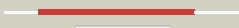




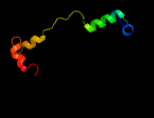
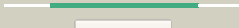
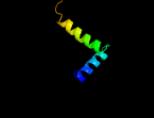


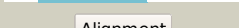

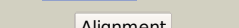

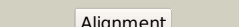

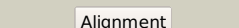

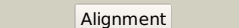



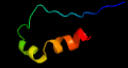










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2550c_(-)_2870129_2870374
Date	Wed Aug 7 12:50:18 BST 2019
Unique Job ID	4d3a7361cd13545b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5jB_	 Alignment		94.0	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	c2h1oH_	 Alignment		59.0	20	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
3	c5x3tA_	 Alignment		45.3	28	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapb26; PDBTitle: vapbc from mycobacterium tuberculosis
4	d2bsqe1	 Alignment		44.2	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
5	c1ea4K_	 Alignment		32.0	33	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
6	d2cpga_	 Alignment		32.0	33	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
7	c4hv0B_	 Alignment		25.6	30	PDB header: transcription, viral protein Chain: B: PDB Molecule: avtr; PDBTitle: structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus
8	d1h9aa2	 Alignment		25.0	24	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
9	c1h9aA_	 Alignment		21.6	24	PDB header: oxidoreductase (choh(d) - nad(p)) Chain: A: PDB Molecule: glucose 6-phosphate 1-dehydrogenase; PDBTitle: complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from l. mesenteroides with coenzyme nadp
10	c4e9iB_	 Alignment		19.5	24	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi
11	c6a6xC_	 Alignment		17.7	46	PDB header: toxin Chain: C: PDB Molecule: antitoxin maze7; PDBTitle: the crystal structure of the mtb maze-mazf-mt9 complex

12	d1qkia2	Alignment		16.2	21	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
13	d1o51a_	Alignment		14.9	50	Fold: Ferredoxin-like Superfamily: GlnB-like Family: DUF190/COG1993
14	c4lqvA_	Alignment		14.4	26	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray crystal structure of glucose-6-phosphate 1-dehydrogenase from2 mycobacterium avium
15	c6g2jY_	Alignment		14.0	30	PDB header: oxidoreductase Chain: Y: PDB Molecule: mcg5603; PDBTitle: mouse mitochondrial complex i in the active state
16	c2kc8B_	Alignment		13.7	44	PDB header: toxin/toxin repressor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: structure of e. coli toxin rele (r81a/r83a) mutant in2 complex with antitoxin relbc (k47-l79) peptide
17	c2bhlB_	Alignment		13.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose-6-phosphate dehydrogenase (deletion2 variant) complexed with glucose-6-phosphate
18	c1qkiE_	Alignment		12.5	21	PDB header: oxidoreductase Chain: E: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose 6-phosphate dehydrogenase (variant2 canton r459l) complexed with structural nadp+
19	c2kqrA_	Alignment		11.0	18	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase, cytoplasmic; PDBTitle: solution structure of the n-terminal domain (residues 1-111) of brugia2 malayi asparaginyl-trna synthetase
20	c2nd4A_	Alignment		10.6	46	PDB header: hydrolase receptor Chain: A: PDB Molecule: amylase-binding protein abpa; PDBTitle: a distinct sortase srtb anchors and processes a streptococcal adhesin2 abpa with a novel structural property
21	c2ql8A_	Alignment	not modelled	10.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative redox protein; PDBTitle: crystal structure of a putative redox protein (lsei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution
22	c6iyaD_	Alignment	not modelled	9.9	22	PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso
23	c2ls01_	Alignment	not modelled	9.5	50	PDB header: hydrolase Chain: 1: PDB Molecule: zoocin a endopeptidase; PDB Fragment: unp residues 170-285; PDBTitle: solution structure of the target recognition domain of zoocin a
24	c5ldwY_	Alignment	not modelled	8.1	23	PDB header: oxidoreductase Chain: Y: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class1
25	c5cmyB_	Alignment	not modelled	7.6	12	PDB header: protein transport Chain: B: PDB Molecule: epsin-5; PDBTitle: crystal structure of yeast ent5 n-terminal domain-native
26	c5ytpA_	Alignment	not modelled	7.3	47	PDB header: dna binding protein Chain: A: PDB Molecule: ttha0139; PDBTitle: crystal structure of ttha0139 l34a from thermus thermophilus hb8
27	d1qwia_	Alignment	not modelled	7.3	13	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
28	d1bh9b_	Alignment	not modelled	7.1	28	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
						PDB header: oxidoreductase

29	c3cjeA_	Alignment	not modelled	7.0	29	Chain: A: PDB Molecule: osmc-like protein; PDBTitle: crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution
30	d1h8ba_	Alignment	not modelled	7.0	32	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
31	c1lqE_	Alignment	not modelled	6.5	21	PDB header: unknown function Chain: E: PDB Molecule: osmotical inducible protein c like family; PDBTitle: crystal structure of osmc like protein from mycoplasma2 pneumoniae
32	d1lqla_	Alignment	not modelled	6.5	21	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
33	d1vlaa_	Alignment	not modelled	6.4	21	Fold: OsmC-like Superfamily: OsmC-like Family: YhfA-like
34	c1g5jB_	Alignment	not modelled	6.1	71	PDB header: apoptosis Chain: B: PDB Molecule: bad protein; PDBTitle: complex of bcl-xl with peptide from bad
35	c4mh4B_	Alignment	not modelled	5.9	21	PDB header: protein binding Chain: B: PDB Molecule: osmc-like protein; PDBTitle: crystal structure of osmc-like protein from burkholderia cenocepacia2 j2315
36	d1p94a_	Alignment	not modelled	5.9	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
37	c2mdvB_	Alignment	not modelled	5.8	32	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
38	d2gf3a2	Alignment	not modelled	5.7	11	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: D-aminoacid oxidase-like
39	c2rsoA_	Alignment	not modelled	5.6	47	PDB header: transcription Chain: A: PDB Molecule: chromatin-associated protein swi6; PDBTitle: solution structure of the chromodomain of swi6
40	d1fexa_	Alignment	not modelled	5.6	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
41	c2rf4B_	Alignment	not modelled	5.5	33	PDB header: transferase Chain: B: PDB Molecule: dna-directed rna polymerase i subunit rpa4; PDBTitle: crystal structure of the rna polymerase i subcomplex a14/43
42	c2bjoA_	Alignment	not modelled	5.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein ohrb; PDBTitle: crystal structure of the organic hydroperoxide resistance2 protein ohrb of bacillus subtilis
43	c2kelB_	Alignment	not modelled	5.5	29	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
44	d1aqtal	Alignment	not modelled	5.4	50	Fold: Long alpha-hairpin Superfamily: Epsilon subunit of F1F0-ATP synthase C-terminal domain Family: Epsilon subunit of F1F0-ATP synthase C-terminal domain
45	c3k9tA_	Alignment	not modelled	5.4	50	PDB header: hydrolase Chain: A: PDB Molecule: putative peptidase; PDBTitle: crystal structure of putative peptidase (np_348812.1) from clostridium2 acetobutylicum at 2.37 a resolution
46	d1ml8a_	Alignment	not modelled	5.3	20	Fold: OsmC-like Superfamily: OsmC-like Family: YhfA-like
47	c5lnkW_	Alignment	not modelled	5.1	38	PDB header: oxidoreductase Chain: W: PDB Molecule: mitochondrial complex i, sgdh subunit; PDBTitle: entire ovine respiratory complex i