



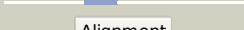

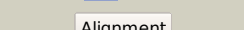

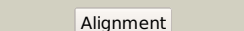
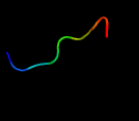







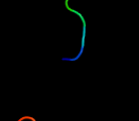
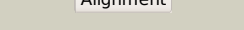

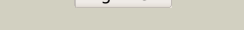



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1688 (mpg)_1912986_1913597
 Date Fri Aug 2 13:30:28 BST 2019
 Unique Job ID bae1795558e1066

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ewna_	 Alignment		100.0	35	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: 3-methyladenine DNA glycosylase (AAG, ANPG, MPG)
2	c3kc2A_	 Alignment		30.2	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from <i>Saccharomyces cerevisiae</i>
3	c4kkkA_	 Alignment		27.9	30	PDB header: hydrolase Chain: A: PDB Molecule: exoglucanase s; PDBTitle: complex structure of catalytic domain of <i>Clostridium cellulovorans</i> exgs and cellotetraose
4	d1g9ga_	 Alignment		26.1	30	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
5	c4el8A_	 Alignment		25.6	30	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of <i>C. bescii</i> celA gh48 module
6	c4jjiA_	 Alignment		25.3	30	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of <i>T. fusca</i> gh48 d224n mutant
7	c4fusA_	 Alignment		24.9	20	PDB header: hydrolase Chain: A: PDB Molecule: rtx toxins and related Ca ²⁺ -binding protein; PDBTitle: the x-ray structure of <i>Haemella chejuensis</i> family 48 glycosyl hydrolase
8	d1l1ya_	 Alignment		24.9	20	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
9	c1l2aD_	 Alignment		24.9	20	PDB header: hydrolase Chain: D: PDB Molecule: cellobiohydrolase; PDBTitle: the crystal structure and catalytic mechanism of 2 cellobiohydrolase cels, the major enzymatic component of 3 the <i>Clostridium thermocellum</i> cellulosome
10	c5bv9A_	 Alignment		23.9	20	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of <i>Bacillus pumilus</i> gh48 in complex with cellobiose
11	c4uzmA_	 Alignment		20.6	35	PDB header: structural protein Chain: A: PDB Molecule: putative membrane protein igaa homolog; PDBTitle: shotgun proteolysis: a practical application

12	d1jga_	Alignment		14.2	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
13	c3fu1B_	Alignment		14.1	33	PDB header: protein transport Chain: B: PDB Molecule: general secretion pathway protein g; PDBTitle: crystal structure of the major pseudopilin from the type 2 secretion2 system of vibrio cholerae
14	c2wtoB_	Alignment		12.1	23	PDB header: metal binding protein Chain: B: PDB Molecule: orf131 protein; PDBTitle: crystal structure of apo-form czce from c. metallidurans ch34
15	c3gf5A_	Alignment		11.0	24	PDB header: structural protein Chain: A: PDB Molecule: major vault protein; PDBTitle: crystal structure of the p21 r1-r7 n-terminal domain of murine mvp
16	d1vkwa_	Alignment		9.1	33	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: Putative nitroreductase TM1586
17	c3zmnA_	Alignment		8.8	30	PDB header: viral protein Chain: A: PDB Molecule: vp17; PDBTitle: vp17, a capsid protein of bacteriophage p23-77
18	c4n77A_	Alignment		8.8	23	PDB header: rna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cas protein
19	d1ob8a_	Alignment		8.4	16	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
20	d1p2za2	Alignment		8.2	21	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group II dsDNA viruses VP Family: Adenovirus hexon
21	d1rrha2	Alignment	not modelled	8.0	17	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Lipoxygenase N-terminal domain
22	c4amsA_	Alignment	not modelled	7.7	19	PDB header: transferase Chain: A: PDB Molecule: mg662; PDBTitle: a megaviridae orfan gene encode a new nucleotidyl transferase
23	c5no7B_	Alignment	not modelled	7.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: lytic polysaccharide monooxygenase; PDBTitle: crystal structure of a xylan-active lytic polysaccharide monooxygenase2 from pycnoporus coccineus.
24	c4amqA_	Alignment	not modelled	7.5	25	PDB header: transferase Chain: A: PDB Molecule: l544; PDBTitle: a megaviridae orfan gene encodes a new nucleotidyl transferase
25	d2jioa1	Alignment	not modelled	7.1	12	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
26	c4z9dA_	Alignment	not modelled	6.8	27	PDB header: transferase Chain: A: PDB Molecule: pertussis toxin-like subunit arta; PDBTitle: ecplta
27	d1t92a_	Alignment	not modelled	6.7	33	Fold: Pili subunits Superfamily: Pili subunits Family: Pseudopilin
28	d1rkia1	Alignment	not modelled	6.5	22	Fold: THUMP domain Superfamily: THUMP domain-like Family: PAE0736-like
						Fold: lambda repressor-like DNA-binding domains

29	d1rzsa_	Alignment	not modelled	6.2	36	Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
30	d2fqla1	Alignment	not modelled	5.7	17	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
31	d1ncfb3	Alignment	not modelled	5.6	30	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
32	c2w9jB_	Alignment	not modelled	5.6	50	PDB header: signaling protein Chain: B; PDB Molecule: signal recognition particle subunit srp14; PDBTitle: the crystal structure of srp14 from the schizosaccharomyces2 pombe signal recognition particle
33	c1wjvA_	Alignment	not modelled	5.6	30	PDB header: dna binding protein Chain: A; PDB Molecule: cell growth regulating nucleolar protein lyar; PDBTitle: solution structure of the n-terminal zinc finger domain of2 mouse cell growth regulating nucleolar protein lyar