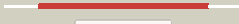


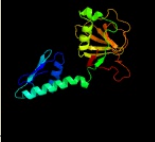
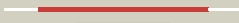
















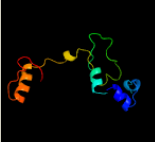








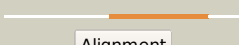
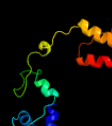
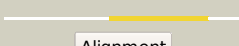
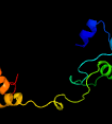


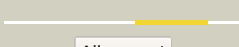

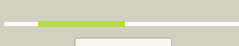


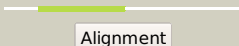
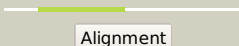
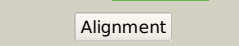
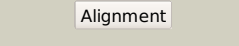
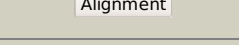
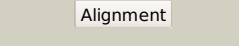
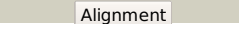


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0264c_(-)_315783_316415
Date	Tue Jul 23 14:50:32 BST 2019
Unique Job ID	4da226e186c97a40

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mmlD	 Alignment		100.0	64	PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
2	c2phcB	 Alignment		100.0	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
3	c3oepA	 Alignment		100.0	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha0988; PDBTitle: crystal structure of ttha0988 in space group p43212
4	c5dudB	 Alignment		100.0	32	PDB header: unknown function Chain: B: PDB Molecule: ybgj; PDBTitle: crystal structure of e. coli ybgjk
5	d2phcb1	 Alignment		100.0	34	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
6	c2zp2B	 Alignment		100.0	37	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis
7	c5i8iD	 Alignment		100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
8	c3va7A	 Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: kla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
9	c2kwaA	 Alignment		99.5	18	PDB header: transferase inhibitor Chain: A: PDB Molecule: kinase a inhibitor; PDBTitle: 1h, 13c and 15n backbone and side chain resonance assignments of the2 n-terminal domain of the histidine kinase inhibitor kipi from3 bacillus subtilis
10	d2phcb2	 Alignment		99.4	14	Fold: DcoH-like Superfamily: PH0987 N-terminal domain-like Family: PH0987 N-terminal domain-like
11	c2qf7A	 Alignment		97.0	15	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli

12	c3bg5B_	 Alignment		95.8	13	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
13	c5vz0D_	 Alignment		95.5	16	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
14	c3hblA_	 Alignment		95.3	13	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
15	c4hnyB_	 Alignment		90.1	11	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
16	c3tw6B_	 Alignment		89.6	10	PDB header: ligase/activator Chain: B: PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
17	c4qskB_	 Alignment		74.9	14	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of I. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
18	d1nzaa_	 Alignment		73.5	14	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
19	c3mmlE_	 Alignment		70.3	24	PDB header: hydrolase Chain: E: PDB Molecule: allophanate hydrolase subunit 2; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
20	d1nwaa_	 Alignment		62.6	18	Fold: Ferredoxin-like Superfamily: Peptide methionine sulfoxide reductase Family: Peptide methionine sulfoxide reductase
21	c1nwaA_	 Alignment	not modelled	62.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
22	c5fa9B_	 Alignment	not modelled	60.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
23	c2j89A_	 Alignment	not modelled	60.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine sulfoxide reductase a; PDBTitle: functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
24	c5dudA_	 Alignment	not modelled	57.4	16	PDB header: unknown function Chain: A: PDB Molecule: ybgk; PDBTitle: crystal structure of e. coli ybgjk
25	c4iyqB_	 Alignment	not modelled	51.5	17	PDB header: protein binding Chain: B: PDB Molecule: divalent ion tolerance protein cuta1; PDBTitle: crystal structure of divalent ion tolerance protein cuta1 from2 ehrlichia chaffeensis
26	d1osce_	 Alignment	not modelled	49.5	15	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
27	c2dy3B_	 Alignment	not modelled	48.5	18	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from corynebacterium glutamicum
28	c2k6zA_	 Alignment	not modelled	45.4	32	PDB header: metal transport Chain: A: PDB Molecule: putative uncharacterized protein ttha1943;

						PDBTitle: solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of 3 p14)
29	c3jt0B_	Alignment	not modelled	45.4	20	PDB header: structural protein Chain: B; PDB Molecule: lamin-b1; PDBTitle: crystal structure of the c-terminal fragment (426-558) lamin-b1 from2 homo sapiens, northeast structural genomics consortium target hr5546a
30	d2cbpa_	Alignment	not modelled	44.1	18	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
31	c1xk8A_	Alignment	not modelled	42.8	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: divalent cation tolerant protein cuta; PDBTitle: divalent cation tolerant protein cuta from homo sapiens o60888
32	d2zfha1	Alignment	not modelled	42.8	13	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
33	d1l0oc_	Alignment	not modelled	42.3	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
34	c1l0oC_	Alignment	not modelled	42.3	30	PDB header: protein binding Chain: C; PDB Molecule: sigma factor; PDBTitle: crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiiab with the sporulation sigma factor3 sigmaf
35	c3zk0A_	Alignment	not modelled	41.7	8	PDB header: chaperone Chain: A; PDB Molecule: sco3965; PDBTitle: the crystal structure of a cu(i) metallochaperone from2 streptomyces lividans in its apo form
36	d1mdah_	Alignment	not modelled	41.0	13	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
37	c2mntA_	Alignment	not modelled	40.9	14	PDB header: isomerase Chain: A; PDB Molecule: tbpar42; PDBTitle: solution structure of the ppiase domain of tbpar42
38	c2zfha_	Alignment	not modelled	39.4	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: cuta; PDBTitle: crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
39	c3ahpA_	Alignment	not modelled	37.4	15	PDB header: electron transport Chain: A; PDB Molecule: cuta1; PDBTitle: crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
40	c4dzaA_	Alignment	not modelled	37.1	28	PDB header: isomerase Chain: A; PDB Molecule: lysine racemase; PDBTitle: crystal structure of a lysine racemase within internal aldimine2 linkage
41	c2zomC_	Alignment	not modelled	36.9	10	PDB header: unknown function Chain: C; PDB Molecule: protein cuta, chloroplast, putative, expressed; PDBTitle: crystal structure of cuta1 from oryza sativa
42	d1whza_	Alignment	not modelled	36.7	18	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: YcfA-like
43	c1yw5A_	Alignment	not modelled	36.0	21	PDB header: isomerase Chain: A; PDB Molecule: peptidyl prolyl cis/trans isomerase; PDBTitle: peptidyl-prolyl isomerase ess1 from candida albicans
44	c4lwaA_	Alignment	not modelled	35.8	14	PDB header: oxidoreductase Chain: A; PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: crystal structure of methionine sulfoxide reductase u16c/e55a from2 clostridium oremlandii
45	d1pina2	Alignment	not modelled	35.6	36	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
46	c1kzIA_	Alignment	not modelled	35.4	15	PDB header: transferase Chain: A; PDB Molecule: riboflavin synthase; PDBTitle: riboflavin synthase from s.pombe bound to2 carboxyethylumazine
47	c3h87D_	Alignment	not modelled	35.4	26	PDB header: toxin/antitoxin Chain: D; PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
48	c6bjuD_	Alignment	not modelled	35.2	11	PDB header: unknown function Chain: D; PDB Molecule: atzh; PDBTitle: the structure of atzh: a little known member of the atrazine breakdown2 pathway
49	d1eq3a_	Alignment	not modelled	34.0	27	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
50	d1m5ya3	Alignment	not modelled	32.9	27	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
51	d1x9la_	Alignment	not modelled	31.2	28	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: DR1885-like metal-binding protein Family: DR1885-like metal-binding protein
52	d1rp3a1	Alignment	not modelled	30.7	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
53	c2lj4A_	Alignment	not modelled	30.6	36	PDB header: isomerase Chain: A; PDB Molecule: peptidyl-prolyl cis-trans isomerase/rotamase, putative; PDBTitle: solution structure of the tbpin1
						PDB header: unknown function

54	c2kz3A_	Alignment	not modelled	30.4	42	Chain: A: PDB Molecule: putative uncharacterized protein rad51i3; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
55	d1naqa_	Alignment	not modelled	30.2	13	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
56	c4e98C_	Alignment	not modelled	30.2	14	PDB header: signaling protein Chain: C: PDB Molecule: cuta1 divalent ion tolerance protein; PDBTitle: crystal structure of possible cuta1 divalent ion tolerance protein2 from cryptosporidium parvum iowa ii
57	d1o7ia_	Alignment	not modelled	30.1	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
58	d1kr4a_	Alignment	not modelled	29.9	9	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
59	c2kqaA_	Alignment	not modelled	28.2	33	PDB header: toxin Chain: A: PDB Molecule: cerato-platanin; PDBTitle: the solution structure of the fungal elicitor cerato-platanin
60	c3dm3A_	Alignment	not modelled	27.5	26	PDB header: replication Chain: A: PDB Molecule: replication factor a; PDBTitle: crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
61	c2nuhA_	Alignment	not modelled	27.2	10	PDB header: unknown function Chain: A: PDB Molecule: periplasmic divalent cation tolerance protein; PDBTitle: crystal structure of cuta from the phytopathgen bacterium xylella2 fastidiosa
62	d1mv8a1	Alignment	not modelled	26.8	18	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
63	c2rqsa_	Alignment	not modelled	26.6	18	PDB header: isomerase Chain: A: PDB Molecule: parvulin-like peptidyl-prolyl isomerase; PDBTitle: 3d structure of pin from the psychrophilic archeon cenarchaeum2 symbiosum (cspin)
64	c1f8aB_	Alignment	not modelled	26.5	36	PDB header: isomerase Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase nima-interacting 1; PDBTitle: structural basis for the phosphoserine-proline recognition by group iv2 ww domains
65	c2jzvA_	Alignment	not modelled	26.3	18	PDB header: isomerase Chain: A: PDB Molecule: foldase protein prsa; PDBTitle: solution structure of s. aureus prsa-ppiase
66	c3e0mB_	Alignment	not modelled	25.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
67	c5d1pB_	Alignment	not modelled	24.9	23	PDB header: ligase Chain: B: PDB Molecule: atp-dependent rna ligase; PDBTitle: archaeal atp-dependent rna ligase - form 2
68	c1zk6A_	Alignment	not modelled	24.6	27	PDB header: isomerase Chain: A: PDB Molecule: foldase protein prsa; PDBTitle: nmr solution structure of b. subtilis prsa ppiase
69	d1wi9a_	Alignment	not modelled	24.6	37	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PCI domain (PINT motif)
70	c2i55A_	Alignment	not modelled	23.8	40	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
71	d1ku2a1	Alignment	not modelled	23.7	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
72	c3a35B_	Alignment	not modelled	23.5	12	PDB header: luminescent protein Chain: B: PDB Molecule: lumazine protein; PDBTitle: crystal structure of lump complexed with riboflavin
73	c2ropA_	Alignment	not modelled	23.4	22	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
74	c4owxB_	Alignment	not modelled	23.3	27	PDB header: dna binding protein/dna Chain: B: PDB Molecule: soSS complex subunit b1; PDBTitle: structural basis of soSS1 in complex with a 12nt ssdna
75	c2kfuA_	Alignment	not modelled	23.0	19	PDB header: protein binding Chain: A: PDB Molecule: rv1827 pthr 22; PDBTitle: pknB-phosphorylated rv1827
76	c4tloB_	Alignment	not modelled	23.0	21	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: alanine racemase from acinetobacter baumannii
77	c4edfC_	Alignment	not modelled	22.1	16	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: dimeric hugdh, k94e
78	d1j6ya_	Alignment	not modelled	22.0	27	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
79	c2q3eH_	Alignment	not modelled	21.7	16	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose

80	d2pv2a1	Alignment	not modelled	21.7	18	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
81	c5b8iB	Alignment	not modelled	21.5	9	PDB header: hydrolase Chain: B: PDB Molecule: calcineurin subunit b, variant; PDBTitle: crystal structure of calcineurin a and calcineurin b in complex with2 fkbp12 and fk506 from coccidioides immitis rs
82	c3mlhA	Alignment	not modelled	21.3	38	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: crystal structure of the 2009 h1n1 influenza virus hemagglutinin2 receptor-binding domain
83	c3m3gA	Alignment	not modelled	21.3	33	PDB header: polysaccharide-binding protein Chain: A: PDB Molecule: ep11 protein; PDBTitle: crystal structure of sm1, an elicitor of plant defence responses from2 trichoderma virens.
84	c1pkvA	Alignment	not modelled	21.2	18	PDB header: transferase Chain: A: PDB Molecule: riboflavin synthase alpha chain; PDBTitle: the n-terminal domain of riboflavin synthase in complex with2 riboflavin
85	c1pkvB	Alignment	not modelled	21.2	18	PDB header: transferase Chain: B: PDB Molecule: riboflavin synthase alpha chain; PDBTitle: the n-terminal domain of riboflavin synthase in complex with2 riboflavin
86	c5e50A	Alignment	not modelled	21.2	17	PDB header: lyase Chain: A: PDB Molecule: aprataxin and pnk-like factor; PDBTitle: aplf/xrcc4 complex
87	c2lciA	Alignment	not modelled	21.0	35	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator rfah; PDBTitle: solution structure of rfah carboxyterminal domain
88	c2k50A	Alignment	not modelled	20.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: replication factor a related protein; PDBTitle: solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
89	c6ar2B	Alignment	not modelled	20.6	14	PDB header: membrane protein Chain: B: PDB Molecule: sarcolemmal membrane-associated protein; PDBTitle: structure of human slmap fha domain in complex with pmst2
90	c2k75A	Alignment	not modelled	20.4	17	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein ta0387; PDBTitle: solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
91	d1jsda	Alignment	not modelled	19.7	31	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
92	c3sumA	Alignment	not modelled	19.6	14	PDB header: unknown function Chain: A: PDB Molecule: cerato-platanin-like protein; PDBTitle: crystal structure of cerato-platanin 5 from m. perniciosa (mpcp5)
93	c4u9rA	Alignment	not modelled	19.4	33	PDB header: hydrolase Chain: A: PDB Molecule: czcp cation efflux p1-atpase; PDBTitle: structure of the n-terminal extension from cupriavidus metallidurans2 czcp
94	c3gpkA	Alignment	not modelled	19.3	18	PDB header: isomerase Chain: A: PDB Molecule: ppic-type peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
95	c2rmlA	Alignment	not modelled	19.3	19	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting p-type atpase copa; PDBTitle: solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
96	c2kkhA	Alignment	not modelled	19.2	15	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
97	c3qqiB	Alignment	not modelled	19.2	23	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin; PDBTitle: crystal structure of the ha1 receptor binding domain of h22 hemagglutinin
98	c2xwxB	Alignment	not modelled	19.2	38	PDB header: chitin-binding protein Chain: B: PDB Molecule: glcnac-binding protein a; PDBTitle: vibrio cholerae colonization factor gbpa crystal structure
99	d3cxa1	Alignment	not modelled	19.1	15	Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like