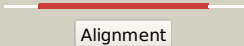

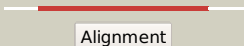

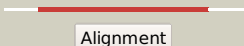







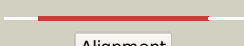














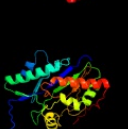


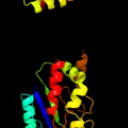


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0433 (-) _520327_521457
Date	Tue Jul 23 14:50:51 BST 2019
Unique Job ID	150839fa93a17cf5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1r8ga_</a>	 Alignment		100.0	28	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamate-cysteine ligase family 2 (GCS2)
2	<a href="#">d1tt4a_</a>	 Alignment		100.0	27	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamate-cysteine ligase family 2 (GCS2)
3	<a href="#">c1tt4B_</a>	 Alignment		100.0	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain: B: PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium
4	<a href="#">c2gwcE_</a>	 Alignment		100.0	21	<b>PDB header:</b> ligase <b>Chain: E: PDB Molecule:</b> glutamate cysteine ligase; <b>PDBTitle:</b> crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue
5	<a href="#">c3nztA_</a>	 Alignment		100.0	16	<b>PDB header:</b> ligase <b>Chain: A: PDB Molecule:</b> glutamate--cysteine ligase; <b>PDBTitle:</b> 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 ffrom francisella tularensis in complex with amp
6	<a href="#">d2d32a1</a>	 Alignment		100.0	15	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamate-cysteine ligase
7	<a href="#">c3ln7A_</a>	 Alignment		100.0	13	<b>PDB header:</b> ligase <b>Chain: A: PDB Molecule:</b> glutathione biosynthesis bifunctional protein gshab; <b>PDBTitle:</b> crystal structure of a bifunctional glutathione synthetase from2 pasteurilla multocida
8	<a href="#">c3ln6A_</a>	 Alignment		100.0	15	<b>PDB header:</b> ligase <b>Chain: A: PDB Molecule:</b> glutathione biosynthesis bifunctional protein gshab; <b>PDBTitle:</b> crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
9	<a href="#">c3lwwA_</a>	 Alignment		99.8	21	<b>PDB header:</b> ligase <b>Chain: A: PDB Molecule:</b> glutamate--cysteine ligase; <b>PDBTitle:</b> glutathione-inhibited scgl
10	<a href="#">c4hppA_</a>	 Alignment		99.2	18	<b>PDB header:</b> ligase <b>Chain: A: PDB Molecule:</b> probable glutamine synthetase; <b>PDBTitle:</b> crystal structure of novel glutamine synthase homolog
11	<a href="#">c5zlpH_</a>	 Alignment		99.1	22	<b>PDB header:</b> ligase <b>Chain: H: PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from helicobacter pylori

12	<a href="#">d2bvca2</a>	Alignment		99.1	20	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamine synthetase catalytic domain
13	<a href="#">d1f52a2</a>	Alignment		99.0	19	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamine synthetase catalytic domain
14	<a href="#">c1fpyE_</a>	Alignment		99.0	19	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
15	<a href="#">c3ng0A_</a>	Alignment		99.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
16	<a href="#">c4s17E_</a>	Alignment		99.0	22	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> the crystal structure of glutamine synthetase from bifidobacterium2 adolescentis atcc 15703
17	<a href="#">c1htoB_</a>	Alignment		98.9	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
18	<a href="#">c5dm3A_</a>	Alignment		98.9	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from chromohalobacter2 salexigens dsm 3043(csal_0679, target efi-550015) with bound adp
19	<a href="#">c3qajL_</a>	Alignment		98.9	17	<b>PDB header:</b> ligase <b>Chain:</b> L: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> x-ray crystal structure of glutamine synthetase from bacillus subtilis2 cocrystallized with atp
20	<a href="#">c3o6xC_</a>	Alignment		98.7	20	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
21	<a href="#">c4is4G_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> ligase <b>Chain:</b> G: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer
22	<a href="#">c4baxH_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of glutamine synthetase from streptomyces2 coelicolor
23	<a href="#">c2j9iL_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> ligase <b>Chain:</b> L: <b>PDB Molecule:</b> glutamate-ammonia ligase domain-containing protein 1; <b>PDBTitle:</b> 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.
24	<a href="#">c2qc8J_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> ligase <b>Chain:</b> J: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
25	<a href="#">c2d3aj_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> ligase <b>Chain:</b> J: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
26	<a href="#">c3fkyD_</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
27	<a href="#">c4bjrA_</a>	Alignment	not modelled	93.3	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pup--protein ligase, prokaryotic ubiquitin-like protein <b>PDBTitle:</b> crystal structure of the complex between prokaryotic2 ubiquitin-like protein pup and its ligase pafa

28	<a href="#">c4b0tB</a>	Alignment	not modelled	68.2	11	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pup--protein ligase; <b>PDBTitle:</b> structure of the pup ligase pafa of the prokaryotic2 ubiquitin-like modification pathway in complex with adp
29	<a href="#">c4b0sA</a>	Alignment	not modelled	45.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deamidase-depupylase dop; <b>PDBTitle:</b> structure of the deamidase-depupylase dop of the prokaryotic2 ubiquitin-like modification pathway in complex with atp
30	<a href="#">c2ebbA</a>	Alignment	not modelled	44.6	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
31	<a href="#">c2v6uB</a>	Alignment	not modelled	30.2	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pterin-4a-carbinolamine dehydratase; <b>PDBTitle:</b> high resolution crystal structure of pterin-4a-2 carbinolamine dehydratase from toxoplasma gondii
32	<a href="#">d1ru0a</a>	Alignment	not modelled	29.9	12	<b>Fold:</b> DCoH-like <b>Superfamily:</b> PCD-like <b>Family:</b> PCD-like
33	<a href="#">d1dcpa</a>	Alignment	not modelled	23.5	9	<b>Fold:</b> DCoH-like <b>Superfamily:</b> PCD-like <b>Family:</b> PCD-like
34	<a href="#">c3jstA</a>	Alignment	not modelled	15.0	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative pterin-4-alpha-carbinolamine dehydratase; <b>PDBTitle:</b> crystal structure of transcriptional coactivator/pterin dehydratase2 from bruceella melitensis
35	<a href="#">d2pw6a1</a>	Alignment	not modelled	13.4	19	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> LigB-like <b>Family:</b> LigB-like
36	<a href="#">c3oqhB</a>	Alignment	not modelled	13.4	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein yvmc; <b>PDBTitle:</b> crystal structure of b. licheniformis cdps yvmc-blic
37	<a href="#">d3ci0k1</a>	Alignment	not modelled	12.5	14	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> GspK insert domain-like <b>Family:</b> GspK insert domain-like
38	<a href="#">c2p7pB</a>	Alignment	not modelled	12.4	16	<b>PDB header:</b> metal binding protein, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> crystal structure of genomically encoded fosfomycin resistance2 protein, fosx, from listeria monocytogenes complexed with mn(ii) and3 sulfate ion
39	<a href="#">c5vb0E</a>	Alignment	not modelled	11.3	9	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> fosfomycin resistance protein fosa3; <b>PDBTitle:</b> crystal structure of fosfomycin resistance protein fosa3
40	<a href="#">c2cp8A</a>	Alignment	not modelled	10.5	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> next to brca1 gene 1 protein; <b>PDBTitle:</b> solution structure of the rsgi ruh-046, a uba domain from2 human next to brca1 gene 1 protein (kiaa0049 protein)3 r923h variant
41	<a href="#">d1nkia</a>	Alignment	not modelled	9.7	13	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
42	<a href="#">d2eg6a1</a>	Alignment	not modelled	9.6	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Dihydroorotase
43	<a href="#">d2d6fc3</a>	Alignment	not modelled	9.4	15	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> GatB/GatE catalytic domain-like
44	<a href="#">d1usma</a>	Alignment	not modelled	9.0	19	<b>Fold:</b> DCoH-like <b>Superfamily:</b> PCD-like <b>Family:</b> PCD-like
45	<a href="#">c2krkA</a>	Alignment	not modelled	8.6	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> 26s protease regulatory subunit 8; <b>PDBTitle:</b> solution nmr structure of 26s protease regulatory subunit 82 from h.sapiens, northeast structural genomics consortium3 target hr3102a
46	<a href="#">c1g5jB</a>	Alignment	not modelled	8.3	67	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bad protein; <b>PDBTitle:</b> complex of bcl-xl with peptide from bad
47	<a href="#">d1r9ca</a>	Alignment	not modelled	7.9	20	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
48	<a href="#">c3rj1G</a>	Alignment	not modelled	7.4	38	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 6; <b>PDBTitle:</b> architecture of the mediator head module
49	<a href="#">d2qkwa1</a>	Alignment	not modelled	7.1	13	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Avirulence protein AvrPto <b>Family:</b> Avirulence protein AvrPto
50	<a href="#">c2qkwa</a>	Alignment	not modelled	7.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> avirulence protein; <b>PDBTitle:</b> structural basis for activation of plant immunity by2 bacterial effector protein avrpto
51	<a href="#">c4gwpG</a>	Alignment	not modelled	6.9	33	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 6; <b>PDBTitle:</b> structure of the mediator head module from s. cerevisiae
52	<a href="#">d1j5ya2</a>	Alignment	not modelled	6.8	18	<b>Fold:</b> HPr-like <b>Superfamily:</b> Putative transcriptional regulator TM1602, C-terminal domain

						<b>Family:</b> Putative transcriptional regulator TM1602, C-terminal domain
53	<a href="#">c3zw5A_</a>	Alignment	not modelled	6.7	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase domain-containing protein 5; <b>PDBTitle:</b> crystal structure of the human glyoxalase domain-containing protein 5
54	<a href="#">c6bu2A_</a>	Alignment	not modelled	6.6	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase; <b>PDBTitle:</b> crystal structure of methylmalonyl-coa epimerase from mycobacterium2 tuberculosis
55	<a href="#">c5oevB_</a>	Alignment	not modelled	6.6	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione synthetase-like effector 22 (gpa-gss22-apo); <b>PDBTitle:</b> the structure of a glutathione synthetase like-effector (gss22) from2 globodera pallida in apoform.
56	<a href="#">c4eacC_</a>	Alignment	not modelled	6.6	7	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> mannonate dehydratase; <b>PDBTitle:</b> crystal structure of mannonate dehydratase from escherichia coli2 strain k12
57	<a href="#">d2f2ab2</a>	Alignment	not modelled	6.5	26	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> GatB/GatE catalytic domain-like
58	<a href="#">c4n0iB_</a>	Alignment	not modelled	6.4	11	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit b, <b>PDBTitle:</b> crystal structure of s. cerevisiae mitochondrial gatfab in complex2 with glutamine
59	<a href="#">c4hc5A_</a>	Alignment	not modelled	6.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of member of glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily from sphaerobacter thermophilus dsm3 20745
60	<a href="#">c6avjB_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cdgsh iron-sulfur domain-containing protein 3, <b>PDBTitle:</b> crystal structure of human mitochondrial inner neet protein (mint)2 /cisd3
61	<a href="#">d1ylea1</a>	Alignment	not modelled	6.1	43	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> AstA-like
62	<a href="#">c2q25C_</a>	Alignment	not modelled	5.9	9	<b>PDB header:</b> virus,hydrolase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> protein alpha; <b>PDBTitle:</b> flock house virus coat protein d75n mutant
63	<a href="#">c5zet2_</a>	Alignment	not modelled	5.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> 2: <b>PDB Molecule:</b> 50s ribosomal protein l31; <b>PDBTitle:</b> m. smegmatis p/p state 50s ribosomal subunit
64	<a href="#">c5zcrB_</a>	Alignment	not modelled	5.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> maltooligosyl trehalose synthase; <b>PDBTitle:</b> dsm5389 glycosyltrehalose synthase
65	<a href="#">c3tbmA_</a>	Alignment	not modelled	5.7	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a type 4 cdgsh iron-sulfur protein.
66	<a href="#">d1zq1c3</a>	Alignment	not modelled	5.7	15	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> GatB/GatE catalytic domain-like
67	<a href="#">c2bzwB_</a>	Alignment	not modelled	5.6	67	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2-antagonist of cell death; <b>PDBTitle:</b> the crystal structure of bcl-xl in complex with full-length bad
68	<a href="#">d2dnaa1</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
69	<a href="#">c3jzeC_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2
70	<a href="#">c3bdkB_</a>	Alignment	not modelled	5.4	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mannonate dehydratase; <b>PDBTitle:</b> crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
71	<a href="#">d1dpsa_</a>	Alignment	not modelled	5.1	5	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin