Phyre2

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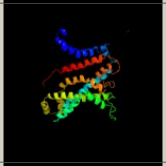
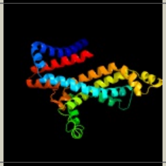
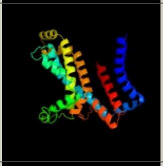
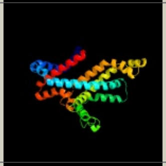
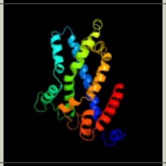
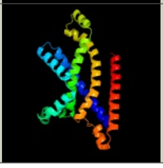
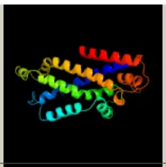
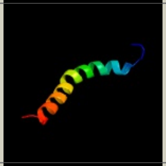
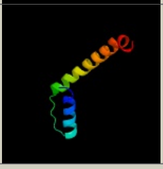
Description	RVBD2398c_(cysW)_2694991_2695809
Date	Mon Aug 5 13:25:55 BST 2019
Unique Job ID	a4eca4ddfcaef5dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4tqvl_	Alignment		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
2	c3fh6F_	Alignment		100.0	17	**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
3	d3d31c1	Alignment		100.0	27	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	c3d31D_	Alignment		100.0	27	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease protein; **PDBTitle:** modbc from methanosarcina acetivorans
5	c2onkC_	Alignment		100.0	26	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
6	d2onkc1	Alignment		100.0	26	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	c2r6gF_	Alignment		100.0	24	**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
8	d2r6gg1	Alignment		100.0	17	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	c4tqvJ_	Alignment		100.0	17	**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
10	d2r6gf2	Alignment		100.0	21	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
11	c4ymuC_	Alignment		99.9	14	**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		99.8	17	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
13	d2r6gf1	Alignment		72.4	8	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
14	c2m8gX_	Alignment		53.4	29	**PDB header:**transcription **Chain:** X: **PDB Molecule:**transcriptional regulator; **PDBTitle:** structure, function, and tethering of dna-binding domains in 542 transcriptional activators
15	c4l5eA_	Alignment		51.8	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of a. aeolicus ntrc1 dna binding domain
16	c1umqA_	Alignment		49.3	6	**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		49.3	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
18	d1ntca_	Alignment		47.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
19	d1fipa_	Alignment		42.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
20	c6an7D_	Alignment		39.3	6	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transport permease protein; **PDBTitle:** crystal structure of o-antigen polysaccharide abc-transporter
21	c5kbuA_	Alignment	not modelled	39.2	17	**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
22	d1etob_	Alignment	not modelled	35.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
23	c3e7lD_	Alignment	not modelled	32.0	23	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
24	d1etxa_	Alignment	not modelled	29.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
25	c6an7C_	Alignment	not modelled	26.6	6	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transport permease protein; **PDBTitle:** crystal structure of o-antigen polysaccharide abc-transporter
26	d1g2ha_	Alignment	not modelled	25.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
27	c1g2hA_	Alignment	not modelled	25.1	13	**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
28	c2hx6A_	Alignment	not modelled	24.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42

						endoribonuclease regb
29	c2ks1A_	Alignment	not modelled	17.4	18	**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
30	c2jwaA_	Alignment	not modelled	17.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
31	c5m7nA_	Alignment	not modelled	16.6	10	**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
32	c2n2aA_	Alignment	not modelled	13.8	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** spatial structure of her2/erbb2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
33	c1ojlD_	Alignment	not modelled	13.7	19	**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
34	c2cw1A_	Alignment	not modelled	11.9	40	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
35	c2rddB_	Alignment	not modelled	9.2	19	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
36	d1cf7a_	Alignment	not modelled	8.4	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
37	c2lhuA_	Alignment	not modelled	7.7	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
38	c2yl4A_	Alignment	not modelled	7.4	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 10, **PDBTitle:** structure of the human mitochondrial abc transporter, abcb10
39	c3s1bA_	Alignment	not modelled	7.3	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**mini-z; **PDBTitle:** the development of peptide-based tools for the analysis of2 angiogenesis
40	c1p7bB_	Alignment	not modelled	7.1	12	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**integral membrane channel and cytosolic domains; **PDBTitle:** crystal structure of an inward rectifier potassium channel
41	c2qksA_	Alignment	not modelled	6.9	5	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**kir3.1-prokaryotic kir channel chimera; **PDBTitle:** crystal structure of a kir3.1-prokaryotic kir channel chimera
42	c4qiwT_	Alignment	not modelled	6.8	21	**PDB header:**transcription **Chain:** T: **PDB Molecule:**dna-directed rna polymerase subunit k; **PDBTitle:** crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
43	d2ns0a1	Alignment	not modelled	6.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
44	c6agfB_	Alignment	not modelled	6.5	9	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**sodium channel subunit beta-1; **PDBTitle:** structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
45	c2oviA_	Alignment	not modelled	6.5	11	**PDB header:**ligand binding protein, metal transport **Chain:** A: **PDB Molecule:**hypothetical protein chux; **PDBTitle:** structure of the heme binding protein chux
46	c1twcF_	Alignment	not modelled	6.4	29	**PDB header:**transcription **Chain:** F: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 23 **PDBTitle:** rna polymerase ii complexed with gtp
47	d1twff_	Alignment	not modelled	6.4	29	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RPB6
48	c3rkoF_	Alignment	not modelled	6.2	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
49	c2rlfA_	Alignment	not modelled	6.2	9	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**matrix protein 2; **PDBTitle:** proton channel m2 from influenza a in complex with2 inhibitor rimantadine
50	c2pmzW_	Alignment	not modelled	6.2	14	**PDB header:**translation, transferase **Chain:** W: **PDB Molecule:**dna-directed rna polymerase subunit k; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
51	c6c14A_	Alignment	not modelled	6.1	13	**PDB header:**membrane protein, metal transport **Chain:** A: **PDB Molecule:**protocadherin-15; **PDBTitle:** cryoem structure of mouse pcdh15-1ec-lhfpl5 complex
52	c4j2nB_	Alignment	not modelled	6.0	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gp37; **PDBTitle:** crystal structure of mycobacteriophage pukovnik xis
53	c4j2nA_	Alignment	not modelled	6.0	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gp37; **PDBTitle:** crystal structure of mycobacteriophage pukovnik xis
						PDB header:transport protein

54	c5xu1M_	Alignment	not modelled	5.9	17	**Chain:** M: **PDB Molecule:**abc transporter permeae; **PDBTitle:** structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
55	c3sjdD_	Alignment	not modelled	5.9	36	**PDB header:**hydrolase/transport protein **Chain:** D: **PDB Molecule:**golgi to er traffic protein 2; **PDBTitle:** crystal structure of s. cerevisiae get3 with bound adp-mg2+ in complex2 with get2 cytosolic domain
56	c3sjdE_	Alignment	not modelled	5.9	36	**PDB header:**hydrolase/transport protein **Chain:** E: **PDB Molecule:**golgi to er traffic protein 2; **PDBTitle:** crystal structure of s. cerevisiae get3 with bound adp-mg2+ in complex2 with get2 cytosolic domain
57	c3zs9C_	Alignment	not modelled	5.9	36	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**golgi to er traffic protein 2; **PDBTitle:** s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
58	c6ic4H_	Alignment	not modelled	5.9	13	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**abc transporter permease; **PDBTitle:** cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
59	c3zs9D_	Alignment	not modelled	5.6	36	**PDB header:**hydrolase/transport protein **Chain:** D: **PDB Molecule:**golgi to er traffic protein 2; **PDBTitle:** s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
60	c5b57B_	Alignment	not modelled	5.6	15	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**putative hemin abc transport system, membrane protein; **PDBTitle:** inward-facing conformation of abc heme importer bhuuv from2 burkholderia cenocepacia
61	c5a40C_	Alignment	not modelled	5.4	19	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**putative fluoride ion transporter crcb; **PDBTitle:** crystal structure of a dual topology fluoride ion channel.
62	d1qkla_	Alignment	not modelled	5.3	29	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RPB6
63	c2d7dB_	Alignment	not modelled	5.1	15	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**40-mer from uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
64	c3tdsC_	Alignment	not modelled	5.1	8	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**formate/nitrite transporter; **PDBTitle:** crystal structure of hsc f194i