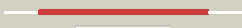









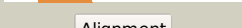
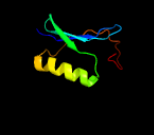

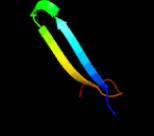






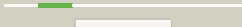
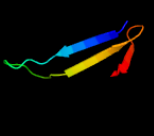
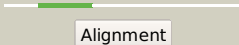

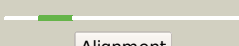
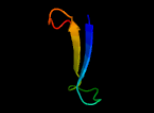
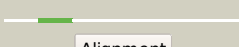



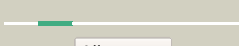
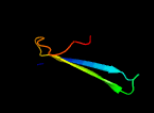





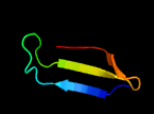
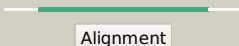

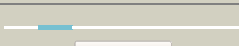
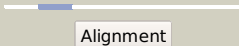
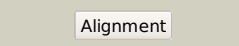



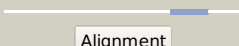




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0776c_(-)_868987_869766
Date	Fri Jul 26 01:50:35 BST 2019
Unique Job ID	da0e33b583485683

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ep5A	 Alignment		96.2	22	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure
2	c4ehtA	 Alignment		89.3	16	PDB header: electron transport Chain: A: PDB Molecule: activator of 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
3	d1huxa	 Alignment		87.9	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
4	d1vhxa	 Alignment		85.1	23	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
5	d3bzka5	 Alignment		84.6	26	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
6	d1iv0a	 Alignment		83.5	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
7	c5nckA	 Alignment		73.7	20	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
8	c2e2pA	 Alignment		73.6	34	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
9	c3eo3B	 Alignment		62.4	21	PDB header: isomerase, transferase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
10	d2aa4a1	 Alignment		61.5	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
11	c3vewA	 Alignment		58.4	18	PDB header: transferase Chain: A: PDB Molecule: o-carbamoyltransferase tobz; PDBTitle: crystal structure of the o-carbamoyltransferase tobz in complex with2 adp

12	c2aa4B_	 Alignment		58.0	16	PDB header: transferase Chain: B: PDB Molecule: putative n-acetylmannosamine kinase; PDBTitle: crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
13	c3ivoC_	 Alignment		54.2	16	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
14	c3zeuE_	 Alignment		54.0	24	PDB header: hydrolase Chain: E: PDB Molecule: probable trna threonylcarbamoyladenine biosynthesis PDBTitle: structure of a salmonella typhimurium ygdj-yeaz heterodimer bound to2 atpgammas
15	c6fpeG_	 Alignment		51.8	23	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
16	c1zc6A_	 Alignment		47.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable n-acetylglucosamine kinase; PDBTitle: crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
17	d2ch5a2	 Alignment		45.6	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
18	c3enoB_	 Alignment		43.7	13	PDB header: hydrolase/unknown function Chain: B: PDB Molecule: putative o-sialoglycoprotein endopeptidase; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
19	c3hz6A_	 Alignment		42.2	24	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
20	d1hjra_	 Alignment		42.0	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
21	c3en9B_	 Alignment	not modelled	32.4	28	PDB header: hydrolase Chain: B: PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
22	c2ch5D_	 Alignment	not modelled	29.7	22	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
23	c3vovC_	 Alignment	not modelled	29.6	22	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
24	d1xw8a_	 Alignment	not modelled	27.5	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
25	d1fnoa3	 Alignment	not modelled	26.7	15	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
26	d2ewsal	 Alignment	not modelled	25.8	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
27	c3giuA_	 Alignment	not modelled	24.1	21	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
28	d1zc6a1	 Alignment	not modelled	22.3	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
		 Alignment				Fold: Ribonuclease H-like motif

29	d1nu0a_	Alignment	not modelled	22.3	17	Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
30	c2ap1A_	Alignment	not modelled	21.7	13	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
31	d1a2za_	Alignment	not modelled	17.6	20	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
32	c2gupA_	Alignment	not modelled	16.1	15	PDB header: transferase Chain: A: PDB Molecule: rok family protein; PDBTitle: structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
33	c5vfbB_	Alignment	not modelled	16.0	16	PDB header: transferase Chain: B: PDB Molecule: malate synthase g; PDBTitle: 1.36 angstrom resolution crystal structure of malate synthase g from2 pseudomonas aeruginosa in complex with glycolic acid.
34	c4idhA_	Alignment	not modelled	15.7	16	PDB header: viral protein Chain: A: PDB Molecule: gene 2 protein; PDBTitle: crystal structure of the large terminase subunit gp2 of bacterial2 virus sf6
35	c3fb9B_	Alignment	not modelled	13.8	63	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein with unknown function from2 streptococcus pneumoniae tigr4
36	d2ap1a2	Alignment	not modelled	13.7	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
37	d1iofa_	Alignment	not modelled	13.4	20	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
38	c2qm1D_	Alignment	not modelled	13.3	19	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
39	d1jzta_	Alignment	not modelled	12.0	15	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
40	d1z6ra2	Alignment	not modelled	11.4	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
41	c3c6aA_	Alignment	not modelled	11.3	11	PDB header: viral protein Chain: A: PDB Molecule: terminase large subunit; PDBTitle: crystal structure of the rb49 gp17 nuclease domain
42	c4gxhC_	Alignment	not modelled	11.2	18	PDB header: hydrolase Chain: C: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of a pyrrolidone-carboxylate peptidase 1 (target id2 nysgrc-012831) from xenorhabdus bovienii ss-2004
43	d1d8ca_	Alignment	not modelled	10.6	31	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
44	c2oceA_	Alignment	not modelled	10.4	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
45	d2gupa1	Alignment	not modelled	8.7	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
46	d2al1a1	Alignment	not modelled	8.5	12	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
47	c3htvA_	Alignment	not modelled	8.4	16	PDB header: transferase Chain: A: PDB Molecule: d-allose kinase; PDBTitle: crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
48	c4o66A_	Alignment	not modelled	8.3	20	PDB header: dna binding protein Chain: A: PDB Molecule: swi/snf-related matrix-associated actin-dependent regulator PDBTitle: crystal structure of smarc11 harp substrate recognition domain
49	c5opqA_	Alignment	not modelled	7.8	31	PDB header: hydrolase Chain: A: PDB Molecule: 3,6-anhydro-d-galactosidase; PDBTitle: a 3,6-anhydro-d-galactosidase produced by zobellia galactanivorans.2 this is an exo-lytic enzyme that hydrolyzes terminal 3,6-anhydro-d-3 galactose from the non-reducing end of carrageenan oligosaccharides.
50	c5m45K_	Alignment	not modelled	7.6	28	PDB header: ligase Chain: K: PDB Molecule: acetone carboxylase beta subunit; PDBTitle: structure of acetone carboxylase purified from xanthobacter2 autotrophicus
51	c4htlA_	Alignment	not modelled	7.2	20	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
52	c3lm2B_	Alignment	not modelled	7.1	11	PDB header: transferase Chain: B: PDB Molecule: putative kinase; PDBTitle: crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
53	c1okjB_	Alignment	not modelled	6.9	25	PDB header: hydrolase Chain: B: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab; PDBTitle: crystal structure of the essential e. coli yeaz2 protein by

						mad method using the gadolinium complex3 "dotma"
54	d1z05a3	Alignment	not modelled	6.6	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
55	c5v5fA	Alignment	not modelled	6.3	9	PDB header: transferase Chain: A: PDB Molecule: at3g11770; PDBTitle: crystal structure of rice1 (pnt2)
56	c1xc3A	Alignment	not modelled	6.0	11	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
57	d1auga	Alignment	not modelled	5.7	15	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
58	d1iu8a	Alignment	not modelled	5.7	17	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
59	c4rkul	Alignment	not modelled	5.5	36	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: crystal structure of plant photosystem i at 3 angstrom resolution
60	c4y28l	Alignment	not modelled	5.3	36	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: the structure of plant photosystem i super-complex at 2.8 angstrom2 resolution.
61	c5z47A	Alignment	not modelled	5.1	12	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of pyrrolidone carboxylate peptidase i with2 disordered loop a from deinococcus radiodurans r1