














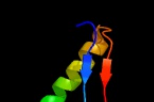






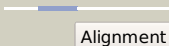

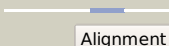

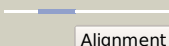
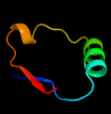
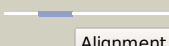

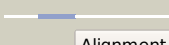

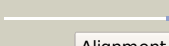







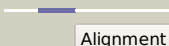
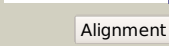
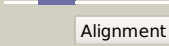
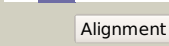
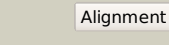
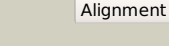
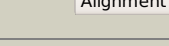



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0434 (-)_521517_522170
Date	Tue Jul 23 14:50:51 BST 2019
Unique Job ID	15cc1507f2319a26

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3m65A_	 Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease la 1; PDBTitle: crystal structure of bacillus subtilis lon n-terminal domain
2	d1zboa1	 Alignment		100.0	24	Fold: PUA domain-like Superfamily: PUA domain-like Family: LON domain-like
3	c3ljcA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease la; PDBTitle: crystal structure of lon n-terminal domain.
4	d2anea1	 Alignment		99.9	19	Fold: PUA domain-like Superfamily: PUA domain-like Family: LON domain-like
5	d1vcoa1	 Alignment		47.6	9	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
6	c3l83A_	 Alignment		45.2	24	PDB header: transferase Chain: A; PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
7	c1vcnA_	 Alignment		40.1	9	PDB header: ligase Chain: A; PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
8	c2w7tA_	 Alignment		38.8	17	PDB header: ligase Chain: A; PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound acivicin
9	c3l7nA_	 Alignment		35.3	15	PDB header: transferase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
10	c1ci6B_	 Alignment		31.8	16	PDB header: transcription Chain: B; PDB Molecule: transcription factor c/ebp beta; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
11	d2a9va1	 Alignment		31.3	11	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

12	d1s1ma1	 Alignment		29.6	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
13	c2ktiA	 Alignment		24.9	8	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of c-terminal domain from mtytyrps of a. nidulans
14	c2issF	 Alignment		23.2	14	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
15	c5ch1B	 Alignment		22.0	27	PDB header: transferase Chain: B: PDB Molecule: putative polycomb protein ezh2,putative polycomb protein PDBTitle: crystal structure of an active polycomb repressive complex 2 in the2 stimulated state
16	d1wl8a1	 Alignment		20.8	6	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
17	c2nz7A	 Alignment		20.7	21	PDB header: apoptosis Chain: A: PDB Molecule: caspase recruitment domain-containing protein 4; PDBTitle: crystal structure analysis of caspase-recruitment domain2 (card) of nod1
18	d1jvna2	 Alignment		18.9	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
19	d1p80a1	 Alignment		17.5	4	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
20	d1k9vf	 Alignment		16.8	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
21	c6gurA	 Alignment	not modelled	16.7	17	PDB header: transferase Chain: A: PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
22	c2b1wA	 Alignment	not modelled	16.7	20	PDB header: apoptosis Chain: A: PDB Molecule: caspase recruitment domain protein 4; PDBTitle: solution structure of the nod1 caspase activating and recruitment2 domain
23	c4gudA	 Alignment	not modelled	15.3	14	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
24	d1ka9h	 Alignment	not modelled	15.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
25	c4l8fA	 Alignment	not modelled	14.8	16	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtX
26	c2ywja	 Alignment	not modelled	14.2	11	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
27	c1utyA	 Alignment	not modelled	13.9	12	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 2; PDBTitle: crystal structure of the rna binding domain of bluetongue virus non-2 structural protein 2(ns2)
28	d1utyA	 Alignment	not modelled	13.9	12	Fold: BTV NS2-like ssRNA-binding domain Superfamily: BTV NS2-like ssRNA-binding domain Family: BTV NS2-like ssRNA-binding domain

29	d1xl3c1	Alignment	not modelled	13.6	8	Fold: Type III secretion system domain Superfamily: Type III secretion system domain Family: TyeA-like
30	d1o1ya	Alignment	not modelled	13.1	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
31	c3uk7B	Alignment	not modelled	13.0	11	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
32	c3l9kX	Alignment	not modelled	12.8	10	PDB header: motor protein Chain: X: PDB Molecule: dynein intermediate chain, cytosolic; PDBTitle: insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
33	c3l9kZ	Alignment	not modelled	12.8	10	PDB header: motor protein Chain: Z: PDB Molecule: dynein intermediate chain, cytosolic; PDBTitle: insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
34	d1q7ra	Alignment	not modelled	12.6	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	c2ip6A	Alignment	not modelled	12.5	9	PDB header: antimicrobial protein Chain: A: PDB Molecule: papb; PDBTitle: crystal structure of pedb
36	c3nvaB	Alignment	not modelled	12.1	6	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
37	c3r74B	Alignment	not modelled	11.9	28	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
38	c3cneD	Alignment	not modelled	11.4	5	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
39	c3fseB	Alignment	not modelled	11.3	16	PDB header: hydrolase Chain: B: PDB Molecule: two-domain protein containing dj-1/thij/pfpi-like and PDBTitle: crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anaebaena variabilis3 atcc 29413 at 1.90 a resolution
40	c4zdiE	Alignment	not modelled	11.1	9	PDB header: ligase Chain: E: PDB Molecule: ctp synthase; PDBTitle: crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
41	c2lxaA	Alignment	not modelled	11.1	13	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit a; PDBTitle: solution nmr structure of glutamine amido transferase subunit of2 gaunosine monophosphate synthetase from methanocaldococcus jannaschii
42	d1i1qb	Alignment	not modelled	10.3	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
43	c3tweA	Alignment	not modelled	10.3	28	PDB header: unknown function Chain: A: PDB Molecule: alpha4h; PDBTitle: crystal structure of the de novo designed peptide alpha4h
44	c3tweB	Alignment	not modelled	10.1	28	PDB header: unknown function Chain: B: PDB Molecule: alpha4h; PDBTitle: crystal structure of the de novo designed peptide alpha4h
45	c2ywdA	Alignment	not modelled	9.9	16	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
46	c1l9xA	Alignment	not modelled	9.8	21	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
47	d1l9xa	Alignment	not modelled	9.8	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
48	d1i7qb	Alignment	not modelled	9.6	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
49	d1cy5a	Alignment	not modelled	8.4	12	Fold: DEATH domain Superfamily: DEATH domain Family: Caspase recruitment domain, CARD
50	c2r47C	Alignment	not modelled	8.1	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein mth_862; PDBTitle: crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
51	c1jvnB	Alignment	not modelled	8.0	19	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
52	c1a3wB	Alignment	not modelled	7.7	17	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
53	c2mn4A	Alignment	not modelled	7.6	20	PDB header: de novo protein Chain: A: PDB Molecule: computational designed protein based on structure template PDBTitle: nmr solution structure of a computational designed

						protein based on2 structure template 1cy5
54	c3katA	Alignment	not modelled	7.4	15	PDB header: apoptosis Chain: A: PDB Molecule: nacht, Irr and pyd domains-containing protein 1; PDBTitle: crystal structure of the card domain of the human nlrp1 protein,2 northeast structural genomics consortium target hr3486e
55	c2ad5B	Alignment	not modelled	7.4	11	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
56	c3n7tA	Alignment	not modelled	7.3	8	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
57	c3l3bA	Alignment	not modelled	7.2	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
58	d1jh3a	Alignment	not modelled	6.9	16	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
59	c3x1mC	Alignment	not modelled	6.8	14	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase/ppat from2 pseudomonas aeruginosa with coa
60	c5tgnA	Alignment	not modelled	6.8	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein sthe_2403 from sphaerobacter thermophilus
61	d1uptd	Alignment	not modelled	6.6	5	Fold: GRIP domain Superfamily: GRIP domain Family: GRIP domain
62	d1qywa	Alignment	not modelled	6.6	5	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/PfpI
63	d1uf0a	Alignment	not modelled	6.6	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
64	c3l0rA	Alignment	not modelled	6.4	14	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: cystatin-2; PDBTitle: crystal structure of salivary cystatin from the soft tick ornithodoros2 moubata
65	d1gpm2	Alignment	not modelled	6.2	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
66	c2mb9A	Alignment	not modelled	6.2	18	PDB header: signaling protein Chain: A: PDB Molecule: b-cell lymphoma/leukemia 10; PDBTitle: human bcl10 card
67	c4lruA	Alignment	not modelled	6.1	8	PDB header: lyase Chain: A: PDB Molecule: glyoxalase iii (glutathione-independent); PDBTitle: crystal structure of glyoxalase iii (orf 19.251) from candida albicans
68	d1sy7a1	Alignment	not modelled	6.1	6	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
69	d1wfa1	Alignment	not modelled	5.8	15	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
70	c4uedB	Alignment	not modelled	5.8	23	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation factor 4e-binding protein 1; PDBTitle: complex of human eif4e with the 4e binding protein 4e-bp1
71	c2lsoA	Alignment	not modelled	5.7	24	PDB header: nuclear protein Chain: A: PDB Molecule: histone h1x; PDBTitle: solution nmr structure of the globular domain of human histone h1x,2 northeast structural genomics consortium (nesg) target hr7057a
72	c3qsjA	Alignment	not modelled	5.5	10	PDB header: hydrolase Chain: A: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
73	d2pa2a1	Alignment	not modelled	5.5	33	Fold: alpha/beta-Hammerhead Superfamily: Ribosomal protein L16p/L10e Family: Ribosomal protein L10e
74	c2vgbB	Alignment	not modelled	5.5	10	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes r/l; PDBTitle: human erythrocyte pyruvate kinase
75	d1qdlb	Alignment	not modelled	5.4	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
76	c3f5dA	Alignment	not modelled	5.2	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from bacillus2 subtilis
77	c4i16A	Alignment	not modelled	5.2	28	PDB header: signaling protein Chain: A: PDB Molecule: caspase recruitment domain-containing protein 11; PDBTitle: crystal structure of carma1 card
78	d1od6a	Alignment	not modelled	5.2	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
						PDB header: actin binding

79	c2qa7B_	Alignment	not modelled	5.2	25	Chain: B; PDB Molecule: huntingtin-interacting protein 1; PDBTitle: crystal structure of huntingtin-interacting protein 12 (hip1) coiled-coil domain with a basic surface suitable3 for hip-protein interactor (hippi)
80	c3mxnA_	Alignment	not modelled	5.1	5	PDB header: replication Chain: A; PDB Molecule: recq-mediated genome instability protein 1; PDBTitle: crystal structure of the rmi core complex