




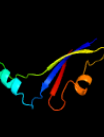







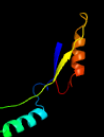



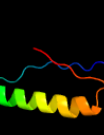
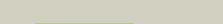
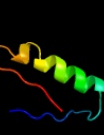

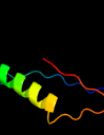
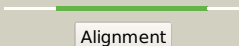

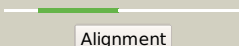
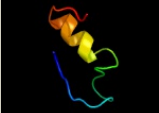
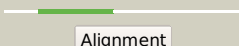

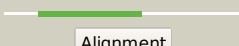
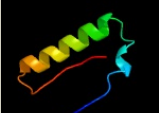
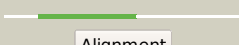
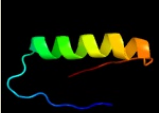
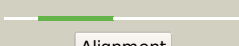
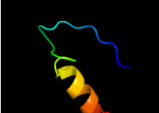

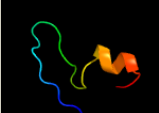

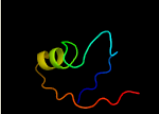


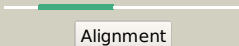
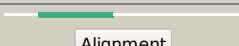


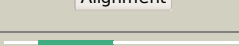
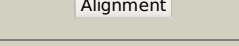
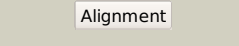

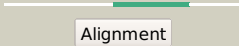


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0787A (-) _882527_882766
Date	Fri Jul 26 01:50:37 BST 2019
Unique Job ID	6dacd63e108d95a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yx5A_	 Alignment		100.0	27	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: upf0062 protein mj1593; PDBTitle: crystal structure of methanocaldococcus jannaschii purs, one of the 2 subunits of formylglycinamide ribonucleotide amidotransferase in the 3 purine biosynthetic pathway
2	d1t4aa_	 Alignment		100.0	40	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
3	d1vq3a_	 Alignment		100.0	25	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
4	c2zw2B_	 Alignment		100.0	22	PDB header: ligase Chain: B; PDB Molecule: putative uncharacterized protein sts178; PDBTitle: crystal structure of formylglycinamide ribonucleotide amidotransferase 2 iii from sulfolobus tokodaii (stpurs)
5	d1gtda_	 Alignment		100.0	25	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
6	c2dgbA_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein purs; PDBTitle: structure of thermus thermophilus purs in the p21 form
7	c1t3tA_	 Alignment		96.7	12	PDB header: ligase Chain: A; PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
8	c5y02D_	 Alignment		77.3	20	PDB header: lyase Chain: D; PDB Molecule: hydroxynitrile lyase; PDBTitle: c-terminal peptide depleted mutant of hydroxynitrile lyase from 2 passiflora edulis (pehnl) bound with (r)-mandelonitrile
9	d1tr0a_	 Alignment		69.6	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
10	c3bn7A_	 Alignment		68.6	16	PDB header: unknown function Chain: A; PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (cc_2267) from 2 caulobacter crescentus cb15 at 1.64 a resolution
11	c3bguA_	 Alignment		63.5	15	PDB header: unknown function Chain: A; PDB Molecule: ferredoxin-like protein of unknown function; PDBTitle: crystal structure of a dimeric ferredoxin-like protein of unknown 2 function (tfu_0763) from thermobifida fusca yx at 1.50 a resolution

12	c2lepA_	 Alignment		58.4	19	PDB header: hydrolase Chain: A: PDB Molecule: rhomboid protease glpg 1; PDBTitle: solution structure of n-terminal cytosolic domain of rhomboid2 intramembrane protease from escherichia coli
13	d1p6ta1	 Alignment		55.6	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
14	d1afia_	 Alignment		55.2	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
15	c2qycA_	 Alignment		54.1	15	PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
16	c5b0aA_	 Alignment		51.6	24	PDB header: lyase Chain: A: PDB Molecule: olivetolic acid cyclase; PDBTitle: polyketide cyclase oac from cannabis sativa, h5q mutant
17	d2qifa1	 Alignment		51.3	23	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
18	c2ofgX_	 Alignment		49.0	15	PDB header: hydrolase, membrane protein Chain: X: PDB Molecule: zinc-transporting atpase; PDBTitle: solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
19	d1s6ua_	 Alignment		47.3	6	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
20	c3ihsB_	 Alignment		46.1	12	PDB header: transport protein Chain: B: PDB Molecule: phosphocarrier protein hpr; PDBTitle: crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
21	d1q8la_	 Alignment	not modelled	45.5	4	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
22	c2ldia_	 Alignment	not modelled	44.1	15	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaan sub mutant
23	c2ofhX_	 Alignment	not modelled	43.6	15	PDB header: hydrolase, membrane protein Chain: X: PDB Molecule: zinc-transporting atpase; PDBTitle: solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
24	d1q4ra_	 Alignment	not modelled	43.6	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
25	d1kvja_	 Alignment	not modelled	43.3	12	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
26	c2lqbA_	 Alignment	not modelled	42.2	8	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: metal binding repeat 2 of the wilson disease protein (atp7b)
27	c6ff2A_	 Alignment	not modelled	42.0	14	PDB header: chaperone Chain: A: PDB Molecule: copper chaperone copz; PDBTitle: copz metallochaperone
28	c5t17A_	 Alignment	not modelled	41.6	23	PDB header: transferase Chain: A: PDB Molecule: phosphocarrier protein npr; PDBTitle: nmr structure of the e. coli protein npr, residues 1-85
29	d1pcha_	 Alignment	not modelled	41.5	14	Fold: HPr-like Superfamily: HPr-like

						Family: HPr-like
30	d2aw0a_	Alignment	not modelled	40.9	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
31	d1ka5a_	Alignment	not modelled	40.3	12	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
32	d1cm3a_	Alignment	not modelled	40.3	8	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
33	d1ptfa_	Alignment	not modelled	40.1	32	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
34	c2rmlA_	Alignment	not modelled	39.9	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
35	d1osda_	Alignment	not modelled	39.7	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
36	c2l3mA_	Alignment	not modelled	39.6	19	PDB header: metal binding protein Chain: A: PDB Molecule: copper-ion-binding protein; PDBTitle: solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
37	d1qr5a_	Alignment	not modelled	38.3	12	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
38	c2kkhA_	Alignment	not modelled	37.9	23	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
39	d1p6ta2	Alignment	not modelled	36.9	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
40	c2ew9A_	Alignment	not modelled	35.8	23	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
41	c1y3kA_	Alignment	not modelled	35.1	19	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the fifth domain of2 menkes protein
42	d2nzul1	Alignment	not modelled	35.0	11	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
43	c2ga7A_	Alignment	not modelled	33.5	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
44	c3bb5B_	Alignment	not modelled	33.3	22	PDB header: unknown function Chain: B: PDB Molecule: stress responsive alpha-beta protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution
45	c3le1B_	Alignment	not modelled	32.9	15	PDB header: transferase Chain: B: PDB Molecule: phosphotransferase system, hpr-related proteins; PDBTitle: crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis
46	c4u9rA_	Alignment	not modelled	32.9	19	PDB header: hydrolase Chain: A: PDB Molecule: czcp cation efflux p1-atpase; PDBTitle: structure of the n-terminal extension from cupriavidus metallidurans2 czcp
47	c3dxxX_	Alignment	not modelled	31.7	12	PDB header: hydrolase Chain: X: PDB Molecule: copper-transporting atpase ran1; PDBTitle: crystal structure of a copper binding domain from hma7, a p-2 type atpase
48	d2fgca2	Alignment	not modelled	29.8	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
49	d2hpra_	Alignment	not modelled	29.1	10	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
50	c5o5fF_	Alignment	not modelled	28.5	18	PDB header: ribosome Chain: F: PDB Molecule: 30s ribosomal protein s6; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
51	c1yjrA_	Alignment	not modelled	27.2	27	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
52	d1mola_	Alignment	not modelled	27.0	16	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
53	d1t3ta3	Alignment	not modelled	27.0	15	Fold: PurS-like Superfamily: PurS-like Family: FGAM synthase PurL, PurS-like domain
54	d1zvvj1	Alignment	not modelled	26.5	15	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
55	d1ffgb_	Alignment	not modelled	24.7	10	Fold: Ferredoxin-like Superfamily: CheY-binding domain of CheA Family: CheY-binding domain of CheA

56	c1a0oH	Alignment	not modelled	24.3	10	PDB header: chemotaxis Chain: H: PDB Molecule: chea; PDBTitle: chey-binding domain of chea in complex with chey
57	d2hmf3	Alignment	not modelled	23.4	25	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
58	c2n7yA	Alignment	not modelled	22.0	15	PDB header: metal binding protein Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: nmr structure of metal-binding domain 1 of atp7b
59	c3bdeA	Alignment	not modelled	21.9	15	PDB header: unknown function Chain: A: PDB Molecule: mll5499 protein; PDBTitle: crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from mesorhizobium loti maff303099 at 1.79 a resolution
60	d1cpza	Alignment	not modelled	21.9	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
61	d1cuka1	Alignment	not modelled	20.7	24	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
62	c3gkuB	Alignment	not modelled	20.7	7	PDB header: rna binding protein Chain: B: PDB Molecule: probable rna-binding protein; PDBTitle: crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
63	c3fmbA	Alignment	not modelled	19.9	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dimeric protein of unknown function and ferredoxin-like PDBTitle: crystal structure of dimeric protein of unknown function and2 ferredoxin-like fold (yp_212648.1) from bacteroides fragilis nctc3 9343 at 1.85 a resolution
64	d2ggpb1	Alignment	not modelled	19.3	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
65	d2pc6a2	Alignment	not modelled	17.7	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
66	c2kt2A	Alignment	not modelled	17.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
67	d2f1fa1	Alignment	not modelled	16.0	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
68	c2fgcA	Alignment	not modelled	15.8	23	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
69	c3r9lA	Alignment	not modelled	14.9	15	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: crystal structure of nucleoside diphosphate kinase from giardia2 lamblia featuring a disordered dinucleotide binding site
70	d1ogda	Alignment	not modelled	14.5	36	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
71	c3lfcC	Alignment	not modelled	14.0	18	PDB header: unknown function Chain: C: PDB Molecule: marr like protein, tvq0766549; PDBTitle: a reported archaeal mechanosensitive channel is a structural2 homolog of marr-like transcriptional regulators
72	c2gcfA	Alignment	not modelled	13.4	20	PDB header: hydrolase Chain: A: PDB Molecule: cation-transporting atpase pacs; PDBTitle: solution structure of the n-terminal domain of the copper(i) atpase2 pacs in its apo form
73	c1yg0A	Alignment	not modelled	12.9	30	PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori
74	c3bjvA	Alignment	not modelled	12.6	6	PDB header: transferase Chain: A: PDB Molecule: rmppa; PDBTitle: the crystal structure of a putative pts iia(ptxa) from streptococcus2 mutans
75	d1sjpa3	Alignment	not modelled	12.6	27	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: GroEL-like chaperone, intermediate domain
76	c2pc6C	Alignment	not modelled	11.4	15	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
77	d1iuea	Alignment	not modelled	11.0	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
78	c3dluA	Alignment	not modelled	10.9	24	PDB header: rna binding protein Chain: A: PDB Molecule: signal recognition particle 19 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
79	c2e1aD	Alignment	not modelled	10.3	10	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
80	d1lnga	Alignment	not modelled	10.3	32	Fold: SRP19 Superfamily: SRP19 Family: SRP19
81	c3hkhA	Alignment	not modelled	9.9	8	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase;

81	c3uk1A	Alignment	not modelled	9.9	0	PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144 PDB header: structural genomics, unknown function
82	c3bqsB	Alignment	not modelled	9.7	15	Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
83	c5xq0B	Alignment	not modelled	9.3	11	PDB header: signaling protein Chain: B: PDB Molecule: fermitin family homolog 2, integrin beta-1; PDBTitle: structural basis of kindlin-mediated integrin recognition and2 activation
84	d1lbuA1	Alignment	not modelled	9.2	0	Fold: PGBD-like Superfamily: PGBD-like Family: Peptidoglycan binding domain, PGBD
85	c6mk7A	Alignment	not modelled	9.2	8	PDB header: membrane protein Chain: A: PDB Molecule: cell division protein ftsx; PDBTitle: solution structure of the large extracellular loop of ftsx in2 streptococcus pneumoniae
86	c3ktwA	Alignment	not modelled	9.0	22	PDB header: rna/rna binding protein Chain: A: PDB Molecule: signal recognition particle 19 kda protein; PDBTitle: crystal structure of the srp19/s-domain srp rna complex of sulfolobus2 solfataricus
87	d1mwza	Alignment	not modelled	9.0	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
88	c3twkB	Alignment	not modelled	8.8	35	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
89	c4c9yB	Alignment	not modelled	8.8	19	PDB header: cell cycle Chain: B: PDB Molecule: spindle and kinetochore-associated protein 1; PDBTitle: structural basis for the microtubule binding of the human2 kinetochore ska complex
90	c3oxpA	Alignment	not modelled	8.8	14	PDB header: transferase Chain: A: PDB Molecule: phosphotransferase enzyme ii, a component; PDBTitle: structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
91	c3oxpB	Alignment	not modelled	8.8	14	PDB header: transferase Chain: B: PDB Molecule: phosphotransferase enzyme ii, a component; PDBTitle: structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
92	c2f1fA	Alignment	not modelled	8.6	16	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetohydroxyacid2 synthase isozyme iii from e. coli
93	d1szpa1	Alignment	not modelled	8.4	26	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
94	c1x60A	Alignment	not modelled	8.4	4	PDB header: hydrolase Chain: A: PDB Molecule: sporulation-specific n-acetylmuramoyl-l-alanine PDBTitle: solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
95	c2ec4A	Alignment	not modelled	8.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fas-associated factor 1; PDBTitle: solution structure of the uas domain from human fas-2 associated factor 1
96	d1zcaa1	Alignment	not modelled	8.1	30	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
97	c3l7pA	Alignment	not modelled	7.9	15	PDB header: transcription Chain: A: PDB Molecule: putative nitrogen regulatory protein pii; PDBTitle: crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
98	c3fp5A	Alignment	not modelled	7.9	20	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa binding protein; PDBTitle: crystal structure of acbp from monilophthora perniciosa
99	c2mjfB	Alignment	not modelled	7.8	23	PDB header: protein binding Chain: B: PDB Molecule: protein hit1; PDBTitle: solution structure of the complex between the yeast rsa1 and hit12 proteins