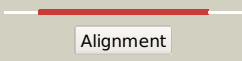



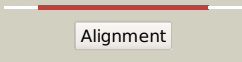





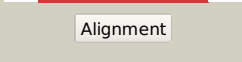

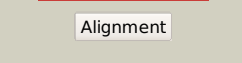

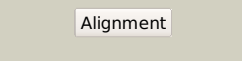

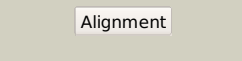

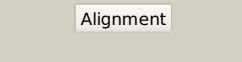

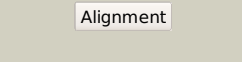



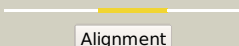
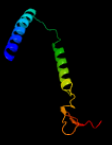


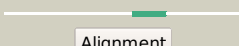

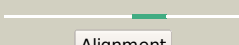

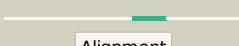










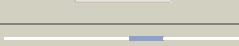
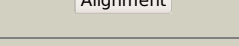
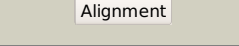




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2834c_(ugpE)_3140497_3141324
 Date Wed Aug 7 12:50:50 BST 2019
 Unique Job ID 8721acdbd2cf0f15

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c4tqvI_ |  |  | 100.0 | 25 | PDB header: transport protein Chain: J; PDB Molecule: algm2; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate |
| 2 | d2r6gg1 |  |  | 100.0 | 29 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 3 | c3fh6F_ |  |  | 100.0 | 15 | PDB header: transport protein Chain: F; PDB Molecule: maltose transport system permease protein malF; PDBTitle: crystal structure of the resting state maltose transporter from e.2 coli |
| 4 | c4tqvI_ |  |  | 100.0 | 17 | PDB header: transport protein Chain: I; PDB Molecule: algm1; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate |
| 5 | c2r6gF_ |  |  | 100.0 | 18 | PDB header: hydrolase/transport protein Chain: F; PDB Molecule: maltose transport system permease protein malF; PDBTitle: the crystal structure of the e. coli maltose transporter |
| 6 | d2onkc1 |  |  | 100.0 | 17 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 7 | c2onkC_ |  |  | 100.0 | 17 | PDB header: membrane protein Chain: C; PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda |
| 8 | d2r6gf2 |  |  | 100.0 | 19 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 9 | d3d31c1 |  |  | 100.0 | 20 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 10 | c3d31D_ |  |  | 100.0 | 20 | PDB header: transport protein Chain: D; PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans |
| 11 | c4ymuC_ |  |  | 100.0 | 13 | PDB header: protein binding/transport protein Chain: C; PDB Molecule: abc-type amino acid transport system, permease component; PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps |

| | | | | | | |
|----|-------------------------|---|---|------|----|--|
| 12 | d3dhwa1 |  Alignment |  | 99.9 | 21 | Fold: MetI-like Superfamily: MetI-like Family: MetI-like |
| 13 | c5kbuA |  Alignment |  | 76.9 | 14 | PDB header: transport protein Chain: A: PDB Molecule: glutamate receptor 2,voltage-dependent calcium channel PDBTitle: cryo-em structure of glua2-2xstz complex at 7.8 angstrom resolution |
| 14 | d2r6gf1 |  Alignment |  | 70.4 | 11 | Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like |
| 15 | c2m8gX |  Alignment |  | 46.7 | 19 | PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators |
| 16 | c1umqA |  Alignment |  | 43.7 | 13 | PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity |
| 17 | d1umqa |  Alignment |  | 43.7 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 18 | c4l5eA |  Alignment |  | 43.5 | 13 | PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain |
| 19 | d1ntca |  Alignment |  | 41.3 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 20 | d1fipa |  Alignment |  | 31.4 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 21 | c3e7ID |  Alignment | not modelled | 26.5 | 10 | PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain |
| 22 | d1etob |  Alignment | not modelled | 26.1 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 23 | d1etxa |  Alignment | not modelled | 25.0 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 24 | c2hx6A |  Alignment | not modelled | 24.6 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb |
| 25 | c2jwaA |  Alignment | not modelled | 22.7 | 21 | PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure |
| 26 | c2ks1A |  Alignment | not modelled | 22.7 | 21 | PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation |
| 27 | d1g2ha |  Alignment | not modelled | 16.1 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like |
| 28 | c1g2hA |  Alignment | not modelled | 16.1 | 10 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c5m7nA_ | Alignment | not modelled | 14.3 | 13 | PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology |
| 30 | c5ir6A_ | Alignment | not modelled | 12.3 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: bd-type quinol oxidase subunit i; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans |
| 31 | c1ojlD_ | Alignment | not modelled | 11.4 | 23 | PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding |
| 32 | c1bctA_ | Alignment | not modelled | 9.8 | 21 | PDB header: photoreceptor Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution |
| 33 | c4huqS_ | Alignment | not modelled | 9.6 | 11 | PDB header: hydrolase Chain: S: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a transporter |
| 34 | c3s1bA_ | Alignment | not modelled | 8.6 | 24 | PDB header: signaling protein Chain: A: PDB Molecule: mini-z; PDBTitle: the development of peptide-based tools for the analysis of2 angiogenesis |
| 35 | c2cw1A_ | Alignment | not modelled | 8.6 | 27 | PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein |
| 36 | c2n2aA_ | Alignment | not modelled | 7.7 | 15 | PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erb2-2; PDBTitle: spatial structure of her2/erb2 dimeric transmembrane domain in the2 presence of cytoplasmic jxtamembrane domains |
| 37 | c4j2nA_ | Alignment | not modelled | 7.1 | 15 | PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis |
| 38 | c4j2nB_ | Alignment | not modelled | 7.1 | 15 | PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis |
| 39 | c2momB_ | Alignment | not modelled | 6.9 | 19 | PDB header: membrane protein Chain: B: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles |
| 40 | c2momC_ | Alignment | not modelled | 6.9 | 19 | PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles |
| 41 | c1pyuD_ | Alignment | not modelled | 6.9 | 15 | PDB header: lyase Chain: D: PDB Molecule: aspartate 1-decarboxylase alfa chain; PDBTitle: processed aspartate decarboxylase mutant with ser25 mutated to cys |
| 42 | c4qiWT_ | Alignment | not modelled | 6.9 | 50 | PDB header: transcription Chain: T: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis |
| 43 | c1twcF_ | Alignment | not modelled | 6.6 | 43 | PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii 23 PDBTitle: rna polymerase ii complexed with gtp |
| 44 | d1twff_ | Alignment | not modelled | 6.5 | 43 | Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6 |
| 45 | c2pmzW_ | Alignment | not modelled | 6.3 | 50 | PDB header: translation, transferase Chain: W: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus |
| 46 | d1cf7a_ | Alignment | not modelled | 5.9 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp |
| 47 | c4xtnJ_ | Alignment | not modelled | 5.5 | 7 | PDB header: membrane protein Chain: J: PDB Molecule: sodium pumping rhodopsin; PDBTitle: crystal structure of the light-driven sodium pump kr2 in the2 pentameric red form, ph 4.9 |
| 48 | c6eyuA_ | Alignment | not modelled | 5.4 | 14 | PDB header: membrane protein Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: crystal structure of the inward h(+) pump xenorhodopsin |
| 49 | d2ns0a1 | Alignment | not modelled | 5.3 | 28 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like |
| 50 | d1qkla_ | Alignment | not modelled | 5.3 | 43 | Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6 |