















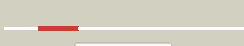











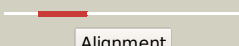

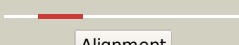
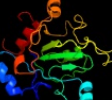
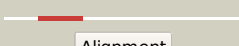

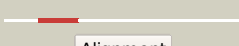






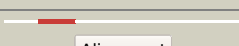

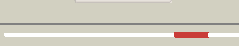
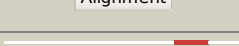
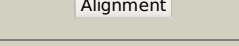
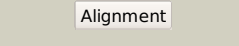




# Phyre2

|               |                                 |
|---------------|---------------------------------|
| Email         | mdejesus@rockefeller.edu        |
| Description   | RVBD1547_(dnaE)_1747700_1751254 |
| Date          | Fri Aug 2 13:30:13 BST 2019     |
| Unique Job ID | 94a68f2e773b2972                |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c5fkvA_</a> |  Alignment   |    | 100.0      | 37     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha;<br><b>PDBTitle:</b> cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)             |
| 2  | <a href="#">c3e0dA_</a> |  Alignment   |    | 100.0      | 42     | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha;<br><b>PDBTitle:</b> insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit              |
| 3  | <a href="#">c5lewA_</a> |  Alignment   |    | 100.0      | 99     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha;<br><b>PDBTitle:</b> dna polymerase   |
| 4  | <a href="#">c2hnhA_</a> |  Alignment   |    | 100.0      | 40     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii alpha subunit;<br><b>PDBTitle:</b> crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii  |
| 5  | <a href="#">c3f2cA_</a> |  Alignment |  | 100.0      | 27     | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> geobacillus kaustophilus dna polc;<br><b>PDBTitle:</b> dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn  |
| 6  | <a href="#">c4gx9A_</a> |  Alignment |  | 100.0      | 37     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit epsilon,dna polymerase iii<br><b>PDBTitle:</b> crystal structure of a dna polymerase iii alpha-epsilon chimera  |
| 7  | <a href="#">c3e0fA_</a> |  Alignment |  | 99.8       | 16     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent phosphoesterase;<br><b>PDBTitle:</b> crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution |
| 8  | <a href="#">c2wjeA_</a> |  Alignment |  | 99.7       | 17     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase cpsb;<br><b>PDBTitle:</b> crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.   |
| 9  | <a href="#">c3dcpB_</a> |  Alignment |  | 99.7       | 20     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphatase;<br><b>PDBTitle:</b> crystal structure of the putative histidinol phosphatase hisk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.             |
| 10 | <a href="#">c2yb1A_</a> |  Alignment |  | 99.7       | 17     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase;<br><b>PDBTitle:</b> structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.   |
| 11 | <a href="#">c3qy6A_</a> |  Alignment |  | 99.6       | 20     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase ywqe;<br><b>PDBTitle:</b> crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases              |

|    |                         |   |   |      |    |   |
|----|-------------------------|---|---|------|----|---|
| 12 | <a href="#">c2yz5B_</a> |  Alignment   |    | 99.6 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> histidinol phosphatase;<br><b>PDBTitle:</b> histidinol phosphate phosphatase complexed with phosphate   |
| 13 | <a href="#">c3umuA_</a> |  Alignment   |    | 99.5 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphatase;<br><b>PDBTitle:</b> crystal structure of l-histidinol phosphate phosphatase (hisk) from <i>lactococcus lactis</i> subsp. <i>lactis</i> il1403 complexed with zn, phosphate3 and l-histidinol  |
| 14 | <a href="#">c3auoB_</a> |  Alignment   |    | 99.5 | 15 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase beta family (x family);<br><b>PDBTitle:</b> dna polymerase x from <i>thermus thermophilus</i> hb8 ternary complex with 1-2 nt gapped dna and ddgtp   |
| 15 | <a href="#">d1m65a_</a> |  Alignment   |    | 99.3 | 18 | <b>Fold:</b> 7-stranded beta/alpha barrel<br><b>Superfamily:</b> PHP domain-like<br><b>Family:</b> PHP domain   |
| 16 | <a href="#">c2anuA_</a> |  Alignment   |    | 99.2 | 19 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm0559;<br><b>PDBTitle:</b> crystal structure of predicted metal-dependent phosphoesterase (php2 family) (tm0559) from <i>thermotoga maritima</i> at 2.40 a resolution   |
| 17 | <a href="#">d2anuA1</a> |  Alignment   |    | 99.2 | 19 | <b>Fold:</b> 7-stranded beta/alpha barrel<br><b>Superfamily:</b> PHP domain-like<br><b>Family:</b> PHP domain   |
| 18 | <a href="#">c5zb8B_</a> |  Alignment |  | 99.1 | 19 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> pfuendoq;<br><b>PDBTitle:</b> crystal structure of the novel lesion-specific endonuclease pfuendoq2 from <i>pyrococcus furiosus</i>   |
| 19 | <a href="#">c2w9mB_</a> |  Alignment |  | 99.0 | 18 | <b>PDB header:</b> dna replication<br><b>Chain:</b> B: <b>PDB Molecule:</b> polymerase x;<br><b>PDBTitle:</b> structure of family x dna polymerase from <i>deinococcus2</i> radiodurans   |
| 20 | <a href="#">c3e38A_</a> |  Alignment |  | 98.8 | 29 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> two-domain protein containing predicted php-like metal-<br><b>PDBTitle:</b> crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bvu_3505) from <i>bacteroides3</i> vulgatus atcc 8482 at 2.20 a resolution |
| 21 | <a href="#">c4joiA_</a> |  Alignment | not modelled  | 97.8 | 20 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cst complex subunit stn1;<br><b>PDBTitle:</b> crystal structure of the human telomeric stn1-ten1 complex  |
| 22 | <a href="#">c6k0aC_</a> |  Alignment | not modelled  | 97.7 | 14 | <b>PDB header:</b> rna binding protein/rna<br><b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease p protein component 3;<br><b>PDBTitle:</b> cryo-em structure of an archaeal ribonuclease p   |
| 23 | <a href="#">d1e1oa1</a> |  Alignment | not modelled  | 97.6 | 12 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain  |
| 24 | <a href="#">c3kf6A_</a> |  Alignment | not modelled  | 97.6 | 21 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein stn1;<br><b>PDBTitle:</b> crystal structure of <i>s. pombe</i> stn1-ten1 complex   |
| 25 | <a href="#">d1c0aa1</a> |  Alignment | not modelled  | 97.6 | 24 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain  |
| 26 | <a href="#">c6ns0A_</a> |  Alignment | not modelled  | 97.6 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from <i>chlamydia trachomatis2</i> complexed with l-lysine and cladosporin   |
| 27 | <a href="#">c5hggD_</a> |  Alignment | not modelled  | 97.5 | 13 | <b>PDB header:</b> ligase/ligase inhibitor<br><b>Chain:</b> D: <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> loa loa lysyl-trna synthetase in complex with cladosporin.   |
| 28 | <a href="#">d1b8aa1</a> |  Alignment | not modelled  | 97.5 | 16 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain  |
| 29 | <a href="#">c5zg8A_</a> |  Alignment | not modelled  | 97.5 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asparagine--trna ligase;   |

|    |                         |           |              |      |   |
|----|-------------------------|-----------|--------------|------|---|
|    |                         |           |              |      | <b>PDBTitle:</b> crystal structure of ttnrs   |
| 30 | <a href="#">d1gm5a2</a> | Alignment | not modelled | 97.5 | 17<br><b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> RecG "wedge" domain   |
| 31 | <a href="#">c4upaA</a>  | Alignment | not modelled | 97.5 | 12<br><b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of entamoeba histolytica lysyl-trna synthetase in2 complex with amppnp  |
| 32 | <a href="#">d1bbua1</a> | Alignment | not modelled | 97.5 | 13<br><b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain  |
| 33 | <a href="#">c3i7fA</a>  | Alignment | not modelled | 97.5 | 12<br><b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> aspartyl-trna synthetase;<br><b>PDBTitle:</b> aspartyl trna synthetase from entamoeba histolytica  |
| 34 | <a href="#">c1b8aB</a>  | Alignment | not modelled | 97.5 | 15<br><b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> protein (aspartyl-trna synthetase);<br><b>PDBTitle:</b> aspartyl-trna synthetase   |
| 35 | <a href="#">c4ex5A</a>  | Alignment | not modelled | 97.5 | 11<br><b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine  |
| 36 | <a href="#">c4h02B</a>  | Alignment | not modelled | 97.5 | 12<br><b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> lysyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of p. falciparum lysyl-trna synthetase  |
| 37 | <a href="#">c4gopB</a>  | Alignment | not modelled | 97.5 | 20<br><b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> B; <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> structure and conformational change of a replication protein a2 heterotrimer bound to ssdna                                 |
| 38 | <a href="#">c3bjuB</a>  | Alignment | not modelled | 97.5 | 14<br><b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> lysyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of tetrameric form of human lysyl-trna synthetase   |
| 39 | <a href="#">c4owxB</a>  | Alignment | not modelled | 97.5 | 15<br><b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> B; <b>PDB Molecule:</b> soxs complex subunit b1;<br><b>PDBTitle:</b> structural basis of soxs1 in complex with a 12nt ssdna   |
| 40 | <a href="#">c4up8A</a>  | Alignment | not modelled | 97.4 | 15<br><b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of entamoeba histolytica lysyl-trna synthetase apo2 form  |
| 41 | <a href="#">c1x55A</a>  | Alignment | not modelled | 97.4 | 16<br><b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> asparaginyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue                        |
| 42 | <a href="#">d2edua1</a> | Alignment | not modelled | 97.4 | 22<br><b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> RuvA domain 2-like<br><b>Family:</b> ComEA-like   |
| 43 | <a href="#">c3e9hB</a>  | Alignment | not modelled | 97.4 | 17<br><b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> lysyl-trna synthetase;<br><b>PDBTitle:</b> lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine   |
| 44 | <a href="#">c5elnC</a>  | Alignment | not modelled | 97.4 | 12<br><b>PDB header:</b> ligase<br><b>Chain:</b> C; <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine   |
| 45 | <a href="#">c5vl1D</a>  | Alignment | not modelled | 97.4 | 25<br><b>PDB header:</b> ligase<br><b>Chain:</b> D; <b>PDB Molecule:</b> lysine--trna ligase;<br><b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from mycobacterium ulcerans2 complexed with l-lysine   |
| 46 | <a href="#">c4j15A</a>  | Alignment | not modelled | 97.4 | 13<br><b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> aspartate--trna ligase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex                              |
| 47 | <a href="#">c5groA</a>  | Alignment | not modelled | 97.3 | 19<br><b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> aspartate--trna(asp/asn) ligase;<br><b>PDBTitle:</b> crystal structure of the n-terminal anticodon-binding domain of non-2 discriminating aspartyl-trna synthetase from helicobacter pylori        |
| 48 | <a href="#">c1eqrC</a>  | Alignment | not modelled | 97.3 | 24<br><b>PDB header:</b> ligase<br><b>Chain:</b> C; <b>PDB Molecule:</b> aspartyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of free aspartyl-trna synthetase from2 escherichia coli  |
| 49 | <a href="#">c4o2dB</a>  | Alignment | not modelled | 97.3 | 23<br><b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> aspartate--trna ligase;<br><b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid   |
| 50 | <a href="#">c6od8A</a>  | Alignment | not modelled | 97.3 | 19<br><b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> putative aspartyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of a putative aspartyl-trna synthetase from2 leishmania major friedlin  |
| 51 | <a href="#">c3dm3A</a>  | Alignment | not modelled | 97.3 | 17<br><b>PDB header:</b> replication<br><b>Chain:</b> A; <b>PDB Molecule:</b> replication factor a;<br><b>PDBTitle:</b> crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjrl18e |
| 52 | <a href="#">c2xgtB</a>  | Alignment | not modelled | 97.2 | 17<br><b>PDB header:</b> ligase<br><b>Chain:</b> B; <b>PDB Molecule:</b> asparaginyl-trna synthetase, cytoplasmic;<br><b>PDBTitle:</b> asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate                      |
| 53 | <a href="#">c3m4qA</a>  | Alignment | not modelled | 97.2 | 11<br><b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> asparaginyl-trna synthetase, putative;<br><b>PDBTitle:</b> entamoeba histolytica asparaginyl-trna synthetase (asnrs)   |
| 54 | <a href="#">c4gn5A</a>  | Alignment | not modelled | 97.2 | 18<br><b>PDB header:</b> de novo protein/hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> obody am3l15;<br><b>PDBTitle:</b> obody am3l15 bound to hen egg-white lysozyme  |
|    |                         |           |              |      | <b>PDB header:</b> replication  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 55 | <a href="#">c3e0eA_</a> | Alignment | not modelled | 97.2 | 11 | <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a;<br><b>PDBTitle:</b> crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targ mrr110b  |
| 56 | <a href="#">c1wydB_</a> | Alignment | not modelled | 97.2 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical aspartyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii  |
| 57 | <a href="#">c1e22A_</a> | Alignment | not modelled | 97.2 | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lysyl-trna synthetase;<br><b>PDBTitle:</b> lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp  |
| 58 | <a href="#">d1l0wa1</a> | Alignment | not modelled | 97.1 | 14 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain  |
| 59 | <a href="#">c5xixD_</a> | Alignment | not modelled | 97.1 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> asparagine--trna ligase, cytoplasmic;<br><b>PDBTitle:</b> the canonical domain of human asparaginyl-trna synthetase  |
| 60 | <a href="#">c4wj4A_</a> | Alignment | not modelled | 97.1 | 23 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartate--trna(asp/asn) ligase;<br><b>PDBTitle:</b> crystal structure of non-discriminating aspartyl-trna synthetase from2 pseudomonas aeruginosa complexed with trna(asn) and aspartic acid  |
| 61 | <a href="#">c2k50A_</a> | Alignment | not modelled | 97.1 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> replication factor a related protein;<br><b>PDBTitle:</b> solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a. |
| 62 | <a href="#">d2pi2a1</a> | Alignment | not modelled | 97.1 | 17 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 63 | <a href="#">c1asyA_</a> | Alignment | not modelled | 97.0 | 12 | <b>PDB header:</b> complex (aminoacyl-trna synthase/trna)<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase;<br><b>PDBTitle:</b> class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp   |
| 64 | <a href="#">d1n9wa1</a> | Alignment | not modelled | 97.0 | 18 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain  |
| 65 | <a href="#">d1eova1</a> | Alignment | not modelled | 97.0 | 13 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain  |
| 66 | <a href="#">c2pi2A_</a> | Alignment | not modelled | 97.0 | 17 | <b>PDB header:</b> replication, dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a 32 kda subunit;<br><b>PDBTitle:</b> full-length replication protein a subunits rpa14 and rpa32   |
| 67 | <a href="#">c1efwA_</a> | Alignment | not modelled | 96.9 | 16 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase;<br><b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli  |
| 68 | <a href="#">c4glaD_</a> | Alignment | not modelled | 96.8 | 19 | <b>PDB header:</b> hydrolase/de novo protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> obody n18;<br><b>PDBTitle:</b> obody n18 bound to hen egg-white lysozyme  |
| 69 | <a href="#">d1o7ia_</a> | Alignment | not modelled | 96.8 | 20 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 70 | <a href="#">c1n9wA_</a> | Alignment | not modelled | 96.7 | 15 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase 2;<br><b>PDBTitle:</b> crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus   |
| 71 | <a href="#">c4ah6B_</a> | Alignment | not modelled | 96.7 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aspartate--trna ligase, mitochondrial;<br><b>PDBTitle:</b> human mitochondrial aspartyl-trna synthetase  |
| 72 | <a href="#">c3vdyA_</a> | Alignment | not modelled | 96.7 | 19 | <b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein ssbb;<br><b>PDBTitle:</b> b. subtilis ssbb/ssdna  |
| 73 | <a href="#">c3kf8C_</a> | Alignment | not modelled | 96.6 | 15 | <b>PDB header:</b> structural protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein stn1;<br><b>PDBTitle:</b> crystal structure of c. tropicalis stn1-ten1 complex   |
| 74 | <a href="#">c5iheB_</a> | Alignment | not modelled | 96.6 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase ii small subunit;<br><b>PDBTitle:</b> d-family dna polymerase - dp1 subunit (3'-5' proof-reading2 exonuclease)   |
| 75 | <a href="#">d2i5ha1</a> | Alignment | not modelled | 96.5 | 15 | <b>Fold:</b> AF1531-like<br><b>Superfamily:</b> AF1531-like<br><b>Family:</b> AF1531-like   |
| 76 | <a href="#">c2i5hA_</a> | Alignment | not modelled | 96.5 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1531;<br><b>PDBTitle:</b> crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655  |
| 77 | <a href="#">c3eivB_</a> | Alignment | not modelled | 96.4 | 16 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> single-stranded dna-binding protein 2;<br><b>PDBTitle:</b> crystal structure of single-stranded dna-binding protein2 from streptomyces coelicolor   |
| 78 | <a href="#">c6i52B_</a> | Alignment | not modelled | 96.3 | 18 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> replication factor a protein 2;<br><b>PDBTitle:</b> yeast rpa bound to ssdna  |
| 79 | <a href="#">c1z9fA_</a> | Alignment | not modelled | 96.3 | 15 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-strand binding protein;<br><b>PDBTitle:</b> crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution   |
| 80 | <a href="#">d1xjva1</a> | Alignment | not modelled | 96.3 | 14 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
|    |                         |           |              |      |    | <b>PDB header:</b> transferase  |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
| 81  | <a href="#">c3tqvA</a>  | Alignment | not modelled | 96.3 | 24 | <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii   |
| 82  | <a href="#">c1gm5A</a>  | Alignment | not modelled | 96.3 | 15 | <b>PDB header:</b> helicase<br><b>Chain:</b> A: <b>PDB Molecule:</b> recg; <b>PDBTitle:</b> structure of recg bound to three-way dna junction   |
| 83  | <a href="#">c5o19A</a>  | Alignment | not modelled | 96.3 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor, mitochondrial; <b>PDBTitle:</b> structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain   |
| 84  | <a href="#">c1ynxA</a>  | Alignment | not modelled | 96.2 | 16 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> replication factor-a protein 1; <b>PDBTitle:</b> solution structure of dna binding domain a (dbd-a) of2 s.cerevisiae replication protein a (rpa)  |
| 85  | <a href="#">c2k75A</a>  | Alignment | not modelled | 96.2 | 20 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ta0387; <b>PDBTitle:</b> solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.                     |
| 86  | <a href="#">c2cwaA</a>  | Alignment | not modelled | 96.1 | 17 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-strand binding protein; <b>PDBTitle:</b> crystal structure of the single-stranded dna binding protein from2 thermus thermophilus hb8   |
| 87  | <a href="#">d1krta</a>  | Alignment | not modelled | 96.1 | 14 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Anticodon-binding domain  |
| 88  | <a href="#">d1v1qa</a>  | Alignment | not modelled | 96.0 | 16 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 89  | <a href="#">c5xgtA</a>  | Alignment | not modelled | 96.0 | 18 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of staphylococcus aureus2 single-stranded dna-binding protein ssba at 1.82 angstrom resolution                 |
| 90  | <a href="#">c2kenA</a>  | Alignment | not modelled | 96.0 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein; <b>PDBTitle:</b> solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazel. northeast structural3 genomics consortium target mar214a. |
| 91  | <a href="#">d1eyga</a>  | Alignment | not modelled | 95.8 | 20 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 92  | <a href="#">c5odnG</a>  | Alignment | not modelled | 95.8 | 15 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> G: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> salinibacter ruber single-strand binding protein  |
| 93  | <a href="#">c1xjvA</a>  | Alignment | not modelled | 95.7 | 14 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> protection of telomeres 1; <b>PDBTitle:</b> crystal structure of human pot1 bound to telomeric single-2 stranded dna (ttagggtag)  |
| 94  | <a href="#">d1wjja</a>  | Alignment | not modelled | 95.7 | 17 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 95  | <a href="#">c2iheA</a>  | Alignment | not modelled | 95.7 | 15 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus  |
| 96  | <a href="#">d3bzka1</a> | Alignment | not modelled | 95.6 | 18 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> RuvA domain 2-like<br><b>Family:</b> Tex HHH-containing domain-like   |
| 97  | <a href="#">d1qvca</a>  | Alignment | not modelled | 95.6 | 20 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 98  | <a href="#">c1qvca</a>  | Alignment | not modelled | 95.6 | 20 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> single stranded dna binding protein monomer; <b>PDBTitle:</b> crystal structure analysis of single stranded dna binding protein2 (ssb) from e.coli  |
| 99  | <a href="#">d1jmca1</a> | Alignment | not modelled | 95.6 | 17 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 100 | <a href="#">c1fguA</a>  | Alignment | not modelled | 95.5 | 18 | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a 70 kda dna-binding subunit; <b>PDBTitle:</b> ssdna-binding domain of the large subunit of replication2 protein a  |
| 101 | <a href="#">c3kojA</a>  | Alignment | not modelled | 95.4 | 8  | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ycf41; <b>PDBTitle:</b> crystal structure of the ssb domain of q5n255_synp6 protein from2 synechococcus sp. northeast structural genomics consortium target3 snr59a.                    |
| 102 | <a href="#">c2ihfA</a>  | Alignment | not modelled | 95.4 | 13 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus                               |
| 103 | <a href="#">d1se8a</a>  | Alignment | not modelled | 95.0 | 14 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 104 | <a href="#">c1se8A</a>  | Alignment | not modelled | 95.0 | 14 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-strand binding protein; <b>PDBTitle:</b> structure of single-stranded dna-binding protein (ssb) from d.2 radiodurans   |
| 105 | <a href="#">d1ue1a</a>  | Alignment | not modelled | 94.9 | 14 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |

|     |                         |           |              |      |    |   |
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| 106 | <a href="#">c1s5lu_</a> | Alignment | not modelled | 94.9 | 17 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> U: <b>PDB Molecule:</b> photosystem ii 12 kda extrinsic protein;<br><b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center   |
| 107 | <a href="#">c5gqoB_</a> | Alignment | not modelled | 94.8 | 10 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> single-stranded dna-binding protein;<br><b>PDBTitle:</b> structure of the second single stranded dna binding protein (ssbb)2 from mycobacterium smegmatis   |
| 108 | <a href="#">d3ulla_</a> | Alignment | not modelled | 94.7 | 15 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 109 | <a href="#">c3lgjA_</a> | Alignment | not modelled | 94.6 | 15 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein;<br><b>PDBTitle:</b> crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae   |
| 110 | <a href="#">c1ue7A_</a> | Alignment | not modelled | 94.5 | 13 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-strand binding protein;<br><b>PDBTitle:</b> crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis  |
| 111 | <a href="#">d1qzga_</a> | Alignment | not modelled | 94.3 | 19 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 112 | <a href="#">c5vbnE_</a> | Alignment | not modelled | 94.3 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> E: <b>PDB Molecule:</b> dna polymerase epsilon subunit 2;<br><b>PDBTitle:</b> crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit   |
| 113 | <a href="#">c1k8gC_</a> | Alignment | not modelled | 94.2 | 8  | <b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> C: <b>PDB Molecule:</b> telomere-binding protein alpha subunit;<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of oxytricha2 nova telomere end binding protein alpha subunit both3 uncomplexed and complexed with telomeric ssdna |
| 114 | <a href="#">c3pgzB_</a> | Alignment | not modelled | 94.2 | 14 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> single-stranded dna-binding protein;<br><b>PDBTitle:</b> crystal structure of a single strand binding protein (ssb) from2 bartonella henselae   |
| 115 | <a href="#">c2vw9B_</a> | Alignment | not modelled | 94.0 | 20 | <b>PDB header:</b> dna-binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> single-stranded dna binding protein;<br><b>PDBTitle:</b> single stranded dna binding protein complex from2 helicobacter pylori  |
| 116 | <a href="#">d1jb7a1</a> | Alignment | not modelled | 93.9 | 8  | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB   |
| 117 | <a href="#">c6hv9B_</a> | Alignment | not modelled | 93.9 | 22 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase epsilon subunit b;<br><b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna   |
| 118 | <a href="#">c6cqoH_</a> | Alignment | not modelled | 93.8 | 15 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> H: <b>PDB Molecule:</b> single-stranded dna-binding protein rim1, mitochondrial;<br><b>PDBTitle:</b> crystal structure of mitochondrial single-stranded dna binding2 proteins from s. cerevisiae (semet labeled), rim1 (form2)                        |
| 119 | <a href="#">c6bwyA_</a> | Alignment | not modelled | 93.5 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protection of telomeres protein 1, dna dc->du-editing<br><b>PDBTitle:</b> dna substrate selection by apobec3g   |
| 120 | <a href="#">d2axtu1</a> | Alignment | not modelled | 93.5 | 17 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> PsbU/PoIX domain-like<br><b>Family:</b> PsbU-like   |