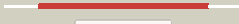
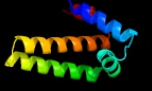


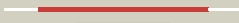


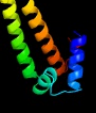

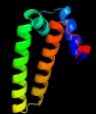

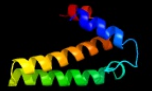







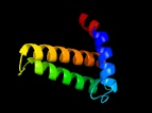


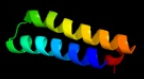










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2122c_(hisE)_2380671_2380952
Date	Mon Aug 5 13:25:24 BST 2019
Unique Job ID	59ad587bffb7f5a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y6xa1	 Alignment		100.0	99	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
2	d2a7wa1	 Alignment		100.0	28	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
3	c2a7wF_	 Alignment		100.0	28	PDB header: hydrolase Chain: F: PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
4	c1yvWd_	 Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp2 pyrophosphohydrolase from bacillus cereus. nesgc target3 bcr13.
5	d1yvwa1	 Alignment		100.0	25	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
6	d1yxbal	 Alignment		100.0	52	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
7	d1vmga_	 Alignment		98.1	23	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
8	c2yxhB_	 Alignment		97.9	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mazg-related protein; PDBTitle: crystal structure of mazg-related protein from thermotoga maritima
9	c2q9lA_	 Alignment		97.7	24	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
10	d2a3qa1	 Alignment		97.7	24	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
11	c3crcB_	 Alignment		97.7	26	PDB header: hydrolase Chain: B: PDB Molecule: protein mazg; PDBTitle: crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response

12	d2gtad1	Alignment		97.6	27	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
13	c3obcB_	Alignment		97.6	16	PDB header: hydrolase Chain: B: PDB Molecule: pyrophosphatase; PDBTitle: crystal structure of a pyrophosphatase (af1178) from archaeoglobus2 fulgidus at 1.80 a resolution
14	c2q4pA_	Alignment		97.6	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein rs21-c6; PDBTitle: ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
15	d2oiea1	Alignment		97.4	25	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
16	d2gtaa1	Alignment		97.4	29	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
17	c2vf3F_	Alignment		94.6	33	PDB header: hydrolase Chain: F: PDB Molecule: mazg-like nucleoside triphosphate pyrophosphohydrolase; PDBTitle: crystal structure of dr2231, the mazg-like protein from deinococcus2 radiodurans, complex with manganese
18	c2rfpA_	Alignment		69.8	14	PDB header: hydrolase Chain: A: PDB Molecule: putative ntp pyrophosphohydrolase; PDBTitle: crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
19	c2p06A_	Alignment		31.1	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af_0060; PDBTitle: crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304
20	d2p06a1	Alignment		31.1	21	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: AF0060-like
21	c4riqU_	Alignment	not modelled	28.0	14	PDB header: transferase/protein binding Chain: U: PDB Molecule: set1/ash2 histone methyltransferase complex subunit ash2; PDBTitle: crystal structure of dpy-30 dimerization/docking domain in complex2 with ash2l sdc1-dpy-30 interacting region (sdi)
22	c4riqI_	Alignment	not modelled	28.0	14	PDB header: transferase/protein binding Chain: I: PDB Molecule: set1/ash2 histone methyltransferase complex subunit ash2; PDBTitle: crystal structure of dpy-30 dimerization/docking domain in complex2 with ash2l sdc1-dpy-30 interacting region (sdi)
23	c4riqC_	Alignment	not modelled	28.0	14	PDB header: transferase/protein binding Chain: C: PDB Molecule: set1/ash2 histone methyltransferase complex subunit ash2; PDBTitle: crystal structure of dpy-30 dimerization/docking domain in complex2 with ash2l sdc1-dpy-30 interacting region (sdi)
24	c4riqR_	Alignment	not modelled	28.0	14	PDB header: transferase/protein binding Chain: R: PDB Molecule: set1/ash2 histone methyltransferase complex subunit ash2; PDBTitle: crystal structure of dpy-30 dimerization/docking domain in complex2 with ash2l sdc1-dpy-30 interacting region (sdi)
25	c4riqF_	Alignment	not modelled	28.0	14	PDB header: transferase/protein binding Chain: F: PDB Molecule: set1/ash2 histone methyltransferase complex subunit ash2; PDBTitle: crystal structure of dpy-30 dimerization/docking domain in complex2 with ash2l sdc1-dpy-30 interacting region (sdi)
26	c4riqO_	Alignment	not modelled	28.0	14	PDB header: transferase/protein binding Chain: O: PDB Molecule: set1/ash2 histone methyltransferase complex subunit ash2; PDBTitle: crystal structure of dpy-30 dimerization/docking domain in complex2 with ash2l sdc1-dpy-30 interacting region (sdi)
						PDB header: transferase/protein binding Chain: L: PDB Molecule: set1/ash2 histone methyltransferase

27	c4riqL_	Alignment	not modelled	28.0	14	complex subunit ash2; PDBTitle: crystal structure of dpy-30 dimerization/docking domain in complex2 with ash2l sdc1-dpy-30 interacting region (sdi)
28	c4riqX_	Alignment	not modelled	28.0	14	PDB header: transferase/protein binding Chain: X: PDB Molecule: set1/ash2 histone methyltransferase complex subunit ash2; PDBTitle: crystal structure of dpy-30 dimerization/docking domain in complex2 with ash2l sdc1-dpy-30 interacting region (sdi)
29	c6dmpA_	Alignment	not modelled	21.4	41	PDB header: de novo protein Chain: A: PDB Molecule: designed orthogonal protein dhd13_xaaa_a; PDBTitle: de novo design of a protein heterodimer with specificity mediated by2 hydrogen bond networks
30	c2a2oG_	Alignment	not modelled	20.1	24	PDB header: transcription Chain: G: PDB Molecule: hypothetical protein bt3146; PDBTitle: crystal structure of a putativetena family transcriptional regulator2 (bt_3146) from bacteroides thetaiotaomicron vpi-5482 at 2.16 a3 resolution
31	c4m3lC_	Alignment	not modelled	19.7	21	PDB header: ligase Chain: C: PDB Molecule: e3 ubiquitin-protein ligase trim63; PDBTitle: crystal structure of the coiled coil domain of murf1
32	c2v75A_	Alignment	not modelled	17.7	33	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: n-terminal domain of nab2
33	c6in7B_	Alignment	not modelled	17.1	15	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto)
34	d2a2ma1	Alignment	not modelled	17.0	24	Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: TENA/THI-4
35	d1w1we_	Alignment	not modelled	16.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rad21/Rec8-like
36	c1w1wF_	Alignment	not modelled	16.7	19	PDB header: cell adhesion Chain: F: PDB Molecule: sister chromatid cohesion protein 1; PDBTitle: sc smc1hd:scc1-c complex, atpgs
37	c3hjlA_	Alignment	not modelled	15.7	13	PDB header: proton transport Chain: A: PDB Molecule: flagellar motor switch protein flig; PDBTitle: the structure of full-length flig from aquifex aeolicus
38	c3pl4A_	Alignment	not modelled	14.2	14	PDB header: motor protein Chain: A: PDB Molecule: flagellar motor switch protein; PDBTitle: crystal structure of flig (residue 116-343) from h. pylori
39	c2z1dA_	Alignment	not modelled	14.2	7	PDB header: metal binding protein Chain: A: PDB Molecule: hydrogenase expression/formation protein hypd; PDBTitle: crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
40	c2l27B_	Alignment	not modelled	14.1	14	PDB header: membrane protein, peptide binding protei Chain: B: PDB Molecule: peptide agonist; PDBTitle: nmr structure of the ecd1 of crf-r1 in complex with a peptide agonist
41	d2zjrk1	Alignment	not modelled	13.5	18	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
42	c2rmfA_	Alignment	not modelled	13.2	11	PDB header: hormone Chain: A: PDB Molecule: urocortin; PDBTitle: human urocortin 1
43	c4uoiB_	Alignment	not modelled	12.9	20	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: unexpected structure for the n-terminal domain of hepatitis c virus2 envelope glycoprotein e1
44	c6huxA_	Alignment	not modelled	12.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: h(2)-forming methylenetetrahydromethanopterin PDBTitle: hmdii from methanocaldococcus jannaschii reconstituted with fe-2 guanylylpyridinol (fegp) cofactor and co-crystallized with methenyl-3 tetrahydromethanopterin at 2.5 a resolution
45	d1ov9a_	Alignment	not modelled	12.0	10	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
46	c6mbdC_	Alignment	not modelled	11.5	26	PDB header: apoptosis Chain: C: PDB Molecule: dm1; PDBTitle: human mcl-1 in complex with the designed peptide dm1
47	c6mbdD_	Alignment	not modelled	11.5	26	PDB header: apoptosis Chain: D: PDB Molecule: dm1; PDBTitle: human mcl-1 in complex with the designed peptide dm1
48	d1bpoa1	Alignment	not modelled	11.1	26	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Clathrin heavy-chain linker domain
49	c2ip6A_	Alignment	not modelled	10.8	18	PDB header: antimicrobial protein Chain: A: PDB Molecule: papb; PDBTitle: crystal structure of pedb
50	c4yddF_	Alignment	not modelled	10.7	8	PDB header: oxidoreductase Chain: F: PDB Molecule: dmsu reductase family type ii enzyme, iron-sulfur subunit; PDBTitle: crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps
51	c6nd4l_	Alignment	not modelled	10.0	16	PDB header: ribosome Chain: I: PDB Molecule: utp8; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
						PDB header: ribosome

52	c5o600_	Alignment	not modelled	10.0	32	Chain: O: PDB Molecule: 50s ribosomal protein l17; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
53	c4uqwA_	Alignment	not modelled	9.7	17	PDB header: chaperone Chain: A: PDB Molecule: protein clpv1; PDBTitle: coevolution of the atpase clpv, the tssb-tssc sheath and2 the accessory hsie protein distinguishes two type vi3 secretion classes
54	c4yt2A_	Alignment	not modelled	9.5	18	PDB header: metal binding protein Chain: A: PDB Molecule: h(2)-forming methylenetetrahydromethanopterin PDBTitle: hmd ii from methanocaldococcus jannaschii
55	c5ipmF_	Alignment	not modelled	9.5	24	PDB header: transcription, transferase/dna/rna Chain: F: PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
56	c6c03A_	Alignment	not modelled	9.2	12	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
57	c2rkka_	Alignment	not modelled	9.1	9	PDB header: lipid transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein vta1; PDBTitle: crystal structure of s.cerevisiae vta1 n-terminal domain
58	c3j3vN_	Alignment	not modelled	9.0	23	PDB header: ribosome Chain: N: PDB Molecule: 50s ribosomal protein l17; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
59	c4xngC_	Alignment	not modelled	8.8	18	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein mg218.1; PDBTitle: central domain of mycoplasma genitalium terminal organelle protein2 mg491
60	c5tgyA_	Alignment	not modelled	8.1	26	PDB header: unknown function Chain: A: PDB Molecule: ps1; PDBTitle: nmr structure of holo-ps1
61	c2lo0B_	Alignment	not modelled	7.9	14	PDB header: protein binding Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the get5 carboxyl domain from a. fumigatus
62	c5fztB_	Alignment	not modelled	7.5	33	PDB header: structural protein Chain: B: PDB Molecule: rho gtpase-activating protein 7; PDBTitle: the crystal structure of r7r8 in complex with a dlc12 fragment.
63	c2ltuA_	Alignment	not modelled	7.5	16	PDB header: transferase Chain: A: PDB Molecule: 5'-amp-activated protein kinase catalytic subunit alpha-2; PDBTitle: solution structure of autoinhibitory domain of human amp-activated2 protein kinase catalytic subunit
64	c5cd6C_	Alignment	not modelled	7.1	20	PDB header: unknown function Chain: C: PDB Molecule: tpr-domain containing protein; PDBTitle: crystal structure of a tpr-domain containing protein (bdi_1685) from2 parabacteroides distazonis atcc 8503 at 2.26 a resolution
65	d1ryga_	Alignment	not modelled	6.8	8	Fold: Rubredoxin-like Superfamily: RNA polymerase subunits Family: RpoE2-like
66	c4wt3A_	Alignment	not modelled	6.5	40	PDB header: chaperone Chain: A: PDB Molecule: rubisco accumulation factor 1, isoform 2; PDBTitle: the n-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana
67	d1hiob_	Alignment	not modelled	6.3	12	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
68	c3zriA_	Alignment	not modelled	6.2	18	PDB header: chaperone Chain: A: PDB Molecule: clpb protein; PDBTitle: n-domain of clpv from vibrio cholerae
69	d1p3mh_	Alignment	not modelled	6.1	14	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
70	c5wurB_	Alignment	not modelled	6.1	10	PDB header: metal binding protein Chain: B: PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
71	c5x6cE_	Alignment	not modelled	6.1	7	PDB header: rna binding protein Chain: E: PDB Molecule: uncharacterized protein mj1481; PDBTitle: crystal structure of seprs-sepcyse from methanocaldococcus jannaschii
72	c5x6cF_	Alignment	not modelled	6.1	7	PDB header: rna binding protein Chain: F: PDB Molecule: uncharacterized protein mj1481; PDBTitle: crystal structure of seprs-sepcyse from methanocaldococcus jannaschii
73	d1vp7a_	Alignment	not modelled	6.0	12	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
74	c2q00B_	Alignment	not modelled	6.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: orf c02003 protein; PDBTitle: crystal structure of the p95883_sulso protein from sulfobolbus2 solfataricus. nesg target ssr10.
75	c4hh5A_	Alignment	not modelled	5.9	16	PDB header: protein binding Chain: A: PDB Molecule: putative type vi secretion protein; PDBTitle: n-terminal domain (1-163) of clpv1 atpase from e.coli eaec sc11 t6ss.
76	c5b52B_	Alignment	not modelled	5.7	44	PDB header: transcription Chain: B: PDB Molecule: h-ns family protein mvat; PDBTitle: crystal structure of the n-terminal domain of h-ns family protein turb
						PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acyl carrier protein;

77	c2kciA_	Alignment	not modelled	5.7	12	PDBTitle: solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
78	c5w82E_	Alignment	not modelled	5.6	29	PDB header: viral protein Chain: E; PDB Molecule: protein delta; PDBTitle: crystal structure of orsay virus delta protein n-terminal fragment (aa2 1-101)
79	c2i7uA_	Alignment	not modelled	5.5	48	PDB header: de novo protein/ligand binding protein Chain: A; PDB Molecule: four-alpha-helix bundle; PDBTitle: structural and dynamical analysis of a four-alpha-helix2 bundle with designed anesthetic binding pockets
80	c5InfA_	Alignment	not modelled	5.5	6	PDB header: chaperone Chain: A; PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: solution nmr structure of farnesylated pex19, c-terminal domain
81	c2jeeA_	Alignment	not modelled	5.4	27	PDB header: cell cycle Chain: A; PDB Molecule: cell division protein zapb; PDBTitle: xray structure of e. coli yjiu
82	c4z6yD_	Alignment	not modelled	5.1	53	PDB header: hydrolase inhibitor/protein binding Chain: D; PDB Molecule: hamartin; PDBTitle: structure of the tbc1d7-tsc1 complex
83	c4z6yC_	Alignment	not modelled	5.1	53	PDB header: hydrolase inhibitor/protein binding Chain: C; PDB Molecule: hamartin; PDBTitle: structure of the tbc1d7-tsc1 complex
84	c4z6yF_	Alignment	not modelled	5.0	53	PDB header: hydrolase inhibitor/protein binding Chain: F; PDB Molecule: hamartin; PDBTitle: structure of the tbc1d7-tsc1 complex
85	d2qamn1	Alignment	not modelled	5.0	41	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17