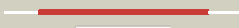



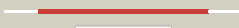


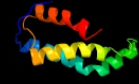



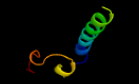

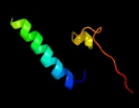

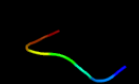



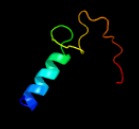


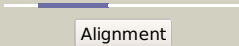


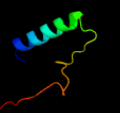
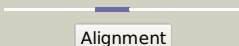



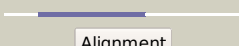
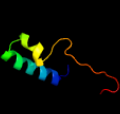
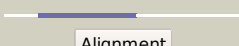

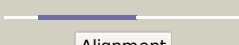

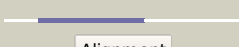
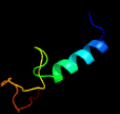

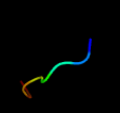

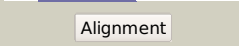
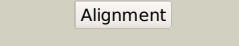
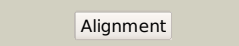
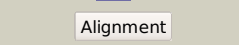
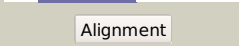

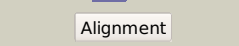


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2975c_(-)_3331368_3331622
Date	Thu Aug 8 16:20:13 BST 2019
Unique Job ID	e544d69e02827186

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3cr3a1	 Alignment		99.7	16	Fold: DhaL-like Superfamily: DhaL-like Family: DhaL-like
2	c2btdA_	 Alignment		99.5	14	PDB header: transferase Chain: A; PDB Molecule: pts-dependent dihydroxyacetone kinase; PDBTitle: crystal structure of dhal from e. coli
3	d1un8a1	 Alignment		99.5	18	Fold: DhaL-like Superfamily: DhaL-like Family: DhaL-like
4	c1un9B_	 Alignment		98.9	17	PDB header: kinase Chain: B; PDB Molecule: dihydroxyacetone kinase; PDBTitle: crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
5	c5m1hA_	 Alignment		42.6	35	PDB header: viral protein Chain: A; PDB Molecule: gag protein; PDBTitle: structure of a spumaretrovirus gag central domain reveals an ancient2 retroviral capsid
6	c1t10A_	 Alignment		30.8	20	PDB header: isomerase Chain: A; PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
7	d1q50a_	 Alignment		27.0	20	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
8	c5wcoC_	 Alignment		25.2	50	PDB header: viral protein Chain: C; PDB Molecule: ns2; PDBTitle: matrix protein (m1) of infectious salmon anaemia virus
9	c3it4B_	 Alignment		20.9	19	PDB header: transferase Chain: B; PDB Molecule: arginine biosynthesis bifunctional protein argj PDBTitle: the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
10	c2vzkD_	 Alignment		19.9	23	PDB header: transferase Chain: D; PDB Molecule: glutamate n-acetyltransferase 2 beta chain; PDBTitle: structure of the acyl-enzyme complex of an n-terminal nucleophile2 (ntn) hydrolase, oat2
11	c1vraB_	 Alignment		18.2	35	PDB header: transferase Chain: B; PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution

12	c5ocdD	 Alignment		17.8	7	PDB header: rna binding protein Chain: D: PDB Molecule: cyclodipeptide synthase; PDBTitle: structure of a cdps from fluoribacter dumoffii
13	c3pr3B	 Alignment		16.8	34	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
14	c6cfzJ	 Alignment		16.2	22	PDB header: nuclear protein Chain: J: PDB Molecule: spc34; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
15	d2r6gf1	 Alignment		15.4	5	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
16	c2wu8A	 Alignment		15.3	28	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
17	c3ujhB	 Alignment		15.1	27	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
18	c2o2cB	 Alignment		14.8	20	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase, glycosomal; PDBTitle: crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
19	d1vz6a	 Alignment		13.9	23	Fold: DmpA/ArgJ-like Superfamily: DmpA/ArgJ-like Family: ArgJ-like
20	c4glkA	 Alignment		13.8	63	PDB header: hydrolase Chain: A: PDB Molecule: abiq; PDBTitle: structure and activity of abiq, a lactococcal anti-phage2 endoribonuclease belonging to the type-iii toxin-antitoxin system
21	c4qfA	 Alignment	not modelled	12.8	22	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of a glucose-6-phosphate isomerase from trypanosoma cruzi
22	c4em6D	 Alignment	not modelled	12.6	20	PDB header: isomerase Chain: D: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: the structure of glucose-6-phosphate isomerase (gpi) from brucella2 melitensis
23	d1xcoa	 Alignment	not modelled	11.9	21	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
24	d2nsfa2	 Alignment	not modelled	11.8	27	Fold: SCP-like Superfamily: SCP-like Family: Microthiol-dependent maleylpyruvate isomerase C-terminal domain-like
25	c4atoA	 Alignment	not modelled	11.6	38	PDB header: toxin/antitoxin Chain: A: PDB Molecule: toxN; PDBTitle: new insights into the mechanism of bacterial type iii toxin-antitoxin2 systems: selective toxin inhibition by a non-coding rna pseudoknot
26	c3hjbA	 Alignment	not modelled	11.2	24	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
27	c5mlqA	 Alignment	not modelled	11.2	11	PDB header: ligase Chain: A: PDB Molecule: cdps; PDBTitle: structure of cdps from nocardia brasiliensis
28	c6cp8D	 Alignment	not modelled	11.2	27	PDB header: toxin/antitoxin Chain: D: PDB Molecule: cdii; PDBTitle: contact-dependent growth inhibition toxin-immunity protein complex2 from from e. coli 3006

29	c5uj6A	Alignment	not modelled	10.8	14	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolases family 2, sugar binding domain protein; PDBTitle: crystal structure of bacteroides uniformis beta-glucuronidase
30	dlzkea1	Alignment	not modelled	10.8	20	Fold: ROP-like Superfamily: HP1531-like Family: HP1531-like
31	c4mqdB	Alignment	not modelled	10.1	29	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: dna-entry nuclease inhibitor; PDBTitle: crystal structure of comj, inhibitor of the dna degrading activity of 2 nuca, from bacillus subtilis
32	dlf61a	Alignment	not modelled	10.0	32	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
33	dlhm5a	Alignment	not modelled	9.7	24	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
34	c2xd0B	Alignment	not modelled	9.5	13	PDB header: toxin/rna Chain: B: PDB Molecule: toxN; PDBTitle: a processed non-coding rna regulates a bacterial antiviral system
35	c4pkfC	Alignment	not modelled	9.1	67	PDB header: lyase Chain: C: PDB Molecule: tutf; PDBTitle: benzylsuccinate synthase alpha-beta-gamma complex
36	c5f9pA	Alignment	not modelled	9.0	44	PDB header: oxidoreductase Chain: A: PDB Molecule: anthrone oxidase-like protein; PDBTitle: crystal structure study of anthrone oxidase-like protein
37	c3fdqB	Alignment	not modelled	9.0	50	PDB header: dna binding protein/dna Chain: B: PDB Molecule: motility gene repressor mogr; PDBTitle: recognition of at-rich dna binding sites by the mogr2 repressor
38	dl1ata	Alignment	not modelled	8.8	22	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
39	c2wzpQ	Alignment	not modelled	8.6	55	PDB header: viral protein Chain: Q: PDB Molecule: lactococcal phage p2 orf15; PDBTitle: structures of lactococcal phage p2 baseplate shed light on 2 a novel mechanism of host attachment and activation in 3 siphoviridae
40	c2x5aT	Alignment	not modelled	8.5	55	PDB header: viral protein Chain: T: PDB Molecule: orf15; PDBTitle: structure of the phage p2 baseplate in its activated 2 conformation with ca (part 2 of 2)
41	c5l6mA	Alignment	not modelled	8.5	43	PDB header: hydrolase Chain: A: PDB Molecule: vapb family protein; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
42	c4esiA	Alignment	not modelled	8.4	88	PDB header: hydrolase/dna Chain: A: PDB Molecule: type-2 restriction enzyme dpni; PDBTitle: restriction endonuclease dpni in complex with target dna
43	c6j54d	Alignment	not modelled	8.1	75	PDB header: membrane protein Chain: D: PDB Molecule: PDBTitle: cryo-em structure of the mammalian e-state atp synthase fo section
44	c6eewC	Alignment	not modelled	7.9	22	PDB header: lyase Chain: C: PDB Molecule: aromatic-l-amino-acid decarboxylase; PDBTitle: crystal structure of catharanthus roseus tryptophan decarboxylase in 2 complex with l-tryptophan
45	c3q9cF	Alignment	not modelled	7.8	6	PDB header: hydrolase Chain: F: PDB Molecule: acetyl polyamine amidohydrolase; PDBTitle: crystal structure of h159a apah complexed with n8-acetylspermidine
46	c6gcjA	Alignment	not modelled	7.6	50	PDB header: structural protein Chain: A: PDB Molecule: hydrophobin; PDBTitle: solution structure of the roda hydrophobin from aspergillus fumigatus
47	c5fcxB	Alignment	not modelled	7.5	4	PDB header: carotenoid binding protein Chain: B: PDB Molecule: red carotenoid protein (rcp); PDBTitle: structure of anabaena (nostoc) sp. pcc 7120 red carotenoid protein 2 binding canthaxanthin
48	c3nbuC	Alignment	not modelled	7.2	27	PDB header: isomerase Chain: C: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of pgi glucose phosphate isomerase
49	c3g8rA	Alignment	not modelled	6.9	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis 2 protein e from chromobacterium violaceum atcc 12472
50	c6emoA	Alignment	not modelled	6.8	40	PDB header: transcription Chain: A: PDB Molecule: pc4 and sfrs1-interacting protein, ledgf/p75 ibd-jpo2 m1; PDBTitle: solution structure of the ledgf/p75 ibd - jpo2 (aa 1-32) complex
51	c3ljkA	Alignment	not modelled	6.8	20	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: glucose-6-phosphate isomerase from francisella tularensis.
52	c6aозD	Alignment	not modelled	6.8	16	PDB header: gene regulation Chain: D: PDB Molecule: casp8-associated protein 2; PDBTitle: crystal structure of human flash n-terminal domain c54s/c83a (crystal 2 form 1)
53	c6fmbA	Alignment	not modelled	6.7	86	PDB header: rna binding protein Chain: A: PDB Molecule: csep0064 putative effector protein; PDBTitle: crystal structure of the bec1054 rnase-like effector from the fungal 2 pathogen blumeria graminis

54	c3kngA	Alignment	not modelled	6.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: snoab; PDBTitle: crystal structure of snoab, a cofactor-independent oxygenase2 from streptomyces nogalater, determined to 1.9 resolution
55	c1ycoA	Alignment	not modelled	6.7	16	PDB header: transferase Chain: A: PDB Molecule: branched-chain phosphotransacylase; PDBTitle: crystal structure of a branched-chain phosphotransacylase from2 enterococcus faecalis v583
56	d2pvaa	Alignment	not modelled	6.6	7	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Penicillin V acylase
57	c3i4eA	Alignment	not modelled	6.4	45	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: crystal structure of isocitrate lyase from burkholderia2 pseudomallei
58	d1u0fa	Alignment	not modelled	6.4	17	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
59	c3e5bB	Alignment	not modelled	6.2	27	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.4 a crystal structure of isocitrate lyase from brucella melitensis
60	c2rilA	Alignment	not modelled	6.1	30	PDB header: oxidoreductase Chain: A: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
61	d1uufa1	Alignment	not modelled	6.1	22	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
62	d1h6za3	Alignment	not modelled	6.1	33	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Pyruvate phosphate dikinase, N-terminal domain
63	c3t0yB	Alignment	not modelled	6.0	44	PDB header: transcription regulator/protein binding Chain: B: PDB Molecule: nepr; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
64	c3menC	Alignment	not modelled	5.9	16	PDB header: hydrolase Chain: C: PDB Molecule: acetylpolymine aminohydrolase; PDBTitle: crystal structure of acetylpolymine aminohydrolase from burkholderia2 pseudomallei, iodide soak
65	c1wozA	Alignment	not modelled	5.9	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 177aa long conserved hypothetical protein (st1454); PDBTitle: crystal structure of uncharacterized protein st1454 from sulfolobus2 tokodaii
66	c5ji5A	Alignment	not modelled	5.8	22	PDB header: hydrolase Chain: A: PDB Molecule: bupha.10154.a.b1; PDBTitle: crystal structure of a histone deacetylase superfamily protein from2 burkholderia phymatumphymatum
67	c6ioxB	Alignment	not modelled	5.7	16	PDB header: transferase Chain: B: PDB Molecule: phosphotransacetylase; PDBTitle: crystal structure of porphyromonas gingivalis phosphotransacetylase in2 complex with acetyl-coa
68	c3tj6B	Alignment	not modelled	5.7	21	PDB header: protein binding/toxin Chain: B: PDB Molecule: antigenic heat-stable 120 kda protein; PDBTitle: human vinculin head domain (vh1, residues 1-258) in complex with the2 vinculin binding site of the surface cell antigen 4 (sca4-vbs-c;3 residues 812-835) from rickettsia rickettsii
69	d1gzda	Alignment	not modelled	5.6	22	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
70	c4q86B	Alignment	not modelled	5.6	14	PDB header: protein binding Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase accessory PDBTitle: ycao with amp bound
71	d1dfma	Alignment	not modelled	5.5	38	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease BgIII
72	c2qffA	Alignment	not modelled	5.4	23	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of staphylococcal complement inhibitor
73	c4e1oC	Alignment	not modelled	5.4	11	PDB header: lyase Chain: C: PDB Molecule: histidine decarboxylase; PDBTitle: human histidine decarboxylase complex with histidine methyl ester2 (hme)
74	d2af4c1	Alignment	not modelled	5.4	26	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
75	c5lnkZ	Alignment	not modelled	5.4	29	PDB header: oxidoreductase Chain: Z: PDB Molecule: mitochondrial complex i, pdsw subunit; PDBTitle: entire ovine respiratory complex i
76	d1s5qb	Alignment	not modelled	5.3	14	Fold: PAH2 domain Superfamily: PAH2 domain Family: PAH2 domain
77	d3bgea1	Alignment	not modelled	5.3	17	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
78	c5o5jO	Alignment	not modelled	5.3	21	PDB header: ribosome Chain: O: PDB Molecule: 30s ribosomal protein s15; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
79	c5aozA	Alignment	not modelled	5.2	67	PDB header: sugar binding protein Chain: A: PDB Molecule: putative cellulosomal scaffoldin protein; PDBTitle: high resolution semet structure of the third cohesin from2

					ruminococcus flavefaciens scaffoldin protein, scab
80	c5uukB_	Alignment	not modelled	5.2	21
81	c1byvA_	Alignment	not modelled	5.1	26

PDB header:apoptosis

Chain: B: **PDB Molecule:**bfl-1-specific selected peptide;

PDBTitle: human bfl-1 in complex with a bfl-1-specific selected peptide

PDB header:hormone/growth factor

Chain: A: **PDB Molecule:**protein (calcitonin);

PDBTitle: glycosylated eel calcitonin