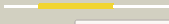

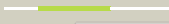









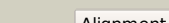

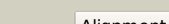









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2281_(pitB)_2553183_2554841
Date	Mon Aug 5 13:25:42 BST 2019
Unique Job ID	e1d8db22c3869213

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w2eA_	 Alignment		73.1	13	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin pip2-7 7; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin, aqy1, in a2 closed conformation at ph 3.5
2	d1j4na_	 Alignment		64.2	17	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
3	c4r0cB_	 Alignment		61.9	11	PDB header: membrane protein Chain: B: PDB Molecule: abgt putative transporter family; PDBTitle: crystal structure of the alcanivorax borkumensis ydah transporter2 reveals an unusual topology
4	d1fx8a_	 Alignment		40.6	17	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
5	c6eu6A_	 Alignment		34.0	15	PDB header: membrane protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: sensor amt protein
6	c2ia2D_	 Alignment		25.1	15	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
7	c1ldaA_	 Alignment		23.4	17	PDB header: transport protein Chain: A: PDB Molecule: glycerol uptake facilitator protein; PDBTitle: crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
8	c2b6pA_	 Alignment		20.0	14	PDB header: membrane protein Chain: A: PDB Molecule: lens fiber major intrinsic protein; PDBTitle: x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state
9	c4g1uB_	 Alignment		17.9	18	PDB header: transport protein/hydrolase Chain: B: PDB Molecule: hemin transport system permease protein hmuu; PDBTitle: x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
10	c2g7uB_	 Alignment		17.7	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
11	c2bruC_	 Alignment		17.4	33	PDB header: oxidoreductase Chain: C: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase

12	c2nuuF_	Alignment		17.3	19	PDB header: transport protein/signaling protein Chain: F: PDB Molecule: ammonia channel; PDBTitle: regulating the escherichia coli ammonia channel: the crystal structure2 of the amtb-glnk complex
13	d1d4oa_	Alignment		15.9	42	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
14	c1pt9B_	Alignment		15.8	42	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase, mitochondrial; PDBTitle: crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
15	d1pnoa_	Alignment		15.6	42	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
16	c3r4kD_	Alignment		15.2	15	PDB header: dna binding protein Chain: D: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
17	c1mkmA_	Alignment		13.8	22	PDB header: transcription Chain: A: PDB Molecule: iclr transcriptional regulator; PDBTitle: crystal structure of the thermotoga maritima iclr
18	c2f2bA_	Alignment		13.3	16	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin aqpm; PDBTitle: crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
19	c2xroE_	Alignment		13.2	30	PDB header: dna-binding protein/dna Chain: E: PDB Molecule: hth-type transcriptional regulator ttgv; PDBTitle: crystal structure of ttgv in complex with its dna operator
20	d2qapa1	Alignment		12.4	31	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
21	c2qapC_	Alignment	not modelled	12.2	31	PDB header: lyase Chain: C: PDB Molecule: fructose-1,6-bisphosphate aldolase; PDBTitle: fructose-1,6-bisphosphate aldolase from leishmania mexicana
22	c6c6lN_	Alignment	not modelled	12.1	16	PDB header: membrane protein Chain: N: PDB Molecule: v0 assembly protein 1; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
23	c5tjA_	Alignment	not modelled	12.0	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of iclr transcriptional regulator from2 alicyclobacillus acidocaldarius
24	c3c02A_	Alignment	not modelled	11.9	15	PDB header: membrane protein Chain: A: PDB Molecule: aquaglyceroporin; PDBTitle: x-ray structure of the aquaglyceroporin from plasmodium falciparum
25	c2kncA_	Alignment	not modelled	11.4	10	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
26	c5h1aC_	Alignment	not modelled	10.8	30	PDB header: transcription regulator Chain: C: PDB Molecule: iclr transcription factor homolog; PDBTitle: crystal structure of an iclr homolog from microbacterium sp. strain2 hm58-2
27	c2o0yB_	Alignment	not modelled	10.3	11	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
28	c5whmB_	Alignment	not modelled	10.2	22	PDB header: transcription Chain: B: PDB Molecule: iclr family transcriptional regulator; PDBTitle: crystal structure of iclr family transcriptional regulator from2 brucella abortus PDB header: hydrolase

29	c3mmtC_	Alignment	not modelled	10.1	33	Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose bisphosphate aldolase from bartonella2 henselae, bound to fructose bisphosphate
30	c3d9sB_	Alignment	not modelled	9.6	15	PDB header: membrane protein Chain: B: PDB Molecule: aquaporin-5; PDBTitle: human aquaporin 5 (aqp5) - high resolution x-ray structure
31	c5y6iB_	Alignment	not modelled	9.5	26	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of pseudomonas aeruginosa hmgr
32	c4o9uB_	Alignment	not modelled	9.2	23	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
33	d1mkma1	Alignment	not modelled	9.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
34	d1a5ca_	Alignment	not modelled	8.5	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
35	c4od5C_	Alignment	not modelled	7.5	14	PDB header: transferase Chain: C: PDB Molecule: 4-hydroxybenzoate octaprenyltransferase; PDBTitle: substrate-bound structure of a ubia homolog from aeropyrum pernix k1
36	d1f2ja_	Alignment	not modelled	7.3	33	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
37	c6cfwl_	Alignment	not modelled	7.1	24	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
38	d1s7ba_	Alignment	not modelled	6.9	22	Fold: Multidrug resistance efflux transporter EmrE Superfamily: Multidrug resistance efflux transporter EmrE Family: Multidrug resistance efflux transporter EmrE
39	c3s0xB_	Alignment	not modelled	6.2	16	PDB header: hydrolase Chain: B: PDB Molecule: peptidase a24b, flak domain protein; PDBTitle: the crystal structure of gxgd membrane protease flak
40	c2vm6A_	Alignment	not modelled	6.1	18	PDB header: immune system Chain: A: PDB Molecule: bcl-2-related protein a1; PDBTitle: human bcl2-a1 in complex with bim-bh3 peptide
41	d1u7ga_	Alignment	not modelled	6.1	21	Fold: Ammonium transporter Superfamily: Ammonium transporter Family: Ammonium transporter
42	c5w1eA_	Alignment	not modelled	6.0	19	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: pobr in complex with phb
43	c5ua4A_	Alignment	not modelled	5.9	16	PDB header: apoptosis Chain: A: PDB Molecule: 5-hl; PDBTitle: crystal structure of a179l:bid bh3 complex
44	c2vofA_	Alignment	not modelled	5.8	19	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-related protein a1; PDBTitle: structure of mouse a1 bound to the puma bh3-domain
45	c2k1aA_	Alignment	not modelled	5.8	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
46	c4o9tH_	Alignment	not modelled	5.7	23	PDB header: membrane protein Chain: H: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
47	d1fdja_	Alignment	not modelled	5.6	31	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
48	c2pc4B_	Alignment	not modelled	5.5	29	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
49	d2f6ua1	Alignment	not modelled	5.5	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
50	c5aexB_	Alignment	not modelled	5.5	24	PDB header: membrane protein Chain: B: PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
51	d1v8ba2	Alignment	not modelled	5.3	17	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
52	c2d57A_	Alignment	not modelled	5.3	12	PDB header: transport protein Chain: A: PDB Molecule: aquaporin-4; PDBTitle: double layered 2d crystal structure of aquaporin-4 (aqp4m23) at 3.2 a2 resolution by electron crystallography
53	c6h1nA_	Alignment	not modelled	5.2	14	PDB header: apoptosis Chain: A: PDB Molecule: bcl2-like 10 (apoptosis facilitator); PDBTitle: crystal structure of a zebra-fish pro-survival protein nrz-apo
54	d1xfba1	Alignment	not modelled	5.1	31	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
55	c4huqS_	Alignment	not modelled	5.1	16	PDB header: hydrolase Chain: S: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a transporter

56	dlybea1	Alignment	not modelled	5.0	27	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
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