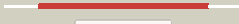



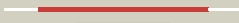

















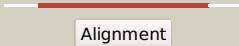

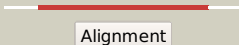

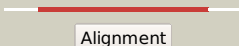



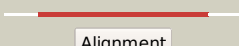

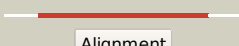

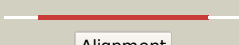






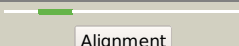
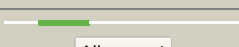

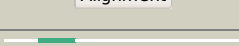
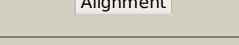
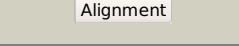
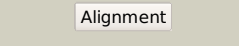


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3393_(iunH)_3808641_3809567
Date	Fri Aug 9 18:20:06 BST 2019
Unique Job ID	8bc378d38730d2d7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2masa_	 Alignment		100.0	28	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
2	c6ba1C_	 Alignment		100.0	33	PDB header: hydrolase Chain: C: PDB Molecule: inosine-uridine preferring nucleoside hydrolase; PDBTitle: purine-preferring ribonucleoside hydrolase from gardnerella vaginalis
3	c3b9xA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine-specific ribonucleoside hydrolase rihb; PDBTitle: crystal structure of the e. coli pyrimidine nucleoside hydrolase yeik2 in complex with inosine
4	c4kpnE_	 Alignment		100.0	33	PDB header: hydrolase Chain: E: PDB Molecule: nucleoside n-ribohydrolase 1; PDBTitle: plant nucleoside hydrolase - pprh1 enzyme
5	d1q8fa_	 Alignment		100.0	29	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
6	c3t8jA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: purine nucleosidase, (iunh-1); PDBTitle: structural analysis of thermostable s. solfataricus pyrimidine-2 specific nucleoside hydrolase
7	d1ezra_	 Alignment		100.0	30	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
8	c4kpoB_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: nucleoside n-ribohydrolase 3; PDBTitle: plant nucleoside hydrolase - zmrh3 enzyme
9	c3t8iC_	 Alignment		100.0	28	PDB header: hydrolase Chain: C: PDB Molecule: purine nucleosidase, (iunh-2); PDBTitle: structural analysis of thermostable s. solfataricus purine-specific2 nucleoside hydrolase
10	c6ba0D_	 Alignment		100.0	32	PDB header: hydrolase Chain: D: PDB Molecule: cytidine/uridine-specific hydrolase; PDBTitle: pyrimidine-specific ribonucleoside hydrolase from gardnerella2 vaginalis
11	c1yoeA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ybek; PDBTitle: crystal structure of a the e. coli pyrimidine nucleoside hydrolase2 ybek with bound ribose

12	c3fz0C_	 Alignment		100.0	30	PDB header: hydrolase Chain: C: PDB Molecule: nucleoside hydrolase, putative; PDBTitle: inosine-guanosine nucleoside hydrolase (ig-nh)
13	c5mj7B_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: structure of the c. elegans nucleoside hydrolase
14	c4wr2A_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine-specific ribonucleoside hydrolase riha; PDBTitle: crystal structure of a putative pyrimidine-specific ribonucleoside2 hydrolase (riha) protein from shewanella loihica pv-4 (shew_0697,3 target psi-029635) with divalent cation and peg 400 bound at the4 active site
15	c2c40B_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: inosine-uridine preferring nucleoside hydrolase family PDBTitle: crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
16	c4i74A_	 Alignment		100.0	22	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: inosine-adenosine-guanosine-nucleoside hydrolase; PDBTitle: crystal structure of the trypanosoma brucei inosine-adenosine-2 guanosine nucleoside hydrolase in complex with compound uamc-003123 and allosterically inhibited by a ni2+ ion
17	d1kica_	 Alignment		100.0	22	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
18	c4kl0A_	 Alignment		100.0	17	PDB header: calcium binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the effector protein xoo4466
19	c2yhqA_	 Alignment		99.5	21	PDB header: hydrolase Chain: A: PDB Molecule: cellulose-binding protein; PDBTitle: ab initio phasing of a nucleoside hydrolase-related hypothetical2 protein from saccharophagus degradans that is associated with3 carbohydrate metabolism
20	c5d8mA_	 Alignment		82.3	18	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
21	d1gpma1	 Alignment	not modelled	60.9	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
22	d1ccwa_	 Alignment	not modelled	57.4	20	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
23	c4ra6A_	 Alignment	not modelled	56.5	17	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of linker less pyrococcus furiosus l-asparaginase
24	c2zyiB_	 Alignment	not modelled	47.8	15	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
25	d7reqa2	 Alignment	not modelled	47.2	22	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
26	d2ocda1	 Alignment	not modelled	45.7	16	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
27	d1tcaa_	 Alignment	not modelled	45.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
28	c2p2dA_	 Alignment	not modelled	34.9	17	PDB header: transferase Chain: A: PDB Molecule: l-asparaginase i; PDBTitle: crystal structure and allosteric regulation of the cytoplasmic2 escherichia coli l-asparaginase i PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein

29	c2c5a_	Alignment	not modelled	34.0	9	thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
30	c3icvA_	Alignment	not modelled	32.2	18	PDB header: hydrolase Chain: A; PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica
31	c4ldaF_	Alignment	not modelled	31.9	22	PDB header: transcription Chain: F; PDB Molecule: tadz; PDBTitle: crystal structure of a chey-like protein (tadz) from pseudomonas2 aeruginosa pao1 at 2.70 a resolution
32	d1nnsa_	Alignment	not modelled	31.4	16	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
33	c4q0mA_	Alignment	not modelled	30.8	17	PDB header: hydrolase Chain: A; PDB Molecule: l-asparaginase; PDBTitle: crystal structure of pyrococcus furiosus l-asparaginase
34	d1o7ja_	Alignment	not modelled	29.7	24	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
35	d4pgaa_	Alignment	not modelled	28.1	22	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
36	c4r8kC_	Alignment	not modelled	26.6	19	PDB header: hydrolase Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the guinea pig l-asparaginase 1 catalytic domain
37	c1wnfA_	Alignment	not modelled	25.8	16	PDB header: hydrolase Chain: A; PDB Molecule: l-asparaginase; PDBTitle: crystal structure of ph0066 from pyrococcus horikoshii
38	d1o94c_	Alignment	not modelled	24.5	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
39	c1ni5A_	Alignment	not modelled	24.2	21	PDB header: cell cycle Chain: A; PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
40	c4kpuB_	Alignment	not modelled	24.1	14	PDB header: electron transport Chain: B; PDB Molecule: electron transfer flavoprotein alpha/beta-subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
41	c5ow0B_	Alignment	not modelled	23.8	21	PDB header: electron transport Chain: B; PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
42	d1wsaa_	Alignment	not modelled	21.4	19	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
43	c5ot0A_	Alignment	not modelled	21.1	14	PDB header: hydrolase Chain: A; PDB Molecule: l-asparaginase; PDBTitle: the thermostable l-asparaginase from thermococcus kodakarensis
44	c5ol2E_	Alignment	not modelled	20.7	15	PDB header: flavoprotein Chain: E; PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
45	c3vrhA_	Alignment	not modelled	20.6	16	PDB header: rna binding protein Chain: A; PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
46	c1y80A_	Alignment	not modelled	20.4	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
47	c3eulB_	Alignment	not modelled	20.3	15	PDB header: transcription Chain: B; PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative response2 regulator narl from mycobacterium tuberculosis
48	c3j26C_	Alignment	not modelled	19.7	26	PDB header: virus Chain: C; PDB Molecule: capsid protein v20; PDBTitle: the 3.5 a resolution structure of the sputnik virophage by cryo-em
49	c2dplA_	Alignment	not modelled	19.7	15	PDB header: ligase Chain: A; PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
50	d1agxa_	Alignment	not modelled	19.2	13	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
51	d2b3ya2	Alignment	not modelled	19.2	23	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
52	c3qz6A_	Alignment	not modelled	18.4	12	PDB header: lyase Chain: A; PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
53	d1ni5a1	Alignment	not modelled	18.4	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase

54	d2c5sa1	Alignment	not modelled	18.0	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
55	c4nzpA	Alignment	not modelled	17.5	13	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
56	d3clsc1	Alignment	not modelled	17.1	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
57	c3ss1A	Alignment	not modelled	16.5	26	PDB header: transferase Chain: A: PDB Molecule: toxin a; PDBTitle: clostridium difficile toxin a (tcda) glucosyltransferase domain
58	c6bs3A	Alignment	not modelled	15.7	20	PDB header: unknown function Chain: A: PDB Molecule: putative atpase rv3679; PDBTitle: crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
59	c2ph1A	Alignment	not modelled	14.4	10	PDB header: ligand binding protein Chain: A: PDB Molecule: nucleotide-binding protein; PDBTitle: crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
60	c4mozC	Alignment	not modelled	14.1	15	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
61	c2d6fA	Alignment	not modelled	13.9	18	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
62	d1vbk1	Alignment	not modelled	13.8	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
63	d1lk6a2	Alignment	not modelled	13.8	21	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
64	c5ghaC	Alignment	not modelled	13.5	15	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
65	c4pfxA	Alignment	not modelled	13.0	18	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: the highly conserved domain of unknown function 1792 has a distinct2 glycosyltransferase fold
66	c5v4aB	Alignment	not modelled	12.9	32	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase (duf1792); PDBTitle: a new glycosyltransferase (duf1792) from streptococcus sanguinis
67	d1qhda1	Alignment	not modelled	12.8	16	Fold: A virus capsid protein alpha-helical domain Superfamily: A virus capsid protein alpha-helical domain Family: vp6, the major capsid protein of group A rotavirus
68	d1ve5a1	Alignment	not modelled	12.8	21	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
69	d2vl8a1	Alignment	not modelled	12.2	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycosylating toxin catalytic domain-like
70	c3hv2B	Alignment	not modelled	12.1	7	PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-containing2 protein from pseudomonas fluorescens pf-5
71	c4ysbB	Alignment	not modelled	11.7	21	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of ethe1 from myxococcus xanthus
72	c4mf4F	Alignment	not modelled	11.7	22	PDB header: lyase Chain: F: PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpai aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
73	c4x91C	Alignment	not modelled	11.7	18	PDB header: transferase Chain: C: PDB Molecule: group xv phospholipase a2; PDBTitle: crystal structure of lysosomal phospholipase a2 in complex with2 isopropyl dodec-11-enylfluorophosphonate (idfp)
74	d1efvb	Alignment	not modelled	11.3	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
75	c1xtyD	Alignment	not modelled	11.2	33	PDB header: hydrolase Chain: D: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of sulfobolus solfataricus peptidyl-trna hydrolase
76	c4eo9A	Alignment	not modelled	10.9	18	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae
77	d2vk9a1	Alignment	not modelled	10.8	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycosylating toxin catalytic domain-like
78	c2d3kA	Alignment	not modelled	10.3	33	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: structural study on project id ph1539 from pyrococcus2 horikoshii ot3 PDB header: hydrolase

79	c2zv3E_	Alignment	not modelled	10.2	33	Chain: E: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
80	c3fkqA_	Alignment	not modelled	10.0	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
81	c3cseA_	Alignment	not modelled	9.8	27	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: candida glabrata dihydrofolate reductase complexed with nadph and 2,4-2 diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b)
82	c2witA_	Alignment	not modelled	9.8	16	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: the crystal structure of helicobacter pylori l-asparaginase at 1.4 a2 resolution
83	c4kr7A_	Alignment	not modelled	9.7	23	PDB header: transferase/rna Chain: A: PDB Molecule: probable trna sulfurtransferase; PDBTitle: crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
84	d2a9pa1	Alignment	not modelled	9.2	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
85	c3kqgB_	Alignment	not modelled	9.1	17	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
86	d1lw7a1	Alignment	not modelled	8.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyllyl transferase Family: Adenylyltransferase
87	d3erja1	Alignment	not modelled	8.9	33	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
88	c1zq1B_	Alignment	not modelled	8.8	18	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
89	c3fiuD_	Alignment	not modelled	8.8	20	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmn synthetase from francisella tularensis
90	c3bl5E_	Alignment	not modelled	8.8	13	PDB header: hydrolase Chain: E: PDB Molecule: queuosine biosynthesis protein quec; PDBTitle: crystal structure of quec from bacillus subtilis: an enzyme2 involved in preg1 biosynthesis
91	c4x96B_	Alignment	not modelled	8.7	12	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
92	d2bvla1	Alignment	not modelled	8.4	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycosylating toxin catalytic domain-like
93	c2j7pA_	Alignment	not modelled	8.3	16	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
94	d2d6fa2	Alignment	not modelled	8.3	14	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
95	d1umdb2	Alignment	not modelled	8.2	21	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
96	d1t1ra2	Alignment	not modelled	8.1	3	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	d2bfdb2	Alignment	not modelled	8.0	11	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
98	d1q7sa_	Alignment	not modelled	8.0	36	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
99	c1ys7B_	Alignment	not modelled	8.0	11	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+