





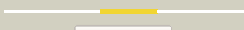

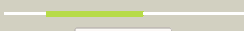

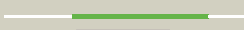
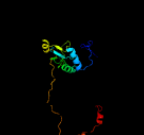




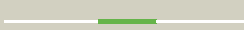





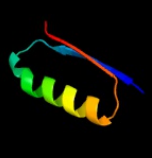

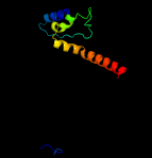

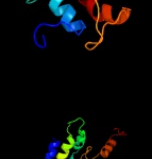
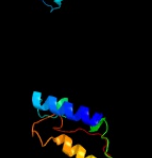


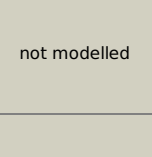


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0695 (-) _794718_795473
Date	Fri Jul 26 01:50:26 BST 2019
Unique Job ID	efdb55ef2e8c7309

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v7za_	 Alignment		100.0	30	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
2	c3no4A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: creatinine amidohydrolase; PDBTitle: crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
3	c3lubE_	 Alignment		100.0	23	PDB header: hydrolase Chain: E; PDB Molecule: putative creatinine amidohydrolase; PDBTitle: crystal structure of putative creatinine amidohydrolase (yp_211512.1)2 from bacteroides fragilis nctc 9343 at 2.11 a resolution
4	c2zqeA_	 Alignment		75.3	23	PDB header: dna binding protein Chain: A; PDB Molecule: muts2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus muts2
5	c2lndA_	 Alignment		65.8	27	PDB header: de novo protein Chain: A; PDB Molecule: de novo designed protein, pfk fold; PDBTitle: solution nmr structure of de novo designed protein, pfk fold,2 northeast structural genomics consortium target or134
6	c1un9B_	 Alignment		57.8	15	PDB header: kinase Chain: B; PDB Molecule: dihydroxyacetone kinase; PDBTitle: crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
7	c2wylF_	 Alignment		57.3	13	PDB header: hydrolase Chain: F; PDB Molecule: l-ascorbate-6-phosphate lactonase ulag; PDBTitle: apo structure of a metallo-b-lactamase
8	c4ochA_	 Alignment		56.0	20	PDB header: hydrolase Chain: A; PDB Molecule: endonuclease muts2; PDBTitle: apo structure of smr domain of muts2 from deinococcus radiodurans
9	c3qd7X_	 Alignment		54.3	16	PDB header: hydrolase Chain: X; PDB Molecule: uncharacterized protein ydal; PDBTitle: crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
10	c5t3oB_	 Alignment		47.1	18	PDB header: transferase Chain: B; PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase ii2 from thermus thermophilus
11	c3dahB_	 Alignment		45.0	20	PDB header: transferase Chain: B; PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei

12	d2qwxal	Alignment		44.6	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
13	c3lotC	Alignment		38.9	27	PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
14	c3eolB	Alignment		37.2	13	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.0a crystal structure of isocitrate lyase from brucella melitensis2 (p43212)
15	c4awaA	Alignment		36.7	13	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: legumain; PDBTitle: crystal structure of active legumain in complex with yvad-cmk2 at ph 5.0
16	c3e02A	Alignment		35.7	25	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
17	c4twbB	Alignment		34.1	20	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: sulfobolus solfataricus ribose-phosphate pyrophosphokinase
18	d1dkua1	Alignment		33.7	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
19	c3efhB	Alignment		31.1	14	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
20	c4s2uA	Alignment		29.6	18	PDB header: transferase Chain: A: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase from2 e. coli
21	c3e49A	Alignment	not modelled	29.1	23	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
22	c3c6cA	Alignment	not modelled	28.9	21	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
23	c2qv5A	Alignment	not modelled	25.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2773; PDBTitle: crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
24	d1j9ja	Alignment	not modelled	21.9	19	Fold: SurE-like Superfamily: SurE-like Family: SurE-like
25	d1u9ya1	Alignment	not modelled	21.9	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
26	c5xtuA	Alignment	not modelled	20.9	9	PDB header: hydrolase Chain: A: PDB Molecule: gdsl-family esterase; PDBTitle: crystal structure of gdsl esterase of photobacterium sp. j15
27	c3d3ja	Alignment	not modelled	20.7	4	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
						PDB header: structural genomics, unknown function

28	c2rbgB_	Alignment	not modelled	20.4	10	Chain: B: PDB Molecule: putative uncharacterized protein st0493; PDBTitle: crystal structure of hypothetical protein(st0493) from <i>Sulfolobus tokodaii</i>
29	c2amjD_	Alignment	not modelled	20.3	25	PDB header: oxidoreductase Chain: D: PDB Molecule: modulator of drug activity b; PDBTitle: crystal structure of modulator of drug activity b from <i>Escherichia coli</i> o157:h7
30	c6nfeB_	Alignment	not modelled	20.1	17	PDB header: ligase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of ribose-phosphate pyrophosphokinase from <i>Legionella pneumophila</i> with bound amp, adp, and ribose-5-phosphate
31	d2c4ka1	Alignment	not modelled	20.1	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
32	c5zbiB_	Alignment	not modelled	20.0	11	PDB header: plant protein Chain: B: PDB Molecule: peptide asparaginyl ligase; PDBTitle: crystal structure of asparaginyl endopeptidases from <i>Viola canadensis</i>
33	c3atyA_	Alignment	not modelled	19.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f2a synthase; PDBTitle: crystal structure of tcoye
34	c2c4kD_	Alignment	not modelled	19.1	14	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase-associated protein PDBTitle: crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39)
35	c5mp7C_	Alignment	not modelled	18.0	22	PDB header: transferase Chain: C: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosylpyrophosphate synthetase from <i>Mycobacterium smegmatis</i>
36	c5czdB_	Alignment	not modelled	18.0	11	PDB header: transferase Chain: B: PDB Molecule: acyl-carrier-protein; PDBTitle: the complex structure of vink with vinl
37	d1l5xa_	Alignment	not modelled	17.6	11	Fold: SurE-like Superfamily: SurE-like Family: SurE-like
38	c2phjA_	Alignment	not modelled	17.1	21	PDB header: hydrolase Chain: A: PDB Molecule: 5'-nucleotidase sure; PDBTitle: crystal structure of sure protein from <i>Aquifex aeolicus</i>
39	c5knkB_	Alignment	not modelled	16.8	13	PDB header: transferase Chain: B: PDB Molecule: lipid a biosynthesis lauroyl acyltransferase; PDBTitle: lipid a secondary acyltransferase lpxm from <i>Acinetobacter baumannii</i> 2 with catalytic residue substitution (e127a)
40	c5vcsB_	Alignment	not modelled	16.6	8	PDB header: transferase Chain: B: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n- PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound acceptor
41	c1u9yD_	Alignment	not modelled	16.5	20	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from <i>Methanocaldococcus jannaschii</i>
42	c3bv6D_	Alignment	not modelled	15.8	18	PDB header: hydrolase Chain: D: PDB Molecule: metal-dependent hydrolase; PDBTitle: crystal structure of uncharacterized metallo protein from <i>Vibrio cholerae</i> with beta-lactamase like fold
43	c2v4oB_	Alignment	not modelled	15.8	16	PDB header: hydrolase Chain: B: PDB Molecule: multifunctional protein sur e; PDBTitle: crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
44	d2cxha1	Alignment	not modelled	15.7	38	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Brix domain
45	c2cxhA_	Alignment	not modelled	15.7	38	PDB header: rna binding protein Chain: A: PDB Molecule: probable brix-domain ribosomal biogenesis protein; PDBTitle: crystal structure of probable ribosomal biogenesis protein from <i>Aeropyrum pernix</i> k1
46	c2l0dA_	Alignment	not modelled	14.8	16	PDB header: cell adhesion Chain: A: PDB Molecule: cell surface protein; PDBTitle: solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from <i>Methanosarcina acetivorans</i> , northeast structural3 genomics consortium target mvr254a
47	c4fguB_	Alignment	not modelled	14.8	9	PDB header: hydrolase Chain: B: PDB Molecule: legumain; PDBTitle: crystal structure of prolegumain
48	c2kxjA_	Alignment	not modelled	14.6	15	PDB header: protein binding Chain: A: PDB Molecule: ubx domain-containing protein 4; PDBTitle: solution structure of ubx domain of human ubxd2 protein
49	c5f34A_	Alignment	not modelled	14.3	21	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannoside acyltransferase; PDBTitle: crystal structure of membrane associated pata from <i>Mycobacterium smegmatis</i> in complex with s-hexadecyl coenzyme a - p21 space group
50	d1q6za1	Alignment	not modelled	13.6	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
51	d2ivya1	Alignment	not modelled	13.2	21	Fold: Ferredoxin-like Superfamily: TTP0101/SSO1404-like Family: TTP0101/SSO1404-like
52	c3i4eA_	Alignment	not modelled	13.0	10	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: crystal structure of isocitrate lyase from <i>Burkholderia pseudomallei</i> PDB header: transferase

53	c1dkrB_	Alignment	not modelled	12.8	21	Chain: B; PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
54	c5xgqB_	Alignment	not modelled	12.4	24	PDB header: ligase Chain: B; PDB Molecule: methionine-trna ligase; PDBTitle: crystal structure of apo form (free-state) mycobacterium tuberculosis2 methionyl-trna synthetase
55	c3d3kD_	Alignment	not modelled	12.4	7	PDB header: protein binding Chain: D; PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
56	c3no5C_	Alignment	not modelled	12.3	11	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
57	d1fxoa_	Alignment	not modelled	12.3	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
58	c5vcmA_	Alignment	not modelled	12.3	9	PDB header: transferase Chain: A; PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n- PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
59	c5jkjA_	Alignment	not modelled	11.9	16	PDB header: hydrolase Chain: A; PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
60	c2v5hB_	Alignment	not modelled	11.9	19	PDB header: transcription Chain: B; PDB Molecule: acetylglutamate kinase; PDBTitle: controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
61	d1vk8a_	Alignment	not modelled	11.8	19	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
62	c4qeaG_	Alignment	not modelled	11.2	21	PDB header: hydrolase Chain: G; PDB Molecule: 5'-nucleotidase sure; PDBTitle: crystal structure of stationary phase survival protein (sure) from2 brucella abortus
63	c4rnxA_	Alignment	not modelled	10.9	7	PDB header: oxidoreductase Chain: A; PDB Molecule: nadph dehydrogenase 1; PDBTitle: k154 circular permutation of old yellow enzyme
64	d2jgra1	Alignment	not modelled	10.9	28	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
65	c5kstA_	Alignment	not modelled	10.6	19	PDB header: hydrolase Chain: A; PDB Molecule: 5'-nucleotidase sure; PDBTitle: stationary phase survival protein e (sure) from xylella fastidiosa-2 xfsure-tsamp (tetramer smaller - crystallization with 3'amp).
66	d1jzta_	Alignment	not modelled	10.4	18	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
67	c1bdgA_	Alignment	not modelled	10.1	12	PDB header: hexokinase Chain: A; PDB Molecule: hexokinase; PDBTitle: hexokinase from schistosoma mansoni complexed with glucose
68	d2jnaa1	Alignment	not modelled	9.8	24	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
69	d1qd1a1	Alignment	not modelled	9.5	24	Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
70	d2noca1	Alignment	not modelled	9.3	27	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
71	c5gnvB_	Alignment	not modelled	9.3	50	PDB header: peptide binding protein Chain: B; PDB Molecule: microtubule-associated protein 1a; PDBTitle: structure of psd-95/map1a complex reveals unique target recognition2 mode of maguk gk domain
72	d3dtoa1	Alignment	not modelled	9.2	11	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
73	d2vbu1	Alignment	not modelled	9.2	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: CTP-dependent riboflavin kinase-like
74	d3eeqa2	Alignment	not modelled	9.1	15	Fold: CbiG N-terminal domain-like Superfamily: CbiG N-terminal domain-like Family: CbiG N-terminal domain-like
75	c6cwxB_	Alignment	not modelled	8.7	18	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease p protein subunit p25; PDBTitle: crystal structure of human ribonuclease p/mrp proteins rpp20/rpp25
76	c30thB_	Alignment	not modelled	8.7	22	PDB header: transferase/antibiotic Chain: B; PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
77	c3uuuA_	Alignment	not modelled	8.6	20	PDB header: hydrolase Chain: A; PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
78	c3bmaC_	Alignment	not modelled	8.6	10	PDB header: ligase Chain: C; PDB Molecule: d-alanyl-lipoteichoic acid synthetase; PDBTitle: crystal structure of d-alanyl-lipoteichoic acid synthetase

						from2 streptococcus pneumoniae r6
79	d1dxqa_	Alignment	not modelled	8.5	26	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
80	d1gwja_	Alignment	not modelled	8.3	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
81	c2m2jA_	Alignment	not modelled	8.2	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative periplasmic protein; PDBTitle: solution nmr structure of the n-terminal domain of stm1478 from2 salmonella typhimurium lt2: target str147a of the northeast3 structural genomics consortium (nesg), and apc101565 of the midwest4 center for structural genomics (mcsg).
82	c5dynA_	Alignment	not modelled	8.1	7	PDB header: hydrolase Chain: A: PDB Molecule: putative peptidase; PDBTitle: b. fragilis cysteine protease
83	c5l20A_	Alignment	not modelled	7.9	23	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: clostripain-related protein; PDBTitle: crystal structure of a clostripain (bt_0727) from bacteroides2 thetaiotaomicron atcc 29148 in complex with peptide inhibitor btn-3 vltk-aomk
84	c3qayC_	Alignment	not modelled	7.9	18	PDB header: lyase Chain: C: PDB Molecule: endolysin; PDBTitle: catalytic domain of cd27l endolysin targeting clostridia difficile
85	c6mywA_	Alignment	not modelled	7.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: gluconobacter ene-reductase (gluer) mutant - t36a
86	c3eeqB_	Alignment	not modelled	7.7	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cobalamin biosynthesis protein g homolog; PDBTitle: crystal structure of a putative cobalamin biosynthesis protein g2 homolog from sulfolobus solfataricus
87	d1qo7a_	Alignment	not modelled	7.7	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxyde hydrolase
88	d1yqha1	Alignment	not modelled	7.6	9	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
89	c3fniA_	Alignment	not modelled	7.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
90	c2l9wA_	Alignment	not modelled	7.4	16	PDB header: splicing, rna binding protein Chain: A: PDB Molecule: u4/u6 snrna-associated-splicing factor prp24; PDBTitle: solution structure of the c-terminal domain of prp24
91	c3ab4K_	Alignment	not modelled	7.4	10	PDB header: transferase Chain: K: PDB Molecule: aspartokinase; PDBTitle: crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
92	d2b61a1	Alignment	not modelled	7.3	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
93	c2ltfA_	Alignment	not modelled	7.3	22	PDB header: viral protein Chain: A: PDB Molecule: tail protein x; PDBTitle: the solution structure of phage p2 gpX
94	c3l1iA_	Alignment	not modelled	7.2	21	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
95	c3gr7A_	Alignment	not modelled	7.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
96	c5kolA_	Alignment	not modelled	7.2	24	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the competence-damaged protein (cina) superfamily2 protein eck1530/ec0983 from escherichia coli
97	d2bufa1	Alignment	not modelled	7.1	21	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
98	d3djba1	Alignment	not modelled	7.1	0	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
99	c2wojD_	Alignment	not modelled	7.0	30	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3