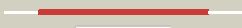


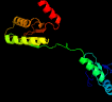
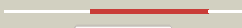






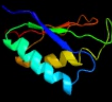

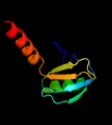







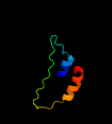
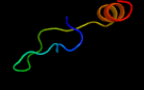
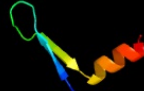

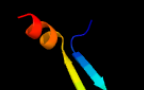

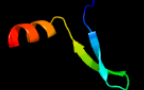
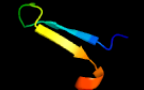
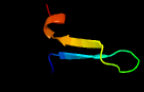
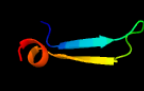


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1641_(infC)_1852280_1852885
 Date Fri Aug 2 13:30:23 BST 2019
 Unique Job ID 547f83da09c8eaf5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5lmtX_	 Alignment		100.0	53	PDB header: ribosome Chain: X: PDB Molecule: translation initiation factor if-3; PDBTitle: structure of bacterial 30s-if1-if3-mrna-trna translation pre-2 initiation complex(state-3)
2	c6nf8z_	 Alignment		100.0	17	PDB header: ribosomal protein Chain: Z: PDB Molecule: PDBTitle: structure of bacterial 30s-if1-if3-mrna-trna translation pre-2 initiation complex(state-3)
3	c2crqA_	 Alignment		100.0	19	PDB header: translation Chain: A: PDB Molecule: mitochondrial translational initiation factor 3; PDBTitle: solution structure of c-terminal domain of riken cdna2 2810012114
4	c2m71A_	 Alignment		100.0	27	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-3; PDBTitle: solution structure of the a c-terminal domain of translation2 initiation factor if-3 from campylobacter jejuni
5	d1tiga_	 Alignment		100.0	48	Fold: IF3-like Superfamily: Translation initiation factor IF3, C-terminal domain Family: Translation initiation factor IF3, C-terminal domain
6	d2ifea_	 Alignment		100.0	41	Fold: IF3-like Superfamily: Translation initiation factor IF3, C-terminal domain Family: Translation initiation factor IF3, C-terminal domain
7	d1tifa_	 Alignment		100.0	53	Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
8	d1i96v_	 Alignment		99.9	55	Fold: IF3-like Superfamily: Translation initiation factor IF3, C-terminal domain Family: Translation initiation factor IF3, C-terminal domain
9	c6o6dA_	 Alignment		99.9	43	PDB header: ligase Chain: A: PDB Molecule: translation initiation factor if-3; PDBTitle: n-terminal domain of translation initiation factor if-3 from2 helicobacter pylori
10	d2ouxax2	 Alignment		50.0	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
11	c2m4iA_	 Alignment		47.8	14	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: solution structure of bacillus subtilis minc n-terminal domain

12	d2yvxa2	Alignment		47.5	28	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
13	d1vr9a3	Alignment		47.5	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
14	c1vr9B_	Alignment		45.9	20	PDB header: unknown function Chain: B: PDB Molecule: cbs domain protein/act domain protein; PDBTitle: crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
15	d1zfja4	Alignment		45.1	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
16	c3lhhA_	Alignment		43.1	20	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
17	c5ks7A_	Alignment		41.1	17	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: carnitine transport atp-binding protein opuca; PDBTitle: crystal structure of listeria monocytogenes opuca cbs domain dimer in2 complex with cyclic-di-amp
18	c3jtfB_	Alignment		39.7	32	PDB header: transport protein Chain: B: PDB Molecule: magnesium and cobalt efflux protein; PDBTitle: the cbs domain pair structure of a magnesium and cobalt efflux protein2 from bordetella parapertussis in complex with amp
19	d2riha1	Alignment		39.6	28	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
20	d2ooxe2	Alignment		38.1	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
21	c2yvxD_	Alignment	not modelled	37.5	28	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
22	d1k4ia_	Alignment	not modelled	36.7	20	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
23	d2yzqa2	Alignment	not modelled	36.1	23	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
24	d3ddja1	Alignment	not modelled	35.3	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
25	c2p9mD_	Alignment	not modelled	32.2	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0922; PDBTitle: crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
26	c3lfrB_	Alignment	not modelled	31.0	32	PDB header: transport protein Chain: B: PDB Molecule: putative metal ion transporter; PDBTitle: the crystal structure of a cbs domain from a putative metal ion2 transporter bound to amp from pseudomonas syringae to 1.55a
27	c3ctuB_	Alignment	not modelled	30.6	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
28	d1t23a_	Alignment	not modelled	30.2	22	Fold: Chromosomal protein MC1 Superfamily: Chromosomal protein MC1 Family: Chromosomal protein MC1

29	d1a9xa3	Alignment	not modelled	29.8	15	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
30	d1pvma4	Alignment	not modelled	28.4	28	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
31	c4gqvA_	Alignment	not modelled	27.5	22	PDB header: protein binding Chain: A: PDB Molecule: cbs domain-containing protein cbsx1, chloroplastic; PDBTitle: crystal structure of cbs-pair protein, cbsx1 from arabidopsis thaliana
32	c2qh1B_	Alignment	not modelled	27.2	28	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ta0289; PDBTitle: structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
33	c5x8oA_	Alignment	not modelled	26.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
34	c4ivnB_	Alignment	not modelled	25.1	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannac-6p
35	c4hg0A_	Alignment	not modelled	24.4	36	PDB header: transport protein Chain: A: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: crystal structure of magnesium and cobalt efflux protein corc,2 northeast structural genomics consortium (nesg) target er40
36	c4p6dA_	Alignment	not modelled	24.1	9	PDB header: lyase Chain: A: PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: structure of ribb complexed with po4 ion
37	c3ju2A_	Alignment	not modelled	24.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from sinorhizobium meliloti 1021
38	c5dotA_	Alignment	not modelled	23.6	28	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
39	c1yavB_	Alignment	not modelled	23.1	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein yukl2 from bacillus subtilis
40	c2emqA_	Alignment	not modelled	22.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
41	c3tsdA_	Alignment	not modelled	22.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
42	d2hc5a1	Alignment	not modelled	22.3	14	Fold: FlaG-like Superfamily: FlaG-like Family: FlaG-like
43	c2x3yA_	Alignment	not modelled	22.2	18	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
44	c3lmzA_	Alignment	not modelled	21.4	14	PDB header: isomerase Chain: A: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
45	c5iipA_	Alignment	not modelled	20.8	17	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter%2c atp- PDBTitle: staphylococcus aureus opuca
46	c4zexA_	Alignment	not modelled	20.0	13	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
47	c2k8vA_	Alignment	not modelled	18.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin domain-containing protein 12; PDBTitle: solution structure of oxidised erp18
48	d1vima_	Alignment	not modelled	18.9	23	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
49	d1rgra_	Alignment	not modelled	18.5	15	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
50	c3shoA_	Alignment	not modelled	18.2	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
51	c5douC_	Alignment	not modelled	18.1	27	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
52	c1zfiA_	Alignment	not modelled	17.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
						PDB header: isomerase Chain: C: PDB Molecule: arabinose 5-phosphate isomerase;

53	c2xhzC_	Alignment	not modelled	17.5	18	PDBTitle: probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
54	d1hf2a2	Alignment	not modelled	16.2	13	Fold: Cell-division inhibitor MinC, N-terminal domain Superfamily: Cell-division inhibitor MinC, N-terminal domain Family: Cell-division inhibitor MinC, N-terminal domain
55	c3owvA_	Alignment	not modelled	16.1	26	PDB header: hydrolase Chain: A: PDB Molecule: dna-entry nuclease; PDBTitle: structural insights into catalytic and substrate binding mechanisms of2 the strategic enda nuclease from streptococcus pneumoniae
56	c4nocA_	Alignment	not modelled	16.1	15	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein with cbs domains; PDBTitle: the crystal structure of a cbs domain-containing protein of unknown2 function from kribbella flavida dsm 17836.
57	c2i6kA_	Alignment	not modelled	15.3	15	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 1; PDBTitle: crystal structure of human type i ipp isomerase complexed with a2 substrate analog
58	c4dqwb_	Alignment	not modelled	15.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
59	d1qs0a_	Alignment	not modelled	14.5	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
60	c4ffnA_	Alignment	not modelled	14.4	26	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
61	c2ouxB_	Alignment	not modelled	13.8	17	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
62	d1ozia_	Alignment	not modelled	13.8	10	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
63	c4qfha_	Alignment	not modelled	13.6	29	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of a glucose-6-phosphate isomerase from trypanosoma cruzi
64	c3ljkA_	Alignment	not modelled	13.0	26	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: glucose-6-phosphate isomerase from francisella tularensis.
65	c4ot7A_	Alignment	not modelled	12.8	27	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
66	c1t10A_	Alignment	not modelled	12.7	29	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
67	c2o2cB_	Alignment	not modelled	12.5	33	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
68	d1m3sa_	Alignment	not modelled	12.5	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
69	c4z87B_	Alignment	not modelled	12.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
70	d1u0fa_	Alignment	not modelled	12.3	21	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
71	c2yvzA_	Alignment	not modelled	12.2	11	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
72	c4qfsc_	Alignment	not modelled	12.2	24	PDB header: signaling protein/inhibitor/activator Chain: C: PDB Molecule: 5'-amp-activated protein kinase subunit gamma-1; PDBTitle: structure of ampk in complex with br2-a769662core activator and2 staurosporine inhibitor
73	c2pfiA_	Alignment	not modelled	12.1	17	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein clc-ka; PDBTitle: crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
74	c6o9l6_	Alignment	not modelled	12.0	20	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
75	d1viza_	Alignment	not modelled	12.0	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
76	c2l8bA_	Alignment	not modelled	11.5	13	PDB header: hydrolase Chain: A: PDB Molecule: protein trai; PDBTitle: trai (381-569)
77	d1hm5a_	Alignment	not modelled	11.4	24	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
						PDB header: isomerase

78	c2kzhA_	Alignment	not modelled	11.1	21	Chain: A; PDB Molecule: tryptophan biosynthesis protein trpcf; PDBTitle: three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
79	d2g0wa1	Alignment	not modelled	11.0	24	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lol1-like
80	d1jr1a4	Alignment	not modelled	10.9	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
81	c3eukC_	Alignment	not modelled	10.8	17	PDB header: cell cycle Chain: C; PDB Molecule: chromosome partition protein mukb, linker; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpgammas complex, asymmetric dimer
82	c3zigA_	Alignment	not modelled	10.5	22	PDB header: cell cycle Chain: A; PDB Molecule: sepf-like protein; PDBTitle: sepf-like protein from pyrococcus furiosus
83	c2zdsB_	Alignment	not modelled	10.4	32	PDB header: dna binding protein Chain: B; PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from streptomyces coelicolor a3(2)
84	c5uqiA_	Alignment	not modelled	10.4	20	PDB header: isomerase Chain: A; PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p
85	c3fxaA_	Alignment	not modelled	10.0	20	PDB header: sugar binding protein Chain: A; PDB Molecule: sis domain protein; PDBTitle: crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
86	c3m1rF_	Alignment	not modelled	9.9	29	PDB header: hydrolase Chain: F; PDB Molecule: formimidoylglutamase; PDBTitle: the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
87	c4p9gA_	Alignment	not modelled	9.8	12	PDB header: oxidoreductase Chain: A; PDB Molecule: 2,4'-dihydroxyacetophenone dioxygenase; PDBTitle: structure of the 2,4'-dihydroxyacetophenone dioxygenase from2 alcaligenes sp.
88	c21liA_	Alignment	not modelled	9.8	27	PDB header: transcription Chain: A; PDB Molecule: hltf protein; PDBTitle: nmr structure of the hltf hiran domain
89	d1x94a_	Alignment	not modelled	9.7	11	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
90	d1vjea_	Alignment	not modelled	9.6	36	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
91	d1gsoa2	Alignment	not modelled	9.6	31	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
92	c4kw2A_	Alignment	not modelled	9.4	7	PDB header: isomerase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein (bd1_1873)2 from parabacteroides distasonis atcc 8503 at 2.32 a resolution
93	d1q50a_	Alignment	not modelled	9.0	29	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
94	d1gzda_	Alignment	not modelled	8.9	24	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
95	c2yt7A_	Alignment	not modelled	8.8	15	PDB header: protein transport Chain: A; PDB Molecule: amyloid beta a4 precursor protein-binding family PDBTitle: solution structure of the pdz domain of amyloid beta a42 precursor protein-binding family a member 3
96	c3k1rA_	Alignment	not modelled	8.8	13	PDB header: structural protein Chain: A; PDB Molecule: harmonin; PDBTitle: structure of harmonin npdz1 in complex with the sam-pbm of2 sans
97	c1hf2A_	Alignment	not modelled	8.7	11	PDB header: cell division protein Chain: A; PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the bacterial cell-division inhibitor minc from2 t. maritima
98	d1iata_	Alignment	not modelled	8.6	24	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
99	c3k2yD_	Alignment	not modelled	8.6	8	PDB header: nucleotide binding protein Chain: D; PDB Molecule: uncharacterized protein lp_0118; PDBTitle: crystal structure of protein lp_0118 from lactobacillus2 plantarum,northeast structural genomics consortium target3 lpr91b