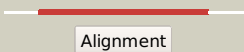

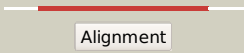

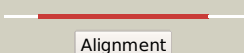

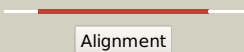






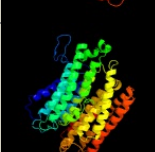

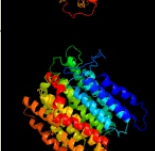


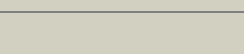
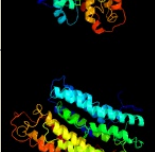

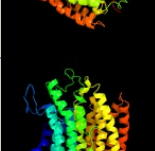
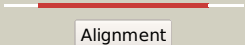

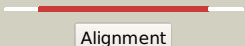

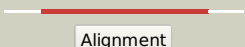



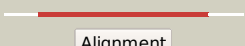

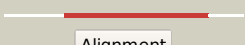
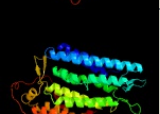





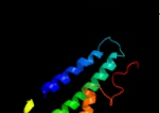
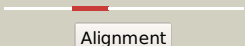
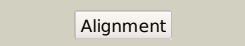

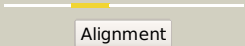
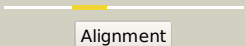
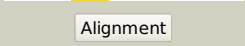
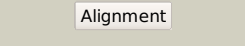
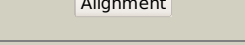


# Phyre2

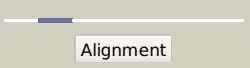
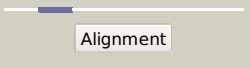
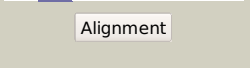
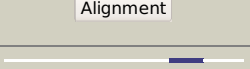
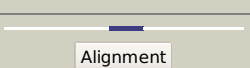
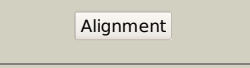
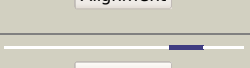
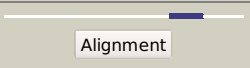
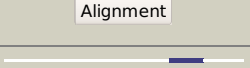
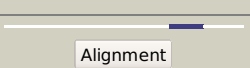
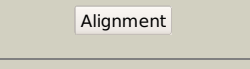
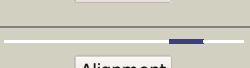
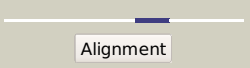
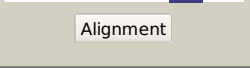
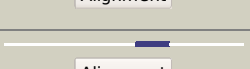
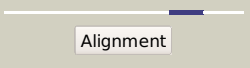
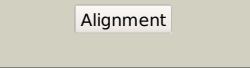
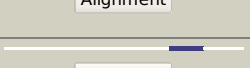
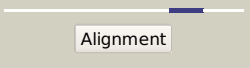

|               |                                 |
|---------------|---------------------------------|
| Email         | mdejesus@rockefeller.edu        |
| Description   | RVBD3158_(nuoN)_3525787_3527382 |
| Date          | Thu Aug 8 16:20:34 BST 2019     |
| Unique Job ID | f69f848f9ab6609f                |

Detailed template information

| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                             |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3rkoL_</a> |  Alignment   |    | 100.0      | 19     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> L; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit l;<br><b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 2  | <a href="#">c4heaT_</a> |  Alignment   |    | 100.0      | 21     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> T; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 12;<br><b>PDBTitle:</b> crystal structure of the entire respiratory complex i from thermus2 thermophilus                          |
| 3  | <a href="#">c6humB_</a> |  Alignment   |    | 100.0      | 34     | <b>PDB header:</b> proton transport<br><b>Chain:</b> B; <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit 2;<br><b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus                         |
| 4  | <a href="#">c3rkoM_</a> |  Alignment   |   | 100.0      | 18     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> M; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit m;<br><b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 5  | <a href="#">c6humF_</a> |  Alignment |  | 100.0      | 21     | <b>PDB header:</b> proton transport<br><b>Chain:</b> F; <b>PDB Molecule:</b> nadh dehydrogenase subunit 5;<br><b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus                                     |
| 6  | <a href="#">c3rkoN_</a> |  Alignment |  | 100.0      | 34     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> N; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit n;<br><b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 7  | <a href="#">c6gcs5_</a> |  Alignment |  | 100.0      | 14     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> 5; <b>PDB Molecule:</b> nd5 subunit (nu5m);<br><b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica                                                           |
| 8  | <a href="#">c6humD_</a> |  Alignment |  | 100.0      | 23     | <b>PDB header:</b> proton transport<br><b>Chain:</b> D; <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase chain 4 1;<br><b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus                         |
| 9  | <a href="#">c4he8M_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> M; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 13;<br><b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus              |
| 10 | <a href="#">c6gcs4_</a> |  Alignment |  | 100.0      | 17     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> 4; <b>PDB Molecule:</b> nd4 subunit (nu4m);<br><b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica                                                           |
| 11 | <a href="#">c5ldwL_</a> |  Alignment |  | 100.0      | 15     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> L; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 5;<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class1                                                      |

|    |                         |                                                                                               |                                                                                     |       |    |                                                                                                                                                                                                                                                  |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|-------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c6cfwH_</a> |  Alignment    |     | 100.0 | 23 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> H: <b>PDB Molecule:</b> monovalent cation/h+ antiporter subunit d;<br><b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase                                         |
| 13 | <a href="#">c6g2jL_</a> |  Alignment   |    | 100.0 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> L: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 5;<br><b>PDBTitle:</b> mouse mitochondrial complex i in the active state                                                         |
| 14 | <a href="#">c5ldwM_</a> |  Alignment   |    | 100.0 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> M: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4;<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class1                                                      |
| 15 | <a href="#">c4he8I_</a> |  Alignment   |    | 100.0 | 37 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> I: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 14;<br><b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus              |
| 16 | <a href="#">c6gcs2_</a> |  Alignment   |    | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> 2: <b>PDB Molecule:</b> nd2 subunit (nu2m);<br><b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica                                                           |
| 17 | <a href="#">c5xtjd_</a> |  Alignment   |    | 100.0 | 21 | <b>PDB header:</b> oxidoreductase/electron transport<br><b>Chain:</b> I: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit<br><b>PDBTitle:</b> cryo-em structure of human respiratory complex i                    |
| 18 | <a href="#">c6g2jN_</a> |  Alignment |   | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> N: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 2;<br><b>PDBTitle:</b> mouse mitochondrial complex i in the active state                                                         |
| 19 | <a href="#">c5ldwN_</a> |  Alignment |  | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> N: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 2;<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class1                                                      |
| 20 | <a href="#">c6gcs1_</a> |  Alignment |  | 92.0  | 9  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> 1: <b>PDB Molecule:</b> nd1 subunit (nu1m);<br><b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica                                                           |
| 21 | <a href="#">c4heaK_</a> |  Alignment | not modelled                                                                        | 91.8  | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> K: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 11;<br><b>PDBTitle:</b> crystal structure of the entire respiratory complex i from thermus2 thermophilus                          |
| 22 | <a href="#">c5lc5H_</a> |  Alignment | not modelled                                                                        | 91.3  | 9  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 1;<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class2                                                      |
| 23 | <a href="#">c6humE_</a> |  Alignment | not modelled                                                                        | 85.6  | 20 | <b>PDB header:</b> proton transport<br><b>Chain:</b> E: <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit 4l;<br><b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus                        |
| 24 | <a href="#">c6cfwG_</a> |  Alignment | not modelled                                                                        | 77.7  | 13 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> G: <b>PDB Molecule:</b> monovalent cation/h+ antiporter subunit c;<br><b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase                                         |
| 25 | <a href="#">c6gcsL_</a> |  Alignment | not modelled                                                                        | 73.8  | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> L: <b>PDB Molecule:</b> nd4l subunit (nulm);<br><b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica                                                          |
| 26 | <a href="#">c3rkoK_</a> |  Alignment | not modelled                                                                        | 72.8  | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> K: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit k;<br><b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 27 | <a href="#">c6g2jK_</a> |  Alignment | not modelled                                                                        | 60.9  | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> K: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4l;<br><b>PDBTitle:</b> mouse mitochondrial complex i in the active state                                                        |
| 28 | <a href="#">c6cfwM_</a> |  Alignment | not modelled                                                                        | 38.0  | 9  | <b>PDB header:</b> membrane protein<br><b>Chain:</b> M: <b>PDB Molecule:</b> mbh13 nadh dehydrogenase subunit;<br><b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase                                                  |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                     |
|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c5lc5K_</a> | Alignment | not modelled | 34.9 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> K: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4;<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class2                                                         |
| 30 | <a href="#">c5ldwK_</a> | Alignment | not modelled | 34.9 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> K: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4;<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class1                                                         |
| 31 | <a href="#">c2l3iA_</a> | Alignment | not modelled | 28.0 | 50 | <b>PDB header:</b> antimicrobial protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> aoxki4a, antimicrobial peptide in spider venom;<br><b>PDBTitle:</b> ooxki4a, spider derived antimicrobial peptide                                                 |
| 32 | <a href="#">d1a6qa1</a> | Alignment | not modelled | 26.1 | 24 | <b>Fold:</b> Another 3-helical bundle<br><b>Superfamily:</b> Protein serine/threonine phosphatase 2C, C-terminal domain<br><b>Family:</b> Protein serine/threonine phosphatase 2C, C-terminal domain                                                |
| 33 | <a href="#">c6humA_</a> | Alignment | not modelled | 15.8 | 14 | <b>PDB header:</b> proton transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit 1;<br><b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus                            |
| 34 | <a href="#">d1s1qa_</a> | Alignment | not modelled | 14.5 | 31 | <b>Fold:</b> UBC-like<br><b>Superfamily:</b> UBC-like<br><b>Family:</b> UEV domain                                                                                                                                                                  |
| 35 | <a href="#">c5o31b_</a> | Alignment | not modelled | 13.4 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 7,<br><b>PDBTitle:</b> mitochondrial complex i in the deactive state                                                 |
| 36 | <a href="#">c5ldxb_</a> | Alignment | not modelled | 13.4 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 7,<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class3.                                         |
| 37 | <a href="#">c5ldwb_</a> | Alignment | not modelled | 13.4 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 7,<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class1                                          |
| 38 | <a href="#">c5lc5b_</a> | Alignment | not modelled | 13.4 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 7,<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class2                                          |
| 39 | <a href="#">c4lnsA_</a> | Alignment | not modelled | 13.1 | 38 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asparagine synthetase a;<br><b>PDBTitle:</b> crystal structure of asparagine synthetase a (asna) from trypanosoma2 brucei                                                        |
| 40 | <a href="#">c6iu3A_</a> | Alignment | not modelled | 12.5 | 5  | <b>PDB header:</b> metal transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> vit1;<br><b>PDBTitle:</b> crystal structure of iron transporter vit1 with zinc ions                                                                                     |
| 41 | <a href="#">c3r24A_</a> | Alignment | not modelled | 11.8 | 56 | <b>PDB header:</b> transferase, viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2'-o-methyl transferase;<br><b>PDBTitle:</b> crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible                                      |
| 42 | <a href="#">c4j15A_</a> | Alignment | not modelled | 11.3 | 38 | <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            |
| 43 | <a href="#">c5n9yB_</a> | Alignment | not modelled | 11.0 | 11 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> zinc transport protein zntb;<br><b>PDBTitle:</b> the full-length structure of zntb                                                                                     |
| 44 | <a href="#">c1sghB_</a> | Alignment | not modelled | 10.8 | 33 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ezrin-radixin-moesin binding phosphoprotein 50;<br><b>PDBTitle:</b> moesin ferm domain bound to ebp50 c-terminal peptide                                             |
| 45 | <a href="#">d1n9wa2</a> | Alignment | not modelled | 10.8 | 50 | <b>Fold:</b> Class II aaRS and biotin synthetases<br><b>Superfamily:</b> Class II aaRS and biotin synthetases<br><b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain                                                    |
| 46 | <a href="#">c1n9wA_</a> | Alignment | not modelled | 10.7 | 50 | <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 |
| 47 | <a href="#">c2d10F_</a> | Alignment | not modelled | 10.1 | 33 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> F: <b>PDB Molecule:</b> ezrin-radixin-moesin binding phosphoprotein 50;<br><b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide      |
| 48 | <a href="#">c2d10G_</a> | Alignment | not modelled | 10.1 | 33 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> G: <b>PDB Molecule:</b> ezrin-radixin-moesin binding phosphoprotein 50;<br><b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide      |
| 49 | <a href="#">c2d10E_</a> | Alignment | not modelled | 10.1 | 33 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> E: <b>PDB Molecule:</b> ezrin-radixin-moesin binding phosphoprotein 50;<br><b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide      |
| 50 | <a href="#">c2d10H_</a> | Alignment | not modelled | 10.1 | 33 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> H: <b>PDB Molecule:</b> ezrin-radixin-moesin binding phosphoprotein 50;<br><b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide      |
| 51 | <a href="#">c3bjuB_</a> | Alignment | not modelled | 10.1 | 50 | <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                                                                   |
| 52 | <a href="#">c4o2dB_</a> | Alignment | not modelled | 10.1 | 38 | <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                                 |
| 53 | <a href="#">c2d11F_</a> | Alignment | not modelled | 10.0 | 33 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> F: <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf2;<br><b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide     |

|    |                        |                                                                                               |              |      |    |                                                                                                                                                                                                                                                  |
|----|------------------------|-----------------------------------------------------------------------------------------------|--------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 54 | <a href="#">c2d11E</a> |  Alignment    | not modelled | 10.0 | 33 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> E: <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf2;<br><b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide  |
| 55 | <a href="#">c2d11G</a> |  Alignment   | not modelled | 10.0 | 33 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> G: <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf2;<br><b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide  |
| 56 | <a href="#">c2d11H</a> |  Alignment   | not modelled | 10.0 | 33 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> H: <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf2;<br><b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide  |
| 57 | <a href="#">c3fq6A</a> |  Alignment   | not modelled | 9.9  | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase;<br><b>PDBTitle:</b> the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi                                        |
| 58 | <a href="#">c5elnC</a> |  Alignment   | not modelled | 9.9  | 50 | <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                                      |
| 59 | <a href="#">c6odmK</a> |  Alignment   | not modelled | 9.8  | 23 | <b>PDB header:</b> viral protein<br><b>Chain:</b> K: <b>PDB Molecule:</b> capsid vertex component 2;<br><b>PDBTitle:</b> herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit                                |
| 60 | <a href="#">c5ynpA</a> |  Alignment   | not modelled | 9.8  | 44 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nsp16 protein;<br><b>PDBTitle:</b> crystal structure of mers-cov nsp16/nsp10 complex bound to sinefungin2 and m7gpppa                                                    |
| 61 | <a href="#">c1vw48</a> |  Alignment   | not modelled | 9.7  | 31 | <b>PDB header:</b> ribosome<br><b>Chain:</b> 8: <b>PDB Molecule:</b> 54s ribosomal protein l13, mitochondrial;<br><b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit                                                  |
| 62 | <a href="#">c4ex5A</a> |  Alignment  | not modelled | 9.6  | 50 | <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                               |
| 63 | <a href="#">c5vl1D</a> |  Alignment | not modelled | 9.6  | 38 | <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                                      |
| 64 | <a href="#">c5hgdD</a> |  Alignment | not modelled | 9.5  | 50 | <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 cladospirin.                                                          |
| 65 | <a href="#">c4upaA</a> |  Alignment | not modelled | 9.5  | 38 | <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                                             |
| 66 | <a href="#">c1b8aB</a> |  Alignment | not modelled | 9.4  | 50 | <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                                                                                              |
| 67 | <a href="#">c4ddpA</a> |  Alignment | not modelled | 9.3  | 55 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> beclin-1;<br><b>PDBTitle:</b> crystal structure of beclin 1 evolutionarily conserved domain(ecd)                                                                    |
| 68 | <a href="#">c5o60M</a> |  Alignment | not modelled | 9.3  | 36 | <b>PDB header:</b> ribosome<br><b>Chain:</b> M: <b>PDB Molecule:</b> 50s ribosomal protein l15;<br><b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis                                                   |
| 69 | <a href="#">c1wydB</a> |  Alignment | not modelled | 9.1  | 50 | <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 sulfobolus tokodaii                                             |
| 70 | <a href="#">c3vp7A</a> |  Alignment | not modelled | 9.1  | 73 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 30;<br><b>PDBTitle:</b> crystal structure of the beta-alpha repeated, autophagy-specific2 (bara) domain of vps30/atg6  |
| 71 | <a href="#">c6ns0A</a> |  Alignment | not modelled | 9.0  | 50 | <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 chlamydia trachomatis2 complexed with l-lysine and cladospirin                       |
| 72 | <a href="#">c5lnkm</a> |  Alignment | not modelled | 9.0  | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> M: <b>PDB Molecule:</b> mitochondrial complex i, nd4 subunit;<br><b>PDBTitle:</b> entire ovine respiratory complex i                                                                          |
| 73 | <a href="#">c5dfzD</a> |  Alignment | not modelled | 8.9  | 73 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 30;<br><b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.                                                    |
| 74 | <a href="#">c2xqtB</a> |  Alignment | not modelled | 8.8  | 25 | <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 |
| 75 | <a href="#">c1x55A</a> |  Alignment | not modelled | 8.7  | 50 | <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   |
| 76 | <a href="#">c6pqhA</a> |  Alignment | not modelled | 8.6  | 50 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asparagine--trna ligase;<br><b>PDBTitle:</b> crystal structure of asparagine-trna ligase from elizabethkingia sp.2 ccug 26117                                                 |
| 77 | <a href="#">c4h02B</a> |  Alignment | not modelled | 8.6  | 50 | <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                                                                           |
| 78 | <a href="#">c5zq8A</a> |  Alignment | not modelled | 8.4  | 50 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> asparagine--trna ligase;<br><b>PDBTitle:</b> crystal structure of ttnrs                                                                                                       |

|    |                         |           |              |     |    |                                                                                                                                                                                                                                                                                                                                       |
|----|-------------------------|-----------|--------------|-----|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 79 | <a href="#">c1asyA_</a> | Alignment | not modelled | 8.3 | 38 | <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                                                           |
| 80 | <a href="#">c1e22A_</a> | Alignment | not modelled | 8.2 | 50 | <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                                                                                                        |
| 81 | <a href="#">c5xixD_</a> | Alignment | not modelled | 8.2 | 25 | <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                                                                                                                                                |
| 82 | <a href="#">c6od8A_</a> | Alignment | not modelled | 8.1 | 38 | <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                                                                                                                    |
| 83 | <a href="#">c4u62D_</a> | Alignment | not modelled | 7.9 | 54 | <b>PDB header:</b> viral protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> structural protein vp1;<br><b>PDBTitle:</b> trichodysplasia spinulosa-associated polyomavirus (tspyv) vp1 in2 complex with 3'-sialyllactose                                                                                                                 |
| 84 | <a href="#">c4up8A_</a> | Alignment | not modelled | 7.8 | 38 | <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                                                                                                                                                |
| 85 | <a href="#">c3j1zP_</a> | Alignment | not modelled | 7.7 | 14 | <b>PDB header:</b> metal transport<br><b>Chain:</b> P: <b>PDB Molecule:</b> cation efflux family protein;<br><b>PDBTitle:</b> inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy                                                                                                          |
| 86 | <a href="#">c3m4qA_</a> | Alignment | not modelled | 7.6 | 25 | <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 (asnr5)                                                                                                                                               |
| 87 | <a href="#">c1efwA_</a> | Alignment | not modelled | 7.5 | 38 | <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                                                                                              |
| 88 | <a href="#">c3c25A_</a> | Alignment | not modelled | 7.5 | 67 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> noti restriction endonuclease;<br><b>PDBTitle:</b> crystal structure of noti restriction endonuclease bound to cognate2 dna                                                                                                                                 |
| 89 | <a href="#">d1j4na_</a> | Alignment | not modelled | 7.5 | 13 | <b>Fold:</b> Aquaporin-like<br><b>Superfamily:</b> Aquaporin-like<br><b>Family:</b> Aquaporin-like                                                                                                                                                                                                                                    |
| 90 | <a href="#">d1o8bb1</a> | Alignment | not modelled | 7.2 | 13 | <b>Fold:</b> NagB/RpiA/CoA transferase-like<br><b>Superfamily:</b> NagB/RpiA/CoA transferase-like<br><b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), catalytic domain                                                                                                                                                           |
| 91 | <a href="#">c3e9hB_</a> | Alignment | not modelled | 7.2 | 50 | <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                                                                                                                       |
| 92 | <a href="#">c2p04B_</a> | Alignment | not modelled | 7.2 | 50 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> signal transduction histidine kinase;<br><b>PDBTitle:</b> 2.1 ang structure of the dimerized pas domain of signal transduction2 histidine kinase from nostoc punctiforme pcc 73102 with homology to3 the h-noxa/h-noba domain of the soluble guanylyl cyclase |
| 93 | <a href="#">c2re3A_</a> | Alignment | not modelled | 7.1 | 38 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution                                                                                             |
| 94 | <a href="#">c4gj4A_</a> | Alignment | not modelled | 7.1 | 43 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> soluble guanylyl cyclase alpha-1 subunit;<br><b>PDBTitle:</b> the crystal structure of the soluble guanylate cyclase pas alpha2 domain from manduca sexta                                                                                                           |
| 95 | <a href="#">c4ah6B_</a> | Alignment | not modelled | 7.0 | 38 | <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                                                                                                                                                            |
| 96 | <a href="#">c3bwrC_</a> | Alignment | not modelled | 6.8 | 46 | <b>PDB header:</b> viral protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> capsid protein vp1;<br><b>PDBTitle:</b> sv40 vp1 pentamer in complex with gm1 oligosaccharide                                                                                                                                                               |
| 97 | <a href="#">c4pcgD_</a> | Alignment | not modelled | 6.6 | 23 | <b>PDB header:</b> viral protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> vp1;<br><b>PDBTitle:</b> structure of human polyomavirus 6 (hpyv6) vp1 pentamer                                                                                                                                                                             |
| 98 | <a href="#">c4j2IC_</a> | Alignment | not modelled | 6.5 | 45 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein capicua homolog;<br><b>PDBTitle:</b> crystal structure of axh domain complexed with capicua                                                                                                                                               |
| 99 | <a href="#">c4j2ID_</a> | Alignment | not modelled | 6.5 | 45 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> protein capicua homolog;<br><b>PDBTitle:</b> crystal structure of axh domain complexed with capicua                                                                                                                                               |