
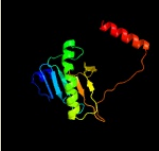







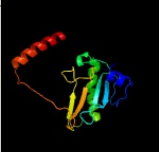







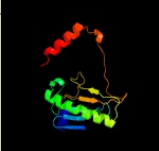
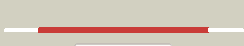
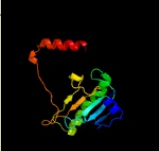




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1262c_(-)_1409944_1410378
Date	Wed Jul 31 22:05:35 BST 2019
Unique Job ID	ddb54c33e3454915

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3l7xA_	 Alignment		100.0	33	PDB header: cell cycle Chain: A: PDB Molecule: putative hit-like protein involved in cell-cycle PDBTitle: the crystal structure of smu.412c from streptococcus mutans ua159
2	c3o0mB_	 Alignment		100.0	75	PDB header: hydrolase Chain: B: PDB Molecule: hit family protein; PDBTitle: crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
3	c2eo4A_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: 150aa long hypothetical histidine triad nucleotide-binding PDBTitle: crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfobolus tokodaii strain7
4	c3p0tB_	 Alignment		100.0	29	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
5	c6iq1A_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: adenosine 5'-monophosphoramidase; PDBTitle: crystal structure of histidine triad nucleotide-binding protein from2 candida albicans
6	c3ksvA_	 Alignment		100.0	30	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: hypothetical protein from leishmania major
7	c3lb5B_	 Alignment		100.0	33	PDB header: cell cycle Chain: B: PDB Molecule: hit-like protein involved in cell-cycle regulation; PDBTitle: crystal structure of hit-like protein involved in cell-cycle2 regulation from bartonella henselae with unknown ligand
8	c3anoA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: ap-4-a phosphorylase; PDBTitle: crystal structure of a novel diadenosine 5',5'''-p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
9	c3imiB_	 Alignment		100.0	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hit family protein; PDBTitle: 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
10	d1y23a_	 Alignment		100.0	33	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
11	c5cs2A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad protein; PDBTitle: crystal structure of plasmodium falciparum diadenosine triphosphate2 hydrolase in complex with cyclomarin a

12	d1kpfA_	Alignment		100.0	32	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
13	c6d6jB_	Alignment		100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of hit family hydrolase from legionella pneumophila2 philadelphia 1
14	c4eguA_	Alignment		100.0	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: histidine triad (hit) protein; PDBTitle: 0.95a resolution structure of a histidine triad protein from2 clostridium difficile
15	d1rzya_	Alignment		100.0	32	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
16	c3n1tE_	Alignment		100.0	25	PDB header: hydrolase Chain: E: PDB Molecule: hit-like protein hint; PDBTitle: crystal structure of the h101a mutant echint gmp complex
17	d1emsal	Alignment		100.0	29	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
18	d2oika1	Alignment		100.0	19	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
19	c1emsB_	Alignment		100.0	31	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
20	c3r6fA_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: hit family protein; PDBTitle: crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
21	d1xqua_	Alignment	not modelled	100.0	32	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
22	c1xquA_	Alignment	not modelled	100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: hit family hydrolase; PDBTitle: hit family hydrolase from clostridium thermocellum cth-393
23	d1z84a2	Alignment	not modelled	100.0	12	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
24	d1fita_	Alignment	not modelled	100.0	30	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
25	c3oj7A_	Alignment	not modelled	100.0	30	PDB header: metal binding protein Chain: A: PDB Molecule: putative histidine triad family protein; PDBTitle: crystal structure of a histidine triad family protein from entamoeba2 histolytica, bound to sulfate
26	d1guqa2	Alignment	not modelled	99.9	17	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
27	c4q6jJ_	Alignment	not modelled	99.9	33	PDB header: cell cycle Chain: J: PDB Molecule: uncharacterized hit-like protein hp_0404; PDBTitle: hit like protein from helicobacter pylori 26695
28	c1zwiA_	Alignment	not modelled	99.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative galactose-1-phosphate uridyl transferase; PDBTitle: x-ray structure of galt-like protein from arabidopsis thaliana2 at5g18200

29	c4incA	Alignment	not modelled	99.9	31	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad nucleotide-binding protein 2; PDBTitle: human histidine triad nucleotide binding protein 2
30	c1gupC	Alignment	not modelled	99.9	17	PDB header: nucleotidyltransferase Chain: C: PDB Molecule: galactose-1-phosphate uridylyltransferase; PDBTitle: structure of nucleotidyltransferase complexed with udp-2 galactose
31	c5in3A	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: galactose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of glucose-1-phosphate bound nucleotidylated human2 galactose-1-phosphate uridylyltransferase
32	c3i24B	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of a hit family hydrolase protein from vibrio2 fischeri. northeast structural genomics consortium target id vfr176
33	c3oheA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
34	c3nrdB	Alignment	not modelled	99.9	19	PDB header: nucleotide binding protein Chain: B: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
35	c3i4sB	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: histidine triad protein; PDBTitle: crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
36	c4ndgB	Alignment	not modelled	99.7	26	PDB header: dna binding protein/rna/dna Chain: B: PDB Molecule: aprataxin; PDBTitle: human aprataxin (aptx) bound to rna-dna and zn - adenosine vanadate2 transition state mimic complex
37	c3splC	Alignment	not modelled	99.6	16	PDB header: hydrolase/dna Chain: C: PDB Molecule: aprataxin-like protein; PDBTitle: crystal structure of aprataxin ortholog hnt3 in complex with dna and2 amp
38	d1z84a1	Alignment	not modelled	99.5	17	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
39	c3jb9c	Alignment	not modelled	99.5	13	PDB header: rna binding protein/rna Chain: C: PDB Molecule: u5 snrna; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
40	c4i5wA	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: 5',5'''-p-1,p-4-tetraphosphate phosphorylase 2; PDBTitle: crystal structure of yeast ap4a phosphorylase apa2 in complex with amp
41	c6id1U	Alignment	not modelled	99.1	18	PDB header: splicing Chain: U: PDB Molecule: cwf19-like protein 2; PDBTitle: cryo-em structure of a human intron lariat spliceosome after prp432 loaded (ils2 complex) at 2.9 angstrom resolution
42	c4qvua	Alignment	not modelled	99.1	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4931 family protein (bce0241) from bacillus2 cereus atcc 10987 at 2.65 a resolution
43	d3bl9a1	Alignment	not modelled	99.1	19	Fold: HIT-like Superfamily: HIT-like Family: mRNA decapping enzyme DcpS C-terminal domain
44	c3bl9B	Alignment	not modelled	99.0	19	PDB header: hydrolase Chain: B: PDB Molecule: scavenger mrna-decapping enzyme dcps; PDBTitle: synthetic gene encoded dcps bound to inhibitor dg157493
45	d1vlra1	Alignment	not modelled	98.9	17	Fold: HIT-like Superfamily: HIT-like Family: mRNA decapping enzyme DcpS C-terminal domain
46	c1xmlA	Alignment	not modelled	98.8	19	PDB header: chaperone Chain: A: PDB Molecule: heat shock-like protein 1; PDBTitle: structure of human dcps
47	c6gbsB	Alignment	not modelled	98.8	22	PDB header: hydrolase Chain: B: PDB Molecule: putative mrna decapping protein; PDBTitle: crystal structure of the c. thermophilum scavenger decapping enzyme2 dcps apo form
48	c5bv3C	Alignment	not modelled	98.7	14	PDB header: hydrolase Chain: C: PDB Molecule: m7gpppx diphosphatase; PDBTitle: yeast scavenger decapping enzyme in complex with m7gdp
49	d1guqa1	Alignment	not modelled	98.3	18	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
50	d2pofa1	Alignment	not modelled	94.7	17	Fold: HIT-like Superfamily: HIT-like Family: CDH-like
51	c4lvjA	Alignment	not modelled	84.1	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: plasmid recombination enzyme; PDBTitle: mobm relaxase domain (mobv; mob_pre) bound to plasmid pmv158 orit dna2 (22nt). mn-bound crystal structure at ph 5.5
52	c3vg8F	Alignment	not modelled	30.8	12	PDB header: unknown function Chain: F: PDB Molecule: hypothetical protein tthb210; PDBTitle: crystal structure of hypothetical protein tthb210 from thermus2 thermophilus hb8
53	c3csqC	Alignment	not modelled	29.1	14	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
54	c2ef0A	Alignment	not modelled	28.7	10	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from

						thermus2 thermophilus
55	c3sdsA	Alignment	not modelled	18.2	17	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, mitochondrial; PDBTitle: crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
56	d1uf0a	Alignment	not modelled	17.7	3	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
57	c4g6uB	Alignment	not modelled	17.6	12	PDB header: toxin Chain: B: PDB Molecule: ec869 cdii; PDBTitle: cdia-ct/cdii toxin and immunity complex from escherichia coli
58	d1duvg1	Alignment	not modelled	16.5	19	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
59	c4zqvA	Alignment	not modelled	16.3	14	PDB header: immune system Chain: A: PDB Molecule: cdii immunity protein; PDBTitle: cdii immunity protein from yersinia kristensenii
60	c3txxD	Alignment	not modelled	16.0	15	PDB header: transferase Chain: D: PDB Molecule: putrescine carbamoyltransferase; PDBTitle: crystal structure of putrescine transcarbamylase from enterococcus2 faecalis
61	d1vlva1	Alignment	not modelled	15.6	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
62	c5mkwA	Alignment	not modelled	14.8	21	PDB header: hydrolase Chain: A: PDB Molecule: dna annealing helicase and endonuclease zranb3; PDBTitle: crystal structure of the human zranb3 hnh domain
63	c3tpfF	Alignment	not modelled	14.6	12	PDB header: transferase Chain: F: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
64	d2at2a1	Alignment	not modelled	13.3	15	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
65	d1otha1	Alignment	not modelled	12.8	11	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
66	d1mg4a	Alignment	not modelled	12.5	3	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
67	c2dnfA	Alignment	not modelled	12.4	10	PDB header: protein binding Chain: A: PDB Molecule: doublecortin domain-containing protein 2; PDBTitle: solution structure of rsgi ruh-062, a dcx domain from human
68	c5nngA	Alignment	not modelled	12.3	13	PDB header: transferase Chain: A: PDB Molecule: ctatc; PDBTitle: aspartate transcarbamoylase from chaetomium thermophilum cad-like2 bound to carbamoyl phosphate
69	c3bddD	Alignment	not modelled	11.6	8	PDB header: transcription Chain: D: PDB Molecule: regulatory protein marr; PDBTitle: crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
70	c2qwwB	Alignment	not modelled	11.6	0	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
71	c4f2gA	Alignment	not modelled	11.6	13	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase 1; PDBTitle: the crystal structure of ornithine carbamoyltransferase from2 burkholderia thailandensis e264
72	d1ml4a1	Alignment	not modelled	11.5	15	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
73	c2rgwD	Alignment	not modelled	11.4	9	PDB header: transferase Chain: D: PDB Molecule: aspartate carbamoyltransferase; PDBTitle: catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
74	d1dxha1	Alignment	not modelled	11.4	15	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
75	c3gd5D	Alignment	not modelled	11.1	11	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
76	d1p4da	Alignment	not modelled	11.1	12	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Relaxase domain
77	d1tuga1	Alignment	not modelled	10.9	15	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
78	d1ekxa1	Alignment	not modelled	10.7	15	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
79	d2it9a1	Alignment	not modelled	10.5	4	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: PMN2A0962/syc2379c-like
						PDB header: hydrolase Chain: I: PDB Molecule: neuronal migration protein doublecortin;

80	c4atul_	Alignment	not modelled	10.4	3	PDBTitle: human doublecortin n-dc repeat plus linker, and tubulin (2xrp) docked2 into an 8a cryo-em map of doublecortin-stabilised microtubules3 reconstructed in absence of kinesin
81	d1pvva1	Alignment	not modelled	10.4	13	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
82	c3zf7a_	Alignment	not modelled	10.2	13	PDB header: ribosome Chain: A: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
83	d2nvna1	Alignment	not modelled	10.0	21	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: PMN2A0962/syc2379c-like
84	c5kevB_	Alignment	not modelled	9.9	14	PDB header: signaling protein Chain: B: PDB Molecule: vtrc protein; PDBTitle: vibrio parahaemolyticus vtra/vtrc complex
85	c4oh7B_	Alignment	not modelled	9.6	20	PDB header: transferase Chain: B: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from brucella2 melitensis
86	c5g1oF_	Alignment	not modelled	9.6	6	PDB header: transferase Chain: F: PDB Molecule: cad protein; PDBTitle: aspartate transcarbamoylase domain of human cad in apo form
87	c5ubaA_	Alignment	not modelled	9.4	14	PDB header: rna binding protein Chain: A: PDB Molecule: rna pseudouridylylase synthase domain-containing protein 4; PDBTitle: human rna pseudouridylylase synthase domain containing 4
88	d1mjda_	Alignment	not modelled	9.3	3	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
89	c1pg5A_	Alignment	not modelled	9.2	15	PDB header: transferase Chain: A: PDB Molecule: aspartate carbamoyltransferase; PDBTitle: crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius
90	c5ilqA_	Alignment	not modelled	9.2	6	PDB header: transferase Chain: A: PDB Molecule: aspartate carbamoyltransferase; PDBTitle: crystal structure of truncated unliganded aspartate transcarbamoylase2 from plasmodium falciparum
91	c3l6tB_	Alignment	not modelled	9.0	25	PDB header: hydrolase Chain: B: PDB Molecule: mobilization protein trai; PDBTitle: crystal structure of an n-terminal mutant of the plasmid pcu1 trai2 relaxase domain
92	c1ortD_	Alignment	not modelled	8.7	15	PDB header: transferase Chain: D: PDB Molecule: ornithine transcarbamoylase; PDBTitle: ornithine transcarbamoylase from pseudomonas aeruginosa
93	c4a18N_	Alignment	not modelled	8.3	8	PDB header: ribosome Chain: N: PDB Molecule: rpl27; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rna and proteins of molecule 1
94	c3grfA_	Alignment	not modelled	8.2	13	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
95	c5ip4E_	Alignment	not modelled	8.2	8	PDB header: transferase Chain: E: PDB Molecule: neuronal migration protein doublecortin; PDBTitle: x-ray structure of the c-terminal domain of human doublecortin
96	c1ml4A_	Alignment	not modelled	8.1	17	PDB header: transferase Chain: A: PDB Molecule: aspartate transcarbamoylase; PDBTitle: the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
97	c3py7A_	Alignment	not modelled	8.0	13	PDB header: viral protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,paxillin ld1,protein e6 PDBTitle: crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
98	d1omha_	Alignment	not modelled	8.0	12	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Relaxase domain
99	c2otcA_	Alignment	not modelled	7.9	17	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine