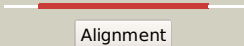

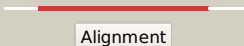

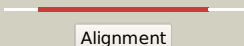







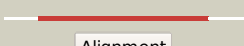











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2131c_(cysQ)_2392525_2393328
Date	Mon Aug 5 13:25:25 BST 2019
Unique Job ID	af11177346bad1cb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5djjA_	 Alignment		100.0	99	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
2	c3t0jB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of inositol monophosphatase - ii from staphylococcus2 aureus mssa476
3	c4j13B_	 Alignment		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
4	c5zonA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: histidinol-phosphatase; PDBTitle: histidinol phosphate phosphatase from mycobacterium tuberculosis
5	c3rydA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal strucutre of ca bound impase family protein from2 staphylococcus aureus
6	c4gdgA_	 Alignment		100.0	19	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
7	c2p3nB_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: thermotoga maritima impase tm1415
8	d1ka1a_	 Alignment		100.0	23	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
9	d1jp4a_	 Alignment		100.0	21	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
10	c2qf1A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of subh: inositol monophosphatase and extragenic2 suppressor from e. coli
11	c4n81A_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase; PDBTitle: another flexible region at the active site of an inositol2 monophosphatase from zymomonas mobilis

12	c5eq9A_	Alignment		100.0	20	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+
13	c3luzA_	Alignment		100.0	21	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
14	d1g0ha_	Alignment		100.0	16	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
15	c3qmfA_	Alignment		100.0	16	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
16	d2hhma_	Alignment		100.0	22	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
17	c3b8bA_	Alignment		100.0	23	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
18	c2czhB_	Alignment		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)
19	c2fvzB_	Alignment		100.0	25	PDB header: hydrolase Chain: B; PDB Molecule: inositol monophosphatase 2; PDBTitle: human inositol monophosphatase 2
20	c5esyA_	Alignment		100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: sal1 phosphatase; PDBTitle: arabidopsis thaliana sal1
21	d1xi6a_	Alignment	not modelled	100.0	18	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
22	c5zhbB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B; PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of inositol monophosphatase from anabaena (nostoc) sp. pcc2 7120
23	d1vdwa_	Alignment	not modelled	100.0	17	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
24	c2q74B_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: B; PDB Molecule: inositol-1-monophosphatase; PDBTitle: mycobacterium tuberculosis subh
25	d1lbva_	Alignment	not modelled	100.0	24	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
26	d1inpa_	Alignment	not modelled	100.0	20	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
27	c2pcrA_	Alignment	not modelled	100.0	21	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
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	99.8	15	PDB header: hydrolase Chain: B; PDB Molecule: sedoheptulose-1,7 bisphosphatase, putative; PDBTitle: 1.85 angstrom crystal structure of putative

						sedoheptulose-1,7,2 bisphosphatase from toxoplasma gondii
30	d1d9qa_	Alignment	not modelled	99.8	15	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
31	c2fhyL_	Alignment	not modelled	99.4	18	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
32	d1nuwa_	Alignment	not modelled	99.3	16	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
33	d1ftaa_	Alignment	not modelled	99.3	18	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
34	c2gq1A_	Alignment	not modelled	99.2	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
35	d1bk4a_	Alignment	not modelled	99.2	16	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
36	c5oezA_	Alignment	not modelled	99.1	17	PDB header: hydrolase Chain: A: PDB Molecule: fbp protein; PDBTitle: crystal structure of leishmania major fructose-1,6-bisphosphatase in2 apo form.
37	d1spia_	Alignment	not modelled	98.9	17	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
38	c3rojD_	Alignment	not modelled	95.8	18	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
39	c6ayyB_	Alignment	not modelled	94.4	19	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
40	d1ni9a_	Alignment	not modelled	85.6	19	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: GlpX-like bacterial fructose-1,6-bisphosphatase
41	d1o12a1	Alignment	not modelled	47.0	55	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
42	c3hjeA_	Alignment	not modelled	32.1	31	PDB header: transferase Chain: A: PDB Molecule: 704aa long hypothetical glycosyltransferase; PDBTitle: crystal structure of sulfolobus tokodaii hypothetical maltooligosyl2 trehalose synthase
43	d1r89a1	Alignment	not modelled	23.1	27	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: Archaeal tRNA CCA-adding enzyme substrate-binding domain
44	c3b0vD_	Alignment	not modelled	22.4	22	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
45	d2dsqg1	Alignment	not modelled	20.5	19	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
46	d1mdah_	Alignment	not modelled	20.3	9	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
47	c3fhkF_	Alignment	not modelled	19.4	26	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
48	c1kqA_	Alignment	not modelled	17.5	40	PDB header: transferase Chain: A: PDB Molecule: exotoxin a; PDBTitle: pseudomonas aeruginosa exotoxin a, wild type
49	d1icfi_	Alignment	not modelled	16.4	25	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
50	c6ei9A_	Alignment	not modelled	15.7	16	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
51	d1m1la_	Alignment	not modelled	14.8	15	Fold: Suppressor of Fused, N-terminal domain Superfamily: Suppressor of Fused, N-terminal domain Family: Suppressor of Fused, N-terminal domain
52	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)
53	c2pncB_	Alignment	not modelled	12.9	15	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
54	d1rmja_	Alignment	not modelled	12.2	25	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
55	d2dsrg1	Alignment	not modelled	11.9	21	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain

56	c4qpwA	Alignment	not modelled	11.1	33	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase family 10; PDBTitle: bixyn10a cbm1 with xylohexaose bound
57	c6bmcA	Alignment	not modelled	10.9	31	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
58	d1kfia4	Alignment	not modelled	10.7	38	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
59	d2j9ga2	Alignment	not modelled	10.1	21	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
60	c5hudA	Alignment	not modelled	9.8	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
61	c4m4xA	Alignment	not modelled	9.1	12	PDB header: transcription Chain: A: PDB Molecule: aryl hydrocarbon receptor; PDBTitle: structure and dimerization properties of the aryl hydrocarbon receptor2 (ahr) pas-a domain
62	c5uxmA	Alignment	not modelled	9.0	31	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: type ii dah7ps from pseudomonas aeruginosa with trp bound
63	c5d28A	Alignment	not modelled	8.6	12	PDB header: viral protein Chain: A: PDB Molecule: gm-csf/il-2 inhibition factor; PDBTitle: complex of gm-csf/il-2 inhibition factor with granulocyte-macrophage2 colony-stimulating factor
64	c5zcrB	Alignment	not modelled	8.6	22	PDB header: hydrolase Chain: B: PDB Molecule: maltooligosyl trehalose synthase; PDBTitle: dsm5389 glycosyltrehalose synthase
65	d3pmgA4	Alignment	not modelled	8.2	19	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
66	c5tw1E	Alignment	not modelled	7.7	11	PDB header: transcription activator/transferase/dna Chain: E: PDB Molecule: dna-directed rna polymerase subunit omega; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
67	d1wdjb	Alignment	not modelled	7.2	17	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein TT1808 (TTHA1514)
68	c4nl8E	Alignment	not modelled	7.1	50	PDB header: dna binding protein Chain: E: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to ssb c-terminal tail peptide
69	d1g3pa2	Alignment	not modelled	7.1	86	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
70	c5hr4J	Alignment	not modelled	6.9	18	PDB header: hydrolase/dna Chain: J: PDB Molecule: mmei; PDBTitle: structure of type iii restriction-modification enzyme mmei in complex2 with dna has implications for engineering of new specificities
71	d1p7ga2	Alignment	not modelled	6.9	10	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
72	d1x4ka1	Alignment	not modelled	6.8	27	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
73	d2b7oa1	Alignment	not modelled	6.8	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
74	c2g29A	Alignment	not modelled	6.7	15	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein nrta; PDBTitle: crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803
75	c4aejA	Alignment	not modelled	6.5	50	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of human fibrillar procollagen type iii c-2 propeptide trimer
76	c1gn4B	Alignment	not modelled	6.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: h145e mutant of mycobacterium tuberculosis iron-superoxide dismutase.
77	d1w96a2	Alignment	not modelled	6.2	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
78	d1chua2	Alignment	not modelled	6.2	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
79	d1lgtA1	Alignment	not modelled	6.2	23	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
80	d1wdja	Alignment	not modelled	6.2	25	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein TT1808 (TTHA1514)

81	d1ps9a1	Alignment	not modelled	6.1	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
82	d1w7ca1	Alignment	not modelled	5.8	23	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
83	d1ulza2	Alignment	not modelled	5.7	24	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
84	c4f2nL_	Alignment	not modelled	5.6	13	PDB header: oxidoreductase Chain: L; PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of iron superoxide dismutase from leishmania major
85	c3ot2B_	Alignment	not modelled	5.6	42	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
86	c3ot2A_	Alignment	not modelled	5.6	42	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
87	c1svfB_	Alignment	not modelled	5.4	45	PDB header: viral protein Chain: B; PDB Molecule: protein (fusion glycoprotein); PDBTitle: paramyxovirus sv5 fusion protein core
88	c3dgsA_	Alignment	not modelled	5.4	60	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
89	c4a3uB_	Alignment	not modelled	5.3	13	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh\flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
90	c5k31E_	Alignment	not modelled	5.3	47	PDB header: structural protein Chain: E; PDB Molecule: collagen alpha-1(i) chain; PDBTitle: crystal structure of human fibrillar procollagen type i c-propeptide2 homo-trimer
91	d1oyaa_	Alignment	not modelled	5.3	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
92	c3knyA_	Alignment	not modelled	5.3	21	PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein bt_3535; PDBTitle: crystal structure of a two domain protein with unknown function2 (bt_3535) from bacteroides thetaiotaomicron vpi-5482 at 2.60 a3 resolution
93	c1sz1A_	Alignment	not modelled	5.2	27	PDB header: transferase/rna Chain: A; PDB Molecule: trna nucleotidyltransferase; PDBTitle: mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
94	d1iv8a2	Alignment	not modelled	5.2	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	c3kruC_	Alignment	not modelled	5.2	11	PDB header: oxidoreductase Chain: C; PDB Molecule: nadh\flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39