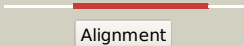

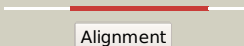

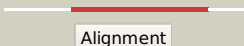







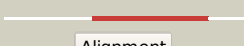




















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0618 (galTa)_711539_712234
 Date Fri Jul 26 01:50:18 BST 2019
 Unique Job ID 02c4ee760a490e10

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5in3A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: galactose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of glucose-1-phosphate bound nucleotidylated human2 galactose-1-phosphate uridylyltransferase
2	c1gupC_	 Alignment		100.0	26	PDB header: nucleotidyltransferase Chain: C: PDB Molecule: galactose-1-phosphate uridylyltransferase; PDBTitle: structure of nucleotidyltransferase complexed with udp-2 galactose
3	d1guqa1	 Alignment		100.0	27	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
4	c1zwwA_	 Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative galactose-1-phosphate uridylyl transferase; PDBTitle: x-ray structure of galt-like protein from arabidopsis thaliana2 at5g18200
5	d1z84a1	 Alignment		100.0	23	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
6	c4qvua_	 Alignment		99.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4931 family protein (bce0241) from bacillus2 cereus atcc 10987 at 2.65 a resolution
7	c4i5wA_	 Alignment		98.4	19	PDB header: transferase Chain: A: PDB Molecule: 5',5'''-p-1,p-4-tetraphosphate phosphorylase 2; PDBTitle: crystal structure of yeast ap4a phosphorylase apa2 in complex with amp
8	c5cs2A_	 Alignment		98.0	16	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad protein; PDBTitle: crystal structure of plasmodium falciparum diadenosine triphosphate2 hydrolase in complex with cyclamarin a
9	c3ksvA_	 Alignment		97.8	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: hypothetical protein from leishmania major
10	c3anoA_	 Alignment		97.6	17	PDB header: transferase Chain: A: PDB Molecule: ap-4-a phosphorylase; PDBTitle: crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
11	c2eo4A_	 Alignment		97.4	13	PDB header: hydrolase Chain: A: PDB Molecule: 150aa long hypothetical histidine triad nucleotide-binding PDBTitle: crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfolobus tokodaii strain7

12	d1emsa1	Alignment		97.3	19	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
13	c3l7xA	Alignment		97.2	16	PDB header: cell cycle Chain: A: PDB Molecule: putative hit-like protein involved in cell-cycle PDBTitle: the crystal structure of smu.412c from streptococcus mutans ua159
14	d1y23a	Alignment		97.2	17	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
15	c3imiB	Alignment		97.2	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hit family protein; PDBTitle: 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
16	d1fita	Alignment		97.2	17	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
17	c3lb5B	Alignment		97.1	13	PDB header: cell cycle Chain: B: PDB Molecule: hit-like protein involved in cell-cycle regulation; PDBTitle: crystal structure of hit-like protein involved in cell-cycle2 regulation from bartonella henselae with unknown ligand
18	c3o0mB	Alignment		97.0	13	PDB header: hydrolase Chain: B: PDB Molecule: hit family protein; PDBTitle: crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
19	c3oj7A	Alignment		97.0	13	PDB header: metal binding protein Chain: A: PDB Molecule: putative histidine triad family protein; PDBTitle: crystal structure of a histidine triad family protein from entamoeba2 histolytica, bound to sulfate
20	c6iq1A	Alignment		96.8	14	PDB header: hydrolase Chain: A: PDB Molecule: adenosine 5'-monophosphoramidase; PDBTitle: crystal structure of histidine triad nucleotide-binding protein from2 candida albicans
21	c1xquA	Alignment	not modelled	96.7	16	PDB header: hydrolase Chain: A: PDB Molecule: hit family hydrolase; PDBTitle: hit family hydrolase from clostridium thermocellum cth-393
22	d1xqua	Alignment	not modelled	96.7	16	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
23	c1emsB	Alignment	not modelled	96.7	20	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
24	d1kpfa	Alignment	not modelled	96.6	11	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
25	d1rzya	Alignment	not modelled	96.6	13	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
26	c4eguA	Alignment	not modelled	96.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: histidine triad (hit) protein; PDBTitle: 0.95a resolution structure of a histidine triad protein from2 clostridium difficile
27	c6d6jB	Alignment	not modelled	96.6	12	PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of hit family hydrolase from legionella pneumophila2 philadelphia 1
28	c4incA	Alignment	not modelled	96.2	11	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad nucleotide-binding protein 2, PDBTitle: human histidine triad nucleotide binding protein 2
						Fold: HIT-like

29	d1z84a2	Alignment	not modelled	95.8	15	Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
30	d2oika1	Alignment	not modelled	95.8	17	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
31	c4q61j_	Alignment	not modelled	95.6	10	PDB header: cell cycle Chain: J: PDB Molecule: uncharacterized hit-like protein hp_0404; PDBTitle: hit like protein from helicobacter pylori 26695
32	c3n1tE_	Alignment	not modelled	95.2	9	PDB header: hydrolase Chain: E: PDB Molecule: hit-like protein hint; PDBTitle: crystal structure of the h101a mutant echint gmp complex
33	c3r6fA_	Alignment	not modelled	94.8	16	PDB header: hydrolase Chain: A: PDB Molecule: hit family protein; PDBTitle: crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
34	c3p0tB_	Alignment	not modelled	94.6	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
35	c3jb9c_	Alignment	not modelled	93.1	16	PDB header: rna binding protein/rna Chain: C: PDB Molecule: u5 snrna; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
36	c3i4sB_	Alignment	not modelled	90.2	8	PDB header: hydrolase Chain: B: PDB Molecule: histidine triad protein; PDBTitle: crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
37	d1guqa2	Alignment	not modelled	89.6	13	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
38	c3oheA_	Alignment	not modelled	88.5	8	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
39	c3i24B_	Alignment	not modelled	85.8	5	PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of a hit family hydrolase protein from vibrio2 fischeri. northeast structural genomics consortium target id vfr176
40	c6id1U_	Alignment	not modelled	83.3	13	PDB header: splicing Chain: U: PDB Molecule: cwf19-like protein 2; PDBTitle: cryo-em structure of a human intron lariat spliceosome after prp432 loaded (ils2 complex) at 2.9 angstrom resolution
41	c3nrdB_	Alignment	not modelled	80.3	10	PDB header: nucleotide binding protein Chain: B: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
42	c5sxyA_	Alignment	not modelled	50.6	41	PDB header: chaperone Chain: A: PDB Molecule: bifunctional coenzyme pqq synthesis protein c/d; PDBTitle: the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqcd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
43	c4ndgB_	Alignment	not modelled	46.4	16	PDB header: dna binding protein/rna/dna Chain: B: PDB Molecule: aprataxin; PDBTitle: human aprataxin (aptx) bound to rna-dna and zn - adenosine vanadate2 transition state mimic complex
44	d1vpra1	Alignment	not modelled	38.4	20	Fold: Lipocalins Superfamily: Lipocalins Family: Dinoflagellate luciferase repeat
45	c3g2bA_	Alignment	not modelled	36.6	41	PDB header: biosynthetic protein Chain: A: PDB Molecule: coenzyme pqq synthesis protein d; PDBTitle: crystal structure of pqqd from xanthomonas campestris
46	c2iqcA_	Alignment	not modelled	26.7	46	PDB header: protein binding Chain: A: PDB Molecule: fanconi anemia group f protein; PDBTitle: crystal structure of human fancf protein that functions in2 the assembly of a dna damage signaling complex
47	c1t3bA_	Alignment	not modelled	26.1	14	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
48	c3pa8A_	Alignment	not modelled	24.7	21	PDB header: toxin/peptide inhibitor Chain: A: PDB Molecule: toxin b; PDBTitle: structure of the c. difficile tcdb cysteine protease domain in complex2 with a peptide inhibitor
49	d1igna2	Alignment	not modelled	24.1	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: DNA-binding domain of rap1
50	c3j6vR_	Alignment	not modelled	22.7	23	PDB header: ribosome Chain: R: PDB Molecule: 28s ribosomal protein s18a, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
51	d1ea9c2	Alignment	not modelled	21.1	24	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
52	c4acvA_	Alignment	not modelled	20.4	40	PDB header: immune system Chain: A: PDB Molecule: prophage lambdalm01, antigen b; PDBTitle: listeria monocytogenes antigen b
53	c4lh9A_	Alignment	not modelled	19.9	12	PDB header: transcription Chain: A: PDB Molecule: heterocyst differentiation control protein; PDBTitle: crystal structure of the refolded hood domain (asp256-gly295) of hetr
54	c5aj3R_	Alignment	not modelled	19.8	43	PDB header: ribosome Chain: R: PDB Molecule: mitoribosomal protein bs18m, mrps18c; PDBTitle: structure of the small subunit of the mammalian

						mitoribosome
55	d1u0la1	Alignment	not modelled	19.8	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
56	d1t9ha1	Alignment	not modelled	18.3	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
57	c5xmca_	Alignment	not modelled	18.2	19	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy; PDBTitle: crystal structure of the auto-inhibited nedd4 family e3 ligase itch
58	d1w2za2	Alignment	not modelled	16.0	6	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
59	c5a3ga_	Alignment	not modelled	16.0	17	PDB header: viral protein Chain: A: PDB Molecule: m50; PDBTitle: structure of herpesvirus nuclear egress complex subunit m50
60	c3t4cD_	Alignment	not modelled	15.7	6	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 1; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
61	c1rfoC_	Alignment	not modelled	15.4	38	PDB header: viral protein Chain: C: PDB Molecule: whisker antigen control protein; PDBTitle: trimeric foldon of the t4 phagehead fibrin
62	c2he3A_	Alignment	not modelled	15.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 2; PDBTitle: crystal structure of the selenocysteine to cysteine mutant of human2 glutathione peroxidase 2 (gpx2)
63	d1n6ja_	Alignment	not modelled	14.6	11	Fold: SRF-like Superfamily: SRF-like Family: SRF-like
64	c5yirG_	Alignment	not modelled	14.6	50	PDB header: protein binding Chain: G: PDB Molecule: ankyrin-2; PDBTitle: crystal structure of ankb lir/gabarap complex
65	c3w6gP_	Alignment	not modelled	14.6	35	PDB header: oxidoreductase Chain: P: PDB Molecule: probable peroxiredoxin; PDBTitle: structure of peroxiredoxin from anaerobic hyperthermophilic archaeon2 pyrococcus horikoshii
66	c5n6yC_	Alignment	not modelled	14.3	4	PDB header: oxidoreductase Chain: C: PDB Molecule: nitrogenase vanadium-iron protein delta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
67	c3epsB_	Alignment	not modelled	14.2	15	PDB header: transferase, hydrolase Chain: B: PDB Molecule: isocitrate dehydrogenase kinase/phosphatase; PDBTitle: the crystal structure of isocitrate dehydrogenase kinase/phosphatase2 from e. coli
68	d1z8ma1	Alignment	not modelled	14.1	20	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
69	d2lhba_	Alignment	not modelled	14.1	24	Fold: Globin-like Superfamily: Globin-like Family: Globins
70	c2riIA_	Alignment	not modelled	13.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
71	c4uhpB_	Alignment	not modelled	13.8	24	PDB header: hydrolase Chain: B: PDB Molecule: bacteriocin immunity protein; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
72	c3znul_	Alignment	not modelled	13.3	14	PDB header: lyase Chain: I: PDB Molecule: 5-chloromuconolactone dehalogenase; PDBTitle: crystal structure of clcf in crystal form 2
73	c2bc4C_	Alignment	not modelled	13.1	40	PDB header: immune system Chain: C: PDB Molecule: hla class ii histocompatibility antigen, dm alpha chain; PDBTitle: crystal structure of hla-dm
74	d1egwa_	Alignment	not modelled	13.0	11	Fold: SRF-like Superfamily: SRF-like Family: SRF-like
75	c1f3jD_	Alignment	not modelled	12.8	40	PDB header: immune system Chain: D: PDB Molecule: h-2 class ii histocompatibility antigen; PDBTitle: histocompatibility antigen i-ag7
76	d1ocya_	Alignment	not modelled	12.7	23	Fold: Receptor-binding domain of short tail fibre protein gp12 Superfamily: Receptor-binding domain of short tail fibre protein gp12 Family: Receptor-binding domain of short tail fibre protein gp12 PDB header: transcription
77	c4ynlB_	Alignment	not modelled	12.6	12	Chain: B: PDB Molecule: heterocyst differentiation control protein; PDBTitle: crystal structure of the hood domain of anabaena hetr in complex with2 the hexapeptide ergsgr derived from pats
78	d1d6za2	Alignment	not modelled	12.4	6	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
79	c3fq6A_	Alignment	not modelled	12.1	29	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
80	d1kwa_	Alignment	not modelled	11.7	32	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain

81	d2f8aa1	Alignment	not modelled	11.7	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
82	c3mlcC	Alignment	not modelled	11.6	13	PDB header: isomerase Chain: C: PDB Molecule: fg41 malonate semialdehyde decarboxylase; PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropiolate
83	c2oruA	Alignment	not modelled	11.6	50	PDB header: de novo protein Chain: A: PDB Molecule: xtz1-peptide; PDBTitle: solution structure of xtz1-peptide, a beta-hairpin peptide2 with a structured extension
84	c1vluB	Alignment	not modelled	11.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: gamma-glutamyl phosphate reductase; PDBTitle: crystal structure of gamma-glutamyl phosphate reductase (yor323c) from2 saccharomyces cerevisiae at 2.40 a resolution
85	d1ua7a1	Alignment	not modelled	11.5	29	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
86	d1zaka2	Alignment	not modelled	11.4	50	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
87	c4qglA	Alignment	not modelled	11.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: acireductone dioxygenase; PDBTitle: acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
88	c1ekmC	Alignment	not modelled	11.3	23	PDB header: oxidoreductase Chain: C: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure at 2.5 a resolution of zinc-substituted2 copper amine oxidase of hansenua polymorpha expressed in3 escherichia coli
89	c5yisC	Alignment	not modelled	11.1	36	PDB header: protein binding Chain: C: PDB Molecule: ankyrin-2; PDBTitle: crystal structure of ankb lir/lc3b complex
90	d1nqua	Alignment	not modelled	11.0	41	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
91	c3sdsA	Alignment	not modelled	11.0	18	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, mitochondrial; PDBTitle: crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
92	c3nbbC	Alignment	not modelled	11.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: peroxisomal primary amine oxidase; PDBTitle: crystal structure of mutant y305f expressed in e. coli in the copper2 amine oxidase from hansenua polymorpha
93	d1w6ga2	Alignment	not modelled	10.9	14	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
94	c2elpA	Alignment	not modelled	10.8	57	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
95	c4xruE	Alignment	not modelled	10.8	11	PDB header: protein binding Chain: E: PDB Molecule: rnl; PDBTitle: structure of pnkp1/rnl/hen1 complex
96	c3ho6B	Alignment	not modelled	10.6	17	PDB header: toxin Chain: B: PDB Molecule: toxin a; PDBTitle: structure-function analysis of inositol hexakisphosphate-2 induced autoprocessing in clostridium difficile toxin a
97	c1yuzB	Alignment	not modelled	10.5	38	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
98	c4q2uH	Alignment	not modelled	10.5	20	PDB header: toxin/toxin repressor Chain: H: PDB Molecule: mrna interferase yafq; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
99	c6jy5B	Alignment	not modelled	10.4	31	PDB header: structural protein Chain: B: PDB Molecule: unidentified carboxysome polypeptide; PDBTitle: structure of csos4b from halothiobacillus neapolitanus