protein htype; <b>PDBTitle:</b> crystal structure of hype from thermococcus kodakaraensis (outward2 form)
20	<a href="#">c2v9yA_</a>	Alignment		100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> human aminoimidazole ribonucleotide synthetase
21	<a href="#">c5avmE_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structures of 5-aminoimidazole ribonucleotide (air)2 synthetase, purm, from thermus thermophilus
22	<a href="#">c3ac6A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase 2; <b>PDBTitle:</b> crystal structure of purl from thermus thermophilus
23	<a href="#">c5l16A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative selenophosphate synthetase; <b>PDBTitle:</b> crystal structure of n-terminus truncated selenophosphate synthetase2 from leishmania major
24	<a href="#">c2hs0A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase ii; <b>PDBTitle:</b> t. maritima purl complexed with atp
25	<a href="#">c3d54I_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> I: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase ii; <b>PDBTitle:</b> structure of purlqs from thermotoga maritima
26	<a href="#">d3c9ua1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
27	<a href="#">c1t3tA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase; <b>PDBTitle:</b> structure of formylglycinamide synthetase
28	<a href="#">d1clib1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like

29	<a href="#">d1clia1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
30	<a href="#">d2zaua1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
31	<a href="#">d3c9ua2</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
32	<a href="#">d2zoda1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
33	<a href="#">c3mdoB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of a putative phosphoribosylformylglycinamide2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution
34	<a href="#">d2z1ea1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
35	<a href="#">d1vk3a2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
36	<a href="#">d2zoda2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
37	<a href="#">c3kizA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of putative phosphoribosylformylglycinamide cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
38	<a href="#">d2z1ea2</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
39	<a href="#">d1vk3a1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
40	<a href="#">d1clia2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
41	<a href="#">d1vk3a3</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
42	<a href="#">d1t3ta4</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
43	<a href="#">d1t3ta6</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
44	<a href="#">d1t3ta5</a>	Alignment	not modelled	99.2	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
45	<a href="#">d1t3ta7</a>	Alignment	not modelled	99.2	23	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
46	<a href="#">c3fokH_</a>	Alignment	not modelled	86.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> uncharacterized protein cgl0159; <b>PDBTitle:</b> crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
47	<a href="#">c3jrkG_</a>	Alignment	not modelled	84.1	15	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tagatose 1,6-diphosphate aldolase 2; <b>PDBTitle:</b> a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
48	<a href="#">d1to3a_</a>	Alignment	not modelled	76.9	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
49	<a href="#">c3qi7A_</a>	Alignment	not modelled	73.1	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
50	<a href="#">c3dzvB_</a>	Alignment	not modelled	42.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-methyl-5-(beta-hydroxyethyl)thiazole kinase; <b>PDBTitle:</b> crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole kinase2 (np_816404.1) from enterococcus faecalis v583 at 2.57 a resolution
51	<a href="#">c2qjhH_</a>	Alignment	not modelled	42.6	19	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400; <b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
52	<a href="#">c4ru1C_</a>	Alignment	not modelled	41.2	5	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> monosaccharide abc transporter substrate-binding protein, <b>PDBTitle:</b> crystal structure of carbohydrate transporter acei_1806 from2 acidothermus cellulolyticus 11b, target efi-510965, in complex with3 myo-inositol
53	<a href="#">d2csua1</a>	Alignment	not modelled	38.6	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain

54	<a href="#">c4mozC</a>	Alignment	not modelled	34.1	18	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
55	<a href="#">c2hqbA</a>	Alignment	not modelled	33.7	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional activator of comk gene; <b>PDBTitle:</b> crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
56	<a href="#">c5jxpA</a>	Alignment	not modelled	32.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
57	<a href="#">c5jxfA</a>	Alignment	not modelled	29.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
58	<a href="#">c5kdmD</a>	Alignment	not modelled	28.2	15	<b>PDB header:</b> chaperone / dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> major tegument protein; <b>PDBTitle:</b> crystal structure of ebv tegument protein bnrf1 in complex with2 histone chaperone daxx and histones h3.3-h4
59	<a href="#">c3gndC</a>	Alignment	not modelled	24.6	18	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> aldolase lsrf; <b>PDBTitle:</b> crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
60	<a href="#">d1fnda1</a>	Alignment	not modelled	23.3	25	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
61	<a href="#">d1wfa1</a>	Alignment	not modelled	22.5	11	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
62	<a href="#">c3g85A</a>	Alignment	not modelled	21.4	5	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (laci family); <b>PDBTitle:</b> crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
63	<a href="#">d1v8aa</a>	Alignment	not modelled	21.0	29	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
64	<a href="#">c3eggC</a>	Alignment	not modelled	20.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> spinophilin; <b>PDBTitle:</b> crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
65	<a href="#">c3lukB</a>	Alignment	not modelled	20.5	9	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein argonaute-2; <b>PDBTitle:</b> crystal structure of mid domain from hago2
66	<a href="#">d1gawa1</a>	Alignment	not modelled	20.1	17	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
67	<a href="#">c5mvrA</a>	Alignment	not modelled	19.9	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna threonylcarbamoyladenosine biosynthesis protein tsae; <b>PDBTitle:</b> crystal structure of bacillus subtilus ydib
68	<a href="#">d2bmwa1</a>	Alignment	not modelled	19.8	22	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
69	<a href="#">c5braA</a>	Alignment	not modelled	19.4	14	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative periplasmic binding protein with substrate ribose; <b>PDBTitle:</b> crystal structure of a putative periplasmic solute binding protein2 (ipr025997) from ochrobactrum anthropi atcc49188 (oant_2843, target3_efi-511085)
70	<a href="#">d1htwa</a>	Alignment	not modelled	19.4	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> YjeE-like
71	<a href="#">c4y01B</a>	Alignment	not modelled	18.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase s46; <b>PDBTitle:</b> crystal structure of dipeptidyl peptidase 11 (dpp11) from2 porphyromonas gingivalis
72	<a href="#">d1ep3b1</a>	Alignment	not modelled	18.7	32	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
73	<a href="#">c2jreA</a>	Alignment	not modelled	18.3	16	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> c60-1 pdz domain peptide; <b>PDBTitle:</b> c60-1, a pdz domain designed using statistical coupling2 analysis
74	<a href="#">c3rotA</a>	Alignment	not modelled	18.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc sugar transporter, periplasmic sugar binding protein; <b>PDBTitle:</b> crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
75	<a href="#">d2byga1</a>	Alignment	not modelled	18.0	23	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
76	<a href="#">c5f67A</a>	Alignment	not modelled	17.9	23	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> inactivation-no-after-potential d protein; <b>PDBTitle:</b> an exquisitely specific pdz/target recognition revealed by the2 structure of inad pdz3 in complex with trp channel tail
77	<a href="#">c6ndiB</a>	Alignment	not modelled	17.7	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.60 angstrom resolution crystal structure of periplasmic binding and2 sugar binding domain of laci family protein from klebsiella3 pneumoniae.
78	<a href="#">c3wolB</a>	Alignment	not modelled	17.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl aminopeptidase bii; <b>PDBTitle:</b> crystal structure of the dap bii dipeptide complex i
						<b>Fold:</b> Periplasmic bindina protein-like I

79	<a href="#">d1jyea_</a>	Alignment	not modelled	17.2	21	<b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
80	<a href="#">c1jyeA_</a>	Alignment	not modelled	17.2	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lactose operon repressor; <b>PDBTitle:</b> structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
81	<a href="#">c6dspB_</a>	Alignment	not modelled	17.1	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> autoinducer 2-binding protein lsrB; <b>PDBTitle:</b> lsrB from clostridium saccharobutylicum in complex with ai-2
82	<a href="#">c3d02A_</a>	Alignment	not modelled	17.1	3	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative lacI-type transcriptional regulator; <b>PDBTitle:</b> crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
83	<a href="#">d2f0aa1</a>	Alignment	not modelled	16.7	25	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
84	<a href="#">d1ujda_</a>	Alignment	not modelled	16.6	17	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
85	<a href="#">c3qz6A_</a>	Alignment	not modelled	16.6	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase; <b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
86	<a href="#">d1oi7a1</a>	Alignment	not modelled	16.0	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
87	<a href="#">d1x5qa1</a>	Alignment	not modelled	15.8	23	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
88	<a href="#">c6fpeE_</a>	Alignment	not modelled	15.6	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> atpase yjee, predicted to have essential role in cell wall <b>PDBTitle:</b> bacterial protein complex
89	<a href="#">c6hyhA_</a>	Alignment	not modelled	15.4	17	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator; <b>PDBTitle:</b> crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucofuranose
90	<a href="#">c3gbvB_</a>	Alignment	not modelled	15.3	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative lacI-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative lacI transcriptional regulator from2 bacteroides fragilis
91	<a href="#">d1tjya_</a>	Alignment	not modelled	14.3	14	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
92	<a href="#">d1wfga_</a>	Alignment	not modelled	13.9	17	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
93	<a href="#">c3dbiA_</a>	Alignment	not modelled	13.8	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of sugar-binding transcriptional regulator (lacI2 family) from escherichia coli complexed with phosphate
94	<a href="#">c4ywkA_</a>	Alignment	not modelled	13.8	31	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 21; <b>PDBTitle:</b> pyrococcus furiosus mcm n-terminal domain with zinc-binding subdomain2 b deleted
95	<a href="#">c4wzzA_</a>	Alignment	not modelled	13.7	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar abc transporter, substrate-binding protein; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
96	<a href="#">c5hqjA_</a>	Alignment	not modelled	13.6	15	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator; <b>PDBTitle:</b> crystal structure of abc transporter solute binding protein b1g1h72 from burkholderia graminis c4d1m, target efi-511179, in complex with3 d-arabinose
97	<a href="#">d1whaa_</a>	Alignment	not modelled	13.6	14	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
98	<a href="#">c3d8uA_</a>	Alignment	not modelled	13.5	6	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> purr transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
99	<a href="#">c4kzka_</a>	Alignment	not modelled	13.5	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinose abc transporter, periplasmic l-arabinose- <b>PDBTitle:</b> the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis