

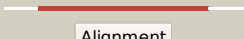

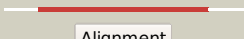









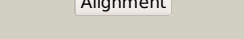

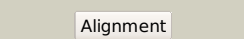
















# Phyre2


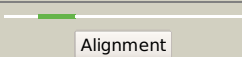
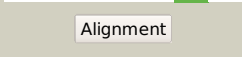
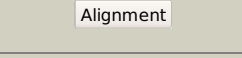
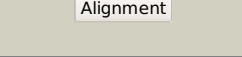
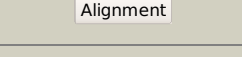
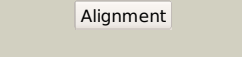
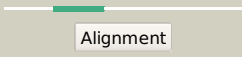
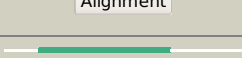
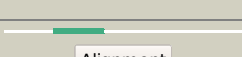
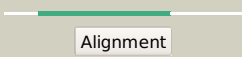
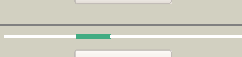
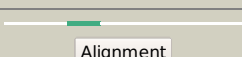
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Description	RVBD2192c_(trpD)_2455639_2456751
Date	Mon Aug 5 13:25:32 BST 2019
Unique Job ID	18fd04fb9fc037a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2bpqB_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
2	<a href="#">c1v8gB_</a>	 Alignment		100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
3	<a href="#">c1khdD_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.9 resolution3 (current name, pectobacterium carotovorum)
4	<a href="#">c4gtnA_</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> structure of anthranilate phosphoribosyl transferase from2 acinetobacter baylyi
5	<a href="#">c5nofB_</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyltransferase from thermococcus kodakaraensis
6	<a href="#">c1o17A_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyl-transferase (trpd)
7	<a href="#">c1vquB_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase 2; <b>PDBTitle:</b> crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
8	<a href="#">c4hkmA_</a>	 Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of an anthranilate phosphoribosyltransferase (target2 id nysgrc-016600) from xanthomonas campestris
9	<a href="#">c4muoB_</a>	 Alignment		100.0	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ybib; <b>PDBTitle:</b> the trpd2 enzyme from e.coli: ybib
10	<a href="#">c3h5qA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine-nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
11	<a href="#">c4ga5H_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> putative thymidine phosphorylase; <b>PDBTitle:</b> crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form

12	<a href="#">c1brwB</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (pyrimidine nucleoside phosphorylase); <b>PDBTitle:</b> the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
13	<a href="#">d2elca2</a>	Alignment		100.0	46	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
14	<a href="#">c2j0fC</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> thymidine phosphorylase; <b>PDBTitle:</b> structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
15	<a href="#">c2dsjA</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine-nucleoside (thymidine) phosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0128 from thermus thermophilus hb8
16	<a href="#">c1otpa</a>	Alignment		100.0	18	<b>PDB header:</b> phosphorylase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine phosphorylase; <b>PDBTitle:</b> structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
17	<a href="#">d1o17a2</a>	Alignment		100.0	29	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
18	<a href="#">d1khda2</a>	Alignment		100.0	33	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
19	<a href="#">d1uoua2</a>	Alignment		100.0	22	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
20	<a href="#">d1brwa2</a>	Alignment		100.0	20	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
21	<a href="#">d2tpta2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
22	<a href="#">d1khda1</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
23	<a href="#">d1brwa1</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
24	<a href="#">d2tpta1</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
25	<a href="#">d1o17a1</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
26	<a href="#">d1uoua1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
27	<a href="#">d1v8ga1</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain

						<b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
28	<a href="#">d2elca1</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
29	<a href="#">c4gijC</a>	Alignment	not modelled	85.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> pseudouridine-5'-phosphate glycosidase; <b>PDBTitle:</b> crystal structure of pseudouridine monophosphate glycosidase complexed2 with sulfate
30	<a href="#">c1qzwC</a>	Alignment	not modelled	85.0	14	<b>PDB header:</b> signaling protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
31	<a href="#">d1vkma</a>	Alignment	not modelled	84.7	18	<b>Fold:</b> Indigoidine synthase A-like <b>Superfamily:</b> Indigoidine synthase A-like <b>Family:</b> Indigoidine synthase A-like
32	<a href="#">c1vmaA</a>	Alignment	not modelled	80.9	15	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
33	<a href="#">c4ex8A</a>	Alignment	not modelled	80.6	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alna; <b>PDBTitle:</b> crystal structure of the prealnumycin c-glycosynthase alna
34	<a href="#">c5zmfA</a>	Alignment	not modelled	78.6	17	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atpase arsa1; <b>PDBTitle:</b> amppnp complex of c. reinhardtii arsa1
35	<a href="#">d1p88a</a>	Alignment	not modelled	77.5	17	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
36	<a href="#">c2v3cC</a>	Alignment	not modelled	74.1	12	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
37	<a href="#">c2qguA</a>	Alignment	not modelled	71.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable signal peptide protein; <b>PDBTitle:</b> three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
38	<a href="#">c2yhsA</a>	Alignment	not modelled	70.3	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the e. coli srp receptor ftsy
39	<a href="#">c3zh3A</a>	Alignment	not modelled	67.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase; <b>PDBTitle:</b> crystal structure of s. pneumoniae d39 native mura1
40	<a href="#">c2kvcA</a>	Alignment	not modelled	65.7	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of the mycobacterium tuberculosis protein rv0543c.2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
41	<a href="#">c3zq6D</a>	Alignment	not modelled	64.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative arsenical pump-driving atpase; <b>PDBTitle:</b> adp-alf4 complex of m. therm. trc40
42	<a href="#">c2m0nA</a>	Alignment	not modelled	62.8	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
43	<a href="#">c5bufA</a>	Alignment	not modelled	62.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase; <b>PDBTitle:</b> 2.37 angstrom structure of epsp synthase from acinetobacter baumannii
44	<a href="#">d1ihua2</a>	Alignment	not modelled	62.0	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
45	<a href="#">c6bs3A</a>	Alignment	not modelled	61.4	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative atpase rv3679; <b>PDBTitle:</b> crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
46	<a href="#">c6bs5B</a>	Alignment	not modelled	61.1	34	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> anion transporter; <b>PDBTitle:</b> crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
47	<a href="#">c3kc2A</a>	Alignment	not modelled	59.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ykr070w; <b>PDBTitle:</b> crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
48	<a href="#">d2afhe1</a>	Alignment	not modelled	57.9	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
49	<a href="#">c3endA</a>	Alignment	not modelled	57.7	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase <b>PDBTitle:</b> crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
50	<a href="#">c2lkyA</a>	Alignment	not modelled	57.0	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of msmeq_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b

51	<a href="#">c5dcfA</a>	 Alignment	not modelled	56.9	13	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine recombinase xerd,dna translocase ftsk; <b>PDBTitle:</b> c-terminal domain of xerd recombinase in complex with gamma domain of f2 ftsk
52	<a href="#">c5uwaB</a>	 Alignment	not modelled	56.4	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable phospholipid-binding protein mlac; <b>PDBTitle:</b> structure of e. coli phospholipid binding protein mlac
53	<a href="#">c5lwcA</a>	 Alignment	not modelled	55.4	21	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin bacsp222; <b>PDBTitle:</b> nmr solution structure of bacteriocin bacsp222 from staphylococcus2 pseudintermedius 222
54	<a href="#">c4rtbA</a>	 Alignment	not modelled	55.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrg protein; <b>PDBTitle:</b> x-ray structure of the fefe-hydrogenase maturase hydrg from2 carboxydotherrnus hydrogenoformans
55	<a href="#">c2pqaA</a>	 Alignment	not modelled	54.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase; <b>PDBTitle:</b> a100g cp4 epsps liganded with (r)-difluoromethyl tetrahedral reaction2 intermediate analog
56	<a href="#">c5ujsB</a>	 Alignment	not modelled	53.5	14	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase; <b>PDBTitle:</b> 2.45 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from campylobacter jejuni.
57	<a href="#">c3ug7D</a>	 Alignment	not modelled	53.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> arsenical pump-driving atpase; <b>PDBTitle:</b> crystal structure of get3 from methanocaldococcus jannaschii
58	<a href="#">d1cp2a</a>	 Alignment	not modelled	53.4	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
59	<a href="#">c3ibgF</a>	 Alignment	not modelled	51.3	34	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> atpase, subunit of the get complex; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus get3 with bound2 adp
60	<a href="#">c5wi5C</a>	 Alignment	not modelled	51.1	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; <b>PDBTitle:</b> 2.0 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from streptococcus pneumoniae in complex3 with uridine-diphosphate-2(n-acetylglucosaminy)l butyric acid, (2r)-4 2-(phosphonoxy)propanoic acid and magnesium.
61	<a href="#">d1rf6a</a>	 Alignment	not modelled	49.6	23	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
62	<a href="#">c1ii0A</a>	 Alignment	not modelled	47.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenical pump-driving atpase; <b>PDBTitle:</b> crystal structure of the escherichia coli arsenite-translocating2 atpase
63	<a href="#">d1a0pa2</a>	 Alignment	not modelled	47.6	13	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
64	<a href="#">c2qy9A</a>	 Alignment	not modelled	47.5	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
65	<a href="#">d1g6sa</a>	 Alignment	not modelled	46.6	17	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
66	<a href="#">c2iy3A</a>	 Alignment	not modelled	45.9	14	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein,signal recognition <b>PDBTitle:</b> structure of the e. coli signal regognition particle
67	<a href="#">c1r71B</a>	 Alignment	not modelled	45.9	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor protein korb; <b>PDBTitle:</b> crystal structure of the dna binding domain of korb in complex with2 the operator dna
68	<a href="#">c2wooc</a>	 Alignment	not modelled	45.2	31	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> nucleotide-free form of s. pombe get3
69	<a href="#">c5xwbB</a>	 Alignment	not modelled	44.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase; <b>PDBTitle:</b> crystal structure of 5-enolpyruvulshikimate-3-phosphate synthase from2 a psychrophilic bacterium, colwellia psychrerythraea
70	<a href="#">c5gafi</a>	 Alignment	not modelled	44.2	15	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein I10; <b>PDBTitle:</b> rnc in complex with srp
71	<a href="#">d1j9ia</a>	 Alignment	not modelled	43.8	19	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Terminase gpNU1 subunit domain
72	<a href="#">c3rmtB</a>	 Alignment	not modelled	43.1	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-phosphoshikimate 1-carboxyvinyltransferase 1; <b>PDBTitle:</b> crystal structure of putative 5-enolpyruvoylshikimate-3-phosphate2 synthase from bacillus halodurans c-125
73	<a href="#">c3igfB</a>	 Alignment	not modelled	43.0	23	<b>PDB header:</b> atp binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> all4481 protein; <b>PDBTitle:</b> crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
74	<a href="#">c4wxcC</a>	Alignment	not modelled	43.0	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> biotin and thiamin synthesis associated; <b>PDBTitle:</b> crystal structure of hydrg: a maturase of the [fefe]-

						hydrogenase
75	<a href="#">c2j37W_</a>	Alignment	not modelled	41.3	9	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein (srp54); <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
76	<a href="#">c4ru8C_</a>	Alignment	not modelled	41.1	32	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of pnob8 para with amppnp
77	<a href="#">c3eegB_</a>	Alignment	not modelled	39.6	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
78	<a href="#">c2mqkA_</a>	Alignment	not modelled	39.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent target dna activator b; <b>PDBTitle:</b> solution structure of n terminal domain of the mub aaa+ atpase
79	<a href="#">d1w4ta1</a>	Alignment	not modelled	38.7	18	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
80	<a href="#">d1byia_</a>	Alignment	not modelled	38.0	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
81	<a href="#">c3vx3A_</a>	Alignment	not modelled	37.7	41	<b>PDB header:</b> adp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atpase involved in chromosome partitioning, para/mind <b>PDBTitle:</b> crystal structure of [nife] hydrogenase maturation protein hy pb from2 thermococcus kodakarensis kod1
82	<a href="#">d1r71a_</a>	Alignment	not modelled	37.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
83	<a href="#">c4gxwA_</a>	Alignment	not modelled	35.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> crystal structure of a cog1816 amidohydrolase (target efi-505188) from2 burkhoderia ambifaria, with bound zn
84	<a href="#">c3of5A_</a>	Alignment	not modelled	34.5	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
85	<a href="#">d1b8za_</a>	Alignment	not modelled	33.7	10	<b>Fold:</b> IHF-like DNA-binding proteins <b>Superfamily:</b> IHF-like DNA-binding proteins <b>Family:</b> Prokaryotic DNA-binding protein
86	<a href="#">c2j289_</a>	Alignment	not modelled	33.5	14	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
87	<a href="#">c3bg3B_</a>	Alignment	not modelled	32.8	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
88	<a href="#">c3katA_</a>	Alignment	not modelled	32.7	20	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> nacht, Irr and pyd domains-containing protein 1; <b>PDBTitle:</b> crystal structure of the card domain of the human nlrp1 protein,2 northeast structural genomics consortium target hr3486e
89	<a href="#">c5lvtC_</a>	Alignment	not modelled	32.2	6	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna-binding protein hu; <b>PDBTitle:</b> structure of hu protein from lactococcus lactis
90	<a href="#">d1mula_</a>	Alignment	not modelled	32.1	17	<b>Fold:</b> IHF-like DNA-binding proteins <b>Superfamily:</b> IHF-like DNA-binding proteins <b>Family:</b> Prokaryotic DNA-binding protein
91	<a href="#">c1nvmG_</a>	Alignment	not modelled	31.7	15	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
92	<a href="#">c2yvqA_</a>	Alignment	not modelled	31.1	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
93	<a href="#">c3kjbB_</a>	Alignment	not modelled	30.9	22	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase complex, accessory <b>PDBTitle:</b> adp-bound state of cooc1
94	<a href="#">c2ozeA_</a>	Alignment	not modelled	30.4	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> orf delta'; <b>PDBTitle:</b> the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
95	<a href="#">c3r38A_</a>	Alignment	not modelled	29.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; <b>PDBTitle:</b> 2.23 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase (mura) from listeria monocytogenes egd-e
96	<a href="#">c3bg3A_</a>	Alignment	not modelled	29.6	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
97	<a href="#">c3ol4B_</a>	Alignment	not modelled	29.4	25	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
98	<a href="#">c2ndpA_</a>	Alignment	not modelled	28.9	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone-like dna-binding superfamily protein; <b>PDBTitle:</b> structure of dna-binding hu protein from micoplasma mycoplasma2 gallisepticum
99	<a href="#">c6drpB_</a>	Alignment	not modelled	28.8	11	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> nlr family card domain-containing protein 4;

						<b>PDBTitle:</b> cryo-em structures of asc and nirc4 card filaments reveal a unified mechanism of nucleation and activation of caspase-1
100	<a href="#">c5hy7D_</a>	Alignment	not modelled	28.6	15	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> ysf3; <b>PDBTitle:</b> sf3b10-sf3b130 from chaetomium thermophilum
101	<a href="#">c5ks8D_</a>	Alignment	not modelled	28.4	20	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from <i>Methylobacillus flagellatus</i>
102	<a href="#">d1ihua1</a>	Alignment	not modelled	28.3	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
103	<a href="#">c4ak9A_</a>	Alignment	not modelled	28.3	12	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cpfts; <b>PDBTitle:</b> structure of chloroplast ftsy from <i>Physcomitrella patens</i>
104	<a href="#">c5bq2C_</a>	Alignment	not modelled	28.1	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylglucosamine 1-carboxyvinyltransferase; <b>PDBTitle:</b> crystal structure of udp-n-acetylglucosamine 1-carboxyvinyltransferase2 (udp-n-acetylglucosamine enolpyruvyl transferase, ept) from <i>Pseudomonas aeruginosa</i>
105	<a href="#">c1rr2A_</a>	Alignment	not modelled	28.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcarboxylase 5s subunit; <b>PDBTitle:</b> propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
106	<a href="#">c2dg2D_</a>	Alignment	not modelled	27.4	15	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> apolipoprotein a-i binding protein; <b>PDBTitle:</b> crystal structure of mouse apolipoprotein a-i binding protein
107	<a href="#">c3rhiB_</a>	Alignment	not modelled	27.4	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein hu; <b>PDBTitle:</b> dna-binding protein hu from <i>Bacillus anthracis</i>
108	<a href="#">c2o8bA_</a>	Alignment	not modelled	27.4	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein msh2; <b>PDBTitle:</b> human mutsalpha (msh2/msh6) bound to adp and a g t mispair
109	<a href="#">c3ewbX_</a>	Alignment	not modelled	27.2	14	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from <i>Listeria monocytogenes</i>
110	<a href="#">c1tuuA_</a>	Alignment	not modelled	27.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase crystallized with atpgs
111	<a href="#">c2xj9B_</a>	Alignment	not modelled	27.1	24	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> mipz; <b>PDBTitle:</b> dimer structure of the bacterial cell division regulator mipz
112	<a href="#">c3stgA_</a>	Alignment	not modelled	26.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from <i>Neisseria meningitidis</i>
113	<a href="#">c2ph1A_</a>	Alignment	not modelled	26.0	29	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide-binding protein; <b>PDBTitle:</b> crystal structure of nucleotide-binding protein af2382 from <i>Archaeoglobus fulgidus</i> , northeast structural genomics target gr165
114	<a href="#">c1hyqA_</a>	Alignment	not modelled	25.8	28	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division inhibitor (mind-1); <b>PDBTitle:</b> mind bacterial cell division regulator from <i>A. fulgidus</i>
115	<a href="#">d1hyqa_</a>	Alignment	not modelled	25.8	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
116	<a href="#">c6iucC_</a>	Alignment	not modelled	25.6	24	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> spooj regulator (soj); <b>PDBTitle:</b> structure of helicobacter pylori soj-atp complex bound to dna
117	<a href="#">d1tuea_</a>	Alignment	not modelled	25.5	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
118	<a href="#">c4fczB_</a>	Alignment	not modelled	25.5	6	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> toluene-tolerance protein; <b>PDBTitle:</b> crystal structure of toluene-tolerance protein from <i>Pseudomonas putida</i> 2 (strain kt2440), northeast structural genomics consortium (nesg)3 target ppr99
119	<a href="#">c5ekaA_</a>	Alignment	not modelled	25.5	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein hu; <b>PDBTitle:</b> hu dna-binding protein from <i>Thermus thermophilus</i>
120	<a href="#">c5x9wA_</a>	Alignment	not modelled	25.2	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> mismatch repair protein