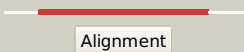

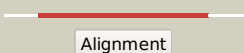

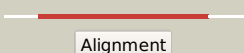

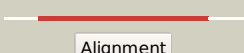





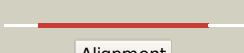

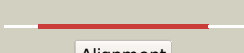





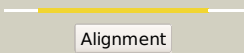

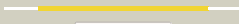







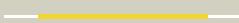

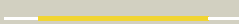

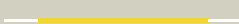






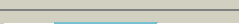

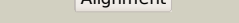
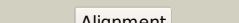

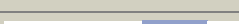



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0992c_(-)_1108582_1109175
Date	Wed Jul 31 22:05:06 BST 2019
Unique Job ID	ba97dc0645f79560

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jcbA_	 Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: 5-formyltetrahydrofolate cyclo-ligase family protein; PDBTitle: the crystal structure of 5-formyl-tetrahydrofolate2 cycloligase from bacillus anthracis (ba4489)
2	c3hy4A_	 Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: 5-formyltetrahydrofolate cyclo-ligase; PDBTitle: structure of human mthfs with n5-iminium phosphate
3	d1soua_	 Alignment		100.0	26	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: Methenyltetrahydrofolate synthetase
4	c1ydmC_	 Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein yqgn; PDBTitle: x-ray structure of northeast structural genomics target sr44
5	c1u3fA_	 Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: 5,10-methenyltetrahydrofolate synthetase; PDBTitle: structural and functional characterization of a 5,10-2 methenyltetrahydrofolate synthetase from mycoplasma3 pneumoniae (gi: 13508087)
6	d1sbqa_	 Alignment		100.0	24	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: Methenyltetrahydrofolate synthetase
7	d1wkca_	 Alignment		100.0	35	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: Methenyltetrahydrofolate synthetase
8	c5b04B_	 Alignment		96.7	23	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
9	c3ecsD_	 Alignment		90.5	14	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
10	c6j3mD_	 Alignment		78.4	13	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
11	c4zemB_	 Alignment		78.3	16	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif2b-like protein, PDBTitle: crystal structure of eif2b beta from chaetomium thermophilum

12	c6i7tB	 Alignment		77.1	13	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: eif2b:eif2 complex
13	c6i3mF	 Alignment		74.8	12	PDB header: translation Chain: F: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
14	d1t9ka	 Alignment		72.7	16	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
15	c1w2wj	 Alignment		72.4	19	PDB header: isomerase Chain: J: PDB Molecule: 5-methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of yeast ypr118w, a methylthioribose-1-phosphate2 isomerase related to regulatory eif2b subunits
16	c5b04G	 Alignment		71.9	10	PDB header: translation Chain: G: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
17	c2yvka	 Alignment		71.7	10	PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
18	c6a34B	 Alignment		70.2	15	PDB header: isomerase Chain: B: PDB Molecule: putative methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate isomerase from2 pyrococcus horikoshii ot3 - form i
19	d1t5oa	 Alignment		60.0	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
20	c6musF	 Alignment		39.6	38	PDB header: rna binding protein/rna Chain: F: PDB Molecule: uncharacterized protein csm5; PDBTitle: cryo-em structure of larger csm-crrna-target rna ternary complex in2 type iii-a crispr-cas system
21	c1vw4K	 Alignment	not modelled	38.3	23	PDB header: ribosome Chain: K: PDB Molecule: 54s ribosomal protein l16, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
22	c3uk7B	 Alignment	not modelled	35.9	12	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
23	d1z7ma1	 Alignment	not modelled	35.0	20	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
24	c5dboA	 Alignment	not modelled	34.7	16	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
25	d1k6da	 Alignment	not modelled	29.3	12	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
26	d1q7ra	 Alignment	not modelled	28.3	11	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
27	c3od1A	 Alignment	not modelled	25.6	22	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase regulatory subunit; PDBTitle: the crystal structure of an atp phosphoribosyltransferase regulatory2 subunit/histidyl-trna synthetase from bacillus halodurans c
28	c4v19C	 Alignment	not modelled	24.8	25	PDB header: ribosome Chain: Q: PDB Molecule: mitoribosomal protein ul16m, mrpl16;

28	c6v130_	Alignment	not modelled	24.8	23	PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2 PDB header: rna binding protein
29	c6ig0H_	Alignment	not modelled	24.5	38	Chain: H: PDB Molecule: type iii-a crispr-associated ramp protein csm5; PDBTitle: type iii-a csm complex, cryo-em structure of csm-ctr1, atp bound
30	d1wu7a2	Alignment	not modelled	24.2	22	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
31	d1e1oa2	Alignment	not modelled	22.8	0	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
32	d1i1qb_	Alignment	not modelled	22.7	9	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
33	c3rr1C_	Alignment	not modelled	22.5	15	PDB header: transferase Chain: C: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; PDBTitle: complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
34	d2e1za1	Alignment	not modelled	22.3	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
35	c3racA_	Alignment	not modelled	22.1	27	PDB header: ligase Chain: A: PDB Molecule: histidine-trna ligase; PDBTitle: crystal structure of histidine--trna ligase subunit from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446.
36	d1vb5a_	Alignment	not modelled	21.4	15	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
37	c3bboO_	Alignment	not modelled	21.3	21	PDB header: ribosome Chain: O: PDB Molecule: ribosomal protein l16; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
38	c2zalD_	Alignment	not modelled	20.6	50	PDB header: hydrolase Chain: D: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
39	d2gfqa1	Alignment	not modelled	20.5	22	Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like
40	c2gfgC_	Alignment	not modelled	19.9	22	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: upf0204 protein ph0006; PDBTitle: structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
41	c1jn9D_	Alignment	not modelled	19.7	50	PDB header: hydrolase Chain: D: PDB Molecule: putative l-asparaginase; PDBTitle: structure of putative asparaginase encoded by escherichia coli ybik2 gene
42	c1k2xB_	Alignment	not modelled	19.7	50	PDB header: hydrolase Chain: B: PDB Molecule: putative l-asparaginase; PDBTitle: crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
43	c1k2xD_	Alignment	not modelled	19.7	50	PDB header: hydrolase Chain: D: PDB Molecule: putative l-asparaginase; PDBTitle: crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
44	c6ezoD_	Alignment	not modelled	19.3	11	PDB header: membrane protein Chain: D: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
45	d2nv0a1	Alignment	not modelled	19.3	9	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
46	c2gacD_	Alignment	not modelled	19.0	40	PDB header: hydrolase Chain: D: PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
47	c2ftcl_	Alignment	not modelled	19.0	26	PDB header: ribosome Chain: I: PDB Molecule: mitochondrial ribosomal protein l16; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
48	d2j01q1	Alignment	not modelled	18.9	23	Fold: alpha/beta-Hammerhead Superfamily: Ribosomal protein L16p/L10e Family: Ribosomal protein L16p
49	d1id3b_	Alignment	not modelled	18.3	16	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
50	d1yqea1	Alignment	not modelled	18.0	15	Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like
51	c1z7nB_	Alignment	not modelled	17.8	22	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase regulatory subunit; PDBTitle: atp phosphoribosyl transferase (hiszg atp-prtase) from2 lactococcus lactis with bound prpp substrate
52	c4wcej_	Alignment	not modelled	17.6	28	PDB header: ribosome Chain: J: PDB Molecule: 50s ribosomal protein l16; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus
53	d1qdlb_	Alignment	not modelled	17.5	10	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
						PDB header: transferase

54	c4ijnB_	Alignment	not modelled	17.0	19	Chain: B: PDB Molecule: acetate kinase; PDBTitle: crystal structure of an acetate kinase from mycobacterium smegmatis2 bound to amp and sulfate
55	c2zalB_	Alignment	not modelled	16.9	50	PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
56	c1jn9B_	Alignment	not modelled	16.6	50	PDB header: hydrolase Chain: B: PDB Molecule: putative l-asparaginase; PDBTitle: structure of putative asparaginase encoded by escherichia coli ybik2 gene
57	c1t3mD_	Alignment	not modelled	16.6	50	PDB header: hydrolase Chain: D: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
58	c1t3mB_	Alignment	not modelled	16.6	50	PDB header: hydrolase Chain: B: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
59	d2zjrj1	Alignment	not modelled	16.4	19	Fold: alpha/beta-Hammerhead Superfamily: Ribosomal protein L16p/L10e Family: Ribosomal protein L16p
60	d1ka9h_	Alignment	not modelled	16.2	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
61	c2gezF_	Alignment	not modelled	15.9	60	PDB header: hydrolase Chain: F: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
62	d2j8ga2	Alignment	not modelled	15.8	4	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: 1,4-beta-N-acetylmuraminidase
63	c6nr5_	Alignment	not modelled	15.6	32	PDB header: chaperone Chain: 5: PDB Molecule: prefoldin subunit 5; PDBTitle: htric-hpfd class2
64	c4zeoH_	Alignment	not modelled	15.3	14	PDB header: translation Chain: H: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of eif2b delta from chaetomium thermophilum
65	c5o60N_	Alignment	not modelled	15.2	21	PDB header: ribosome Chain: N: PDB Molecule: 50s ribosomal protein l16; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
66	c1x3nA_	Alignment	not modelled	15.1	23	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
67	c3rqsB_	Alignment	not modelled	14.9	45	PDB header: oxidoreductase Chain: B: PDB Molecule: hydroxyacyl-coenzyme a dehydrogenase, mitochondrial; PDBTitle: crystal structure of human l-3- hydroxyacyl-coa dehydrogenase2 (ec1.1.1.35) from mitochondria at the resolution 2.0 a, northeast3 structural genomics consortium target hr487, mitochondrial protein4 partnership
68	c4pv3D_	Alignment	not modelled	14.7	50	PDB header: hydrolase Chain: D: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with na+ cations
69	d1ooya1	Alignment	not modelled	14.5	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
70	c2ywdA_	Alignment	not modelled	14.4	15	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
71	c3ejhF_	Alignment	not modelled	14.3	33	PDB header: cell adhesion Chain: F: PDB Molecule: collagen type-i a1 chain; PDBTitle: crystal structure of the fibronectin 8-9fni domain pair in complex2 with a type-i collagen peptide
72	c6gg0G_	Alignment	not modelled	14.2	10	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model 1)
73	c3khyA_	Alignment	not modelled	13.8	21	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of a propionate kinase from francisella tularensis2 subsp. tularensis schu s4
74	d1qe0a2	Alignment	not modelled	13.7	22	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
75	c5bu3A_	Alignment	not modelled	13.7	67	PDB header: lyase Chain: A: PDB Molecule: pyri4; PDBTitle: crystal structure of diels-alderase pyri4 in complex with its product
76	d2gyck1	Alignment	not modelled	13.4	24	Fold: alpha/beta-Hammerhead Superfamily: Ribosomal protein L16p/L10e Family: Ribosomal protein L16p
77	c5ldxh_	Alignment	not modelled	13.2	55	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-ubiquinone oxidoreductase chain 1; PDBTitle: structure of mammalian respiratory complex i, class3.
78	c5ldwh_	Alignment	not modelled	13.2	55	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-ubiquinone oxidoreductase chain 1; PDBTitle: structure of mammalian respiratory complex i, class1
						PDB header: oxidoreductase

79	c5lc5h_	Alignment	not modelled	13.2	55	Chain: H: PDB Molecule: nadh-ubiquinone oxidoreductase chain 1; PDBTitle: structure of mammalian respiratory complex i, class2
80	c2issF_	Alignment	not modelled	13.1	11	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
81	d1kx5b_	Alignment	not modelled	13.1	15	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
82	d1w7ab4	Alignment	not modelled	13.1	18	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
83	c4ce4O_	Alignment	not modelled	12.8	26	PDB header: ribosome Chain: Q: PDB Molecule: mrp16; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
84	c3p4iA_	Alignment	not modelled	12.7	21	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium
85	c2vduE_	Alignment	not modelled	12.4	19	PDB header: transferase Chain: E: PDB Molecule: trna (guanine-n(7)-)-methyltransferase; PDBTitle: structure of trm8-trm82, the yeast trna m7g methylation2 complex
86	d1bbua2	Alignment	not modelled	11.4	0	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
87	c3d3uA_	Alignment	not modelled	11.2	21	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
88	c4aaqA_	Alignment	not modelled	11.0	37	PDB header: viral protein Chain: A: PDB Molecule: l2 protein iii (penton base); PDBTitle: dodecahedron formed of penton base protein from adenovirus ad3
89	d1lbqa_	Alignment	not modelled	10.8	15	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
90	c1apzB_	Alignment	not modelled	10.7	30	PDB header: complex (hydrolase/peptide) Chain: B: PDB Molecule: aspartylglucosaminidase; PDBTitle: human aspartylglucosaminidase complex with reaction product
91	d1gk8i_	Alignment	not modelled	10.7	19	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
92	d1ytlal	Alignment	not modelled	10.2	35	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: ACDE2-like
93	c2rnmC_	Alignment	not modelled	10.1	55	PDB header: protein fibril Chain: C: PDB Molecule: small s protein; PDBTitle: structure of the het-s(218-289) prion in its amyloid form obtained by2 solid-state nmr
94	d2huec1	Alignment	not modelled	9.9	15	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
95	d3pmga2	Alignment	not modelled	9.9	33	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
96	d2hrca1	Alignment	not modelled	9.8	11	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
97	d1hiod_	Alignment	not modelled	9.8	15	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
98	d1oi4a1	Alignment	not modelled	9.7	8	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
99	c5mqrA_	Alignment	not modelled	9.7	29	PDB header: hydrolase Chain: A: PDB Molecule: beta-l-arabinobiosidase; PDBTitle: sialidase bt_1020