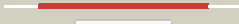
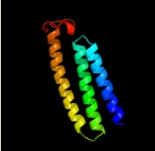

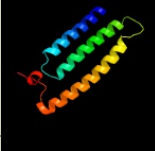
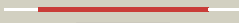
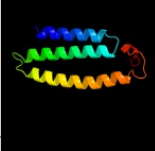

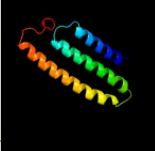

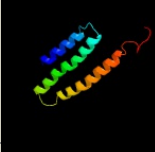



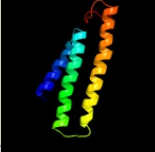

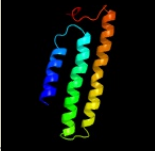

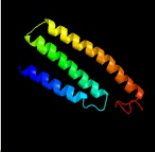

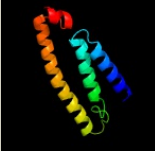

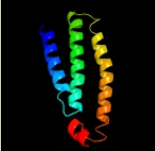
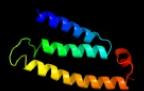





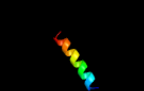

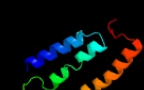


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3155\_(nuoK)\_3521921\_3522220  
 Date Thu Aug 8 16:20:34 BST 2019  
 Unique Job ID caa0c6c471e395b6

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c3rkoK_</a> |  Alignment   |    | 100.0      | 31     | <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 |
| 2  | <a href="#">c6humE_</a> |  Alignment   |    | 100.0      | 45     | <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                        |
| 3  | <a href="#">c4heaK_</a> |  Alignment   |    | 100.0      | 53     | <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                          |
| 4  | <a href="#">c6cfwG_</a> |  Alignment   |   | 100.0      | 19     | <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   |
| 5  | <a href="#">c6gcsL_</a> |  Alignment |  | 100.0      | 23     | <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  |
| 6  | <a href="#">c6g2jK_</a> |  Alignment |  | 99.8       | 24     | <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  |
| 7  | <a href="#">c5ldwK_</a> |  Alignment |  | 99.8       | 24     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> K; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4l;<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class1   |
| 8  | <a href="#">c5lc5K_</a> |  Alignment |  | 99.7       | 24     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> K; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4l;<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class2   |
| 9  | <a href="#">c6humF_</a> |  Alignment |  | 89.5       | 13     | <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                                     |
| 10 | <a href="#">c3rkoL_</a> |  Alignment |  | 87.2       | 14     | <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 |
| 11 | <a href="#">c4heaT_</a> |  Alignment |  | 87.2       | 13     | <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                          |

|    |                         |           |   |      |    |  |
|----|-------------------------|-----------|---|------|----|--|
| 12 | <a href="#">c6gcs5_</a> | Alignment |    | 77.3 | 12 | <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   |
| 13 | <a href="#">c5ldwL_</a> | Alignment |    | 73.6 | 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  |
| 14 | <a href="#">c6cfwH_</a> | Alignment |    | 73.1 | 14 | <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   |
| 15 | <a href="#">c6g2jL_</a> | Alignment |    | 64.9 | 14 | <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   |
| 16 | <a href="#">c6gcs2_</a> | Alignment |    | 62.9 | 17 | <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="#">c3rkoM_</a> | Alignment |    | 59.0 | 16 | <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 |
| 18 | <a href="#">c2mkvA_</a> | Alignment |  | 58.6 | 37 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma;<br><b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in micelles                         |
| 19 | <a href="#">c2jo1A_</a> | Alignment |  | 58.4 | 42 | <b>PDB header:</b> hydrolase regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman;<br><b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles  |
| 20 | <a href="#">c6gcs4_</a> | Alignment |  | 57.3 | 14 | <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   |
| 21 | <a href="#">c5ldwM_</a> | Alignment | not modelled  | 55.2 | 8  | <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  |
| 22 | <a href="#">c2jp3A_</a> | Alignment | not modelled  | 52.0 | 26 | <b>PDB header:</b> transcription regulator 4;<br><b>Chain:</b> A: <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4;<br><b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles               |
| 23 | <a href="#">c6humB_</a> | Alignment | not modelled  | 45.6 | 13 | <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                         |
| 24 | <a href="#">c2zxeG_</a> | Alignment | not modelled  | 44.7 | 26 | <b>PDB header:</b> hydrolase/transport protein<br><b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein;<br><b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state                                 |
| 25 | <a href="#">c5xtdi_</a> | Alignment | not modelled  | 43.4 | 13 | <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                    |
| 26 | <a href="#">c4he8M_</a> | Alignment | not modelled  | 41.8 | 15 | <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              |
| 27 | <a href="#">c3rkoN_</a> | Alignment | not modelled  | 39.2 | 14 | <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 |
| 28 | <a href="#">c4he8I_</a> | Alignment | not modelled  | 24.5 | 15 | <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              |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | <a href="#">c3kdpH</a>  | Alignment | not modelled | 22.4 | 32 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> H: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a;<br><b>PDBTitle:</b> crystal structure of the sodium-potassium pump   |
| 30 | <a href="#">c3kdpG</a>  | Alignment | not modelled | 22.4 | 32 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> G: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a;<br><b>PDBTitle:</b> crystal structure of the sodium-potassium pump   |
| 31 | <a href="#">c4hkrB</a>  | Alignment | not modelled | 15.1 | 9  | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> calcium release-activated calcium channel protein 1;<br><b>PDBTitle:</b> calcium release-activated calcium (crac) channel orai   |
| 32 | <a href="#">c1iflA</a>  | Alignment | not modelled | 13.9 | 19 | <b>PDB header:</b> virus<br><b>Chain:</b> A: <b>PDB Molecule:</b> inovirus;<br><b>PDBTitle:</b> molecular models and structural comparisons of native and2 mutant class i filamentous bacteriophages ff (fd, f1, m13),3 if1 and ike                              |
| 33 | <a href="#">c3n23E</a>  | Alignment | not modelled | 13.1 | 31 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> E: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a;<br><b>PDBTitle:</b> crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump        |
| 34 | <a href="#">c4ecdB</a>  | Alignment | not modelled | 12.5 | 16 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> chorismate synthase;<br><b>PDBTitle:</b> 2.5 angstrom resolution crystal structure of bifidobacterium longum2 chorismate synthase  |
| 35 | <a href="#">d1xmec1</a> | Alignment | not modelled | 12.3 | 30 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> Bacterial ba3 type cytochrome c oxidase subunit Ila<br><b>Family:</b> Bacterial ba3 type cytochrome c oxidase subunit Ila   |
| 36 | <a href="#">c3bvdC</a>  | Alignment | not modelled | 12.3 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 2a;<br><b>PDBTitle:</b> structure of surface-engineered cytochrome ba3 oxidase from thermus2 thermophilus under xenon pressure, 100psi 5min          |
| 37 | <a href="#">d1v54m</a>  | Alignment | not modelled | 11.1 | 24 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)<br><b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)   |
| 38 | <a href="#">c5ldwN</a>  | Alignment | not modelled | 11.0 | 10 | <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  |
| 39 | <a href="#">c2y69Z</a>  | Alignment | not modelled | 10.0 | 24 | <b>PDB header:</b> electron transport<br><b>Chain:</b> Z: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 8h;<br><b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen   |
| 40 | <a href="#">c5z62M</a>  | Alignment | not modelled | 8.8  | 29 | <b>PDB header:</b> electron transport<br><b>Chain:</b> M: <b>PDB Molecule:</b> cytochrome c oxidase subunit 8a, mitochondrial;<br><b>PDBTitle:</b> structure of human cytochrome c oxidase   |
| 41 | <a href="#">c1ztbA</a>  | Alignment | not modelled | 8.7  | 13 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> chorismate synthase;<br><b>PDBTitle:</b> crystal structure of chorismate synthase from mycobacterium2 tuberculosis  |
| 42 | <a href="#">d1qxoA</a>  | Alignment | not modelled | 8.7  | 16 | <b>Fold:</b> Chorismate synthase, AroC<br><b>Superfamily:</b> Chorismate synthase, AroC<br><b>Family:</b> Chorismate synthase, AroC  |
| 43 | <a href="#">c4heaJ</a>  | Alignment | not modelled | 7.9  | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> J: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 10;<br><b>PDBTitle:</b> crystal structure of the entire respiratory complex i from thermus2 thermophilus  |
| 44 | <a href="#">c4u4cB</a>  | Alignment | not modelled | 7.5  | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein air2,poly(a) rna polymerase protein 2;<br><b>PDBTitle:</b> the molecular architecture of the tramp complex reveals the2 organization and interplay of its two catalytic activities |
| 45 | <a href="#">c6gcs6</a>  | Alignment | not modelled | 7.5  | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> 6: <b>PDB Molecule:</b> nd6 subunit (nu6m);<br><b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica   |
| 46 | <a href="#">c6humD</a>  | Alignment | not modelled | 7.4  | 11 | <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   |
| 47 | <a href="#">c6nbxG</a>  | Alignment | not modelled | 7.3  | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j;<br><b>PDBTitle:</b> t.elongatus ndh (data-set 2)   |
| 48 | <a href="#">c3ctoE</a>  | Alignment | not modelled | 7.0  | 33 | <b>PDB header:</b> toxin inhibitor<br><b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein rv3357/mt3465;<br><b>PDBTitle:</b> crystal structure of m. tuberculosis yefm antitoxin   |
| 49 | <a href="#">c4hkrA</a>  | Alignment | not modelled | 6.3  | 9  | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> calcium release-activated calcium channel protein 1;<br><b>PDBTitle:</b> calcium release-activated calcium (crac) channel orai   |
| 50 | <a href="#">c6humG</a>  | Alignment | not modelled | 6.0  | 12 | <b>PDB header:</b> proton transport<br><b>Chain:</b> G: <b>PDB Molecule:</b> nadh dehydrogenase subunit 6;<br><b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus   |
| 51 | <a href="#">c4cimP</a>  | Alignment | not modelled | 5.7  | 14 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> P: <b>PDB Molecule:</b> bcl-2-like protein 2;<br><b>PDBTitle:</b> complex of a bcl-w bh3 mutant with a bh3 domain  |
| 52 | <a href="#">c4cimQ</a>  | Alignment | not modelled | 5.7  | 14 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> Q: <b>PDB Molecule:</b> bcl-2-like protein 2;<br><b>PDBTitle:</b> complex of a bcl-w bh3 mutant with a bh3 domain  |
| 53 | <a href="#">c2lowA</a>  | Alignment | not modelled | 5.7  | 50 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> apelin receptor;<br><b>PDBTitle:</b> solution structure of ar55 in 50% hfip   |