Phyre^2

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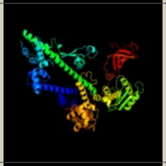
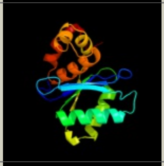
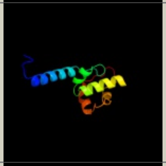
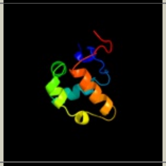
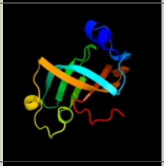
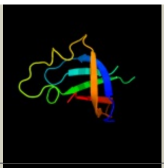
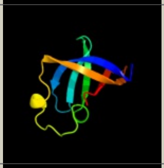
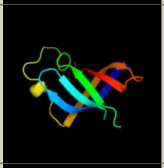
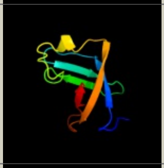
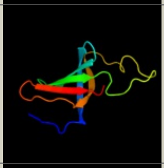
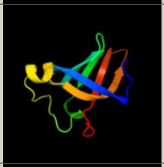
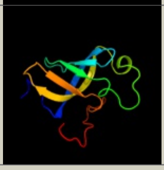
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oceA_	 Alignment		100.0	67	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
2	c3psiA_	 Alignment		100.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
3	c3psfA_	 Alignment		100.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
4	d3bzka3	 Alignment		100.0	63	**Fold:**Tex N-terminal region-like **Superfamily:**Tex N-terminal region-like **Family:**Tex N-terminal region-like
5	d3bzka5	 Alignment		100.0	73	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
6	d3bzka1	 Alignment		99.9	70	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
7	d3bzka2	 Alignment		99.8	64	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
8	d3bzka4	 Alignment		99.7	73	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
9	c2k4kA_	 Alignment		99.6	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**general stress protein 13; **PDBTitle:** solution structure of gsp13 from bacillus subtilis
10	c2cqoA_	 Alignment		99.6	31	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**nucleolar protein of 40 kda; **PDBTitle:** solution structure of the s1 rna binding domain of human2 hypothetical protein flj11067
11	c2khjA_	 Alignment		99.6	31	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1

12	c1q8kA_	Alignment		99.6	25	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 **PDBTitle:** solution structure of alpha subunit of human eif2
13	c1q46A_	Alignment		99.6	24	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
14	d1q46a2	Alignment		99.6	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
15	c1yz6A_	Alignment		99.6	28	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 alpha **PDBTitle:** crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi
16	d1sroa_	Alignment		99.6	43	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
17	d1wi5a_	Alignment		99.5	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
18	c2khiA_	Alignment		99.5	39	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
19	c2k52A_	Alignment		99.5	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1198; **PDBTitle:** structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b
20	c2eqsA_	Alignment		99.5	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dhx8; **PDBTitle:** solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8
21	d2ba0a1	Alignment	not modelled	99.5	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	d2z0sa1	Alignment	not modelled	99.5	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	d2je6i1	Alignment	not modelled	99.5	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
24	d1go3e1	Alignment	not modelled	99.4	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
25	d1kl9a2	Alignment	not modelled	99.4	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	c2ahoB_	Alignment	not modelled	99.4	25	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** structure of the archaeal initiation factor eif2 alpha-2 gamma heterodimer from sulfolobus solfataricus complexed3 with gdpnp
27	d2ahob2	Alignment	not modelled	99.3	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
28	c2z0sA_	Alignment	not modelled	99.3	26	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**probable exosome complex rna-binding protein 1; **PDBTitle:** crystal structure of putative exosome complex rna-

						binding2 protein
29	c1kl9A_	Alignment	not modelled	99.3	25	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 subunit 1; **PDBTitle:** crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha
30	d1y14b1	Alignment	not modelled	99.3	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
31	d2nn6h1	Alignment	not modelled	99.3	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
32	c2ba0A_	Alignment	not modelled	99.2	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4; **PDBTitle:** archaeal exosome core
33	d2nn6i1	Alignment	not modelled	99.1	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
34	c2je6I_	Alignment	not modelled	99.1	24	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**exosome complex rna-binding protein 1; **PDBTitle:** structure of a 9-subunit archaeal exosome
35	c3go5A_	Alignment	not modelled	99.1	16	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**multidomain protein with s1 rna-binding domains; **PDBTitle:** crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
36	c1go3E_	Alignment	not modelled	99.0	35	**PDB header:**transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** structure of an archeal homolog of the eukaryotic rna2 polymerase ii rpb4/rpb7 complex
37	d1hh2p1	Alignment	not modelled	99.0	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
38	d2c35b1	Alignment	not modelled	99.0	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
39	c1hh2P_	Alignment	not modelled	99.0	28	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
40	c1l2fA_	Alignment	not modelled	98.9	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
41	c2pmzE_	Alignment	not modelled	98.9	41	**PDB header:**translation, transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
42	c2ba1B_	Alignment	not modelled	98.9	21	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
43	c2nn6I_	Alignment	not modelled	98.9	21	**PDB header:**hydrolase/transferase **Chain:** I: **PDB Molecule:**3'-5' exoribonuclease csl4 homolog; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
44	c2c35F_	Alignment	not modelled	98.9	20	**PDB header:**polymerase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii
45	d1smxa_	Alignment	not modelled	98.8	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	d2edua1	Alignment	not modelled	98.8	25	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
47	d2duya1	Alignment	not modelled	98.8	33	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
48	c2b8kG_	Alignment	not modelled	98.7	18	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii
49	c3h0gS_	Alignment	not modelled	98.7	23	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
50	d2axtu1	Alignment	not modelled	98.7	19	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like
51	c1nt9G_	Alignment	not modelled	98.5	17	**PDB header:**transcription, transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kd polypeptide; **PDBTitle:** complete 12-subunit rna polymerase ii
52	c2bh8B_	Alignment	not modelled	98.5	31	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
53	c1s5lu_	Alignment	not modelled	98.4	22	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
54	c2ix1A_	Alignment	not modelled	98.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoribonuclease 2; **PDBTitle:** rnase ii d209n mutant

55	c2ckzB_	Alignment	not modelled	98.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase iii 25 kd **PDBTitle:** x-ray structure of rna polymerase iii subcomplex c17-c25.
56	d1iv0a_	Alignment	not modelled	97.8	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
57	c2wp8J_	Alignment	not modelled	97.7	28	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
58	d1vhxa_	Alignment	not modelled	97.7	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
59	d1nu0a_	Alignment	not modelled	97.6	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
60	c2nn6H_	Alignment	not modelled	97.5	21	**PDB header:**hydrolase/transferase **Chain:** H: **PDB Molecule:**exosome complex exonuclease rrp4; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
61	d2ch5a2	Alignment	not modelled	97.5	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
62	d2nn6g1	Alignment	not modelled	97.5	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	c3ayhB_	Alignment	not modelled	97.4	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc8; **PDBTitle:** crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
64	c2c4rL_	Alignment	not modelled	97.3	23	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
65	c2vnuD_	Alignment	not modelled	97.3	28	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp44; **PDBTitle:** crystal structure of sc rrp44
66	d2ja9a1	Alignment	not modelled	97.1	8	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
67	d1hjra_	Alignment	not modelled	97.1	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**RuvC resolvase
68	c2nn6G_	Alignment	not modelled	97.0	14	**PDB header:**hydrolase/transferase **Chain:** G: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
69	d2bgwa1	Alignment	not modelled	96.9	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
70	c2asbA_	Alignment	not modelled	96.8	19	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** structure of a mycobacterium tuberculosis nusa-rna complex
71	c2ja9A_	Alignment	not modelled	96.7	9	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the n-terminal deletion of yeast exosome2 component rrp40
72	d2asba1	Alignment	not modelled	96.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
73	d1zc6a1	Alignment	not modelled	96.5	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
74	c2r7fA_	Alignment	not modelled	96.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease ii family protein; **PDBTitle:** crystal structure of ribonuclease ii family protein from2 deinococcus radiodurans, hexagonal crystal form. northeast3 structural genomics target drr63
75	c2rf4A_	Alignment	not modelled	96.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
76	c1k0rB_	Alignment	not modelled	95.4	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nusa; **PDBTitle:** crystal structure of mycobacterium tuberculosis nusa
77	c3eo3B_	Alignment	not modelled	95.3	15	**PDB header:**isomerase, transferase **Chain:** B: **PDB Molecule:**bifunctional udp-n-acetylglucosamine 2-epimerase/n- **PDBTitle:** crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
78	c1kftA_	Alignment	not modelled	95.3	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
79	d1kfta_	Alignment	not modelled	95.3	15	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
80	d1x2ia1	Alignment	not modelled	95.2	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like

81	c1zbsA_	Alignment	not modelled	94.3	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg1100; **PDBTitle:** crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
82	c2ch5D_	Alignment	not modelled	94.1	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
83	d2gupa1	Alignment	not modelled	94.1	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
84	c2gupA_	Alignment	not modelled	94.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rok family protein; **PDBTitle:** structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
85	d1ixra1	Alignment	not modelled	93.9	27	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
86	c1zxoB_	Alignment	not modelled	93.9	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein q8a1p1; **PDBTitle:** x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
87	d1k3ra1	Alignment	not modelled	93.8	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
88	c2hnhA_	Alignment	not modelled	93.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
89	d1cuka2	Alignment	not modelled	93.6	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
90	c3ifrB_	Alignment	not modelled	93.2	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
91	c2e2pA_	Alignment	not modelled	93.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
92	d1bvsa2	Alignment	not modelled	93.0	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
93	c3f2cA_	Alignment	not modelled	92.9	22	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
94	c1xc3A_	Alignment	not modelled	92.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructokinase; **PDBTitle:** structure of a putative fructokinase from bacillus subtilis
95	d1e3pa2	Alignment	not modelled	92.8	49	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
96	d2p3ra1	Alignment	not modelled	92.7	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
97	c3d0fA_	Alignment	not modelled	92.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
98	c2aa4B_	Alignment	not modelled	92.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative n-acetylmannosamine kinase; **PDBTitle:** crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
99	c2h5xA_	Alignment	not modelled	92.1	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
100	d2aa4a1	Alignment	not modelled	92.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
101	c1ixrA_	Alignment	not modelled	92.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
102	d2a1jb1	Alignment	not modelled	91.9	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
103	c1d8lA_	Alignment	not modelled	91.7	22	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (holliday junction dna helicase ruva); **PDBTitle:** e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii
104	c3e0dA_	Alignment	not modelled	91.5	20	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
105	c3aqqD_	Alignment	not modelled	91.4	21	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**calcium-regulated heat stable protein 1; **PDBTitle:** crystal structure of human crhsp-24

106	c3gbtA_	Alignment	not modelled	91.2	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
107	d1dgsa1	Alignment	not modelled	90.9	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
108	d2ix0a2	Alignment	not modelled	90.8	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
109	c3g25B_	Alignment	not modelled	90.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
110	d2i1qa1	Alignment	not modelled	90.6	19	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
111	c1zc6A_	Alignment	not modelled	90.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable n-acetylglucosamine kinase; **PDBTitle:** crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
112	d1q18a1	Alignment	not modelled	89.9	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
113	c1kcfB_	Alignment	not modelled	89.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical 30.2 kd protein c25g10.02 in **PDBTitle:** crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
114	c3htvA_	Alignment	not modelled	89.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-allose kinase; **PDBTitle:** crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
115	c1glbG_	Alignment	not modelled	89.3	27	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
116	d1wfqa_	Alignment	not modelled	88.7	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
117	c3jvpA_	Alignment	not modelled	88.5	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
118	d2aq0a1	Alignment	not modelled	88.5	9	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
119	d1huxa_	Alignment	not modelled	88.3	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
120	c3ezwD_	Alignment	not modelled	88.0	26	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices