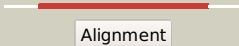



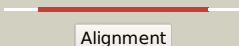

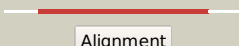

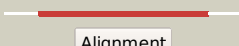

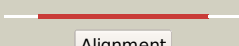

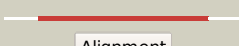

















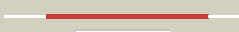













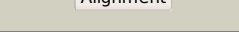
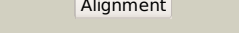
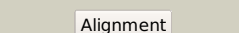
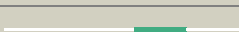


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1878_glnA3_2128029_2129381
Date	Fri Aug 2 13:30:49 BST 2019
Unique Job ID	f0b2ee2410d8c715

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fpyE_	 Alignment		100.0	27	PDB header: ligase Chain: E; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
2	c4hpaA_	 Alignment		100.0	29	PDB header: ligase Chain: A; PDB Molecule: probable glutamine synthetase; PDBTitle: crystal structure of novel glutamine synthase homolog
3	c1htoB_	 Alignment		100.0	26	PDB header: ligase Chain: B; PDB Molecule: glutamine synthetase; PDBTitle: crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
4	c3ng0A_	 Alignment		100.0	23	PDB header: ligase Chain: A; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
5	c5zlpH_	 Alignment		100.0	22	PDB header: ligase Chain: H; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from helicobacter pylori
6	c3qajL_	 Alignment		100.0	25	PDB header: ligase Chain: L; PDB Molecule: glutamine synthetase; PDBTitle: x-ray crystal structure of glutamine synthetase from bacillus subtilis2 cocrystallized with atp
7	c4s17E_	 Alignment		100.0	25	PDB header: ligase Chain: E; PDB Molecule: glutamine synthetase; PDBTitle: the crystal structure of glutamine synthetase from bifidobacterium2 adolescentis atcc 15703
8	c2j9iL_	 Alignment		100.0	23	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.
9	c5dm3A_	 Alignment		100.0	26	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	d1f52a2	 Alignment		100.0	28	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
11	d2bvca2	 Alignment		100.0	28	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain

12	c2qc8J_	 Alignment		100.0	19	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	20	PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from streptomyces2 coelicolor
14	c2d3aj_	 Alignment		100.0	19	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	21	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	21	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	23	PDB header: ligase Chain: G: PDB Molecule: glutamine synthetase; PDBTitle: the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer
18	d1f52a1	 Alignment		99.8	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain
19	d2bvca1	 Alignment		99.8	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain
20	c1tt4B_	 Alignment		99.1	20	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	99.0	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	21	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
23	c2gwcE_	 Alignment	not modelled	98.3	19	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	d1nxia_	 Alignment	not modelled	63.5	19	Fold: Ferredoxin-like Superfamily: Hypothetical protein VC0424 Family: Hypothetical protein VC0424
25	c5op0B_	 Alignment	not modelled	56.4	11	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ligd, polymerase domain; PDBTitle: structure of prim-polc from mycobacterium smegmatis
26	c2qw5B_	 Alignment	not modelled	56.2	12	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
27	c3ln6A_	 Alignment	not modelled	46.5	21	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from streptococcus agalactiae
28	d1u8sa2	 Alignment	not modelled	44.6	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor

29	d1chua3	Alignment	not modelled	40.7	15	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
30	c4aghA	Alignment	not modelled	35.8	20	PDB header: transcription Chain: A: PDB Molecule: mosub1, transcription cofactor; PDBTitle: structural features of ssdna binding protein mosub1 from magnaporthe2 oryzae
31	c3d3aA	Alignment	not modelled	35.2	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
32	d1ur4a	Alignment	not modelled	29.0	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
33	c3ke2A	Alignment	not modelled	28.5	33	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
34	d2bs2a3	Alignment	not modelled	28.4	23	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
35	c3p2oA	Alignment	not modelled	28.4	24	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
36	c3p2oB	Alignment	not modelled	27.7	24	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
37	c2y0fD	Alignment	not modelled	26.8	39	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
38	c3ln7A	Alignment	not modelled	26.5	14	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
39	c1gvhA	Alignment	not modelled	23.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoheмоprotein; PDBTitle: the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket
40	d1u8sa1	Alignment	not modelled	21.2	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
41	d1foba	Alignment	not modelled	21.1	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
42	c3it5B	Alignment	not modelled	20.8	32	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
43	d1tg7a5	Alignment	not modelled	20.5	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Glycosyl hydrolases family 35 catalytic domain
44	d1zpa1	Alignment	not modelled	19.8	10	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
45	c2jy5A	Alignment	not modelled	19.5	16	PDB header: signaling protein Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr structure of ubiquilin 1 uba domain
46	d1tz9a	Alignment	not modelled	17.4	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
47	c5iwvD	Alignment	not modelled	17.2	22	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 subtilis complexed with cmp and mg2+
48	c2jepB	Alignment	not modelled	16.5	11	PDB header: hydrolase Chain: B: PDB Molecule: xyloglucanase; PDBTitle: native family 5 xyloglucanase from paenibacillus pabuli
49	c2c2xB	Alignment	not modelled	16.3	25	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase- PDBTitle: three dimensional structure of bifunctional methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase from mycobacterium tuberculosis
50	c2nyiB	Alignment	not modelled	15.5	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
51	c4ae5C	Alignment	not modelled	15.4	11	PDB header: signaling protein Chain: C: PDB Molecule: signal transduction protein trap; PDBTitle: structure of a major regulator of staphylococcal pathogenesis
52	d1nka3	Alignment	not modelled	14.7	12	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase

52	v11e6a2	Alignment	not modelled	14.7	42	flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
53	c4madA	Alignment	not modelled	14.5	25	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of beta-galactosidase c (bgac) from bacillus2 circulans atcc 31382
54	c4s1aB	Alignment	not modelled	14.0	11	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein cthe_0052 from2 ruminiclostridium thermocellum atcc 27405
55	d1nqua	Alignment	not modelled	14.0	21	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
56	c4e8cA	Alignment	not modelled	13.8	21	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 35; PDBTitle: crystal structure of streptococcal beta-galactosidase in complex with2 galactose
57	c6eonA	Alignment	not modelled	13.8	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: galactanase bt0290
58	d2c0ra1	Alignment	not modelled	13.8	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
59	c4o9uB	Alignment	not modelled	13.8	19	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
60	c2dr1A	Alignment	not modelled	13.2	14	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
61	c3noyA	Alignment	not modelled	13.2	32	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
62	c4bt7A	Alignment	not modelled	13.1	33	PDB header: lyase Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: acetolactate decarboxylase with a bound phosphate ion
63	d1jcb2	Alignment	not modelled	12.6	15	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
64	c1u8sB	Alignment	not modelled	12.3	8	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
65	c5f5sB	Alignment	not modelled	12.2	25	PDB header: splicing Chain: B: PDB Molecule: microfibrillar-associated protein 1; PDBTitle: crystal structure of the prp38-mfap1 complex of homo sapiens
66	d2ez9a2	Alignment	not modelled	12.1	48	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
67	c3qm2A	Alignment	not modelled	12.1	21	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	d1di0a	Alignment	not modelled	12.0	21	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
69	d2z1ea1	Alignment	not modelled	11.7	13	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
70	c4x0vH	Alignment	not modelled	11.5	12	PDB header: hydrolase Chain: H: PDB Molecule: beta-1,3-1,4-glucanase; PDBTitle: structure of a gh5 family lichenase from caldicellulosiruptor sp. f32
71	c2z2vA	Alignment	not modelled	11.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
72	d1z2la2	Alignment	not modelled	11.0	8	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
73	c5yhkB	Alignment	not modelled	10.8	33	PDB header: metal binding protein Chain: B: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterbacter2 aerogenes
74	c1x31D	Alignment	not modelled	10.6	21	PDB header: oxidoreductase Chain: D: PDB Molecule: sarcosine oxidase delta subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
75	d1q6za2	Alignment	not modelled	10.6	26	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
76	d2ch1a1	Alignment	not modelled	10.6	7	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
77	c6k0aC	Alignment	not modelled	10.2	20	PDB header: rna binding protein/rna Chain: C: PDB Molecule: ribonuclease p protein component 3; PDBTitle: cryo-em structure of an archaeal ribonuclease p
						Fold: TBP-like

78	d2qrda1	Alignment	not modelled	10.2	21	Superfamily: KA1-like Family: Ssp2 C-terminal domain-like
79	c6dtfA	Alignment	not modelled	10.1	13	PDB header: peptide binding protein Chain: A: PDB Molecule: periplasmic oligopeptide-binding protein; PDBTitle: crystal structure of haemophilus influenzae oppa complex with kkk
80	d1xv2a	Alignment	not modelled	9.9	39	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: Alpha-acetolactate decarboxylase-like
81	c3htnA	Alignment	not modelled	9.8	14	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
82	d1pvdA2	Alignment	not modelled	9.8	24	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
83	c1a4iB	Alignment	not modelled	9.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
84	d1jqoa	Alignment	not modelled	9.5	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
85	c1jqoA	Alignment	not modelled	9.5	20	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
86	c2gu1A	Alignment	not modelled	9.5	25	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
87	c2igoG	Alignment	not modelled	9.5	15	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
88	d1rvv1	Alignment	not modelled	9.5	13	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
89	c4biyD	Alignment	not modelled	9.3	13	PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
90	c3bdkB	Alignment	not modelled	9.3	18	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
91	d1pcfa	Alignment	not modelled	9.3	15	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Transcriptional coactivator PC4 C-terminal domain
92	c3zxaA	Alignment	not modelled	9.2	15	PDB header: transferase Chain: A: PDB Molecule: hypoxia sensor histidine kinase response regulator dost; PDBTitle: crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
93	d1oiza1	Alignment	not modelled	9.1	17	Fold: RuvA C-terminal domain-like Superfamily: CRAL/TRIO N-terminal domain Family: CRAL/TRIO N-terminal domain
94	c3re3B	Alignment	not modelled	9.1	19	PDB header: lyase Chain: B: 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 francisella tularensis
95	d1a4ia2	Alignment	not modelled	9.0	15	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
96	d1prtc1	Alignment	not modelled	8.8	22	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
97	c5yhoA	Alignment	not modelled	8.5	33	PDB header: metal binding protein Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterobacter2 cloacae
98	d1gvha3	Alignment	not modelled	8.5	21	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavo-hemoglobin, C-terminal domain
99	c4zonB	Alignment	not modelled	8.4	31	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: verruculogen synthase; PDBTitle: structure of ftmox1 with fumitremorgen b complex