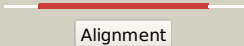
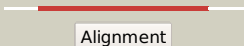
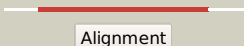



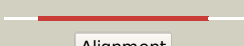







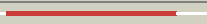
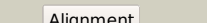
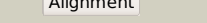

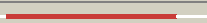

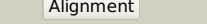


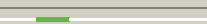

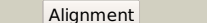
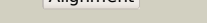



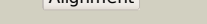


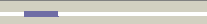


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1604_(impA)_1804046_1804858
Date	Fri Aug 2 13:30:19 BST 2019
Unique Job ID	af9e29d416519147

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rydA_			100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of ca bound impase family protein from2 staphylococcus aureus
2	d2hhma_			100.0	21	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
3	c2qfIA_			100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of subh: inositol monophosphatase and extragenic2 suppressor from e. coli
4	c3t0jB_			100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of inositol monophosphatase - ii from staphylococcus2 aureus mssa476
5	c3qmfA_			100.0	21	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	c2p3nB_			100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: thermotoga maritima impase tm1415
7	c3luzA_			100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: extragenic suppressor protein subh; PDBTitle: crystal structure of extragenic suppressor protein subh from2 bartonella henselae, via combined iodide sad molecular replacement
8	c5zonA_			100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: histidinol-phosphatase; PDBTitle: histidinol phosphate phosphatase from mycobacterium tuberculosis
9	c2czhB_			100.0	24	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	c4n81A_			100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase; PDBTitle: another flexible region at the active site of an inositol2 monophosphatase from zymomonas mobilis
11	c5zhbB_			100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of inositol monophosphatase from anabaena (nostoc) sp. pcc2 7120

12	c2fvzB_	Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase 2; PDBTitle: human inositol monophosphatase 2
13	c5eq9A_	Alignment		100.0	24	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+
14	d1g0ha_	Alignment		100.0	24	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
15	c2pcrA_	Alignment		100.0	29	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	c2q74B_	Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: mycobacterium tuberculosis subh
17	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
18	d1vdwa_	Alignment		100.0	23	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
19	d1xi6a_	Alignment		100.0	21	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
20	c5djjA_	Alignment		100.0	20	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
21	d1kala_	Alignment	not modelled	100.0	25	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
22	c4j13B_	Alignment	not modelled	100.0	19	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
23	c5esyA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: sal1 phosphatase; PDBTitle: arabidopsis thaliana sal1
24	d1jp4a_	Alignment	not modelled	100.0	19	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
25	c3b8bA_	Alignment	not modelled	100.0	19	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	24	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
27	d1inpa_	Alignment	not modelled	100.0	22	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
28	c5iz3B_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: predicted protein; PDBTitle: p. patens sedoheptulose-1,7-bisphosphatase

29	c3uksB	 Alignment	not modelled	99.9	16	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	99.8	17	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
31	d1nuwa	 Alignment	not modelled	99.4	17	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
32	c2fhyL	 Alignment	not modelled	99.3	16	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	99.3	16	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
34	c5oezA	 Alignment	not modelled	99.2	14	PDB header: hydrolase Chain: A: PDB Molecule: fbp protein; PDBTitle: crystal structure of leishmania major fructose-1,6-bisphosphatase in2 apo form.
35	c2gq1A	 Alignment	not modelled	99.2	19	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
36	d1bk4a	 Alignment	not modelled	99.1	16	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
37	d1spia	 Alignment	not modelled	98.9	20	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
38	c6aayB	 Alignment	not modelled	96.8	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	96.5	19	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	93.9	23	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: GlpX-like bacterial fructose-1,6-bisphosphatase
41	d1o12a1	 Alignment	not modelled	59.0	55	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	37.0	21	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
43	d1r89a1	 Alignment	not modelled	35.8	24	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: Archaeal tRNA CCA-adding enzyme substrate-binding domain
44	c1ikqA	 Alignment	not modelled	19.0	47	PDB header: transferase Chain: A: PDB Molecule: exotoxin a; PDBTitle: pseudomonas aeruginosa exotoxin a, wild type
45	c3bbaB	 Alignment	not modelled	17.7	21	PDB header: hydrolase Chain: B: PDB Molecule: interpain a; PDBTitle: structure of active wild-type prevotella intermedia interpain a2 cysteine protease
46	d2dsqg1	 Alignment	not modelled	17.3	27	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
47	d1icfi	 Alignment	not modelled	16.7	23	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
48	c2pncB	 Alignment	not modelled	16.7	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
49	d1mdah	 Alignment	not modelled	14.9	11	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
50	c2h7tA	 Alignment	not modelled	14.2	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)
51	d1g4ma1	 Alignment	not modelled	13.9	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
52	c4onyB	Alignment	not modelled	13.7	15	PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein family 5; PDBTitle: crystal structure of a abc transporter, periplasmic substrate-binding2 protein from brucella melitensis
53	c1sz1A	Alignment	not modelled	13.5	22	PDB header: transferase/rna Chain: A: PDB Molecule: trna nucleotidyltransferase; PDBTitle: mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
54	c5jpwA	Alignment	not modelled	12.0	18	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic oligopeptide- PDBTitle: oligopeptide-binding protein oppa

55	d2dsrg1	Alignment	not modelled	11.5	21	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
56	c4m4xA	Alignment	not modelled	10.7	29	PDB header: transcription Chain: A: PDB Molecule: aryl hydrocarbon receptor; PDBTitle: structure and dimerization properties of the aryl hydrocarbon receptor2 (ahr) pas-a domain
57	d1w7ca1	Alignment	not modelled	10.7	31	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
58	c6bmcA	Alignment	not modelled	10.3	36	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
59	d1rmja	Alignment	not modelled	9.8	21	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
60	d3pmga4	Alignment	not modelled	9.4	50	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
61	d1kfia4	Alignment	not modelled	9.4	38	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
62	c5hudA	Alignment	not modelled	9.4	36	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
63	d2b7oa1	Alignment	not modelled	9.2	36	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
64	c4xq7A	Alignment	not modelled	9.0	42	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
65	d1w6ga1	Alignment	not modelled	8.8	46	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
66	c5uxmA	Alignment	not modelled	8.6	36	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: type ii dah7ps from pseudomonas aeruginosa with trp bound
67	c3pamB	Alignment	not modelled	8.5	16	PDB header: transport protein Chain: B: PDB Molecule: transmembrane protein; PDBTitle: crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
68	c3qf4A	Alignment	not modelled	8.5	20	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
69	c5icqA	Alignment	not modelled	8.5	21	PDB header: periplasmic binding protein Chain: A: PDB Molecule: methylocystis parvus obbp mbne; PDBTitle: methanobactin periplasmic binding protein
70	d1cf1a1	Alignment	not modelled	8.0	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
71	c6a4zA	Alignment	not modelled	7.9	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: chap protein; PDBTitle: oxidase chap
72	d1g3pa2	Alignment	not modelled	7.5	57	Fold: N-terminal domains of the minor coat protein g3p Superfamily: N-terminal domains of the minor coat protein g3p Family: N-terminal domains of the minor coat protein g3p
73	c1w7cA	Alignment	not modelled	7.2	31	PDB header: oxidoreductase Chain: A: PDB Molecule: lysyl oxidase; PDBTitle: pplo at 1.23 angstroms
74	c5swiD	Alignment	not modelled	7.0	17	PDB header: hydrolase Chain: D: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of spgh92 in complex with mannose
75	c3equB	Alignment	not modelled	6.9	32	PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
76	c5lxuA	Alignment	not modelled	6.9	16	PDB header: dna binding protein Chain: A: PDB Molecule: transcription factor lux; PDBTitle: structure of the dna-binding domain of lux arrhythmo
77	c5ochH	Alignment	not modelled	6.8	20	PDB header: hydrolase Chain: H: PDB Molecule: atp-binding cassette sub-family b member 8, mitochondrial; PDBTitle: the crystal structure of human abcb8 in an outward-facing state
78	d2oqa1	Alignment	not modelled	6.6	46	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
79	c4nl8E	Alignment	not modelled	6.6	67	PDB header: dna binding protein Chain: E: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to ssb c-terminal tail peptide
80	c3uc3A	Alignment	not modelled	6.5	18	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding

80	c3ue3A_	Alignment	not modelled	6.3	18	protein 3, PDB header: crystal structure of acinetobacter baumannii pbp3 PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-1,2-mannosidase;
81	c6f92B_	Alignment	not modelled	6.3	22	PDBTitle: structure of the family gh92 alpha-mannosidase bt3965 from bacteroides thetaiotaomicron in complex with mannoimidazole (mani)
82	d1h6la_	Alignment	not modelled	6.2	17	Fold: 6-bladed beta-propeller Superfamily: Thermostable phytase (3-phytase) Family: Thermostable phytase (3-phytase)
83	c3dgsA_	Alignment	not modelled	6.2	40	PDB header: viral protein Chain: A: PDB Molecule: coat protein a; PDBTitle: changing the determinants of protein stability from covalent to non-2 covalent interactions by in-vitro evolution: a structural and3 energetic analysis
84	c5ochF_	Alignment	not modelled	6.2	20	PDB header: hydrolase Chain: F: PDB Molecule: atp-binding cassette sub-family b member 8, mitochondrial; PDBTitle: the crystal structure of human abcb8 in an outward-facing state
85	d1umka2	Alignment	not modelled	6.1	29	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
86	d1wdjb_	Alignment	not modelled	6.0	17	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein TT1808 (TTHA1514)
87	c2ww1B_	Alignment	not modelled	6.0	22	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-1,2-mannosidase; PDBTitle: structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
88	d1w2za1	Alignment	not modelled	5.9	54	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
89	d1d6za1	Alignment	not modelled	5.9	38	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
90	c3higB_	Alignment	not modelled	5.9	31	PDB header: oxidoreductase Chain: B: PDB Molecule: amiloride-sensitive amine oxidase; PDBTitle: crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
91	c1svfB_	Alignment	not modelled	5.6	45	PDB header: viral protein Chain: B: PDB Molecule: protein (fusion glycoprotein); PDBTitle: paramyxovirus sv5 fusion protein core
92	c2c10D_	Alignment	not modelled	5.6	23	PDB header: oxidoreductase Chain: D: PDB Molecule: membrane copper amine oxidase; PDBTitle: the structure of a truncated, soluble version of semicarbazide-2 sensitive amine oxidase
93	c3ot2A_	Alignment	not modelled	5.5	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
94	c3ot2B_	Alignment	not modelled	5.5	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
95	c3qf4B_	Alignment	not modelled	5.4	18	PDB header: transport protein Chain: B: PDB Molecule: uncharacterized abc transporter atp-binding protein PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
96	d1wdja_	Alignment	not modelled	5.4	25	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein TT1808 (TTHA1514)
97	c2r6hC_	Alignment	not modelled	5.4	21	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:ubiquinone oxidoreductase, na translocating, f PDBTitle: crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
98	c3nbbC_	Alignment	not modelled	5.4	46	PDB header: oxidoreductase Chain: C: PDB Molecule: peroxisomal primary amine oxidase; PDBTitle: crystal structure of mutant y305f expressed in e. coli in the copper2 amine oxidase from hansenula polymorpha
99	d1ijdb_	Alignment	not modelled	5.3	57	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits