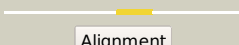

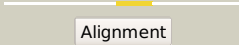

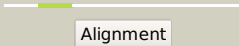



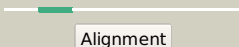



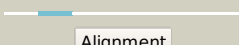

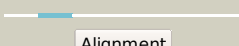
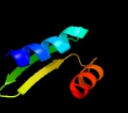
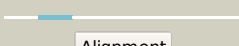


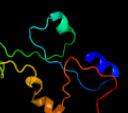




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0806c_(cpsY)_899735_901333
 Date Fri Jul 26 01:50:39 BST 2019
 Unique Job ID f2dd7cb2c8236a92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ga8a_	 Alignment		73.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Galactosyltransferase LgtC
2	c1ga8A_	 Alignment		73.0	18	PDB header: transferase Chain: A: PDB Molecule: galactosyl transferase lgtc; PDBTitle: crystal structure of galactosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
3	c2y9jt_	 Alignment		66.8	13	PDB header: protein transport Chain: T: PDB Molecule: protein prgh; PDBTitle: three-dimensional model of salmonella's needle complex at subnanometer2 resolution
4	d1zvpa2	 Alignment		58.0	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: VC0802-like
5	d1zhva2	 Alignment		49.3	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
6	c1zvpB_	 Alignment		47.9	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein vc0802; PDBTitle: crystal structure of a protein of unknown function vc0802 from vibrio2 cholerae, possible transport protein
7	c1vj7A_	 Alignment		37.5	9	PDB header: protein transport Chain: A: PDB Molecule: escj; PDBTitle: crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
8	c4e8iA_	 Alignment		35.4	11	PDB header: transferase Chain: A: PDB Molecule: lincosamide resistance protein; PDBTitle: crystal structure of lincosamide antibiotic adenylyltransferase lina,2 apo
9	c2hfvA_	 Alignment		34.1	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa1041; PDBTitle: solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
10	c1zcyA_	 Alignment		33.9	12	PDB header: transferase Chain: A: PDB Molecule: glycogenin-1; PDBTitle: apo form of a mutant of glycogenin in which asp159 is replaced by ser
11	d1vh3a_	 Alignment		29.6	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase

12	c1r8uA_	Alignment		26.3	36	PDB header: transcription/transcription activator Chain: A: PDB Molecule: cbp/p300-interacting transactivator 2; PDBTitle: nmr structure of cbp taz1/cited2 complex
13	c1p4qA_	Alignment		23.7	32	PDB header: transcription/transferase Chain: A: PDB Molecule: cbp/p300-interacting transactivator 2; PDBTitle: solution structure of the cited2 transactivation domain in complex2 with the p300 ch1 domain
14	c5l6sF_	Alignment		23.6	19	PDB header: transferase Chain: F: PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: crystal structure of e. coli adp-glucose pyrophosphorylase (agpase) in2 complex with a positive allosteric regulator beta-fructose-1,6-3 diphosphate (fbp) - agpase*fbp
15	d1w77a1	Alignment		21.7	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
16	d2hfvA1	Alignment		21.1	25	Fold: Ferredoxin-like Superfamily: GlnB-like Family: RPA1041-like
17	c2n37A_	Alignment		21.1	47	PDB header: unknown function Chain: A: PDB Molecule: avr-pia protein; PDBTitle: solution structure of avr-pia
18	c5gvvF_	Alignment		20.2	15	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
19	c1zhvA_	Alignment		19.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu0741; PDBTitle: x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
20	c2xmhB_	Alignment		18.9	18	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate cytidyltransferase2 from archaeoglobus fulgidus
21	c6bxjA_	Alignment	not modelled	18.9	46	PDB header: cell adhesion Chain: A: PDB Molecule: chimera protein of integrin beta-3 and integrin alpha-I; PDBTitle: structure of a single-chain beta3 integrin
22	d1qs0a_	Alignment	not modelled	18.0	23	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
23	c6ezoF_	Alignment	not modelled	17.5	16	PDB header: membrane protein Chain: F: PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
24	c4jd0A_	Alignment	not modelled	17.4	14	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
25	d2hmfA2	Alignment	not modelled	16.4	9	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
26	c2fkKA_	Alignment	not modelled	16.1	15	PDB header: viral protein Chain: A: PDB Molecule: baseplate structural protein gp10; PDBTitle: crystal structure of the c-terminal domain of the bacteriophage t42 gene product 10
27	c1zctB_	Alignment	not modelled	15.5	14	PDB header: transferase Chain: B: PDB Molecule: glycogenin-1; PDBTitle: structure of glycogenin truncated at residue 270 in a complex with udp
28	c6gf8B_	Alignment	not modelled	15.4	20	PDB header: cell adhesion Chain: B: PDB Molecule: zona pellucida sperm-binding protein 1,zona pellucida PDBTitle: molecular basis of egg coat filament cross-linking: structure of the2 glycosylated zp1 zp-n1 domain homodimer

29	d1ou0a_	Alignment	not modelled	14.5	23	Fold: Flavodoxin-like Superfamily: Precorrin-8X methylmutase CbiC/CobH Family: Precorrin-8X methylmutase CbiC/CobH
30	d1v9ca_	Alignment	not modelled	14.3	19	Fold: Flavodoxin-like Superfamily: Precorrin-8X methylmutase CbiC/CobH Family: Precorrin-8X methylmutase CbiC/CobH
31	d1yp2a2	Alignment	not modelled	14.1	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
32	d1iioa_	Alignment	not modelled	14.0	27	Fold: EF Hand-like Superfamily: Hypothetical protein MTH865 Family: Hypothetical protein MTH865
33	c6b5kA_	Alignment	not modelled	13.1	18	PDB header: transferase Chain: A; PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
34	c3mcuF_	Alignment	not modelled	13.1	15	PDB header: oxidoreductase Chain: F; PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
35	c3wxvA_	Alignment	not modelled	12.7	18	PDB header: membrane protein/immune system Chain: A; PDB Molecule: adiponectin receptor protein 1; PDBTitle: crystal structure of the human adiponectin receptor 1
36	d2cdqa3	Alignment	not modelled	12.5	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
37	c3kw0D_	Alignment	not modelled	12.2	10	PDB header: hydrolase Chain: D; PDB Molecule: cysteine peptidase; PDBTitle: crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
38	d1xg8a_	Alignment	not modelled	12.0	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: YuzD-like
39	c5vitC_	Alignment	not modelled	11.9	15	PDB header: transferase Chain: C; PDB Molecule: mdcc; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with malonate
40	c1junB_	Alignment	not modelled	11.7	33	PDB header: transcription regulation Chain: B; PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
41	c4ltyD_	Alignment	not modelled	11.3	8	PDB header: hydrolase Chain: D; PDB Molecule: exonuclease subunit sbcd; PDBTitle: crystal structure of e.coli sbcd at 1.8 a resolution
42	c4au1A_	Alignment	not modelled	11.2	8	PDB header: isomerase Chain: A; PDB Molecule: precorrin-8x methylmutase; PDBTitle: crystal structure of cobh (precorrin-8x methyl mutase)2 complexed with c5 desmethyl-hba
43	d1fxoa_	Alignment	not modelled	11.1	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
44	c3m92B_	Alignment	not modelled	10.3	39	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: protein ycin; PDBTitle: the structure of ycin, an uncharacterized protein from shigella2 flexneri.
45	c4wqkA_	Alignment	not modelled	9.7	18	PDB header: transferase Chain: A; PDB Molecule: 2"-aminoglycoside nucleotidyltransferase; PDBTitle: crystal structure of aminoglycoside nucleotidyltransferase ant(2")-2 ia, apo form
46	c6c8zA_	Alignment	not modelled	9.2	25	PDB header: transferase Chain: A; PDB Molecule: adp-dependent phosphofructokinase; PDBTitle: last common ancestor of adp-dependent phosphofructokinases from2 methanosarcinales
47	c6az5A_	Alignment	not modelled	9.1	70	PDB header: sugar binding protein Chain: A; PDB Molecule: alpha-amylase; PDBTitle: crystal structure of cbmd (family cbm41) from eubacterium rectale2 amy13k
48	c3qq5A_	Alignment	not modelled	9.1	23	PDB header: oxidoreductase Chain: A; PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hydF
49	d2guka1	Alignment	not modelled	9.0	23	Fold: PG1857-like Superfamily: PG1857-like Family: PG1857-like
50	d1ss6a_	Alignment	not modelled	9.0	21	Fold: NSFL1 (p97 ATPase) cofactor p47, SEP domain Superfamily: NSFL1 (p97 ATPase) cofactor p47, SEP domain Family: NSFL1 (p97 ATPase) cofactor p47, SEP domain
51	c3j1wU_	Alignment	not modelled	8.9	17	PDB header: cell invasion Chain: U; PDB Molecule: protein prgh; PDBTitle: a refined model of the prototypical salmonella typhimurium t3ss basal2 body reveals the molecular basis for its assembly
52	d2v0fa1	Alignment	not modelled	8.8	26	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
53	d1l2a_	Alignment	not modelled	8.8	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycogenin
54	d1snna_	Alignment	not modelled	8.8	21	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB

55	d1kxpd3	Alignment	not modelled	8.8	21	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
56	d2fj6a1	Alignment	not modelled	8.8	13	Fold: SAM domain-like Superfamily: YozE-like Family: YozE-like
57	d1lhta	Alignment	not modelled	8.7	13	Fold: Head-binding domain of phage P22 tailspike protein Superfamily: Head-binding domain of phage P22 tailspike protein Family: Head-binding domain of phage P22 tailspike protein
58	c5i2cA	Alignment	not modelled	8.6	10	PDB header: signaling protein Chain: A: PDB Molecule: gats-like protein 3; PDBTitle: arginine-bound castor1 from homo sapiens
59	c5ifgC	Alignment	not modelled	8.5	15	PDB header: hydrolase/antitoxin Chain: C: PDB Molecule: mrna interferase high; PDBTitle: crystal structure of higa-high complex from e. coli
60	c5b04l	Alignment	not modelled	8.5	12	PDB header: translation Chain: I: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
61	c4cvhA	Alignment	not modelled	8.5	23	PDB header: transferase Chain: A: PDB Molecule: isoprenoid synthase domain-containing protein; PDBTitle: crystal structure of human isoprenoid synthase domain-containing2 protein
62	c5z34A	Alignment	not modelled	8.5	19	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: the structure of a chitin deacetylase from bombyx mori provide the2 first insight into insect chitin deacetylation mechanism
63	c5znsA	Alignment	not modelled	8.5	15	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: insect chitin deacetylase
64	c3drwA	Alignment	not modelled	8.4	13	PDB header: transferase Chain: A: PDB Molecule: adp-specific phosphofructokinase; PDBTitle: crystal structure of a phosphofructokinase from pyrococcus horikoshii2 ot3 with amp
65	c4kkpA	Alignment	not modelled	8.4	12	PDB header: structural protein Chain: A: PDB Molecule: rbma protein; PDBTitle: crystal structure of vibrio cholerae rbma (crystal form 2)
66	c3s1tB	Alignment	not modelled	8.4	15	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis
67	c2afvB	Alignment	not modelled	8.3	27	PDB header: isomerase Chain: B: PDB Molecule: cobalamin biosynthesis precorrin isomerase; PDBTitle: the crystal structure of putative precorrin isomerase cbic2 in cobalamin biosynthesis
68	d2nxfA1	Alignment	not modelled	7.7	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: ADPRibase-Mn-like
69	c5w65P	Alignment	not modelled	7.7	16	PDB header: transcription Chain: P: PDB Molecule: rna polymerase i-specific transcription initiation factor PDBTitle: rna polymerase i initial transcribing complex state 2
70	c3tqdA	Alignment	not modelled	7.7	16	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
71	d1vaza	Alignment	not modelled	7.6	21	Fold: NSFL1 (p97 ATPase) cofactor p47, SEP domain Superfamily: NSFL1 (p97 ATPase) cofactor p47, SEP domain Family: NSFL1 (p97 ATPase) cofactor p47, SEP domain
72	c2p73A	Alignment	not modelled	7.5	14	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (mannosyltransferase) involved PDBTitle: crystal structure of a glycosyltransferase involved in the2 glycosylation of the major capsid of pbcv-1
73	d1nc7a	Alignment	not modelled	7.4	25	Fold: Hypothetical protein TM1070 Superfamily: Hypothetical protein TM1070 Family: Hypothetical protein TM1070
74	c5y59B	Alignment	not modelled	7.4	21	PDB header: protein binding Chain: B: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku80 and sir4
75	c2mhcA	Alignment	not modelled	7.3	11	PDB header: recombination Chain: A: PDB Molecule: tnpx; PDBTitle: nmr structure of the catalytic domain of the large serine resolvase2 tnpx
76	d1vmha	Alignment	not modelled	6.9	17	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like
77	d1ny711	Alignment	not modelled	6.8	19	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
78	d1pgl11	Alignment	not modelled	6.8	25	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
79	d1ewqa2	Alignment	not modelled	6.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
						PDB header: transferase

80	c2re1A_	Alignment	not modelled	6.8	15	Chain: A: PDB Molecule: aspartokinase, alpha and beta subunits; PDBTitle: crystal structure of aspartokinase alpha and beta subunits
81	d2h80a1	Alignment	not modelled	6.5	33	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
82	d1f2va_	Alignment	not modelled	6.5	12	Fold: Flavodoxin-like Superfamily: Precorrin-8X methylmutase CbiC/CobH Family: Precorrin-8X methylmutase CbiC/CobH
83	d1jeva2	Alignment	not modelled	6.5	27	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
84	d1ul3a_	Alignment	not modelled	6.4	16	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
85	c5k27B_	Alignment	not modelled	6.4	19	PDB header: transferase Chain: B: PDB Molecule: ancmt; PDBTitle: crystal structure of ancestral protein ancmt of adp-dependent sugar2 kinases family.
86	c6f2sB_	Alignment	not modelled	6.3	18	PDB header: virus Chain: B: PDB Molecule: capsid protein; PDBTitle: cryoem structure of ageratum yellow vein virus (ayvv)
87	c3e7dC_	Alignment	not modelled	6.3	19	PDB header: isomerase Chain: C: PDB Molecule: cobh, precorrin-8x methylmutase; PDBTitle: crystal structure of precorrin-8x methyl mutase cbiC/cobh from2 brucella melitensis
88	d2nn6c2	Alignment	not modelled	6.3	13	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
89	d3ci0j1	Alignment	not modelled	6.2	18	Fold: Pili subunits Superfamily: Pili subunits Family: Epsj-like
90	c6g41j_	Alignment	not modelled	6.2	63	PDB header: viral protein Chain: J: PDB Molecule: minor capsid protein; PDBTitle: crystal structure of semet-labeled mavirus penton protein
91	c3kxqB_	Alignment	not modelled	6.1	12	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from bartonella2 henselae at 1.6a resolution
92	c4egvC_	Alignment	not modelled	6.0	18	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of a monomeric scp2-thiolase like protein type 12 (stp1) from mycobacterium smegmatis
93	d1vg5a_	Alignment	not modelled	6.0	22	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
94	c4hrzA_	Alignment	not modelled	5.9	31	PDB header: hydrolase Chain: A: PDB Molecule: tail lysozyme; PDBTitle: phage t4 sheath initiation protein gp25
95	c6gnyA_	Alignment	not modelled	5.9	36	PDB header: structural protein Chain: A: PDB Molecule: membrane-anchored junction protein; PDBTitle: crystal structure of the majin-terb2 heterotetrameric complex
96	d1ju8a_	Alignment	not modelled	5.8	18	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Albumin 1
97	d3erja1	Alignment	not modelled	5.8	13	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
98	d1v95a_	Alignment	not modelled	5.7	12	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
99	d1p8ba_	Alignment	not modelled	5.7	27	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Albumin 1