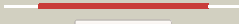



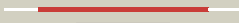






















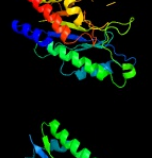
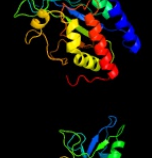
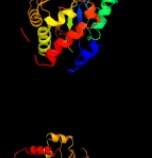
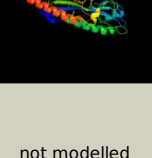


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3698 (-) _4140671_4142200
Date	Fri Aug 9 18:20:39 BST 2019
Unique Job ID	e9ea493e3abe65ce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lvwA_	 Alignment		100.0	17	PDB header: ligase Chain: A; PDB Molecule: glutamate--cysteine ligase; PDBTitle: glutathione-inhibited scgcl
2	d1r8ga_	 Alignment		100.0	19	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
3	d1tt4a_	 Alignment		100.0	18	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
4	c1tt4B_	 Alignment		100.0	18	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative cytoplasmic protein; PDBTitle: structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium
5	c2gwcE_	 Alignment		100.0	20	PDB header: ligase Chain: E; PDB Molecule: glutamate cysteine ligase; PDBTitle: crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue
6	d2d32a1	 Alignment		99.9	16	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase
7	c3nztA_	 Alignment		99.8	13	PDB header: ligase Chain: A; PDB Molecule: glutamate--cysteine ligase; PDBTitle: 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 from francisella tularensis in complex with amp
8	c3ln6A_	 Alignment		99.6	13	PDB header: ligase Chain: A; PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
9	c3ln7A_	 Alignment		99.5	13	PDB header: ligase Chain: A; PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurilla multocida
10	d2bvca2	 Alignment		98.9	22	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
11	c1htoB_	 Alignment		98.8	24	PDB header: ligase Chain: B; PDB Molecule: glutamine synthetase; PDBTitle: crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis

12	d1f52a2	Alignment		98.8	22	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
13	c3ng0A	Alignment		98.8	21	PDB header: ligase Chain: A: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
14	c4hppA	Alignment		98.7	19	PDB header: ligase Chain: A: PDB Molecule: probable glutamine synthetase; PDBTitle: crystal structure of novel glutamine synthase homolog
15	c5zlpH	Alignment		98.7	25	PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from helicobacter pylori
16	c4s17E	Alignment		98.7	23	PDB header: ligase Chain: E: PDB Molecule: glutamine synthetase; PDBTitle: the crystal structure of glutamine synthetase from bifidobacterium2 adolescentis atcc 15703
17	c5dm3A	Alignment		98.6	21	PDB header: ligase Chain: A: PDB Molecule: l-glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from chromohalobacter2 salexigens dsm 3043(csa1_0679, target efi-550015) with bound adp
18	c1fpyE	Alignment		98.6	26	PDB header: ligase Chain: E: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
19	c3qajL	Alignment		98.5	18	PDB header: ligase Chain: L: PDB Molecule: glutamine synthetase; PDBTitle: x-ray crystal structure of glutamine synthetase from bacillus subtilis2 cocrystallized with atp
20	c3o6xC	Alignment		98.2	15	PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
21	c2j9iL	Alignment	not modelled	98.1	17	PDB header: ligase Chain: L: PDB Molecule: glutamate-ammonia ligase domain-containing protein 1; PDBTitle: lengsin is a survivor of an ancient family of class i glutamine2 synthetases in eukaryotes that has undergone evolutionary re-3 engineering for a tissue-specific role in the vertebrate eye lens.
22	c2qc8J	Alignment	not modelled	98.0	18	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
23	c2d3ajL	Alignment	not modelled	97.8	18	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
24	c4baxH	Alignment	not modelled	97.2	19	PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from streptomyces2 coelicolor
25	c4is4G	Alignment	not modelled	97.0	22	PDB header: ligase Chain: G: PDB Molecule: glutamine synthetase; PDBTitle: the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer
26	c3fkyD	Alignment	not modelled	96.9	20	PDB header: ligase Chain: D: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
27	c5gorE	Alignment	not modelled	53.1	25	PDB header: hydrolase Chain: E: PDB Molecule: alkaline invertase; PDBTitle: crystal structure of alkaline invertase inva from anabaena sp. pcc2 7120
						PDB header: hydrolase

28	c5z73A_	Alignment	not modelled	49.4	20	Chain: A: PDB Molecule: alr0819 protein; PDBTitle: crystal structure of alkaline/neutral invertase invb from anabaena sp.2 pcc 7120
29	d1he1a_	Alignment	not modelled	33.7	23	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
30	d1udxa3	Alignment	not modelled	25.7	19	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
31	c5d0fB_	Alignment	not modelled	20.2	27	PDB header: sugar binding protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the candida glabrata glycogen debranching enzyme2 (e564q) in complex with maltopentaose
32	c1g5jB_	Alignment	not modelled	16.2	67	PDB header: apoptosis Chain: B: PDB Molecule: bad protein; PDBTitle: complex of bcl-xl with peptide from bad
33	c2bzwB_	Alignment	not modelled	13.3	67	PDB header: transcription Chain: B: PDB Molecule: bcl2-antagonist of cell death; PDBTitle: the crystal structure of bcl-xl in complex with full-length bad
34	d2g39a2	Alignment	not modelled	12.9	29	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
35	c3cqyA_	Alignment	not modelled	12.7	17	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetylmuramic acid kinase; PDBTitle: crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
36	c5zet2_	Alignment	not modelled	11.3	22	PDB header: ribosome Chain: 2: PDB Molecule: 50s ribosomal protein l31; PDBTitle: m. smegmatis p/p state 50s ribosomal subunit
37	d1wjpa2	Alignment	not modelled	10.3	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
38	d1k82a1	Alignment	not modelled	8.7	10	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
39	d1k3xa1	Alignment	not modelled	8.3	14	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
40	c3r87A_	Alignment	not modelled	7.7	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf6 protein from photobacterium profundum
41	c2kw0A_	Alignment	not modelled	7.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: ccmh protein; PDBTitle: solution structure of n-terminal domain of ccmh from escherichia.coli
42	d2eg6a1	Alignment	not modelled	7.5	27	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
43	d1tdza1	Alignment	not modelled	7.1	10	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
44	c2wfoA_	Alignment	not modelled	6.8	16	PDB header: viral protein Chain: A: PDB Molecule: glycoprotein 1; PDBTitle: crystal structure of machupo virus envelope glycoprotein gp1
45	c2g39A_	Alignment	not modelled	6.7	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: acetyl-coa hydrolase; PDBTitle: crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
46	c5dlcC_	Alignment	not modelled	6.7	15	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
47	c2bf9A_	Alignment	not modelled	6.7	14	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic polypeptide at 0.2 99 angstroms resolution.
48	c4bptC_	Alignment	not modelled	6.6	18	PDB header: oxidoreductase Chain: C: PDB Molecule: phenylalanine-4-hydroxylase (pah) (phe-4-monooxygenase); PDBTitle: structural and thermodynamic insight into phenylalanine2 hydroxylase from the human pathogen legionella pneumophila
49	c2c6rA_	Alignment	not modelled	6.5	9	PDB header: dna-binding protein Chain: A: PDB Molecule: dna-binding stress response protein, dps family; PDBTitle: fe-soaked crystal structure of the dps92 from deinococcus2 radiodurans
50	d1m5wa_	Alignment	not modelled	6.4	28	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
51	c3a46B_	Alignment	not modelled	6.4	8	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex
52	c2yjkF_	Alignment	not modelled	6.4	13	PDB header: metal-binding protein Chain: F: PDB Molecule: afp; PDBTitle: structure of dps from microbacterium arborescens in the2 high iron form
53	c2xgwA_	Alignment	not modelled	6.3	16	PDB header: metal binding protein Chain: A: PDB Molecule: peroxide resistance protein; PDBTitle: zinc-bound crystal structure of streptococcus pyogenes dpr
						PDB header: dna binding protein Chain: C: PDB Molecule: metalloregulation dna-binding stress

54	c2chpC	Alignment	not modelled	6.2	13	protein; PDBTitle: crystal structure of the dodecameric ferritin mrga from b. subtilis2 168
55	c2d5kC	Alignment	not modelled	6.1	15	PDB header: metal binding protein Chain: C: PDB Molecule: dps family protein; PDBTitle: crystal structure of dps from staphylococcus aureus
56	d1vs6z1	Alignment	not modelled	5.9	29	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
57	c4tq0D	Alignment	not modelled	5.8	20	PDB header: protein binding Chain: D: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
58	c1tz5A	Alignment	not modelled	5.8	10	PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
59	c4tq0B	Alignment	not modelled	5.7	20	PDB header: protein binding Chain: B: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
60	d1dpsa	Alignment	not modelled	5.7	7	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin
61	c2k47A	Alignment	not modelled	5.7	17	PDB header: replication Chain: A: PDB Molecule: phosphoprotein; PDBTitle: solution structure of the c-terminal n-rna binding domain2 of the vesicular stomatitis virus phosphoprotein
62	d1ee8a1	Alignment	not modelled	5.6	10	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
63	d1aopa4	Alignment	not modelled	5.6	21	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
64	c5npvB	Alignment	not modelled	5.6	20	PDB header: cell cycle Chain: B: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16i1(atg5bd) complex (i4)
65	c4eu4A	Alignment	not modelled	5.6	29	PDB header: transferase Chain: A: PDB Molecule: succinyl-coa:acetate coenzyme a transferase; PDBTitle: succinyl-coa: acetate coa-transferase (aarch6) in complex with coa2 (hexagonal lattice)
66	c2nvvF	Alignment	not modelled	5.5	24	PDB header: hydrolase Chain: F: PDB Molecule: acetyl-coa hydrolase/transferase family protein; PDBTitle: crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
67	d1w96c1	Alignment	not modelled	5.5	22	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
68	c2hl7A	Alignment	not modelled	5.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein cmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
69	c2gbbA	Alignment	not modelled	5.5	12	PDB header: isomerase Chain: A: PDB Molecule: putative chorismate mutase; PDBTitle: crystal structure of secreted chorismate mutase from yersinia pestis
70	c5npvD	Alignment	not modelled	5.5	20	PDB header: cell cycle Chain: D: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16i1(atg5bd) complex (i4)
71	c5npwF	Alignment	not modelled	5.5	20	PDB header: cell cycle Chain: F: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16i1(atg5bd) complex (c2)
72	c1ee8A	Alignment	not modelled	5.4	10	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
73	c5xs5B	Alignment	not modelled	5.4	58	PDB header: virus Chain: B: PDB Molecule: genome polyprotein; PDBTitle: structure of coxsackievirus a6 (cva6) virus procapsid particle
74	c2i9vA	Alignment	not modelled	5.3	21	PDB header: rna binding protein Chain: A: PDB Molecule: pre-mrna-processing factor 40 homolog a; PDBTitle: nmr structure of the ff domain l24a mutant's folding transition state
75	c4a25A	Alignment	not modelled	5.3	12	PDB header: metal binding protein Chain: A: PDB Molecule: ferritin dps family protein; PDBTitle: x-ray structure dps from kineococcus radiotolerans in2 complex with mn (ii) ions.
76	c1nnjA	Alignment	not modelled	5.3	10	PDB header: hydrolase Chain: A: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
77	c3iq1A	Alignment	not modelled	5.2	16	PDB header: metal transport Chain: A: PDB Molecule: dps family protein; PDBTitle: crystal structure of dps protein from vibrio cholerae o1, a member of2 a broad superfamily of ferritin-like diiron-carboxylate proteins
78	c4wk1A	Alignment	not modelled	5.2	32	PDB header: signaling protein Chain: A: PDB Molecule: psta; PDBTitle: crystal structure of staphylococcus aureus psta in complex with c-di-2 amp
79	c1ronA	Alignment	not modelled	5.1	9	PDB header: neuropeptide Chain: A: PDB Molecule: neuropeptide y;

					PDBTitle: nmr solution structure of human neuropeptide y
80	c5lbgG_	Alignment	not modelled	5.1	7 PDB header: transport protein Chain: G: PDB Molecule: caip; PDBTitle: crystal structure of helicobacter cinaedi caip
81	d1rj9b1	Alignment	not modelled	5.1	22 Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
82	c5ir6C_	Alignment	not modelled	5.1	20 PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
83	c5doqC_	Alignment	not modelled	5.1	20 PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
84	c2vxxB_	Alignment	not modelled	5.1	14 PDB header: dna-binding protein Chain: B: PDB Molecule: starvation induced dna binding protein; PDBTitle: x-ray structure of dpsa from thermosynechococcus elongatus
85	c3gk0H_	Alignment	not modelled	5.1	17 PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
86	c2dezA_	Alignment	not modelled	5.0	5 PDB header: neuropeptide Chain: A: PDB Molecule: peptide yy; PDBTitle: structure of human pyy