



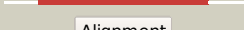

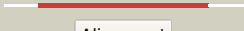




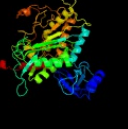




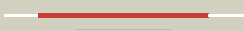





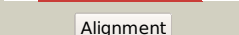







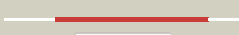











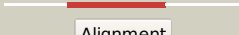


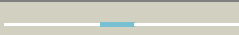




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2220_glnA1_2487623_2489059
Date	Mon Aug 5 13:25:35 BST 2019
Unique Job ID	f99ee6aeaa2693ae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1htoB_	 Alignment		100.0	100	PDB header: ligase Chain: B; PDB Molecule: glutamine synthetase; PDBTitle: crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
2	c1fpyE_	 Alignment		100.0	52	PDB header: ligase Chain: E; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
3	c3ng0A_	 Alignment		100.0	58	PDB header: ligase Chain: A; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
4	c5zlpH_	 Alignment		100.0	45	PDB header: ligase Chain: H; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from helicobacter pylori
5	c4s17E_	 Alignment		100.0	61	PDB header: ligase Chain: E; PDB Molecule: glutamine synthetase; PDBTitle: the crystal structure of glutamine synthetase from bifidobacterium2 adolescentis atcc 15703
6	c3qajL_	 Alignment		100.0	41	PDB header: ligase Chain: L; PDB Molecule: glutamine synthetase; PDBTitle: x-ray crystal structure of glutamine synthetase from bacillus subtilis2 cocrystallized with atp
7	c2j9iL_	 Alignment		100.0	21	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.
8	c4hppA_	 Alignment		100.0	28	PDB header: ligase Chain: A; PDB Molecule: probable glutamine synthetase; PDBTitle: crystal structure of novel glutamine synthase homolog
9	c5dm3A_	 Alignment		100.0	30	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
10	d2bvca2	 Alignment		100.0	100	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
11	d1f52a2	 Alignment		100.0	53	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain

12	c2qc8J_	 Alignment		100.0	23	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
13	c4baxH_	 Alignment		100.0	21	PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from streptomyces2 coelicolor
14	c2d3aj_	 Alignment		100.0	21	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
15	c3fkyD_	 Alignment		100.0	24	PDB header: ligase Chain: D: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
16	c3o6xC_	 Alignment		100.0	22	PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from bacteroides fragilis
17	c4is4G_	 Alignment		100.0	26	PDB header: ligase Chain: G: PDB Molecule: glutamine synthetase; PDBTitle: the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer
18	d2bvca1	 Alignment		99.9	100	Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain
19	d1f52a1	 Alignment		99.9	45	Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain
20	c1tt4B_	 Alignment		99.1	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cytoplasmic protein; PDBTitle: structure of np459575, a predicted glutathione synthase from salmonella typhimurium
21	d1tt4a_	 Alignment	not modelled	99.1	20	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
22	d1r8ga_	 Alignment	not modelled	98.9	19	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
23	c2gwcE_	 Alignment	not modelled	98.0	17	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
24	d1u8sa2	 Alignment	not modelled	41.8	8	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
25	c2qw5B_	 Alignment	not modelled	41.0	19	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
26	c2dr1A_	 Alignment	not modelled	34.8	21	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
27	c3it5B_	 Alignment	not modelled	29.5	32	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
28	c2p6yA_	 Alignment	not modelled	28.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein vca0587; PDBTitle: x-ray structure of the protein q9km02_vibch from vibrio

						cholerae at2 the resolution 1.63 a. northeast structural genomics consortium3 target vcr80.
29	c3ke2A_	Alignment	not modelled	28.7	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yp_928783.1; PDBTitle: crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
30	c5op0B_	Alignment	not modelled	22.2	10	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ligd, polymerase domain; PDBTitle: structure of prim-polc from mycobacterium smegmatis
31	c1a8pA_	Alignment	not modelled	22.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph\;ferredoxin oxidoreductase; PDBTitle: ferredoxin reductase from azotobacter vinelandii
32	d2z1ea1	Alignment	not modelled	20.2	11	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
33	d1vkia_	Alignment	not modelled	19.3	13	Fold: YbaK/ProRS associated domain Superfamily: YbaK/ProRS associated domain Family: YbaK/ProRS associated domain
34	c3bzjA_	Alignment	not modelled	19.1	10	PDB header: hydrolase Chain: A: PDB Molecule: uv endonuclease; PDBTitle: uvde k229l
35	c3hwuA_	Alignment	not modelled	19.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of putative dna-binding protein (yp_299413.1) from2 ralstonia eutropha jmp134 at 1.30 a resolution
36	c2jy5A_	Alignment	not modelled	17.6	17	PDB header: signaling protein Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr structure of ubiquilin 1 uba domain
37	c4bt7A_	Alignment	not modelled	17.5	28	PDB header: lyase Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: acetolactate decarboxylase with a bound phosphate ion
38	d1z2la2	Alignment	not modelled	17.1	8	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
39	c3htnA_	Alignment	not modelled	16.5	12	PDB header: metal binding protein Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: crystal structure of a putative dna binding protein (bt_1116) from2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution
40	c2gu1A_	Alignment	not modelled	16.0	25	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
41	c5knwA_	Alignment	not modelled	15.7	18	PDB header: rna binding protein Chain: A: PDB Molecule: la-related protein 7; PDBTitle: solution nmr structure of human larp7 xrrm2
42	c3ln7A_	Alignment	not modelled	15.5	18	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
43	c1u8sB_	Alignment	not modelled	15.3	3	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
44	c1y1oC_	Alignment	not modelled	15.3	13	PDB header: recombination Chain: C: PDB Molecule: penicillin-binding protein-related factor a; PDBTitle: x-ray crystal structure of penicillin-binding protein-2 related factor a from bacillus stearothermophilus
45	d1y1oa_	Alignment	not modelled	15.3	13	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: RecU-like
46	d2fhqa1	Alignment	not modelled	14.7	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
47	d1owxa_	Alignment	not modelled	14.7	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
48	d1ysja2	Alignment	not modelled	14.5	9	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
49	c3tc3B_	Alignment	not modelled	14.3	9	PDB header: hydrolase Chain: B: PDB Molecule: uv damage endonuclease; PDBTitle: crystal structure of sacuvde
50	c5yhkB_	Alignment	not modelled	14.3	33	PDB header: metal binding protein Chain: B: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterbacter2 aerogenes
51	c3ln6A_	Alignment	not modelled	14.2	16	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
52	c3uz0D_	Alignment	not modelled	13.8	39	PDB header: transport protein Chain: D: PDB Molecule: stage ii sporulation protein q; PDBTitle: crystal structure of spoiiiah and spoiiq complex
53	c2igoG_	Alignment	not modelled	13.7	18	PDB header: oxidoreductase Chain: G: PDB Molecule: pyranose oxidase; PDBTitle: crystal structure of pyranose 2-oxidase h167a mutant with 2-fluoro-2-2 deoxy-d-glucose
54	d1u8sa1	Alignment	not modelled	13.6	5	Fold: Ferredoxin-like Superfamily: ACT-like

						Family: Glycine cleavage system transcriptional repressor
55	d1zpa1	Alignment	not modelled	13.6	7	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
56	c5j1A	Alignment	not modelled	12.7	25	PDB header: hydrolase Chain: A: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer i
57	d1xv2a	Alignment	not modelled	12.6	33	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: Alpha-acetolactate decarboxylase-like
58	d1jqoa	Alignment	not modelled	12.2	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
59	c1jqoA	Alignment	not modelled	12.2	18	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
60	c5kqbA	Alignment	not modelled	11.7	32	PDB header: hydrolase Chain: A: PDB Molecule: peptidase m23; PDBTitle: identification and structural characterization of lytu
61	d1a8pa2	Alignment	not modelled	11.4	20	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
62	c2hsiB	Alignment	not modelled	11.3	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
63	c3p2oB	Alignment	not modelled	11.2	19	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
64	c3tufB	Alignment	not modelled	11.0	44	PDB header: signaling protein Chain: B: PDB Molecule: stage ii sporulation protein q; PDBTitle: structure of the spoIii-spoIIiAh pore forming complex.
65	c5yhoA	Alignment	not modelled	10.8	33	PDB header: metal binding protein Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterobacter2 cloacae
66	c5xneA	Alignment	not modelled	10.3	33	PDB header: lyase Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: x-ray crystal structure of alpha-acetolactate decarboxylase from2 bacillus subtilis strain 168
67	c3qm2A	Alignment	not modelled	10.2	17	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
68	d2c0ra1	Alignment	not modelled	10.2	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
69	c4pmuD	Alignment	not modelled	10.2	8	PDB header: hydrolase Chain: D: PDB Molecule: endo-1,4-beta-xylanase a; PDBTitle: crystal structure of a novel reducing-end xylose-releasing exo-2 oligoxylanase (xyna) belonging to gh10 family (space group p1211)
70	c3ixzB	Alignment	not modelled	9.9	21	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
71	c6ithA	Alignment	not modelled	9.4	23	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
72	c5mwwA	Alignment	not modelled	9.4	20	PDB header: transferase Chain: A: PDB Molecule: rna polymerase sigma factor sigma; PDBTitle: sigma1.1 domain of sigmaa from bacillus subtilis
73	c2z2vA	Alignment	not modelled	9.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
74	c2dt4A	Alignment	not modelled	9.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph0802; PDBTitle: crystal structure of pyrococcus horikoshii a plant- and prokaryote-2 conserved (ppc) protein at 1.60 resolution
75	c5w7gV	Alignment	not modelled	9.0	21	PDB header: virus Chain: V: PDB Molecule: orf132; PDBTitle: an envelope of a filamentous hyperthermophilic virus carries lipids in2 a horseshoe conformation
76	d1a4ia2	Alignment	not modelled	8.7	16	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
77	c5iwvD	Alignment	not modelled	8.6	8	PDB header: lyase Chain: D: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from bacillus subtitis complexed with cmp and mg2+
78	c5u4nA	Alignment	not modelled	8.6	17	PDB header: lyase Chain: A: PDB Molecule: fructose-1; PDBTitle: crystal structure of a fructose-bisphosphate aldolase from neisseria2 gonorrhoeae
79	d1jcb2	Alignment	not modelled	8.3	20	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain

				Family: Domains B1 and B5 of PheRS-beta, PheT	
80	d1bjna_	Alignment	not modelled	8.3	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
81	c2btwA_	Alignment	not modelled	8.2	17 PDB header: transferase Chain: A: PDB Molecule: alr0975 protein; PDBTitle: crystal structure of alr0975
82	c2jepB_	Alignment	not modelled	8.0	13 PDB header: hydrolase Chain: B: PDB Molecule: xyloglucanase; PDBTitle: native family 5 xyloglucanase from paenibacillus pabuli
83	c4bh5B_	Alignment	not modelled	7.9	6 PDB header: cell cycle Chain: B: PDB Molecule: murein hydrolase activator envc; PDBTitle: lytm domain of envc, an activator of cell wall amidases in2 escherichia coli
84	c4owtB_	Alignment	not modelled	7.8	24 PDB header: dna binding protein Chain: B: PDB Molecule: soxs complex subunit b1; PDBTitle: structural basis of soxs1 complex assembly
85	d1rvga_	Alignment	not modelled	7.8	10 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
86	d2cyga1	Alignment	not modelled	7.7	21 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
87	c2k6xA_	Alignment	not modelled	7.5	18 PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
88	c3p2oA_	Alignment	not modelled	7.4	19 PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
89	d2ch1a1	Alignment	not modelled	7.3	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
90	c2nyiB_	Alignment	not modelled	7.3	8 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
91	c3tnfF_	Alignment	not modelled	7.2	47 PDB header: translation, toxin Chain: F: PDB Molecule: antitoxin vapb; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
92	c2iyfA_	Alignment	not modelled	7.2	14 PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
93	c5j1mD_	Alignment	not modelled	7.1	25 PDB header: hydrolase Chain: D: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer ii
94	c2wbrA_	Alignment	not modelled	7.0	25 PDB header: dna-binding protein Chain: A: PDB Molecule: gw182; PDBTitle: the rrm domain in gw182 proteins contributes to mirna-2 mediated gene silencing
95	c2fyfB_	Alignment	not modelled	6.8	8 PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
96	c3sluB_	Alignment	not modelled	6.7	31 PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
97	c3b8eB_	Alignment	not modelled	6.7	13 PDB header: hydrolase/transport protein Chain: B: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
98	d1aq0a_	Alignment	not modelled	6.6	11 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
99	c2f59B_	Alignment	not modelled	6.6	27 PDB header: transferase Chain: B: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione