
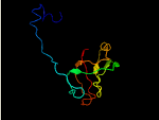

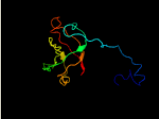
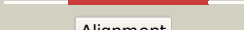

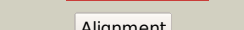

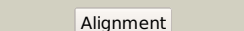













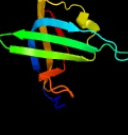

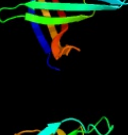


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2694c (-)_3011409_3011777
Date	Wed Aug 7 12:50:34 BST 2019
Unique Job ID	d41e46f7cd577f55

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gm5a2	 Alignment		99.8	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
2	c1gm5A_	 Alignment		99.7	24	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
3	c3e0eA_	 Alignment		99.1	11	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 target mrr110b
4	c3dm3A_	 Alignment		99.0	18	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 mjrr118e
5	c4owxB_	 Alignment		98.6	14	PDB header: dna binding protein/dna Chain: B: PDB Molecule: soxs complex subunit b1; PDBTitle: structural basis of soxs1 in complex with a 12nt ssdna
6	c2k50A_	 Alignment		98.6	12	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.
7	c2kenA_	 Alignment		98.6	12	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 mazei. northeast structural3 genomics consortium target mar214a.
8	c2k75A_	 Alignment		98.4	12	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.
9	c4joiA_	 Alignment		98.2	23	PDB header: dna binding protein Chain: A: PDB Molecule: cst complex subunit stn1; PDBTitle: crystal structure of the human telomeric stn1-ten1 complex
10	d1o7ia_	 Alignment		98.1	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
11	c3m4qA_	 Alignment		97.9	21	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase, putative; PDBTitle: entamoeba histolytica asparaginyl-trna synthetase (asnrs)

12	c4gopB	Alignment		97.9	20	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
13	c5zg8A	Alignment		97.8	22	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase; PDBTitle: crystal structure of ttnrs
14	c3bjub	Alignment		97.8	14	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna synthetase
15	c5elnC	Alignment		97.8	14	PDB header: ligase Chain: C: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine
16	c5groA	Alignment		97.8	29	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
17	d1jmca1	Alignment		97.8	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
18	d1e1oa1	Alignment		97.7	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
19	d1bbua1	Alignment		97.7	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
20	d1wjja	Alignment		97.7	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
21	c6ns0A	Alignment	not modelled	97.7	15	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
22	d1xjva1	Alignment	not modelled	97.7	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
23	d1n9wa1	Alignment	not modelled	97.7	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
24	d1l0wa1	Alignment	not modelled	97.7	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
25	c1n9wA	Alignment	not modelled	97.7	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
26	c4h02B	Alignment	not modelled	97.7	13	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of p. falciparum lysyl-trna synthetase
27	c4j15A	Alignment	not modelled	97.6	18	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
28	c3kf6A	Alignment	not modelled	97.6	16	PDB header: structural protein Chain: A: PDB Molecule: protein stn1; PDBTitle: crystal structure of s. pombe stn1-ten1 complex
						PDB header: ligase

29	c3i7fA_	Alignment	not modelled	97.6	15	Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: aspartyl trna synthetase from entamoeba histolytica
30	c6od8A_	Alignment	not modelled	97.6	20	PDB header: ligase Chain: A: PDB Molecule: putative aspartyl-trna synthetase; PDBTitle: crystal structure of a putative aspartyl-trna synthetase from2 leishmania major friedlin
31	c1b8aB_	Alignment	not modelled	97.6	20	PDB header: ligase Chain: B: PDB Molecule: protein (aspartyl-trna synthetase); PDBTitle: aspartyl-trna synthetase
32	d1b8aa1	Alignment	not modelled	97.5	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
33	c1ynxA_	Alignment	not modelled	97.5	13	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)
34	c4gopC_	Alignment	not modelled	97.5	15	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
35	c4upaA_	Alignment	not modelled	97.5	16	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of entamoeba histolytica lysyl-trna synthetase in2 complex with amppnp
36	c1eqrC_	Alignment	not modelled	97.5	16	PDB header: ligase Chain: C: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of free aspartyl-trna synthetase from2 escherichia coli
37	c5fkvA_	Alignment	not modelled	97.5	17	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)
38	c4wj4A_	Alignment	not modelled	97.5	19	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
39	c1e22A_	Alignment	not modelled	97.5	24	PDB header: ligase Chain: A: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolyzable atp analogue amp-ppc
40	c6i52B_	Alignment	not modelled	97.5	21	PDB header: dna binding protein Chain: B: PDB Molecule: replication factor a protein 2; PDBTitle: yeast rpa bound to ssdna
41	d1eova1	Alignment	not modelled	97.5	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
42	c1xjvA_	Alignment	not modelled	97.5	12	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 (ttagggtag)
43	c4ex5A_	Alignment	not modelled	97.4	19	PDB header: transferase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine
44	d2pi2a1	Alignment	not modelled	97.4	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
45	c2pi2A_	Alignment	not modelled	97.4	18	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
46	d1c0aa1	Alignment	not modelled	97.4	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
47	c5hggD_	Alignment	not modelled	97.3	13	PDB header: ligase/ligase inhibitor Chain: D: PDB Molecule: lysine--trna ligase; PDBTitle: loa loa lysyl-trna synthetase in complex with cladosporin.
48	c1efwA_	Alignment	not modelled	97.3	21	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
49	c3e9hB_	Alignment	not modelled	97.3	26	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
50	c1asyA_	Alignment	not modelled	97.3	13	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
51	c4up8A_	Alignment	not modelled	97.3	16	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of entamoeba histolytica lysyl-trna synthetase apo2 form
52	c1wydB_	Alignment	not modelled	97.2	19	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfobolus tokodaai
53	c1fguA_	Alignment	not modelled	97.2	17	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
54	c4o2dB_	Alignment	not modelled	97.2	20	PDB header: ligase Chain: B: PDB Molecule: aspartate--trna ligase; PDBTitle: crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid

55	c2xqtB	Alignment	not modelled	97.1	16	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
56	c3f2cA	Alignment	not modelled	97.1	17	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
57	c1x55A	Alignment	not modelled	97.1	16	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
58	c4glaD	Alignment	not modelled	97.0	14	PDB header: hydrolase/de novo protein Chain: D: PDB Molecule: obody n18; PDBTitle: obody n18 bound to hen egg-white lysozyme
59	c5v11D	Alignment	not modelled	97.0	23	PDB header: ligase Chain: D: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from mycobacterium ulcerans2 complexed with l-lysine
60	c5xixD	Alignment	not modelled	96.9	27	PDB header: ligase Chain: D: PDB Molecule: asparagine--trna ligase, cytoplasmic; PDBTitle: the canonical domain of human asparaginyl-trna synthetase
61	c4gn5A	Alignment	not modelled	96.9	13	PDB header: de novo protein/hydrolase Chain: A: PDB Molecule: obody am3115; PDBTitle: obody am3115 bound to hen egg-white lysozyme
62	c1k8gC	Alignment	not modelled	96.8	22	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
63	d1jb7a1	Alignment	not modelled	96.7	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
64	c4ah6B	Alignment	not modelled	96.5	19	PDB header: ligase Chain: B: PDB Molecule: aspartate--trna ligase, mitochondrial; PDBTitle: human mitochondrial aspartyl-trna synthetase
65	c6pqhA	Alignment	not modelled	96.5	25	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase; PDBTitle: crystal structure of asparagine-trna ligase from elizabethkingia sp.2 ccug 26117
66	d1krta	Alignment	not modelled	96.4	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
67	c1ph4A	Alignment	not modelled	95.8	19	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
68	c1jb7A	Alignment	not modelled	95.8	19	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
69	c3e0jG	Alignment	not modelled	95.7	18	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
70	c5iheB	Alignment	not modelled	95.2	14	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ii small subunit; PDBTitle: d-family dna polymerase - dp1 subunit (3'-5' proof-reading2 exonuclease)
71	d1jmca2	Alignment	not modelled	92.4	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
72	d1nnxa	Alignment	not modelled	92.0	17	Fold: OB-fold Superfamily: Hypothetical protein YgiW Family: Hypothetical protein YgiW
73	c2cwaA	Alignment	not modelled	90.8	21	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
74	c3e0dA	Alignment	not modelled	90.6	19	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
75	c4jbmA	Alignment	not modelled	90.1	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: interferon-inducible protein aim2; PDBTitle: structure of murine dna binding protein bound with ds dna
76	d2oq0a1	Alignment	not modelled	89.5	12	Fold: OB-fold Superfamily: HIN-2000 domain-like Family: HIN-200/IF120x domain
77	c1qvCA	Alignment	not modelled	88.7	19	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
78	d1qvca	Alignment	not modelled	88.7	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
79	d1eyga	Alignment	not modelled	88.5	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
80	c4l5tB	Alignment	not modelled	87.5	19	PDB header: immune system Chain: B: PDB Molecule: interferon-activable protein 202;

						PDBTitle: crystal structure of the tetrameric p202 hin2
81	c6cqoH_	Alignment	not modelled	87.4	10	PDB header: dna binding protein Chain: H: PDB Molecule: single-stranded dna-binding protein rim1, mitochondrial; PDBTitle: crystal structure of mitochondrial single-stranded dna binding2 proteins from s. cerevisiae (semet labeled), rim1 (form2)
82	c3b6yB_	Alignment	not modelled	87.3	13	PDB header: protein binding Chain: B: PDB Molecule: gamma-interferon-inducible protein ifi-16; PDBTitle: crystal structure of the second hin-200 domain of interferon-inducible2 protein 16
83	c5yzwA_	Alignment	not modelled	87.2	12	PDB header: immune system Chain: A: PDB Molecule: ifi204; PDBTitle: crystal structure of p204 hinb domain
84	c3rn5A_	Alignment	not modelled	87.2	12	PDB header: immune system/dna Chain: A: PDB Molecule: interferon-inducible protein aim2; PDBTitle: structural basis of cytosolic dna recognition by innate immune2 receptors
85	c3eivB_	Alignment	not modelled	86.8	23	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
86	c3k8aA_	Alignment	not modelled	86.5	12	PDB header: dna binding protein Chain: A: PDB Molecule: putative primosomal replication protein; PDBTitle: neisseria gonorrhoeae prib
87	c3vdyA_	Alignment	not modelled	86.1	20	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded dna-binding protein ssbb; PDBTitle: b. subtilis ssbb/ssdna
88	c3pgzB_	Alignment	not modelled	85.9	13	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of a single strand binding protein (ssb) from2 bartonella henselae
89	c6bwyA_	Alignment	not modelled	85.7	12	PDB header: hydrolase Chain: A: PDB Molecule: protection of telomeres protein 1, dna dc->du-editing PDBTitle: dna substrate selection by apobec3g
90	c5xgtA_	Alignment	not modelled	85.3	24	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
91	c5yzpA_	Alignment	not modelled	83.2	17	PDB header: immune system Chain: A: PDB Molecule: ifi204; PDBTitle: crystal structure of p204 hina domain
92	c1z9fA_	Alignment	not modelled	82.5	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
93	c3ulpC_	Alignment	not modelled	82.3	22	PDB header: dna binding protein/dna Chain: C: PDB Molecule: single-strand binding protein; PDBTitle: plasmodium falciparum ssb complex with ssdna
94	c3mxnB_	Alignment	not modelled	81.9	17	PDB header: replication Chain: B: PDB Molecule: recq-mediated genome instability protein 2; PDBTitle: crystal structure of the rmi core complex
95	c3kojA_	Alignment	not modelled	81.8	9	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.
96	d1qzga_	Alignment	not modelled	81.4	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
97	c2oq0D_	Alignment	not modelled	80.7	12	PDB header: protein binding Chain: D: PDB Molecule: gamma-interferon-inducible protein ifi-16; PDBTitle: crystal structure of the first hin-200 domain of interferon-inducible2 protein 16
98	c3nbiA_	Alignment	not modelled	80.6	11	PDB header: protein binding Chain: A: PDB Molecule: recq-mediated genome instability protein 1; PDBTitle: crystal structure of human rmi1 n-terminus
99	c3lgiA_	Alignment	not modelled	80.1	20	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
100	d1sr3a_	Alignment	not modelled	79.6	21	Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE
101	c5gqoB_	Alignment	not modelled	78.3	22	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
102	c5odnG_	Alignment	not modelled	78.0	18	PDB header: dna binding protein Chain: G: PDB Molecule: single-stranded dna-binding protein; PDBTitle: salinibacter ruber single-strand binding protein
103	d1txya_	Alignment	not modelled	77.9	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
104	c3tqyA_	Alignment	not modelled	77.7	15	PDB header: transferase Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii
105	c1se8A_	Alignment	not modelled	76.6	15	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
						Fold: OB-fold

106	d1se8a_	Alignment	not modelled	76.6	15	Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
107	c5z7dA_	Alignment	not modelled	75.5	17	PDB header: immune system Chain: A: PDB Molecule: interferon-activable protein 204; PDBTitle: p204hinab-dsdna complex structure
108	d1ue1a_	Alignment	not modelled	71.9	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
109	c2vw9B_	Alignment	not modelled	70.9	25	PDB header: dna-binding protein Chain: B: PDB Molecule: single-stranded dna binding protein; PDBTitle: single stranded dna binding protein complex from2 helicobacter pylori
110	c2wkdA_	Alignment	not modelled	70.8	29	PDB header: dna binding protein Chain: A: PDB Molecule: orf34p2; PDBTitle: crystal structure of a double ile-to-met mutant of protein orf34 from2 lactococcus phage p2
111	c3fhwB_	Alignment	not modelled	67.7	13	PDB header: dna binding protein Chain: B: PDB Molecule: primosomal replication protein n; PDBTitle: crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
112	c4damA_	Alignment	not modelled	66.4	20	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein 1; PDBTitle: crystal structure of small single-stranded dna-binding protein from2 streptomyces coelicolor
113	c2iheA_	Alignment	not modelled	63.0	17	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
114	c5gvdB_	Alignment	not modelled	61.0	14	PDB header: protein binding Chain: B: PDB Molecule: tudor domain-containing protein 3; PDBTitle: human tdrd3 duf1767-ob domains
115	d3ulla_	Alignment	not modelled	59.0	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
116	d1l1oc_	Alignment	not modelled	56.4	5	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
117	c3en2A_	Alignment	not modelled	55.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable primosomal replication protein n; PDBTitle: three-dimensional structure of the protein prib from ralstonia2 solanacearum at the resolution 2.3a. northeast structural genomics3 consortium target rsr213c.
118	c2ihfA_	Alignment	not modelled	55.2	18	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
119	c6bs8C_	Alignment	not modelled	52.2	12	PDB header: hydrolase Chain: C: PDB Molecule: replicative dna helicase; PDBTitle: the class 3 dnab intein from mycobacterium smegmatis
120	c1ue7A_	Alignment	not modelled	50.5	20	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis