Phyre2

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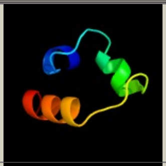
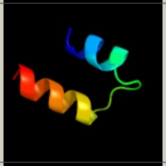
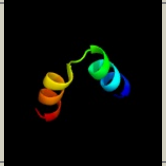
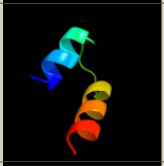
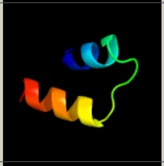
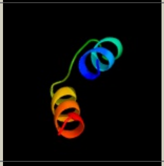
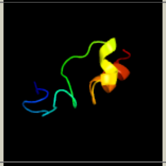
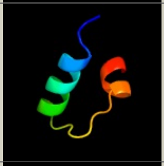
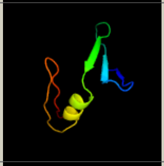
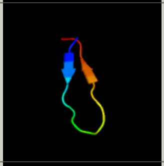
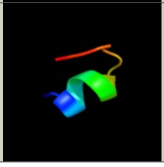
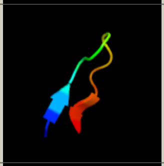
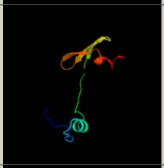
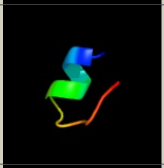
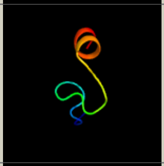
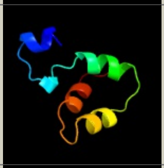
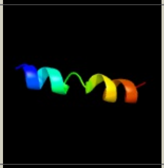
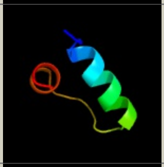
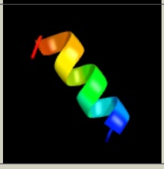
Description	RVBD3753c_(-)_4199899_4200399
Date	Fri Aug 9 18:20:45 BST 2019
Unique Job ID	abde109f49c6705f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6b9rD_	Alignment		20.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**hydroxyethylphosphonate dioxygenase; **PDBTitle:** streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
2	c5lc5E_	Alignment		17.5	12	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nadh dehydrogenase [ubiquinone] flavoprotein 2, **PDBTitle:** structure of mammalian respiratory complex i, class2
3	d1q1aa_	Alignment		17.0	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
4	c6gcsH_	Alignment		15.9	8	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**24-kda subunit (nuhm); **PDBTitle:** cryo-em structure of respiratory complex i from yarrowia lipolytica
5	c5lnk2_	Alignment		14.8	12	**PDB header:**oxidoreductase **Chain:** 2: **PDB Molecule:**mitochondrial complex i, 24 kda subunit; **PDBTitle:** entire ovine respiratory complex i
6	d2fug21	Alignment		12.9	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
7	c2l9fA_	Alignment		11.7	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
8	c6f3tK_	Alignment		11.5	22	**PDB header:**transcription **Chain:** K: **PDB Molecule:**transcription initiation factor tfiid subunit 6; **PDBTitle:** crystal structure of the human taf5-taf6-taf9 complex
9	c3cm1C_	Alignment		11.3	12	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**ssga-like sporulation-specific cell division protein; **PDBTitle:** crystal structure of ssga-like sporulation-specific cell division2 protein (yp_290167.1) from thermobifida fusca yx-er1 at 2.60 a3 resolution
10	c2mmpA_	Alignment		11.3	25	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of a ribosomal protein
11	d1bl0a2	Alignment		11.1	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator

12	c6hl2C_	Alignment		10.4	19	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase subunit e; **PDBTitle:** wild-type nuoef from aquifex aeolicus - oxidized form
13	c5up5A_	Alignment		10.0	54	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ehee_rd1_0284; **PDBTitle:** solution structure of the de novo mini protein ehee_rd1_0284
14	c3d0fA_	Alignment		9.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
15	d1d5ya2	Alignment		8.9	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
16	c4h2uC_	Alignment		7.7	22	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aminoacyl carrier protein 1; **PDBTitle:** crystal structure of bradyrhizobium japonicum glycine:[carrier2 protein] ligase complexed with cognate carrier protein and atp
17	c4yf1D_	Alignment		7.6	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**lmo0812 protein; **PDBTitle:** 1.85 angstrom crystal structure of lmo0812 from listeria monocytogenes2 egd-e
18	c5vwxB_	Alignment		7.5	32	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** bak core latch dimer in complex with bim-h0-h3glt
19	d1tafb_	Alignment		6.8	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
20	c4dkkA_	Alignment		6.6	43	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**double-stranded rna-binding protein staufen homolog 1; **PDBTitle:** the x-ray crystal structure of the human stau1 ssm-'rbd'5 domain-2 swapped dimer
21	c5fyqB_	Alignment	not modelled	6.6	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent protein deacetylase sirtuin-2; **PDBTitle:** sirt2 in complex with a 13-mer trifluoroacetylated ran peptide
22	d1g3wa2	Alignment	not modelled	6.2	25	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
23	c3tkaA_	Alignment	not modelled	6.1	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase h; **PDBTitle:** crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
24	d2isya2	Alignment	not modelled	5.9	22	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
25	d3cu3a1	Alignment	not modelled	5.7	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
26	c5vwxD_	Alignment	not modelled	5.3	35	**PDB header:**apoptosis **Chain:** D: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** bak core latch dimer in complex with bim-h0-h3glt
27	d1tmoa2	Alignment	not modelled	5.3	25	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
28	c5chhA_	Alignment	not modelled	5.3	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arac family transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator cdpr from