



































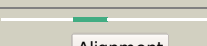
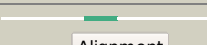


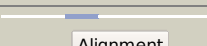
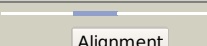
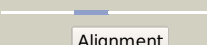
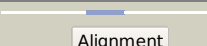

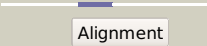
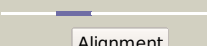



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2701c_suhB_3015873_3016745
Date	Wed Aug 7 12:50:35 BST 2019
Unique Job ID	317cb5d592adcbbd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2q74B_	 Alignment		100.0	98	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: mycobacterium tuberculosis suhb
2	c3rydA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of ca bound impase family protein from2 staphylococcus aureus
3	d2hhma_	 Alignment		100.0	30	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
4	c2qf1A_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of suhb: inositol monophosphatase and extragenic2 suppressor from e. coli
5	c3qmfA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of an inositol monophosphatase family protein2 (sas2203) from staphylococcus aureus mssa476
6	c3t0jB_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of inositol monophosphatase - ii from staphylococcus2 aureus mssa476
7	c5zonA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: histidinol-phosphatase; PDBTitle: histidinol phosphate phosphatase from mycobacterium tuberculosis
8	c4n81A_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase; PDBTitle: another flexible region at the active site of an inositol2 monophosphatase from zymomonas mobilis
9	c2czhB_	 Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase 2; PDBTitle: crystal structure of human myo-inositol monophosphatase 22 (impa2) with phosphate ion (orthorhombic form)
10	c5eq9A_	 Alignment		100.0	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol monophosphatase; PDBTitle: crystal structure of medicago truncatula histidinol-phosphate2 phosphatase (mthpp) in complex with l-histidinol phosphate and mg2+
11	c3luzA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: extragenic suppressor protein suhb; PDBTitle: crystal structure of extragenic suppressor protein suhb from2 bartonella henselae, via combined iodide sad molecular replacement

12	c2p3nB_	Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: thermotoga maritima impase tm1415
13	c2fvzB_	Alignment		100.0	33	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase 2; PDBTitle: human inositol monophosphatase 2
14	c5zhbB_	Alignment		100.0	35	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of inositol monophosphatase from anabaena (nostoc) sp. pcc2 7120
15	c2pcrA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: inositol-1-monophosphatase; PDBTitle: crystal structure of myo-inositol-1(or 4)-monophosphatase (aq_1983)2 from aquifex aeolicus vf5
16	c4gdgA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: 3'(2'),5'-bisphosphate nucleotidase, putative; PDBTitle: structural and functional characterization of 3'(2'),5'-bisphosphate2 nucleotidase1 from entamoeba histolytica
17	d1g0ha_	Alignment		100.0	26	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
18	d1ka1a_	Alignment		100.0	24	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
19	c5djjA_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: 3'-phosphoadenosine 5'-phosphate phosphatase; PDBTitle: structure of m. tuberculosis cysq, a pap phosphatase with po4 and 2mg2 bound
20	d1jp4a_	Alignment		100.0	23	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
21	c4j13B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: 3'(2'),5'-bisphosphate nucleotidase, putative; PDBTitle: structural and functional characterization of 3'(2'),5'-bisphosphate2 nucleotidase2 from entamoeba histolytica
22	d1vdwa_	Alignment	not modelled	100.0	24	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
23	c5esyA_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: sal1 phosphatase; PDBTitle: arabidopsis thaliana sal1
24	d1xi6a_	Alignment	not modelled	100.0	26	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
25	c3b8bA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: cysq, sulfite synthesis pathway protein; PDBTitle: crystal structure of cysq from bacteroides thetaiotaomicron, a2 bacterial member of the inositol monophosphatase family
26	d1lbva_	Alignment	not modelled	100.0	29	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
27	d1inpa_	Alignment	not modelled	100.0	19	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
28	c5iz3B_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: predicted protein; PDBTitle: p. patens sedoheptulose-1,7-bisphosphatase

29	c3uksB	 Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: sedoheptulose-1,7 bisphosphatase, putative; PDBTitle: 1.85 angstrom crystal structure of putative sedoheptulose-1,72 bisphosphatase from toxoplasma gondii
30	d1d9qa	 Alignment	not modelled	99.9	18	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
31	d1nuwa	 Alignment	not modelled	99.6	17	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
32	c2fhyL	 Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: L: PDB Molecule: fructose-1,6-bisphosphatase 1; PDBTitle: structure of human liver fpbase complexed with a novel benzoxazole as2 allosteric inhibitor
33	d1ftaa	 Alignment	not modelled	99.5	15	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
34	d1bk4a	 Alignment	not modelled	99.4	16	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
35	c5oezA	 Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: A: PDB Molecule: fbp protein; PDBTitle: crystal structure of leishmania major fructose-1,6-bisphosphatase in2 apo form.
36	c2gq1A	 Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphatase; PDBTitle: crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
37	d1spia	 Alignment	not modelled	99.2	19	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
38	c6aayB	 Alignment	not modelled	96.5	24	PDB header: hydrolase Chain: B: PDB Molecule: fructose-1,6-bisphosphatase class 2; PDBTitle: crystal structure of apo fructose-1,6-bisphosphatase from2 mycobacterium tuberculosis
39	c3rojD	 Alignment	not modelled	96.0	22	PDB header: hydrolase Chain: D: PDB Molecule: d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7- PDBTitle: d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase2 of synechocystis sp. pcc 6803
40	d1ni9a	 Alignment	not modelled	90.9	22	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: GlpX-like bacterial fructose-1,6-bisphosphatase
41	d1o12a1	 Alignment	not modelled	49.6	45	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
42	c3fhkF	 Alignment	not modelled	45.2	17	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
43	c4jqfA	 Alignment	not modelled	36.4	17	PDB header: dna binding protein Chain: A: PDB Molecule: csst complex subunit stn1; PDBTitle: structure of the c-terminal domain of human telomeric stn1
44	d1g4ma1	 Alignment	not modelled	32.1	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
45	d1icfi	 Alignment	not modelled	24.7	24	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
46	d1mdah	 Alignment	not modelled	23.5	14	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
47	d1r89a1	 Alignment	not modelled	22.4	33	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: Archaeal tRNA CCA-adding enzyme substrate-binding domain
48	d1cf1a1	 Alignment	not modelled	20.9	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
49	d2dsqg1	 Alignment	not modelled	20.2	27	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
50	c1ikqA	 Alignment	not modelled	19.8	35	PDB header: transferase Chain: A: PDB Molecule: exotoxin a; PDBTitle: pseudomonas aeruginosa exotoxin a, wild type
51	c3hjeA	 Alignment	not modelled	18.0	28	PDB header: transferase Chain: A: PDB Molecule: 704aa long hypothetical glycosyltransferase; PDBTitle: crystal structure of sulfolobus tokodaii hypothetical maltooligosyl2 trehalose synthase
52	d3pmga4	 Alignment	not modelled	16.3	16	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
53	c2h7tA	 Alignment	not modelled	13.0	21	PDB header: protein binding Chain: A: PDB Molecule: insulin-like growth factor-binding protein 2; PDBTitle: solution structure of the c-terminal domain of insulin-like2 growth factor binding protein 2 (igfbp-2)
54	c1cf1B	 Alignment	not modelled	11.7	25	PDB header: structural protein Chain: B: PDB Molecule: protein (arrestin); PDBTitle: arrestin from bovine rod outer segments

55	d2dsrg1	Alignment	not modelled	11.5	23	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
56	c2la3A	Alignment	not modelled	11.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
57	c1ayrA	Alignment	not modelled	10.9	23	PDB header: sensory transduction Chain: A: PDB Molecule: arrestin; PDBTitle: arrestin from bovine rod outer segments
58	d2jn4a1	Alignment	not modelled	10.5	12	Fold: NifT/FixU barrel-like Superfamily: NifT/FixU-like Family: NifT/FixU
59	c2jn4A	Alignment	not modelled	10.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein fixu, nift; PDBTitle: solution nmr structure of protein rp4601 from rhodopseudomonas2 palustris. northeast structural genomics consortium target rpt2;3 ontario center for structural proteomics target rp4601.
60	c3h87D	Alignment	not modelled	9.9	34	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
61	c1sz1A	Alignment	not modelled	9.5	25	PDB header: transferase/rna Chain: A: PDB Molecule: trna nucleotidyltransferase; PDBTitle: mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
62	c4m4xA	Alignment	not modelled	9.5	18	PDB header: transcription Chain: A: PDB Molecule: aryl hydrocarbon receptor; PDBTitle: structure and dimerization properties of the aryl hydrocarbon receptor2 (ahr) pas-a domain
63	c5hudA	Alignment	not modelled	9.3	31	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate (dahp) PDBTitle: non-covalent complex of and dahp synthase and chorismate mutase from2 corynebacterium glutamicum with bound transition state analog
64	d2b7oa1	Alignment	not modelled	9.3	31	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
65	c2k2wA	Alignment	not modelled	9.1	18	PDB header: cell cycle Chain: A: PDB Molecule: recombination and dna repair protein; PDBTitle: second brct domain of nbs1
66	c6bmcA	Alignment	not modelled	8.9	38	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: the structure of a dimeric type ii dah7ps associated with pyocyanin2 biosynthesis in pseudomonas aeruginosa
67	c5uxmA	Alignment	not modelled	8.6	31	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: type ii dah7ps from pseudomonas aeruginosa with trp bound
68	d1rmja	Alignment	not modelled	8.4	25	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
69	c2js3B	Alignment	not modelled	7.9	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein q6n9a4_rhopa. northeast structural genomics2 consortium target rpt8
70	c5lxuA	Alignment	not modelled	7.8	9	PDB header: dna binding protein Chain: A: PDB Molecule: transcription factor lux; PDBTitle: structure of the dna-binding domain of lux arrhythmo
71	c1jsyA	Alignment	not modelled	7.6	15	PDB header: signaling protein Chain: A: PDB Molecule: bovine arrestin-2 (full length); PDBTitle: crystal structure of bovine arrestin-2
72	c2pncB	Alignment	not modelled	7.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase, liver isozyme; PDBTitle: crystal structure of bovine plasma copper-containing amine oxidase in2 complex with clonidine
73	c4xwzA	Alignment	not modelled	7.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine:oxygen oxidoreductase; PDBTitle: the crystal structure of fructosyl amine: oxygen oxidoreductase2 (amadoriase i) from aspergillus fumigatus in complex with the3 substrate fructosyl lysine
74	c4xq7A	Alignment	not modelled	5.8	37	PDB header: transferase Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthase-like protein; PDBTitle: the crystal structure of the oas-like domain (old) of human oasl
75	c1px5A	Alignment	not modelled	5.8	44	PDB header: transferase Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthetase 1; PDBTitle: crystal structure of the 2'-specific and double-stranded2 rna-activated interferon-induced antiviral protein 2'-5'-3 oligoadenylate synthetase
76	c5zcrB	Alignment	not modelled	5.7	32	PDB header: hydrolase Chain: B: PDB Molecule: maltoooligosyl trehalose synthase; PDBTitle: dsm5389 glycosyltrehalose synthase
77	c4zwc	Alignment	not modelled	5.2	21	PDB header: signaling protein Chain: C: PDB Molecule: chimera protein of human rhodopsin, mouse s-arrestin, and PDBTitle: crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser