
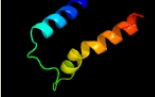



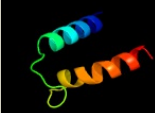

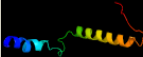
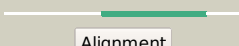
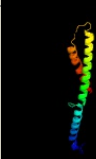
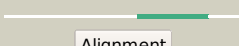

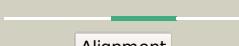
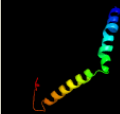







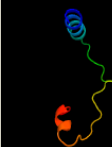
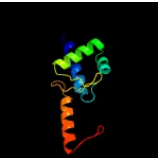
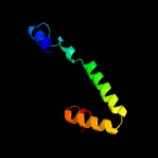


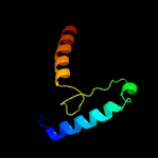

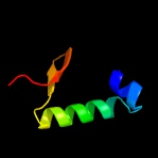
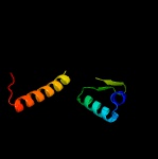
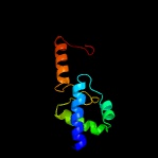


# Phyre2

Email	mdejesus@rockefeller.edu
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Date	Wed Aug 7 12:50:30 BST 2019
Unique Job ID	991ab596b34215ac

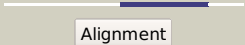
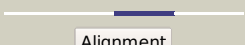
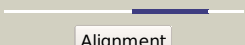


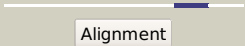
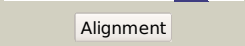



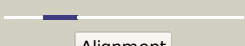

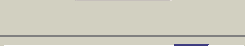
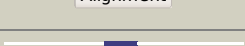
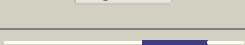





Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3fybA_</a>	 Alignment		91.2	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function (duf1244); <b>PDBTitle:</b> crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
2	<a href="#">c2o35A_</a>	 Alignment		90.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf1244; <b>PDBTitle:</b> protein of unknown function (duf1244) from sinorhizobium melliloti
3	<a href="#">d2o35a1</a>	 Alignment		90.8	16	<b>Fold:</b> SMc04008-like <b>Superfamily:</b> SMc04008-like <b>Family:</b> SMc04008-like
4	<a href="#">c5d6aA_</a>	 Alignment		64.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted atpase of the abc class; <b>PDBTitle:</b> 2.7 angstrom crystal structure of abc transporter atpase from vibrio2 vulnificus in complex with adenylyl-imidodiphosphate (amp-pnp)
5	<a href="#">d16vpa_</a>	 Alignment		48.0	24	<b>Fold:</b> Conserved core of transcriptional regulatory protein vp16 <b>Superfamily:</b> Conserved core of transcriptional regulatory protein vp16 <b>Family:</b> Conserved core of transcriptional regulatory protein vp16
6	<a href="#">c6sbsB_</a>	 Alignment		46.8	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> ytra from sulfolobus acidocaldarius, a gntn-family transcription2 factor
7	<a href="#">c4yivA_</a>	 Alignment		43.4	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> krna editing a6 specific protein; <b>PDBTitle:</b> structure of mrb1590 bound to amp-pnp
8	<a href="#">c2g3nA_</a>	 Alignment		40.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of the sulfolobus solfataricus alpha-2 glucosidase mala in complex with beta-octyl-glucopyranoside
9	<a href="#">c3neuA_</a>	 Alignment		39.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin1836 protein; <b>PDBTitle:</b> the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
10	<a href="#">c4xjnM_</a>	 Alignment		34.9	28	<b>PDB header:</b> viral protein/rna <b>Chain:</b> M: <b>PDB Molecule:</b> nucleocapsid; <b>PDBTitle:</b> structure of the parainfluenza virus 5 nucleocapsid-rna complex: an2 insight into paramyxovirus polymerase activity
11	<a href="#">c3qviB_</a>	 Alignment		30.2	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydantoin racemase; <b>PDBTitle:</b> allantoin racemase from klebsiella pneumoniae

12	<a href="#">c1wsuA</a>	Alignment		26.6	13	<b>PDB header:</b> translation/rna <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> c-terminal domain of elongation factor selB complexed with 2 secis rna
13	<a href="#">c6j52A</a>	Alignment		26.0	18	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> caspase recruitment domain-only protein; <b>PDBTitle:</b> crystal structure of card-only protein in frog virus 3
14	<a href="#">c5e4vA</a>	Alignment		25.3	29	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein,phosphoprotein; <b>PDBTitle:</b> crystal structure of measles n0-p complex
15	<a href="#">d1chka</a>	Alignment		25.3	12	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Chitosanase
16	<a href="#">c5oeiA</a>	Alignment		25.1	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein family upf0065:tat pathway signal; <b>PDBTitle:</b> r. palustris rpa4515 with oxoadipate
17	<a href="#">c2k29A</a>	Alignment		23.5	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin relB; <b>PDBTitle:</b> structure of the dbd domain of e. coli antitoxin relB
18	<a href="#">d2hs5a1</a>	Alignment		22.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
19	<a href="#">c4r1hA</a>	Alignment		20.7	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0741 protein; <b>PDBTitle:</b> gntR family transcriptional regulator from listeria monocytogenes
20	<a href="#">c2plyB</a>	Alignment		19.5	11	<b>PDB header:</b> translation/rna <b>Chain:</b> B: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna binding fragment of elongation factor 2 selB in complex with secis rna.
21	<a href="#">c4fxeB</a>	Alignment	not modelled	19.1	20	<b>PDB header:</b> toxin/toxin inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin relB; <b>PDBTitle:</b> crystal structure of the intact e. coli relBE toxin-antitoxin complex
22	<a href="#">c4q2uM</a>	Alignment	not modelled	17.2	15	<b>PDB header:</b> toxin/toxin repressor <b>Chain:</b> M: <b>PDB Molecule:</b> antitoxin dinJ; <b>PDBTitle:</b> crystal structure of the e. coli dinJ-yafq toxin-antitoxin complex
23	<a href="#">d1w7pd1</a>	Alignment	not modelled	16.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Vacuolar sorting protein domain
24	<a href="#">c3nzpA</a>	Alignment	not modelled	15.8	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine decarboxylase; <b>PDBTitle:</b> crystal structure of the biosynthetic arginine decarboxylase speA from 2 campylobacter jejuni, northeast structural genomics consortium target3 br53
25	<a href="#">c2gf5A</a>	Alignment	not modelled	15.2	14	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> fadd protein; <b>PDBTitle:</b> structure of intact fadd (mort1)
26	<a href="#">c5zi9B</a>	Alignment	not modelled	14.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cytokinin riboside 5'-monophosphate phosphoribohydrolase; <b>PDBTitle:</b> crystal structure of type-II log from streptomyces coelicolor a3
27	<a href="#">c5aj3k</a>	Alignment	not modelled	14.0	14	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> mitoribosomal protein us11m, mrps11; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
28	<a href="#">c2mqbA</a>	Alignment	not modelled	14.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable beta-lactamase; <b>PDBTitle:</b> nmr structure of putative beta-lactamase (np_372339.1)

						from2 staphylococcus aureus mu50 <b>PDB header:</b> translation/rna <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
29	<a href="#">c2pjpA_</a>	Alignment	not modelled	13.6	13	<b>PDB header:</b> hydrolase/replication <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase processivity factor component a20; <b>PDBTitle:</b> crystal structure of the vaccinia virus dna polymerase holoenzyme2 subunit d4 in complex with the a20 n-terminus
30	<a href="#">c4odaD_</a>	Alignment	not modelled	13.5	30	<b>PDB header:</b> hydrolase/replication <b>Chain:</b> C: <b>PDB Molecule:</b> dna polymerase processivity factor component a20; <b>PDBTitle:</b> crystal structure of the vaccinia virus dna polymerase holoenzyme2 subunit d4 in complex with the a20 n-terminus
31	<a href="#">c4odaC_</a>	Alignment	not modelled	13.5	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> predicted transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator from oenococcus oeni
32	<a href="#">c3by6C_</a>	Alignment	not modelled	13.4	9	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein vta1 homolog; <b>PDBTitle:</b> lip5-chmp5
33	<a href="#">c2lxmA_</a>	Alignment	not modelled	12.2	17	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> Double-stranded DNA-binding domain <b>Family:</b> Double-stranded DNA-binding domain
34	<a href="#">d1eija_</a>	Alignment	not modelled	11.5	33	<b>PDB header:</b> transcription/dna <b>Chain:</b> E: <b>PDB Molecule:</b> putative marr-family transcriptional repressor; <b>PDBTitle:</b> crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
35	<a href="#">c3zplE_</a>	Alignment	not modelled	11.5	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> biosynthetic arginine decarboxylase; <b>PDBTitle:</b> x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
36	<a href="#">c3n2oA_</a>	Alignment	not modelled	10.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> chorismate mutase protein; <b>PDBTitle:</b> crystal structure of chorismate mutase from bartonella henselae str.2 houston-1 in complex with malate
37	<a href="#">c3rmiA_</a>	Alignment	not modelled	10.7	8	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase complex repressor; <b>PDBTitle:</b> x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073
38	<a href="#">c5kvrA_</a>	Alignment	not modelled	10.6	13	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> Caspase recruitment domain, CARD
39	<a href="#">d3ygsP_</a>	Alignment	not modelled	10.4	15	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein vta1; <b>PDBTitle:</b> crystal structure of s.cerevisiae vta1 n-terminal domain
40	<a href="#">c2rkkA_</a>	Alignment	not modelled	10.3	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
41	<a href="#">d3bwga1</a>	Alignment	not modelled	9.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
42	<a href="#">d1fjlb_</a>	Alignment	not modelled	9.6	19	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
43	<a href="#">d1z0xa2</a>	Alignment	not modelled	9.4	25	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> crystal structure of a c-terminal fragment of moorella2 thermoacetica elongation factor selb
44	<a href="#">c1lvaA_</a>	Alignment	not modelled	9.2	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein sso0352; <b>PDBTitle:</b> wild-type programmed cell death 5 protein from sulfolobus solfataricus
45	<a href="#">c6iqcA_</a>	Alignment	not modelled	9.1	31	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> D: <b>PDB Molecule:</b> clathrin heavy chain; <b>PDBTitle:</b> clathrin d6 coat
46	<a href="#">c1xi4D_</a>	Alignment	not modelled	9.0	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 16.0 kda protein in abf2-chl12 <b>PDBTitle:</b> nmr ensemble of the yeast saccharomyces cerevisiae protein2 ymr074cp core region
47	<a href="#">c2fh0A_</a>	Alignment	not modelled	8.9	30	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
48	<a href="#">d1ryia1</a>	Alignment	not modelled	8.7	22	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> yr26_sds; <b>PDBTitle:</b> yr26_sds
49	<a href="#">c6a8yA_</a>	Alignment	not modelled	8.4	67	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
50	<a href="#">d2cg4a1</a>	Alignment	not modelled	8.4	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yydk; <b>PDBTitle:</b> the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
51	<a href="#">c3bwgA_</a>	Alignment	not modelled	8.2	14	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> Double-stranded DNA-binding domain <b>Family:</b> Double-stranded DNA-binding domain
52	<a href="#">d2crua1</a>	Alignment	not modelled	8.2	31	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> tfub1; <b>PDBTitle:</b> lasso peptide synthetase b1 complexed with the leader peptide
53	<a href="#">c6ix3B_</a>	Alignment	not modelled	8.2	15	

54	<a href="#">c2z3xC</a>	Alignment	not modelled	8.1	28	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> small, acid-soluble spore protein c; <b>PDBTitle:</b> structure of a protein-dna complex essential for dna protection in2 spore of bacillus species
55	<a href="#">c2jxnA</a>	Alignment	not modelled	7.9	31	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ymr074c; <b>PDBTitle:</b> solution structure of s. cerevisiae pdcd5-like protein ymr074cp
56	<a href="#">c5ldeB</a>	Alignment	not modelled	7.9	22	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> immunoglobulin g-binding protein g,viral flce protein; <b>PDBTitle:</b> crystal structure of a vflip-ikkgamma stapled peptide dimer
57	<a href="#">c4z2cA</a>	Alignment	not modelled	7.6	32	<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
58	<a href="#">d1cy5a</a>	Alignment	not modelled	7.5	5	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> Caspase recruitment domain, CARD
59	<a href="#">c5kkoD</a>	Alignment	not modelled	7.4	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterised protein; <b>PDBTitle:</b> a 1.55a x-ray structure from vibrio cholerae o1 biovar el tor of a2 hypothetical protein
60	<a href="#">c1izlM</a>	Alignment	not modelled	7.3	27	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> photosystem ii: subunit psbc; <b>PDBTitle:</b> crystal structure of photosystem ii
61	<a href="#">d1aopa2</a>	Alignment	not modelled	7.2	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
62	<a href="#">c2wl2B</a>	Alignment	not modelled	7.0	36	<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
63	<a href="#">c6e28D</a>	Alignment	not modelled	7.0	17	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> caspase recruitment domain-containing protein 9; <b>PDBTitle:</b> the card9 card domain-swapped dimer
64	<a href="#">d2cyya1</a>	Alignment	not modelled	6.9	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
65	<a href="#">d1ab4a</a>	Alignment	not modelled	6.9	36	<b>Fold:</b> Type II DNA topoisomerase <b>Superfamily:</b> Type II DNA topoisomerase <b>Family:</b> Type II DNA topoisomerase
66	<a href="#">c4o2xA</a>	Alignment	not modelled	6.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, atp-dependent clp <b>PDBTitle:</b> structure of a malarial protein
67	<a href="#">c5xmeA</a>	Alignment	not modelled	6.9	22	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor type 1-associated death <b>PDBTitle:</b> solution structure of c-terminal domain of tradd
68	<a href="#">c4rl4B</a>	Alignment	not modelled	6.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gtp cyclohydrolase-2; <b>PDBTitle:</b> crystal structure of gtp cyclohydrolase ii from helicobacter pylori2 26695
69	<a href="#">c5l7aA</a>	Alignment	not modelled	6.7	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> the crystal structure of the human snf5/ini1 domain
70	<a href="#">c3ic7A</a>	Alignment	not modelled	6.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator of gntR family2 from bacteroides thetaiotaomicron
71	<a href="#">c4p96B</a>	Alignment	not modelled	6.6	8	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from vibrio cholerae
72	<a href="#">d1au7a1</a>	Alignment	not modelled	6.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
73	<a href="#">d1wh5a</a>	Alignment	not modelled	6.6	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
74	<a href="#">c2du9A</a>	Alignment	not modelled	6.5	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> predicted transcriptional regulators; <b>PDBTitle:</b> crystal structure of the transcriptional factor from c.glutamicum
75	<a href="#">c2nz7A</a>	Alignment	not modelled	6.5	12	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> caspase recruitment domain-containing protein 4; <b>PDBTitle:</b> crystal structure analysis of caspase-recruitment domain2 (card) of nod1
76	<a href="#">c3t5vC</a>	Alignment	not modelled	6.5	50	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> 26s proteasome complex subunit sem1; <b>PDBTitle:</b> sac3:thp1:sem1 complex
77	<a href="#">d1g3nc2</a>	Alignment	not modelled	6.3	100	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
78	<a href="#">c2jrbA</a>	Alignment	not modelled	6.2	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> orf 1 protein; <b>PDBTitle:</b> c-terminal domain of orf1p from mouse line-1
79	<a href="#">c2x2iB</a>	Alignment	not modelled	6.2	33	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,4-glucan lyase isozyme 1; <b>PDBTitle:</b> crystal structure of the gracilariopsis lemaneiformis alpha-1,4-2 glucan lyase with acarbose

80	<a href="#">c2nx9B_</a>	 Alignment	not modelled	6.1	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
81	<a href="#">c4ovtA_</a>	 Alignment	not modelled	6.0	8	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trap dicarboxylate transporter, dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 ochrobacterium anthropi (oant_3902), target efi-510153, with bound l-3 fucionate
82	<a href="#">c3me5A_</a>	 Alignment	not modelled	6.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosine-specific methyltransferase; <b>PDBTitle:</b> crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 2457t
83	<a href="#">c4yk3B_</a>	 Alignment	not modelled	6.0	30	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bepe protein; <b>PDBTitle:</b> crystal structure of the bid domain of bepe from bartonella henselae
84	<a href="#">c3uifA_</a>	 Alignment	not modelled	6.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfonate abc transporter, periplasmic sulfonate-binding <b>PDBTitle:</b> crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
85	<a href="#">d1o4xa1</a>	 Alignment	not modelled	6.0	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
86	<a href="#">d1s7ea1</a>	 Alignment	not modelled	6.0	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
87	<a href="#">c4napD_</a>	 Alignment	not modelled	5.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> extracellular solute-binding protein, family 7; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio alaskensis g20 (dde_0634), target efi-510102, with3 bound d-tryptophan
88	<a href="#">c5toiB_</a>	 Alignment	not modelled	5.9	100	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of the marburg virus vp35 oligomerization domain2 p4222
89	<a href="#">c4gmgA_</a>	 Alignment	not modelled	5.8	32	<b>PDB header:</b> ribosome-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative ribosome associated protein; <b>PDBTitle:</b> ribosome-binding domain of zuo1
90	<a href="#">c2xcsD_</a>	 Alignment	not modelled	5.7	26	<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
91	<a href="#">c6q52A_</a>	 Alignment	not modelled	5.6	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cca-adding enzyme; <b>PDBTitle:</b> structure of a psychrophilic cca-adding enzyme in complex with cmpcpp2 at room temperature in chipx microfluidic device
92	<a href="#">c1iyjC_</a>	 Alignment	not modelled	5.5	56	<b>PDB header:</b> gene regulation/antitumor protein <b>Chain:</b> C: <b>PDB Molecule:</b> deleted in split hand/split foot protein 1; <b>PDBTitle:</b> structure of a brca2-dss1 complex
93	<a href="#">c5jqkA_</a>	 Alignment	not modelled	5.5	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase, putative; <b>PDBTitle:</b> the xray crystal structure of p. falciparum aminopeptidase p
94	<a href="#">c6j4uA_</a>	 Alignment	not modelled	5.5	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tubulinytl-tyr carboxypeptidase 1; <b>PDBTitle:</b> structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
95	<a href="#">c3we3B_</a>	 Alignment	not modelled	5.4	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bloom syndrome protein; <b>PDBTitle:</b> structure of blm rqc domain bound to an arsenate ion
96	<a href="#">d1t3la2</a>	 Alignment	not modelled	5.4	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
97	<a href="#">d1t0hb_</a>	 Alignment	not modelled	5.4	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
98	<a href="#">d1bw5a_</a>	 Alignment	not modelled	5.4	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
99	<a href="#">c4wt3A_</a>	 Alignment	not modelled	5.3	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco accumulation factor 1, isoform 2; <b>PDBTitle:</b> the n-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana