

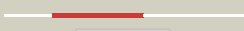






















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2289_(cdh)_2561685_2562467
Date	Mon Aug 5 13:25:43 BST 2019
Unique Job ID	c612d6fd7ba61fb2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pofa1	 Alignment		100.0	29	Fold: HIT-like Superfamily: HIT-like Family: CDH-like
2	c4q61j_	 Alignment		96.7	17	PDB header: cell cycle Chain: J: PDB Molecule: uncharacterized hit-like protein hp_0404; PDBTitle: hit like protein from helicobacter pylori 26695
3	c4incA_	 Alignment		96.5	21	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad nucleotide-binding protein 2, PDBTitle: human histidine triad nucleotide binding protein 2
4	c3n1tE_	 Alignment		96.3	12	PDB header: hydrolase Chain: E: PDB Molecule: hit-like protein hint; PDBTitle: crystal structure of the h101a mutant echint gmp complex
5	d1xqua_	 Alignment		96.0	19	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
6	c1xquA_	 Alignment		96.0	19	PDB header: hydrolase Chain: A: PDB Molecule: hit family hydrolase; PDBTitle: hit family hydrolase from clostridium thermocellum cth-393
7	d1rzva_	 Alignment		95.7	15	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
8	c6d6jB_	 Alignment		95.6	20	PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of hit family hydrolase from legionella pneumophila2 philadelphia 1
9	c3anoA_	 Alignment		95.5	15	PDB header: transferase Chain: A: PDB Molecule: ap-4-a phosphorylase; PDBTitle: crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
10	c3lb5B_	 Alignment		95.5	16	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
11	c6iq1A_	 Alignment		95.4	17	PDB header: hydrolase Chain: A: PDB Molecule: adenosine 5'-monophosphoramidase; PDBTitle: crystal structure of histidine triad nucleotide-binding protein from2 candida albicans

12	c1emsB_	 Alignment		95.3	15	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
13	d1emsa1	 Alignment		95.3	15	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
14	d1kpfa_	 Alignment		95.3	16	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
15	c4eguA_	 Alignment		95.1	17	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
16	c4ndgB_	 Alignment		95.0	15	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
17	c3oj7A_	 Alignment		94.9	21	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
18	d1z84a2	 Alignment		94.8	14	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
19	d1vlra1	 Alignment		94.7	16	Fold: HIT-like Superfamily: HIT-like Family: mRNA decapping enzyme Dcp5 C-terminal domain
20	c3l7xA_	 Alignment		94.6	13	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
21	c3ksvA_	 Alignment	not modelled	94.3	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: hypothetical protein from leishmania major
22	d3bl9a1	 Alignment	not modelled	94.1	16	Fold: HIT-like Superfamily: HIT-like Family: mRNA decapping enzyme Dcp5 C-terminal domain
23	d1fita_	 Alignment	not modelled	94.1	14	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
24	c3bl9B_	 Alignment	not modelled	93.7	16	PDB header: hydrolase Chain: B: PDB Molecule: scavenger mrna-decapping enzyme dcps; PDBTitle: synthetic gene encoded dcps bound to inhibitor dg157493
25	c2eo4A_	 Alignment	not modelled	93.6	22	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
26	c3r6fA_	 Alignment	not modelled	92.9	14	PDB header: hydrolase Chain: A: PDB Molecule: hit family protein; PDBTitle: crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
27	c3o0mB_	 Alignment	not modelled	92.4	17	PDB header: hydrolase Chain: B: PDB Molecule: hit family protein; PDBTitle: crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
28	c1xmIA_	 Alignment	not modelled	92.4	16	PDB header: chaperone Chain: A: PDB Molecule: heat shock-like protein 1; PDBTitle: structure of human dcps

29	c3splC	Alignment	not modelled	91.7	10	PDB header: hydrolase/dna Chain: C: PDB Molecule: aprataxin-like protein; PDBTitle: crystal structure of aprataxin ortholog hnt3 in complex with dna and2 amp
30	c5cs2A	Alignment	not modelled	91.4	16	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad protein; PDBTitle: crystal structure of plasmodium falciparum diadenosine triphosphate2 hydrolase in complex with cyclomarin a
31	d1guqa2	Alignment	not modelled	90.8	19	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
32	c3imiB	Alignment	not modelled	90.7	19	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'
33	d1y23a	Alignment	not modelled	90.6	15	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
34	c3p0tB	Alignment	not modelled	89.7	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
35	c1zwlA	Alignment	not modelled	88.8	14	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
36	c3i24B	Alignment	not modelled	87.5	17	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
37	d2oika1	Alignment	not modelled	86.6	15	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
38	c3nrdB	Alignment	not modelled	83.5	12	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
39	c3i4sB	Alignment	not modelled	82.7	17	PDB header: hydrolase Chain: B: PDB Molecule: histidine triad protein; PDBTitle: crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
40	c3oheA	Alignment	not modelled	81.6	13	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
41	c5bv3C	Alignment	not modelled	79.5	19	PDB header: hydrolase Chain: C: PDB Molecule: m7gpppx diphosphatase; PDBTitle: yeast scavenger decapping enzyme in complex with m7gdp
42	c1gupC	Alignment	not modelled	79.3	20	PDB header: nucleotidyltransferase Chain: C: PDB Molecule: galactose-1-phosphate uridylyltransferase; PDBTitle: structure of nucleotidyltransferase complexed with udp-2 galactose
43	c6gbsB	Alignment	not modelled	76.2	20	PDB header: hydrolase Chain: B: PDB Molecule: putative mrna decapping protein; PDBTitle: crystal structure of the c. thermophilum scavenger decapping enzyme2 dcps apo form
44	c5in3A	Alignment	not modelled	66.7	16	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
45	d1z84a1	Alignment	not modelled	40.7	10	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
46	c3bdIA	Alignment	not modelled	34.8	18	PDB header: hydrolase Chain: A: PDB Molecule: staphylococcal nuclease domain-containing PDBTitle: crystal structure of a truncated human tudor-sn
47	d1rkna	Alignment	not modelled	33.9	11	Fold: OB-fold Superfamily: Staphylococcal nuclease Family: Staphylococcal nuclease
48	c3jb9c	Alignment	not modelled	33.6	14	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
49	d2soba	Alignment	not modelled	33.1	12	Fold: OB-fold Superfamily: Staphylococcal nuclease Family: Staphylococcal nuclease
50	c4i5wA	Alignment	not modelled	30.5	21	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
51	c6ii7A	Alignment	not modelled	26.9	24	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: crystal structure of plasmodium falciparum adenosine deaminase2 c27q+l227i mutant co-complexed with zn ion, hypoxanthine and inosine
52	c2jvaA	Alignment	not modelled	26.3	19	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase domain protein; PDBTitle: nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
53	c2lufA	Alignment	not modelled	24.8	31	PDB header: de novo protein Chain: A: PDB Molecule: retro trp-cage peptide; PDBTitle: retro trp-cage peptide

54	d1vdla_	Alignment	not modelled	24.1	45	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
55	d2amxa1	Alignment	not modelled	21.3	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
56	c6n91A_	Alignment	not modelled	20.2	24	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: crystal structure of adenosine deaminase from vibrio cholerae2 complexed with pentostatin (deoxycoformycin)
57	c3gwhB_	Alignment	not modelled	18.8	18	PDB header: transcription Chain: B: PDB Molecule: transcriptional antiterminator (bgf family); PDBTitle: crystallographic ab initio protein solution far below atomic2 resolution
58	d1qpma_	Alignment	not modelled	18.4	0	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
59	d1tnsa_	Alignment	not modelled	17.0	13	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
60	d1k8kd2	Alignment	not modelled	15.2	36	Fold: Secretion chaperone-like Superfamily: Arp2/3 complex subunits Family: Arp2/3 complex subunits
61	c4waaA_	Alignment	not modelled	14.7	24	PDB header: protein binding/rna Chain: A: PDB Molecule: branchpoint-bridging protein; PDBTitle: crystal structure of selenomethionine msl5 protein in complex with rna2 at 2.2 a
62	c5el3D_	Alignment	not modelled	14.7	24	PDB header: rna binding protein Chain: D: PDB Molecule: kh domain-containing, rna-binding, signal transduction- PDBTitle: structure of the kh domain of t-star
63	c3dwlI_	Alignment	not modelled	14.4	27	PDB header: structural protein Chain: I: PDB Molecule: actin-related protein 2/3 complex subunit 2; PDBTitle: crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
64	c2i34B_	Alignment	not modelled	12.7	11	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: the crystal structure of class c acid phosphatase from bacillus2 anthracis with tungstate bound
65	c4qpiA_	Alignment	not modelled	12.2	32	PDB header: virus Chain: A: PDB Molecule: capsid protein vp1; PDBTitle: crystal structure of hepatitis a virus
66	c3u1dA_	Alignment	not modelled	11.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the structure of a protein with a gntr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei.
67	d1jz8a1	Alignment	not modelled	11.5	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
68	c3dnlB_	Alignment	not modelled	11.4	18	PDB header: viral protein Chain: B: PDB Molecule: hiv-1 envelope glycoprotein gp120; PDBTitle: molecular structure for the hiv-1 gp120 trimer in the b12-bound state
69	c5eltB_	Alignment	not modelled	11.3	30	PDB header: rna binding protein Chain: B: PDB Molecule: kh domain-containing, rna-binding, signal transduction- PDBTitle: structure of the qua1-kh domain of t-star in complex with uauu rna
70	d1tafa_	Alignment	not modelled	11.1	15	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
71	d1yq2a2	Alignment	not modelled	11.0	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
72	c2lvaA_	Alignment	not modelled	11.0	55	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 28; PDBTitle: nmr solution structure of the n-terminal domain of human usp28,2 northeast structural genomics consortium target ht8470a
73	c4gxwA_	Alignment	not modelled	10.9	29	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: crystal structure of a cog1816 amidohydrolase (target efi-505188) from2 burkholderia ambifaria, with bound zn
74	c2muxA_	Alignment	not modelled	10.9	50	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 25; PDBTitle: sumo2 non-covalently interacts with usp25 and downregulates its2 activity
75	d1snoa_	Alignment	not modelled	10.7	16	Fold: OB-fold Superfamily: Staphylococcal nuclease Family: Staphylococcal nuclease
76	c6giyA_	Alignment	not modelled	10.0	20	PDB header: structural protein Chain: A: PDB Molecule: tsfs; PDBTitle: the baseplate complex from the type vi secretion system
77	c2rrIA_	Alignment	not modelled	10.0	16	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik
78	c2lugA_	Alignment	not modelled	9.8	50	PDB header: lipid binding protein Chain: A: PDB Molecule: myelin basic protein; PDBTitle: solution nmr structure of a s72-s107 peptide of 18.5kda murine myelin2 basic protein (mbp) in association with dodecylphosphocholine3 micelles
79	d2fnaa1	Alignment	not modelled	9.8	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

						Family: Helicase DNA-binding domain
80	d1a4ma_	Alignment	not modelled	9.8	24	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
81	c2p9ID_	Alignment	not modelled	9.8	36	PDB header: structural protein Chain: D; PDB Molecule: actin-related protein 2/3 complex subunit 2; PDBTitle: crystal structure of bovine arp2/3 complex
82	c3rysA_	Alignment	not modelled	9.3	33	PDB header: hydrolase Chain: A; PDB Molecule: adenosine deaminase 1; PDBTitle: the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
83	d2h8pc1	Alignment	not modelled	9.1	17	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
84	d2qlia1	Alignment	not modelled	8.9	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
85	c5ow4A_	Alignment	not modelled	8.8	11	PDB header: membrane protein Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protease-resistant fragment of the trypanosoma2 cruzi gamete fusion protein hap2 ectodomain
86	d1vfla1	Alignment	not modelled	8.7	24	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
87	d1j26a_	Alignment	not modelled	8.5	16	Fold: dsRBD-like Superfamily: Peptidyl-tRNA hydrolase domain-like Family: Peptidyl-tRNA hydrolase domain
88	c6b8pG_	Alignment	not modelled	8.3	15	PDB header: metal transport Chain: G; PDB Molecule: potassium voltage-gated channel subfamily kqt member 4; PDBTitle: crystal structure of the mg2+/cam:kv7.4 (kcnq4) ab domain complex
89	d1t0ga_	Alignment	not modelled	8.3	22	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Steroid-binding domain
90	d1es6a2	Alignment	not modelled	8.3	43	Fold: EV matrix protein Superfamily: EV matrix protein Family: EV matrix protein
91	d1iufa1	Alignment	not modelled	8.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
92	d2fhzb1	Alignment	not modelled	7.2	12	Fold: Colicin D/E5 nuclease domain Superfamily: Colicin D/E5 nuclease domain Family: Colicin E5 nuclease domain
93	c3gwrA_	Alignment	not modelled	7.1	17	PDB header: protein binding Chain: A; PDB Molecule: putative calcium/calmodulin-dependent protein kinase type PDBTitle: crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
94	d2ihoa2	Alignment	not modelled	6.9	29	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: MOA C-terminal domain-like
95	c2k2wA_	Alignment	not modelled	6.9	20	PDB header: cell cycle Chain: A; PDB Molecule: recombination and dna repair protein; PDBTitle: second brct domain of nbs1
96	c4jvhA_	Alignment	not modelled	6.9	19	PDB header: rna binding protein Chain: A; PDB Molecule: protein quaking; PDBTitle: structure of the star domain of quaking protein in complex with rna
97	d2b1xa1	Alignment	not modelled	6.9	11	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
98	c6b0nG_	Alignment	not modelled	6.7	19	PDB header: viral protein/immune system Chain: G; PDB Molecule: envelope glycoprotein gp140; PDBTitle: crystal structure of the cleavage-independent prefusion hiv env2 glycoprotein trimer of the clade a bg505 isolate (nfl construct) in3 complex with fabs pgt122 and pgv19 at 3.39 a
99	c3et4A_	Alignment	not modelled	6.5	14	PDB header: hydrolase Chain: A; PDB Molecule: outer membrane protein p4, nadp phosphatase; PDBTitle: structure of recombinant haemophilus influenzae e(p4) acid phosphatase