







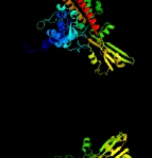

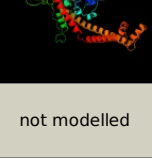


# Phyre2

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 Description RVBD0006\_(gyrA)\_7302\_9818  
 Date Tue Jul 23 14:50:03 BST 2019  
 Unique Job ID 47686c88ac10f2c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zvuA_</a>	 Alignment		100.0	35	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv subunit a; <b>PDBTitle:</b> structure of the full-length e. coli parc subunit
2	<a href="#">c3rafA_</a>	 Alignment		100.0	42	<b>PDB header:</b> isomerase/dna/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> quinazolinedione-dna cleavage complex of type iv topoisomerase from s.2 pneumoniae
3	<a href="#">c4i3hA_</a>	 Alignment		100.0	42	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv subunit b, dna topoisomerase 4 subunit a <b>PDBTitle:</b> a three-gate structure of topoisomerase iv from streptococcus2 pneumoniae
4	<a href="#">c6gauB_</a>	 Alignment		100.0	99	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b,dna gyrase subunit a; <b>PDBTitle:</b> extremely 'open' clamp structure of dna gyrase: role of the2 corynebacteriales gyrb specific insert
5	<a href="#">c4z2cA_</a>	 Alignment		100.0	54	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> quinolone(moxifloxacin)-dna cleavage complex of gyrase from s.2 pneumoniae
6	<a href="#">c2xcsD_</a>	 Alignment		100.0	56	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> dna gyrase subunit b, dna gyrase subunit a; <b>PDBTitle:</b> the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
7	<a href="#">c3ifzA_</a>	 Alignment		100.0	99	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
8	<a href="#">c2wl2B_</a>	 Alignment		100.0	52	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
9	<a href="#">c3ilwA_</a>	 Alignment		100.0	100	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> structure of dna gyrase subunit a n-terminal domain
10	<a href="#">c2xcqA_</a>	 Alignment		100.0	57	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit b, dna gyrase subunit a; <b>PDBTitle:</b> the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
11	<a href="#">c2xkjE_</a>	 Alignment		100.0	41	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> topoisomerase iv; <b>PDBTitle:</b> crystal structure of catalytic core of a. baumannii topo iv (pare-2 parc fusion truncate)

12	<a href="#">d1ab4a_</a>	Alignment		100.0	51	<b>Fold:</b> Type II DNA topoisomerase <b>Superfamily:</b> Type II DNA topoisomerase <b>Family:</b> Type II DNA topoisomerase
13	<a href="#">c5eixB_</a>	Alignment		100.0	42	<b>PDB header:</b> isomerase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna topoisomerase 4 subunit b,dna topoisomerase 4 subunit <b>PDBTitle:</b> quinolone-stabilized cleavage complex of topoisomerase iv from2 klebsiella pneumoniae
14	<a href="#">c5eixG_</a>	Alignment		100.0	42	<b>PDB header:</b> isomerase/dna <b>Chain:</b> G: <b>PDB Molecule:</b> dna topoisomerase 4 subunit b,dna topoisomerase 4 subunit <b>PDBTitle:</b> quinolone-stabilized cleavage complex of topoisomerase iv from2 klebsiella pneumoniae
15	<a href="#">c2inrA_</a>	Alignment		100.0	48	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
16	<a href="#">c2novD_</a>	Alignment		100.0	44	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> breakage-reunion domain of s.pneumoniae topo iv: crystal structure of 2 a gram-positive quinolone target
17	<a href="#">c6ca8A_</a>	Alignment		100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 2; <b>PDBTitle:</b> crystal structure of plasmodium falciparum topoisomerase ii dna-2 binding, cleavage and re-ligation domain
18	<a href="#">c4fm9A_</a>	Alignment		100.0	21	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 2-alpha; <b>PDBTitle:</b> human topoisomerase ii alpha bound to dna
19	<a href="#">c3qx3B_</a>	Alignment		100.0	23	<b>PDB header:</b> isomerase/dna/isomerase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> dna topoisomerase 2-beta; <b>PDBTitle:</b> human topoisomerase iibeta in complex with dna and etoposide
20	<a href="#">c4gfhA_</a>	Alignment		100.0	22	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 2; <b>PDBTitle:</b> topoisomerase ii-dna-amppnp complex
21	<a href="#">d1bjta_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Type II DNA topoisomerase <b>Superfamily:</b> Type II DNA topoisomerase <b>Family:</b> Type II DNA topoisomerase
22	<a href="#">c1bjtA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> topoisomerase <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase ii; <b>PDBTitle:</b> topoisomerase ii residues 409-1201
23	<a href="#">c3l6vA_</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> crystal structure of the xanthomonas campestris gyrase a c-2 terminal domain
24	<a href="#">c3uc1A_</a>	Alignment	not modelled	100.0	100	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> mycobacterium tuberculosis gyrase type iia topoisomerase c-terminal2 domain
25	<a href="#">d1wp5a_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> GyrA/ParC C-terminal domain-like <b>Family:</b> GyrA/ParC C-terminal domain-like
26	<a href="#">d1suua_</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> GyrA/ParC C-terminal domain-like <b>Family:</b> GyrA/ParC C-terminal domain-like
27	<a href="#">c1zi0A_</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> isomerase, dna bindng protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> a superhelical spiral in escherichia coli dna gyrase a c-2 terminal domain imparts unidirectional supercoiling bias
28	<a href="#">c3no0B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> aquifex aeolicus type iia topoisomerase c-terminal domain
						<b>PDB header:</b> isomerase

29	<a href="#">c1zvtA</a>	Alignment	not modelled	100.0	19	<b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv subunit a; <b>PDBTitle:</b> structure of the e. coli parC c-terminal domain
30	<a href="#">d1x75a1</a>	Alignment	not modelled	99.9	46	<b>Fold:</b> Type II DNA topoisomerase <b>Superfamily:</b> Type II DNA topoisomerase <b>Family:</b> Type II DNA topoisomerase
31	<a href="#">c3ku8A</a>	Alignment	not modelled	99.9	45	<b>PDB header:</b> toxin/isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> ccdbvf:gyra14ec
32	<a href="#">c6chgD</a>	Alignment	not modelled	87.3	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> kla0a08800p; <b>PDBTitle:</b> crystal structure of the yeast compass catalytic module
33	<a href="#">c1t3jA</a>	Alignment	not modelled	85.7	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitofusin 1; <b>PDBTitle:</b> mitofusin domain hr2 v686m/i708m mutant
34	<a href="#">c6nd4O</a>	Alignment	not modelled	82.6	15	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> utp1; <b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
35	<a href="#">c2oajA</a>	Alignment	not modelled	82.1	11	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> protein sn1; <b>PDBTitle:</b> crystal structure of sro7 from s. cerevisiae
36	<a href="#">c6nd4H</a>	Alignment	not modelled	78.3	15	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> utp17; <b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
37	<a href="#">c4uuyA</a>	Alignment	not modelled	76.6	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar membrane protein pep3; <b>PDBTitle:</b> structural identification of the vps18 beta-propeller reveals2 a critical role in the hops complex stability and function.
38	<a href="#">c6n8sA</a>	Alignment	not modelled	75.3	16	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lethal(2) giant larvae protein homolog 2; <b>PDBTitle:</b> crystal structure of the human cell polarity protein lethal giant2 larvae 2 (lg2). apkc phosphorylated, crystal form 3.
39	<a href="#">c3dm0A</a>	Alignment	not modelled	71.8	15	<b>PDB header:</b> sugar binding protein,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein fused with rack1; <b>PDBTitle:</b> maltose binding protein fusion with rack1 from a. thaliana
40	<a href="#">c5haxA</a>	Alignment	not modelled	69.4	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin nup170; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum nup170 ntd-nup53 complex
41	<a href="#">c5a1vK</a>	Alignment	not modelled	68.7	10	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> the structure of the copi coat linkage i
42	<a href="#">c3jb9U</a>	Alignment	not modelled	68.4	14	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> U: <b>PDB Molecule:</b> pre-mrna-processing factor 19; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
43	<a href="#">c2q6tB</a>	Alignment	not modelled	67.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dnab replication fork helicase; <b>PDBTitle:</b> crystal structure of the thermus aquaticus dnab monomer
44	<a href="#">c6nd4O</a>	Alignment	not modelled	67.5	14	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> utp12; <b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
45	<a href="#">c5a1vL</a>	Alignment	not modelled	65.2	13	<b>PDB header:</b> transport protein <b>Chain:</b> L: <b>PDB Molecule:</b> coatomer subunit beta; <b>PDBTitle:</b> the structure of the copi coat linkage i
46	<a href="#">c3fokH</a>	Alignment	not modelled	63.8	20	<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="#">c3a7pB</a>	Alignment	not modelled	63.2	16	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg16
48	<a href="#">c5gvbA</a>	Alignment	not modelled	63.1	15	<b>PDB header:</b> replication, peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> wd repeat and hmg-box dna-binding protein 1; <b>PDBTitle:</b> sepb domain of human and-1
49	<a href="#">c5dfzB</a>	Alignment	not modelled	49.6	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase vps15; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
50	<a href="#">c2pbiB</a>	Alignment	not modelled	48.2	10	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> guanine nucleotide-binding protein subunit beta 5; <b>PDBTitle:</b> the multifunctional nature of gbeta5/rgs9 revealed from its crystal2 structure
51	<a href="#">d2v8qb1</a>	Alignment	not modelled	47.5	25	<b>Fold:</b> AMPKBI-like <b>Superfamily:</b> AMPKBI-like <b>Family:</b> AMPKBI-like
52	<a href="#">c2vyeA</a>	Alignment	not modelled	46.9	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dnac-ssdna complex
53	<a href="#">c6qelB</a>	Alignment	not modelled	46.0	20	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> e. coli dnabc apo complex
54	<a href="#">d2g0da1</a>	Alignment	not modelled	46.0	13	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> LanC-like <b>Family:</b> LanC-like
55	<a href="#">c6girA</a>	Alignment	not modelled	45.3	17	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine--trna ligase, cytoplasmic; <b>PDBTitle:</b> arabidopsis thaliana cytosolic seryl-trna synthetase

56	<a href="#">c2lmiA</a>	Alignment	not modelled	44.3	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sg-rich sequence factor 1; <b>PDBTitle:</b> nmr structure of the protein bc040485 from homo sapiens
57	<a href="#">c4e8lC</a>	Alignment	not modelled	42.2	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> virginiamycin a acetyltransferase; <b>PDBTitle:</b> crystal structure of streptogramin group a antibiotic2 acetyltransferase vata from staphylococcus aureus
58	<a href="#">c4qt8A</a>	Alignment	not modelled	40.7	14	<b>PDB header:</b> hydrolase/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage-stimulating protein receptor; <b>PDBTitle:</b> crystal structure of ron sema-psi-ipt1 extracellular domains in2 complex with msp beta-chain
59	<a href="#">c4a2lD</a>	Alignment	not modelled	40.1	12	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> two-component system sensor histidine kinase/response; <b>PDBTitle:</b> structure of the periplasmic domain of the heparin and heparan2 sulphate sensing hybrid two component system bt4663 in apo and3 ligand bound forms
60	<a href="#">c3jroA</a>	Alignment	not modelled	39.9	13	<b>PDB header:</b> transport protein, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of protein transport protein sec13 and <b>PDBTitle:</b> nup84-nup145c-sec13 edge element of the npc lattice
61	<a href="#">d2ayuA1</a>	Alignment	not modelled	39.8	14	<b>Fold:</b> NAP-like <b>Superfamily:</b> NAP-like <b>Family:</b> NAP-like
62	<a href="#">c2ayuA</a>	Alignment	not modelled	39.8	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> nucleosome assembly protein; <b>PDBTitle:</b> the structure of nucleosome assembly protein suggests a mechanism for2 histone binding and shuttling
63	<a href="#">d1jwea</a>	Alignment	not modelled	39.7	20	<b>Fold:</b> N-terminal domain of DnaB helicase <b>Superfamily:</b> N-terminal domain of DnaB helicase <b>Family:</b> N-terminal domain of DnaB helicase
64	<a href="#">c1q1hA</a>	Alignment	not modelled	39.3	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor e; <b>PDBTitle:</b> an extended winged helix domain in general transcription2 factor e/ie alpha
65	<a href="#">d1q1ha</a>	Alignment	not modelled	39.3	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcription factor E/Ile-alpha, N-terminal domain
66	<a href="#">c3zjA</a>	Alignment	not modelled	39.2	36	<b>PDB header:</b> zinc-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pneumococcal histidine triad protein d; <b>PDBTitle:</b> n-terminal domain of pneumococcal phtd protein with bound2 zn(ii)
67	<a href="#">c5mg8B</a>	Alignment	not modelled	39.1	20	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> structural maintenance of chromosomes protein 6; <b>PDBTitle:</b> crystal structure of the s.pombe smc5/6 hinge domain
68	<a href="#">d3dm8a1</a>	Alignment	not modelled	39.1	26	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
69	<a href="#">c2lq3A</a>	Alignment	not modelled	37.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of syc0711_d from synechococcus sp., northeast2 structural genomics consortium (nesg) target snr212
70	<a href="#">c6bbmA</a>	Alignment	not modelled	37.4	20	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
71	<a href="#">d1ivsa1</a>	Alignment	not modelled	37.3	27	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> tRNA-binding arm <b>Family:</b> Valyl-tRNA synthetase (ValRS) C-terminal domain
72	<a href="#">c4h5jB</a>	Alignment	not modelled	37.1	12	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> guanine nucleotide-exchange factor sec12; <b>PDBTitle:</b> crystal structure of the guanine nucleotide exchange factor sec12 (p642 form)
73	<a href="#">c5nzvC</a>	Alignment	not modelled	36.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> coatomer subunit beta'; <b>PDBTitle:</b> the structure of the copi coat linkage iv
74	<a href="#">c1u0iA</a>	Alignment	not modelled	36.4	38	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> iaal-e3; <b>PDBTitle:</b> iaal-e3/k3 heterodimer
75	<a href="#">c4dznC</a>	Alignment	not modelled	36.3	32	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coiled-coil peptide cc-pil; <b>PDBTitle:</b> a de novo designed coiled coil cc-pil
76	<a href="#">c4dznA</a>	Alignment	not modelled	36.3	32	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil peptide cc-pil; <b>PDBTitle:</b> a de novo designed coiled coil cc-pil
77	<a href="#">c4dznB</a>	Alignment	not modelled	36.3	32	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coiled-coil peptide cc-pil; <b>PDBTitle:</b> a de novo designed coiled coil cc-pil
78	<a href="#">c5a9qB</a>	Alignment	not modelled	34.2	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear pore complex protein nup155; <b>PDBTitle:</b> human nuclear pore complex
79	<a href="#">c6ch2E</a>	Alignment	not modelled	34.1	15	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> flagellar hook-associated protein 2,flagellar protein flit; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of flha and flit-flid2 complex
80	<a href="#">c5a1uC</a>	Alignment	not modelled	33.0	10	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> the structure of the copi coat triad
						<b>PDB header:</b> gene regulation

81	<a href="#">c5yjeA</a>	Alignment	not modelled	32.0	16	<b>Chain:</b> A: <b>PDB Molecule:</b> protein hira; <b>PDBTitle:</b> crystal structure of hira(644-1017)
82	<a href="#">c2pqaB</a>	Alignment	not modelled	31.7	29	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> replication protein a 14 kda subunit; <b>PDBTitle:</b> crystal structure of full-length human rpa 14/32 heterodimer
83	<a href="#">d2qrdB1</a>	Alignment	not modelled	31.3	17	<b>Fold:</b> AMPKBI-like <b>Superfamily:</b> AMPKBI-like <b>Family:</b> AMPKBI-like
84	<a href="#">c1dpuA</a>	Alignment	not modelled	31.2	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a (rpa32) c-terminal domain; <b>PDBTitle:</b> solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
85	<a href="#">d1dpuA</a>	Alignment	not modelled	31.2	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal domain of RPA32
86	<a href="#">d1k32a3</a>	Alignment	not modelled	30.0	9	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> Tricorn protease domain 2 <b>Family:</b> Tricorn protease domain 2
87	<a href="#">c3ushB</a>	Alignment	not modelled	29.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the q2s0r5 protein from salinibacter ruber,2 northeast structural genomics consortium target srr207
88	<a href="#">d2dloa1</a>	Alignment	not modelled	29.7	71	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
89	<a href="#">c4q9tB</a>	Alignment	not modelled	29.2	15	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin nup133; <b>PDBTitle:</b> crystal structure of vanderwaltozyma polyspora nup133 beta-propeller2 domain
90	<a href="#">c5tzsT</a>	Alignment	not modelled	29.0	10	<b>PDB header:</b> translation <b>Chain:</b> T: <b>PDB Molecule:</b> utp21; <b>PDBTitle:</b> architecture of the yeast small subunit processome
91	<a href="#">c3a7mA</a>	Alignment	not modelled	28.9	15	<b>PDB header:</b> gene regulation, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein flit; <b>PDBTitle:</b> structure of flit, the flagellar type iii chaperone for flid
92	<a href="#">c6nd4N</a>	Alignment	not modelled	28.4	10	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> utp4; <b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
93	<a href="#">d2pi2e1</a>	Alignment	not modelled	28.3	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
94	<a href="#">c5cwtB</a>	Alignment	not modelled	27.9	18	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin nup57; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum nup57
95	<a href="#">c3qo8A</a>	Alignment	not modelled	27.8	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from candida albicans
96	<a href="#">c5ax7A</a>	Alignment	not modelled	27.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvyl transferase 1; <b>PDBTitle:</b> yeast pyruvyltransferase pvg1p
97	<a href="#">d1mlda2</a>	Alignment	not modelled	27.6	15	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
98	<a href="#">c2p9mD</a>	Alignment	not modelled	27.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein mj0922; <b>PDBTitle:</b> crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
99	<a href="#">c1yadD</a>	Alignment	not modelled	27.2	19	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein teni; <b>PDBTitle:</b> structure of teni from bacillus subtilis
100	<a href="#">c4eacC</a>	Alignment	not modelled	27.1	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> mannonate dehydratase; <b>PDBTitle:</b> crystal structure of mannonate dehydratase from escherichia coli2 strain k12
101	<a href="#">d1b4ua</a>	Alignment	not modelled	26.5	7	<b>Fold:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Superfamily:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Family:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB
102	<a href="#">c4w7yB</a>	Alignment	not modelled	26.4	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> b-cell receptor-associated protein 29; <b>PDBTitle:</b> dimeric bap29 vded with disulfide bonds in crystal contacts
103	<a href="#">c2dfdD</a>	Alignment	not modelled	26.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of human malate dehydrogenase type 2
104	<a href="#">d1wi9a</a>	Alignment	not modelled	26.1	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PCI domain (PINT motif)
105	<a href="#">c4iohA</a>	Alignment	not modelled	25.6	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tl11086 protein; <b>PDBTitle:</b> crystal structure of the tl1086 protein from thermosynechococcus2 elongatus, northeast structural genomics consortium target ter258
106	<a href="#">d2f2ac1</a>	Alignment	not modelled	25.3	9	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Glu-tRNAGln amidotransferase C subunit <b>Family:</b> Glu-tRNAGln amidotransferase C subunit
107	<a href="#">c5n80A</a>	Alignment	not modelled	24.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipopolysaccharide 1,6-galactosyltransferase;

						<b>PDBTitle:</b> glycosyltransferase lps biosynthesis in complex with udp <b>PDB header:</b> unknown function
108	<a href="#">c3kpbA_</a>	Alignment	not modelled	24.7	19	<b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein mj0100; <b>PDBTitle:</b> crystal structure of the cbs domain pair of protein mj01002 in complex with 5'-methylthioadenosine and s-adenosyl-l-3 methionine.
109	<a href="#">d1dlca1</a>	Alignment	not modelled	24.6	27	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> delta-Endotoxin, C-terminal domain
110	<a href="#">c3lssa_</a>	Alignment	not modelled	24.5	13	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> trypanosoma brucei seryl-trna synthetase in complex with atp
111	<a href="#">c3mkqA_</a>	Alignment	not modelled	24.2	13	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> coatomer beta'-subunit; <b>PDBTitle:</b> crystal structure of yeast alpha/betaprime-cop subcomplex of the cop12 vesicular coat
112	<a href="#">c2hpcF_</a>	Alignment	not modelled	23.8	11	<b>PDB header:</b> blood clotting <b>Chain:</b> F; <b>PDB Molecule:</b> fibrinogen, gamma polypeptide; <b>PDBTitle:</b> crystal structure of fragment d from human fibrinogen complexed with 2 gly-pro-arg-pro-amide.
113	<a href="#">d1a06a_</a>	Alignment	not modelled	23.6	30	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
114	<a href="#">c3whlB_</a>	Alignment	not modelled	23.1	13	<b>PDB header:</b> hydrolase/chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> probable 26s proteasome regulatory subunit p27; <b>PDBTitle:</b> crystal structure of nas2 n-terminal domain complexed with pan-rpt5c2 chimera
115	<a href="#">d1n0ua3</a>	Alignment	not modelled	23.0	30	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
116	<a href="#">c4i92A_</a>	Alignment	not modelled	22.6	8	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable serine/threonine-protein kinase at5g41260; <b>PDBTitle:</b> structure of the bsk8 kinase domain
117	<a href="#">c5cwtC_</a>	Alignment	not modelled	22.5	19	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> nucleoporin nup57; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum nup57
118	<a href="#">c4pehC_</a>	Alignment	not modelled	22.5	15	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> C; <b>PDB Molecule:</b> rna lariat debranching enzyme, putative; <b>PDBTitle:</b> dbr1 in complex with synthetic linear rna
119	<a href="#">c3hnwB_</a>	Alignment	not modelled	22.4	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
120	<a href="#">c2pwzG_</a>	Alignment	not modelled	22.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of the apo form of e.coli malate dehydrogenase