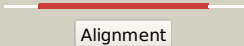

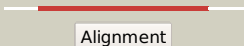

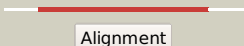







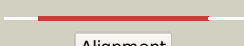




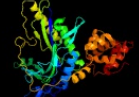















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3009c_gatB_3367274_3368803
Date	Thu Aug 8 16:20:17 BST 2019
Unique Job ID	05c1b1f11f72dc73

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ip4B_	 Alignment		100.0	43	PDB header: ligase Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: the high resolution structure of gatcab
2	c3al0B_	 Alignment		100.0	40	PDB header: ligase/rna Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
3	c2g5iB_	 Alignment		100.0	45	PDB header: ligase Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase PDBTitle: structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
4	c3h0mE_	 Alignment		100.0	46	PDB header: ligase Chain: E: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
5	c4wj3E_	 Alignment		100.0	43	PDB header: ligase/rna Chain: E: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
6	c4wj3B_	 Alignment		100.0	43	PDB header: ligase/rna Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
7	c4wj3H_	 Alignment		100.0	43	PDB header: ligase/rna Chain: H: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
8	c4wj3K_	 Alignment		100.0	43	PDB header: ligase/rna Chain: K: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
9	c3kfuF_	 Alignment		100.0	45	PDB header: ligase/rna Chain: F: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the transamidosome
10	c3kfuL_	 Alignment		100.0	46	PDB header: ligase/rna Chain: L: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the transamidosome
11	d2f2ab2	 Alignment		100.0	54	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: GatB/GatE catalytic domain-like

12	c2d6fD	Alignment		100.0	31	PDB header: ligase/rna Chain: D: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit e; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
13	c1zq1D	Alignment		100.0	32	PDB header: lyase Chain: D: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit e; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
14	c2d6fC	Alignment		100.0	31	PDB header: ligase/rna Chain: C: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit e; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
15	c4n0iB	Alignment		100.0	36	PDB header: ligase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit b, PDBTitle: crystal structure of s. cerevisiae mitochondrial gatfab in complex2 with glutamine
16	d2d6fc3	Alignment		100.0	32	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: GatB/GatE catalytic domain-like
17	d1zq1c3	Alignment		100.0	28	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: GatB/GatE catalytic domain-like
18	d2f2ab1	Alignment		99.9	23	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
19	d1ng6a	Alignment		98.5	17	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/YqeY domain
20	c3tl4X	Alignment		97.8	11	PDB header: ligase Chain: X: PDB Molecule: glutamyl-trna synthetase; PDBTitle: crystal structure of the trna binding domain of glutamyl-trna2 synthetase from saccharomyces cerevisiae
21	d1zq1c1	Alignment	not modelled	97.3	24	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
22	c4ye6A	Alignment	not modelled	95.6	14	PDB header: ligase Chain: A: PDB Molecule: glutamine--trna ligase; PDBTitle: the crystal structure of the intact human glnrs
23	d2d6fc1	Alignment	not modelled	90.2	32	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
24	c2v27A	Alignment	not modelled	45.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine hydroxylase; PDBTitle: structure of the cold active phenylalanine hydroxylase from colwellia2 psychrerythraea 34h
25	c3tcyA	Alignment	not modelled	44.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: crystallographic structure of phenylalanine hydroxylase from2 chromobacterium violaceum (cpah) bound to phenylalanine in a site3 distal to the active site
26	c1ixrB	Alignment	not modelled	43.7	19	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
27	d1ltza	Alignment	not modelled	42.9	29	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
28	c1hjpA	Alignment	not modelled	40.3	10	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli

29	c4bptC	Alignment	not modelled	38.7	24	PDB header: oxidoreductase Chain: C: PDB Molecule: phenylalanine-4-hydroxylase (pah) (phe-4-monoxygenase); PDBTitle: structural and thermodynamic insight into phenylalanine2 hydroxylase from the human pathogen legionella pneumophila
30	c2lcrA	Alignment	not modelled	38.2	40	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
31	c3ep3A	Alignment	not modelled	38.0	17	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase alpha chain; PDBTitle: human adometdc d174n mutant with no putrescine bound
32	d2d32a1	Alignment	not modelled	37.5	22	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase
33	c2pnmA	Alignment	not modelled	35.2	31	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (phenylalanine-4-hydroxylase); PDBTitle: structure of phenylalanine hydroxylase dephosphorylated
34	d1xrsb2	Alignment	not modelled	34.0	25	Fold: Dodecin subunit-like Superfamily: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain Family: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
35	c3nztA	Alignment	not modelled	33.3	26	PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase; PDBTitle: 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 ftom francisella tularensis in complex with amp
36	c2wzr2	Alignment	not modelled	33.1	17	PDB header: virus Chain: 2: PDB Molecule: polyprotein; PDB Fragment: residues 200-284 PDBTitle: the structure of foot and mouth disease virus serotype sat1
37	c1lvaA	Alignment	not modelled	32.9	14	PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of a c-terminal fragment of moorella2 thermoacetica elongation factor selb
38	c2wff2	Alignment	not modelled	32.9	29	PDB header: virus Chain: 2: PDB Molecule: p1; PDB Fragment: capsid protein vp2, residues 81-310; PDBTitle: equine rhinitis a virus
39	d2pw6a1	Alignment	not modelled	32.6	17	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
40	c2mev2	Alignment	not modelled	32.5	29	PDB header: virus Chain: 2: PDB Molecule: mengo virus coat protein (subunit vp2); PDBTitle: structural refinement and analysis of mengo virus
41	c5a8fC	Alignment	not modelled	32.0	24	PDB header: viral protein Chain: C: PDB Molecule: human saffold virus-3 vp2; PDBTitle: structure and genome release mechanism of human cardiovirus saffold2 virus-3
42	c2c8iB	Alignment	not modelled	32.0	41	PDB header: virus/receptor Chain: B: PDB Molecule: echovirus 11 coat protein vp2; PDBTitle: complex of echovirus type 12 with domains 1, 2, 3 and 4 of its2 receptor decay accelerating factor (cd55) by cryo electron microscopy3 at 16 a
43	c2mroB	Alignment	not modelled	32.0	21	PDB header: transport protein/signaling protein Chain: B: PDB Molecule: dna damage-inducible protein 1; PDBTitle: structure of the complex of ubiquitin and the uba domain from dna-2 damage-inducible 1 protein (ddl1)
44	c1c8m2	Alignment	not modelled	32.0	41	PDB header: virus Chain: 2: PDB Molecule: human rhinovirus 16 coat protein; PDB Fragment: residues 2-78; PDBTitle: refined crystal structure of human rhinovirus 16 complexed with2 vp63843 (pleconaril), an anti-picornaviral drug currently in clinical3 trials
45	c1emxA	Alignment	not modelled	30.2	56	PDB header: toxin Chain: A: PDB Molecule: heteropodatoxin 2; PDBTitle: solution structure of hptx2, a toxin from heteropoda2 venatoria spider venom that blocks kv4.2 potassium channel
46	c2oq0D	Alignment	not modelled	29.2	12	PDB header: protein binding Chain: D: PDB Molecule: gamma-interferon-inducible protein ifi-16; PDBTitle: crystal structure of the first hin-200 domain of interferon-inducible2 protein 16
47	c5xs5B	Alignment	not modelled	29.1	35	PDB header: virus Chain: B: PDB Molecule: genome polyprotein; PDBTitle: structure of coxsackievirus a6 (cva6) virus procapsid particle
48	d1jkea	Alignment	not modelled	29.1	24	Fold: DTD-like Superfamily: DTD-like Family: DTD-like
49	c4x82A	Alignment	not modelled	28.9	22	PDB header: transport protein Chain: A: PDB Molecule: zinc transporter zip4; PDBTitle: crystal structure of the extracellular domain of zip4
50	d1mlwa	Alignment	not modelled	28.8	33	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
51	d2oq0a2	Alignment	not modelled	28.7	12	Fold: OB-fold Superfamily: HIN-2000 domain-like Family: HIN-200/IF120x domain
52	c5yzpA	Alignment	not modelled	28.1	17	PDB header: immune system Chain: A: PDB Molecule: ifi204; PDBTitle: crystal structure of p204 hina domain
53	c1ncpB	Alignment	not modelled	28.1	53	PDB header: virus Chain: B: PDB Molecule: coat protein vp2;

53	c1ncqB_	Alignment	not modelled	28.1	33	PDBTitle: the structure of hrv14 when complexed with pleconaril, an2 antiviral compound PDB header: virus
54	c5j98B_	Alignment	not modelled	28.0	18	Chain: B: PDB Molecule: vp2; PDBTitle: crystal structure of slow bee paralysis virus at 2.6a resolution
55	c3tbxB_	Alignment	not modelled	27.8	23	PDB header: immune system/agonist Chain: B: PDB Molecule: beta-2-microglobulin; PDBTitle: crystal structure of the murine class i major histocompatibility2 complex h-2db in complex with lcmv-derived gp33 altered peptide3 ligand v3p
56	c1bev2_	Alignment	not modelled	27.7	47	PDB header: virus Chain: 2: PDB Molecule: bovine enterovirus coat proteins vp1 to vp4; PDBTitle: bovine enterovirus vg-5-27
57	c3b6yB_	Alignment	not modelled	27.4	20	PDB header: protein binding Chain: B: PDB Molecule: gamma-interferon-inducible protein ifi-16; PDBTitle: crystal structure of the second hin-200 domain of interferon-inducible2 protein 16
58	d1phza2	Alignment	not modelled	26.9	31	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
59	c2v9vA_	Alignment	not modelled	26.9	15	PDB header: transcription Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of moorella thermoacetica selb(377-511)
60	c2x7pA_	Alignment	not modelled	26.7	12	PDB header: unknown function Chain: A: PDB Molecule: possible thiamine biosynthesis enzyme; PDBTitle: the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
61	c4jkbA_	Alignment	not modelled	26.6	20	PDB header: dna binding protein/dna Chain: A: PDB Molecule: interferon-activable protein 202; PDBTitle: molecular basis for abrogation of activation of pro-inflammatory2 cytokines
62	d1j7ga_	Alignment	not modelled	26.5	23	Fold: DTD-like Superfamily: DTD-like Family: DTD-like
63	d1mwpa_	Alignment	not modelled	26.4	23	Fold: SRCR-like Superfamily: A heparin-binding domain Family: A heparin-binding domain
64	c4qpqB_	Alignment	not modelled	26.4	17	PDB header: virus Chain: B: PDB Molecule: capsid protein vp0; PDBTitle: crystal structure of empty hepatitis a virus
65	c3e2tA_	Alignment	not modelled	26.2	33	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 5-hydroxylase 1; PDBTitle: the catalytic domain of chicken tryptophan hydroxylase 12 with bound tryptophan
66	c3jb4B_	Alignment	not modelled	26.0	29	PDB header: virus Chain: B: PDB Molecule: vp0; PDBTitle: structure of ljungan virus: insight into picornavirus packaging
67	c3cjc_	Alignment	not modelled	26.0	29	PDB header: virus Chain: C: PDB Molecule: polyprotein; PDBTitle: structure of seneca valley virus-001
68	d1j8ua_	Alignment	not modelled	25.9	31	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
69	d1vcca_	Alignment	not modelled	25.4	56	Fold: DNA topoisomerase I domain Superfamily: DNA topoisomerase I domain Family: Vaccinia DNA topoisomerase I, 9 kDa N-terminal fragment
70	c4l5tB_	Alignment	not modelled	25.3	20	PDB header: immune system Chain: B: PDB Molecule: interferon-activable protein 202; PDBTitle: crystal structure of the tetrameric p202 hin2
71	c5yzaA_	Alignment	not modelled	25.1	22	PDB header: immune system Chain: A: PDB Molecule: ifi204; PDBTitle: crystal structure of p204 hinb domain
72	c5k0uC_	Alignment	not modelled	24.9	35	PDB header: virus Chain: C: PDB Molecule: capsid protein vp2; PDBTitle: cryoem structure of the full virion of a human rhinovirus c
73	c5jzgC_	Alignment	not modelled	24.7	35	PDB header: virus Chain: C: PDB Molecule: capsid protein vp0; PDBTitle: cryoem structure of the native empty particle of a human rhinovirus c
74	c4hw9E_	Alignment	not modelled	24.6	11	PDB header: membrane protein Chain: E: PDB Molecule: mechanosensitive channel mscs; PDBTitle: crystal structure of helicobacter pylori mscs (closed state)
75	c3vbfB_	Alignment	not modelled	24.5	35	PDB header: virus Chain: B: PDB Molecule: genome polyprotein, capsid protein vp2; PDBTitle: crystal structure of formaldehyde treated human enterovirus 71 (space2 group i23)
76	c2i1vB_	Alignment	not modelled	23.4	18	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
77	c3e4rA_	Alignment	not modelled	23.2	15	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes PDB header: oxidoreductase

78	c5denA_	Alignment	not modelled	22.5	31	Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: the first structure of a full-length mammalian phenylalanine2 hydroxylase reveals the architecture of an auto-inhibited tetramer
79	c4v06A_	Alignment	not modelled	22.5	31	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 5-hydroxylase 2; PDBTitle: crystal structure of human tryptophan hydroxylase 2 (tph2), catalytic2 domain
80	c3rn5A_	Alignment	not modelled	22.3	15	PDB header: immune system/dna Chain: A: PDB Molecule: interferon-inducible protein aim2; PDBTitle: structural basis of cytosolic dna recognition by innate immune2 receptors
81	d1toha_	Alignment	not modelled	22.3	26	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
82	c4z92C_	Alignment	not modelled	22.1	18	PDB header: virus Chain: C: PDB Molecule: capsid subunit vp0; PDBTitle: crystal structure of parechovirus-1 virion
83	c3t79A_	Alignment	not modelled	21.6	56	PDB header: dna binding protein/dna Chain: A: PDB Molecule: klla0e03807p; PDBTitle: ndc10: a platform for inner kinetochore assembly in budding yeast
84	c3sqiA_	Alignment	not modelled	21.5	56	PDB header: dna binding protein/dna Chain: A: PDB Molecule: klla0e03807p; PDBTitle: dna binding domain of ndc10
85	c2avuF_	Alignment	not modelled	21.4	26	PDB header: transcription activator Chain: F: PDB Molecule: flagellar transcriptional activator flhc; PDBTitle: structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription
86	c5jk5A_	Alignment	not modelled	21.3	31	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: phenylalanine hydroxylase from dictyostelium - bh2 complex
87	d2avue1	Alignment	not modelled	21.2	26	Fold: FlhC-like Superfamily: FlhC-like Family: FlhC-like
88	c5ekqA_	Alignment	not modelled	20.7	16	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein assembly factor bama; PDBTitle: the structure of the bamacde subcomplex from e. coli
89	d2b8ta2	Alignment	not modelled	20.0	27	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
90	d2nt0a2	Alignment	not modelled	19.9	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
91	c3j3vO_	Alignment	not modelled	19.9	11	PDB header: ribosome Chain: O: PDB Molecule: 50s ribosomal protein l18; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
92	c1bbt2_	Alignment	not modelled	19.7	29	PDB header: virus Chain: 2: PDB Molecule: foot-and-mouth disease virus (subunit vp2); PDBTitle: methods used in the structure determination of foot and2 mouth disease virus
93	c4jbmA_	Alignment	not modelled	18.8	10	PDB header: dna binding protein/dna Chain: A: PDB Molecule: interferon-inducible protein aim2; PDBTitle: structure of murine dna binding protein bound with ds dna
94	c1tmf2_	Alignment	not modelled	18.2	19	PDB header: virus Chain: 2: PDB Molecule: theiler's murine encephalomyelitis virus PDBTitle: three-dimensional structure of theiler murine2 encephalomyelitis virus (bean strain)
95	c2dboA_	Alignment	not modelled	18.0	14	PDB header: hydrolase Chain: A: PDB Molecule: d-tyrosyl-trna(tyr) deacylase; PDBTitle: crystal structure of d-tyr-trna(tyr) deacylase from aquifex aeolicus
96	c5c9aB_	Alignment	not modelled	17.8	41	PDB header: virus Chain: B: PDB Molecule: vp0; PDBTitle: crystal structure of empty coxsackievirus a16 particle
97	c4mzuG_	Alignment	not modelled	17.7	20	PDB header: isomerase, transferase Chain: G: PDB Molecule: wxcm-like protein; PDBTitle: crystal structure of fdtd, a bifunctional ketoisomerase/n-2 acetyltransferase from shewanella denitrificans
98	d1zunb1	Alignment	not modelled	17.7	12	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
99	c5tvoA_	Alignment	not modelled	17.5	24	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase proenzyme; PDBTitle: crystal structure of trypanosoma brucei adometdc-delta26 monomer