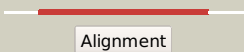

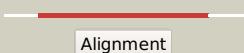

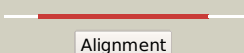

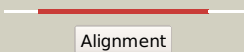





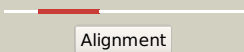

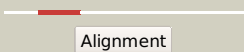

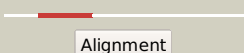







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3370c_(dnaE2)_3781681_3784920
Date	Fri Aug 9 18:20:03 BST 2019
Unique Job ID	eabfe877561355a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fkvA_	 Alignment		100.0	31	PDB header: transferase Chain: A; PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
2	c3e0dA_	 Alignment		100.0	34	PDB header: transferase/dna Chain: A; PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
3	c2hnhA_	 Alignment		100.0	34	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
4	c5lewA_	 Alignment		100.0	31	PDB header: transferase Chain: A; PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: dna polymerase
5	c3f2cA_	 Alignment		100.0	21	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
6	c4gx9A_	 Alignment		100.0	31	PDB header: transferase Chain: A; PDB Molecule: dna polymerase iii subunit epsilon,dna polymerase iii PDBTitle: crystal structure of a dna polymerase iii alpha-epsilon chimera
7	c3e0fA_	 Alignment		99.8	21	PDB header: hydrolase Chain: A; PDB Molecule: putative metal-dependent phosphoesterase; PDBTitle: crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution
8	c2yb1A_	 Alignment		99.6	28	PDB header: hydrolase Chain: A; PDB Molecule: amidohydrolase; PDBTitle: structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
9	c2wjeA_	 Alignment		99.6	18	PDB header: hydrolase Chain: A; PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
10	c3dcpB_	 Alignment		99.6	17	PDB header: hydrolase Chain: B; PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of the putative histidinol phosphatase hisk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
11	c3umuA_	 Alignment		99.6	16	PDB header: hydrolase Chain: A; PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of l-histidinol phosphate phosphatase (hisk) from2 lactococcus lactis subsp. lactis il1403 complexed with zn, phosphate3 and l-histidinol

12	c3qy6A_	Alignment		99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
13	c2yz5B_	Alignment		99.5	19	PDB header: hydrolase Chain: B: PDB Molecule: histidinol phosphatase; PDBTitle: histidinol phosphate phosphatase complexed with phosphate
14	c3auoB_	Alignment		99.4	27	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase beta family (x family); PDBTitle: dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
15	d1m65a_	Alignment		99.3	16	Fold: 7-stranded beta/alpha barrel Superfamily: PHP domain-like Family: PHP domain
16	d2anuA1	Alignment		99.1	19	Fold: 7-stranded beta/alpha barrel Superfamily: PHP domain-like Family: PHP domain
17	c2anuA_	Alignment		99.1	19	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein tm0559; PDBTitle: crystal structure of predicted metal-dependent phosphoesterase (php2 family) (tm0559) from thermotoga maritima at 2.40 a resolution
18	c5zb8B_	Alignment		99.1	16	PDB header: dna binding protein Chain: B: PDB Molecule: pfuendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus
19	c2w9mB_	Alignment		99.0	19	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
20	c3e38A_	Alignment		98.8	33	PDB header: hydrolase Chain: A: PDB Molecule: two-domain protein containing predicted php-like metal- PDBTitle: crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bvu_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
21	d1c0aa1	Alignment	not modelled	98.0	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
22	c4upaA_	Alignment	not modelled	97.9	17	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of entamoeba histolytica lysyl-trna synthetase in2 complex with amppnp
23	d1b8aa1	Alignment	not modelled	97.9	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
24	c6ns0A_	Alignment	not modelled	97.9	19	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from chlamydia trachomatis2 complexed with l-lysine and cladosporin
25	c4joiA_	Alignment	not modelled	97.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: cst complex subunit stn1; PDBTitle: crystal structure of the human telomeric stn1-ten1 complex
26	d1e1oa1	Alignment	not modelled	97.8	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
27	c1b8aB_	Alignment	not modelled	97.8	19	PDB header: ligase Chain: B: PDB Molecule: protein (aspartyl-trna synthetase); PDBTitle: aspartyl-trna synthetase
28	c3i7fA_	Alignment	not modelled	97.8	14	PDB header: ligase Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: aspartyl trna synthetase from entamoeba histolytica
29	c3bjuB_	Alignment	not modelled	97.8	12	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna

						synthetase
30	c4h02B_	Alignment	not modelled	97.8	17	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of p. falciparum lysyl-trna synthetase
31	c4j15A_	Alignment	not modelled	97.8	14	PDB header: ligase Chain: A: PDB Molecule: aspartate--trna ligase, cytoplasmic; PDBTitle: crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex
32	c5hggD_	Alignment	not modelled	97.8	16	PDB header: ligase/ligase inhibitor Chain: D: PDB Molecule: lysine--trna ligase; PDBTitle: loa loa lysyl-trna synthetase in complex with cladosporin.
33	d1bbua1	Alignment	not modelled	97.8	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
34	c5groA_	Alignment	not modelled	97.7	23	PDB header: ligase Chain: A: PDB Molecule: aspartate--trna(asp/asn) ligase; PDBTitle: crystal structure of the n-terminal anticodon-binding domain of non-2 discriminating aspartyl-trna synthetase from helicobacter pylori
35	c1x55A_	Alignment	not modelled	97.7	20	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase; PDBTitle: crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
36	c4o2dB_	Alignment	not modelled	97.7	26	PDB header: ligase Chain: B: PDB Molecule: aspartate--trna ligase; PDBTitle: crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid
37	c5zg8A_	Alignment	not modelled	97.7	17	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase; PDBTitle: crystal structure of ttnrs
38	c2xgtB_	Alignment	not modelled	97.7	21	PDB header: ligase Chain: B: PDB Molecule: asparaginyl-trna synthetase, cytoplasmic; PDBTitle: asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
39	c3m4qA_	Alignment	not modelled	97.6	16	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase, putative; PDBTitle: entamoeba histolytica asparaginyl-trna synthetase (asnr3)
40	c4up8A_	Alignment	not modelled	97.6	17	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of entamoeba histolytica lysyl-trna synthetase apo2 form
41	c4ex5A_	Alignment	not modelled	97.6	20	PDB header: transferase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine
42	c5elnC_	Alignment	not modelled	97.6	12	PDB header: ligase Chain: C: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine
43	d1l0wa1	Alignment	not modelled	97.6	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
44	c3kf6A_	Alignment	not modelled	97.6	11	PDB header: structural protein Chain: A: PDB Molecule: protein stn1; PDBTitle: crystal structure of s. pombe stn1-ten1 complex
45	c5xixD_	Alignment	not modelled	97.6	20	PDB header: ligase Chain: D: PDB Molecule: asparagine--trna ligase, cytoplasmic; PDBTitle: the canonical domain of human asparaginyl-trna synthetase
46	c3e9hB_	Alignment	not modelled	97.5	18	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
47	c5vl1D_	Alignment	not modelled	97.5	22	PDB header: ligase Chain: D: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from mycobacterium ulcerans2 complexed with l-lysine
48	d1eova1	Alignment	not modelled	97.5	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
49	c6od8A_	Alignment	not modelled	97.5	16	PDB header: ligase Chain: A: PDB Molecule: putative aspartyl-trna synthetase; PDBTitle: crystal structure of a putative aspartyl-trna synthetase from2 leishmania major friedlin
50	c1e22A_	Alignment	not modelled	97.5	21	PDB header: ligase Chain: A: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
51	c4gn5A_	Alignment	not modelled	97.5	20	PDB header: de novo protein/hydrolase Chain: A: PDB Molecule: obody am3l15; PDBTitle: obody am3l15 bound to hen egg-white lysozyme
52	c1eqrC_	Alignment	not modelled	97.5	24	PDB header: ligase Chain: C: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of free aspartyl-trna synthetase from2 escherichia coli
53	c1wydB_	Alignment	not modelled	97.5	25	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfolobus tokodaïi
54	c4wj4A_	Alignment	not modelled	97.5	28	PDB header: ligase/rna Chain: A: PDB Molecule: aspartate--trna(asp/asn) ligase; PDBTitle: crystal structure of non-discriminating aspartyl-trna synthetase from2 pseudomonas aeruginosa complexed with trna(asn) and aspartic acid
						Fold: OB-fold

55	d1n9wa1	Alignment	not modelled	97.5	27	Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
56	c4gopB	Alignment	not modelled	97.5	16	PDB header: dna binding protein/dna Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
57	d2eduA1	Alignment	not modelled	97.4	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
58	c1asyA	Alignment	not modelled	97.4	14	PDB header: complex (aminoacyl-trna synthase/trna) Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
59	c4glaD	Alignment	not modelled	97.4	19	PDB header: hydrolase/de novo protein Chain: D: PDB Molecule: obody n18; PDBTitle: obody n18 bound to hen egg-white lysozyme
60	c1efwA	Alignment	not modelled	97.3	22	PDB header: ligase/rna Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
61	c3e0eA	Alignment	not modelled	97.2	13	PDB header: replication Chain: A: PDB Molecule: replication protein a; PDBTitle: crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 large mrr110b
62	c4ah6B	Alignment	not modelled	97.2	23	PDB header: ligase Chain: B: PDB Molecule: aspartate--trna ligase, mitochondrial; PDBTitle: human mitochondrial aspartyl-trna synthetase
63	c6k0aC	Alignment	not modelled	97.2	15	PDB header: rna binding protein/rna Chain: C: PDB Molecule: ribonuclease p protein component 3; PDBTitle: cryo-em structure of an archaeal ribonuclease p
64	c4owxB	Alignment	not modelled	97.2	21	PDB header: dna binding protein/dna Chain: B: PDB Molecule: soxx complex subunit b1; PDBTitle: structural basis of soxx1 in complex with a 12nt ssdna
65	c1n9wA	Alignment	not modelled	97.1	27	PDB header: biosynthetic protein Chain: A: PDB Molecule: aspartyl-trna synthetase 2; PDBTitle: crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
66	d1gm5a2	Alignment	not modelled	97.1	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
67	d2pi2a1	Alignment	not modelled	97.1	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
68	c2pi2A	Alignment	not modelled	97.0	17	PDB header: replication, dna binding protein Chain: A: PDB Molecule: replication protein a 32 kda subunit; PDBTitle: full-length replication protein a subunits rpa14 and rpa32
69	c3dm3A	Alignment	not modelled	97.0	22	PDB header: replication Chain: A: PDB Molecule: replication factor a; PDBTitle: crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjrl18e
70	c2k50A	Alignment	not modelled	97.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: replication factor a related protein; PDBTitle: solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
71	c6pqhA	Alignment	not modelled	96.7	22	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase; PDBTitle: crystal structure of asparagine-trna ligase from elizabethkingia sp.2 ccug 26117
72	d1o7ia	Alignment	not modelled	96.7	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
73	c5iheB	Alignment	not modelled	96.7	22	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ii small subunit; PDBTitle: d-family dna polymerase - dp1 subunit (3'-5' proof-reading2 exonuclease)
74	c1z9fA	Alignment	not modelled	96.7	16	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution
75	d1krta	Alignment	not modelled	96.5	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
76	c5o19A	Alignment	not modelled	96.4	23	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
77	c2i5hA	Alignment	not modelled	96.4	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
78	d2i5ha1	Alignment	not modelled	96.4	22	Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like
79	c2kenA	Alignment	not modelled	96.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazel. northeast structural3 genomics consortium target mar214a.
80	c6i52B	Alignment	not modelled	96.1	15	PDB header: dna binding protein Chain: B: PDB Molecule: replication factor a protein 2; PDBTitle: yeast rpa bound to ssdna

81	c3kf8C_	Alignment	not modelled	96.1	12	PDB header: structural protein Chain: C: PDB Molecule: protein stn1; PDBTitle: crystal structure of c. tropicalis stn1-ten1 complex
82	c1ynxA_	Alignment	not modelled	95.9	10	PDB header: dna binding protein Chain: A: PDB Molecule: replication factor-a protein 1; PDBTitle: solution structure of dna binding domain a (dbd-a) of2 s.cerevisiae replication protein a (rpa)
83	d1xjva1	Alignment	not modelled	95.9	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
84	c2cwaA_	Alignment	not modelled	95.8	19	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of the single-stranded dna binding protein from2 thermus thermophilus hb8
85	d3bzka1	Alignment	not modelled	95.8	33	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
86	d1jmca2	Alignment	not modelled	95.7	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
87	c1xjvA_	Alignment	not modelled	95.5	15	PDB header: transcription/dna Chain: A: PDB Molecule: protection of telomeres 1; PDBTitle: crystal structure of human pot1 bound to telomeric single-2 stranded dna (ttagggttag)
88	d1jmca1	Alignment	not modelled	95.4	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
89	c1s5lu_	Alignment	not modelled	95.4	29	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
90	c2k75A_	Alignment	not modelled	95.2	17	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein ta0387; PDBTitle: solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
91	d1wjja_	Alignment	not modelled	95.1	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
92	c1gm5A_	Alignment	not modelled	95.0	12	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
93	c1fguA_	Alignment	not modelled	94.8	15	PDB header: replication Chain: A: PDB Molecule: replication protein a 70 kda dna-binding subunit; PDBTitle: ssdna-binding domain of the large subunit of replication2 protein a
94	d2axtu1	Alignment	not modelled	94.4	29	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: PsbU-like
95	d2duya1	Alignment	not modelled	94.0	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
96	c3vdyA_	Alignment	not modelled	93.8	16	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded dna-binding protein ssbb; PDBTitle: b. subtilis ssbb/ssdna
97	d1v1qa_	Alignment	not modelled	93.7	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
98	c1k8gC_	Alignment	not modelled	93.6	8	PDB header: dna binding protein/dna Chain: C: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: crystal structure of the n-terminal domain of oxytricha2 nova telomere end binding protein alpha subunit both3 uncomplexed and complexed with telomeric ssdna
99	c3kojA_	Alignment	not modelled	93.6	13	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein ycf41; PDBTitle: crystal structure of the ssb domain of q5n255_synp6 protein from2 synechococcus sp. northeast structural genomics consortium target3 snr59a.
100	c3e0jG_	Alignment	not modelled	93.3	17	PDB header: transferase Chain: G: PDB Molecule: dna polymerase subunit delta-2; PDBTitle: x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
101	d1jb7a1	Alignment	not modelled	92.8	7	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
102	c5gqoB_	Alignment	not modelled	92.7	10	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein; PDBTitle: structure of the second single stranded dna binding protein (ssbb)2 from mycobacterium smegmatis
103	c2iheA_	Alignment	not modelled	92.6	21	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
104	d1nnxa_	Alignment	not modelled	92.3	18	Fold: OB-fold Superfamily: Hypothetical protein YgiW Family: Hypothetical protein YgiW
105	c2ihfA_	Alignment	not modelled	92.1	23	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
106	c4gopC_	Alignment	not modelled	91.8	18	PDB header: dna binding protein/dna Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication

						protein a2 heterotrimer bound to ssdna
107	d1qzga_	Alignment	not modelled	91.4	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
108	c3eivB_	Alignment	not modelled	91.1	10	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein 2; PDBTitle: crystal structure of single-stranded dna-binding protein2 from streptomyces coelicolor
109	d1eyga_	Alignment	not modelled	90.6	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
110	c2oceA_	Alignment	not modelled	90.1	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
111	d1se8a_	Alignment	not modelled	90.1	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
112	c1se8A_	Alignment	not modelled	90.1	17	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: structure of single-stranded dna-binding protein (ssb) from d.2 radiodurans
113	c3lgjA_	Alignment	not modelled	90.0	15	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
114	c5odnG_	Alignment	not modelled	88.7	18	PDB header: dna binding protein Chain: G: PDB Molecule: single-stranded dna-binding protein; PDBTitle: salinibacter ruber single-strand binding protein
115	c6gmhM_	Alignment	not modelled	88.5	16	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
116	c1ph4A_	Alignment	not modelled	88.5	8	PDB header: dna binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggtttggcg
117	c1jb7A_	Alignment	not modelled	88.5	8	PDB header: dna-binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
118	c5xgtA_	Alignment	not modelled	88.2	22	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of the n-terminal domain of staphylococcus aureus2 single-stranded dna-binding protein ssba at 1.82 angstrom resolution
119	c1qvca_	Alignment	not modelled	87.6	16	PDB header: dna binding protein Chain: A: PDB Molecule: single stranded dna binding protein monomer; PDBTitle: crystal structure analysis of single stranded dna binding protein2 (ssb) from e.coli
120	d1qvca_	Alignment	not modelled	87.6	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB