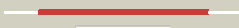




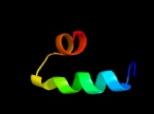











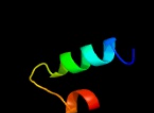

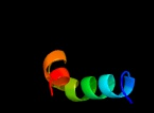




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2136c_(uppP)_2396016_2396846
Date	Mon Aug 5 13:25:25 BST 2019
Unique Job ID	3fb4119c76ed7c91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5oonA_	 Alignment		100.0	34	PDB header: membrane protein Chain: A: PDB Molecule: undecaprenyl-diphosphatase; PDBTitle: structure of undecaprenyl-pyrophosphate phosphatase, bac
2	c2y96A_	 Alignment		86.8	28	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27
3	d1vhra_	 Alignment		86.4	32	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
4	c2r0bA_	 Alignment		83.6	28	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine/tyrosine-interacting protein; PDBTitle: crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
5	c2esbA_	 Alignment		82.9	32	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 18; PDBTitle: crystal structure of human dusp18
6	c1wrmA_	 Alignment		82.8	32	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 22; PDBTitle: crystal structure of jsp-1
7	c2imgA_	 Alignment		82.7	28	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 23; PDBTitle: crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
8	c4ki9A_	 Alignment		82.2	44	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 12; PDBTitle: crystal structure of the catalytic domain of human dusp12 at 2.0 a2 resolution
9	c3s4eA_	 Alignment		81.9	24	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 19; PDBTitle: crystal structrue of a novel mitogen-activated protein kinase2 phosphatase, skrp1
10	c3emuA_	 Alignment		80.8	24	PDB header: hydrolase Chain: A: PDB Molecule: leucine rich repeat and phosphatase domain containing PDBTitle: crystal structure of a leucine rich repeat and phosphatase domain2 containing protein from entamoeba histolytica
11	c6i28A_	 Alignment		80.6	32	PDB header: viral protein Chain: A: PDB Molecule: orf98 ptp-2; PDBTitle: crystal structure of cydia pomonella ptp-2 phosphatase

12	d1m3ga_	Alignment		80.2	32	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
13	c2g6zB_	Alignment		79.8	28	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 5; PDBTitle: crystal structure of human dusp5
14	c4jmKA_	Alignment		79.8	36	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 8; PDBTitle: structure of dusp8
15	c1zzwA_	Alignment		79.7	36	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of catalytic domain of human map kinase2 phosphatase 5
16	c2gwoC_	Alignment		79.7	32	PDB header: hydrolase Chain: C: PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmpd
17	c3rgqA_	Alignment		78.9	32	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
18	c2e0tA_	Alignment		78.4	36	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 26; PDBTitle: crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
19	c3nmeA_	Alignment		78.4	20	PDB header: hydrolase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
20	c2oudA_	Alignment		77.6	36	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
21	d1mkpa_	Alignment	not modelled	77.5	36	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
22	c2nt2C_	Alignment	not modelled	77.4	40	PDB header: hydrolase Chain: C: PDB Molecule: protein phosphatase slingshot homolog 2; PDBTitle: crystal structure of slingshot phosphatase 2
23	d1xria_	Alignment	not modelled	77.4	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
24	c5xjvA_	Alignment	not modelled	77.3	40	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 13 isoform a; PDBTitle: two intermediate states of conformation switch in dual specificity2 phosphatase 13a
25	c4r30C_	Alignment	not modelled	76.5	28	PDB header: hydrolase Chain: C: PDB Molecule: laforin; PDBTitle: structure of human laforin dual specificity phosphatase domain
26	c1yz4A_	Alignment	not modelled	76.3	28	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase-like 15 isoform a; PDBTitle: crystal structure of dusp15
27	c2wgpA_	Alignment	not modelled	75.9	32	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 14; PDBTitle: crystal structure of human dual specificity phosphatase 14
28	c2hcmA_	Alignment	not modelled	75.1	32	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase; PDBTitle: crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural

						genomics3 consortium
29	d1ohea2	Alignment	not modelled	74.3	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
30	c1yn9B	Alignment	not modelled	74.3	28	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
31	c1fpzF	Alignment	not modelled	74.2	28	PDB header: hydrolase Chain: F: PDB Molecule: cyclin-dependent kinase inhibitor 3; PDBTitle: crystal structure analysis of kinase associated phosphatase (kap) with2 a substitution of the catalytic site cysteine (cys140) to a serine
32	d1i9sa	Alignment	not modelled	74.1	32	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
33	c4rkkA	Alignment	not modelled	70.9	28	PDB header: hydrolase Chain: A: PDB Molecule: laforin; PDBTitle: structure of a product bound phosphatase
34	c2j17A	Alignment	not modelled	69.7	28	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase yil113w; PDBTitle: tyr bound form of sdp-1
35	c2c46B	Alignment	not modelled	67.5	32	PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and 5'-2 phosphatase
36	d1rxda	Alignment	not modelled	63.0	28	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
37	c4kyrA	Alignment	not modelled	62.5	20	PDB header: hydrolase, sugar binding protein Chain: A: PDB Molecule: phosphoglucan phosphatase Isf2, chloroplastic; PDBTitle: structure of a product bound plant phosphatase
38	c4nyhB	Alignment	not modelled	62.2	28	PDB header: hydrolase Chain: B: PDB Molecule: rna/rnp complex-1-interacting phosphatase; PDBTitle: orthorhombic crystal form of pir1 dual specificity phosphatase core
39	c2m3vA	Alignment	not modelled	60.7	24	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of tyrosine phosphatase related to biofilm2 formation a (tpba) from pseudomonas aeruginosa
40	c2i6oA	Alignment	not modelled	60.3	28	PDB header: hydrolase Chain: A: PDB Molecule: sulfolobus solfataricus protein tyrosine phosphatase PDBTitle: crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
41	d1v3aa	Alignment	not modelled	59.9	28	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
42	c3s4oB	Alignment	not modelled	56.1	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major
43	c3rz2B	Alignment	not modelled	55.0	28	PDB header: hydrolase Chain: B: PDB Molecule: protein tyrosine phosphatase type iva 1; PDBTitle: crystal of prl-1 complexed with peptide
44	d1fpza	Alignment	not modelled	54.5	24	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
45	c5m43A	Alignment	not modelled	48.7	36	PDB header: ribosome Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of yvh1 phosphatase domain from chaetomium2 thermophilum
46	c5ncrA	Alignment	not modelled	45.6	20	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine phosphatase; PDBTitle: oh1 from the orf virus: a tyrosine phosphatase that displays distinct2 structural features and triple substrate specificity
47	c5z5bA	Alignment	not modelled	44.4	36	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase; PDBTitle: crystal structure of tk-ptp in the g95a mutant form
48	c6byfl	Alignment	not modelled	38.1	17	PDB header: transferase Chain: I: PDB Molecule: tyrosine-protein phosphatase siw14; PDBTitle: crystal structure of the core catalytic domain of pp-ip phosphatase2 siw14 from s. cerevisiae in complex with citrate
49	c2p4dA	Alignment	not modelled	34.8	32	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase; PDBTitle: structure-assisted discovery of variola major h1 phosphatase2 inhibitors
50	c6apxA	Alignment	not modelled	32.9	32	PDB header: hydrolase Chain: A: PDB Molecule: maltose-binding periplasmic protein,dual specificity PDBTitle: crystal structure of human dual specificity phosphatase 1 catalytic2 domain (c258s) as a maltose binding protein fusion in complex with3 the monocbody ysx1
51	c3ux4C	Alignment	not modelled	32.3	13	PDB header: transport protein Chain: C: PDB Molecule: acid-activated urea channel; PDBTitle: crystal structure of the urea channel from the human gastric pathogen2 helicobacter pylori
52	d1d5ra2	Alignment	not modelled	29.4	40	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
53	d1kcfA1	Alignment	not modelled	25.3	40	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
						Fold: Recombination protein RecR

54	d1vdda_	Alignment	not modelled	24.8	18	Superfamily: Recombination protein RecR Family: Recombination protein RecR
55	d1texa_	Alignment	not modelled	22.0	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
56	c5xw4A_	Alignment	not modelled	21.5	32	PDB header: cell cycle Chain: A: PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
57	c5z2vB_	Alignment	not modelled	20.1	18	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
58	c4gbmA_	Alignment	not modelled	19.8	36	PDB header: transferase Chain: A: PDB Molecule: curm sulfotransferase; PDBTitle: sulfotransferase domain from the curacin biosynthetic pathway
59	c5xamA_	Alignment	not modelled	18.5	20	PDB header: membrane protein Chain: A: PDB Molecule: protein translocase subunit secdf; PDBTitle: crystal structure of secdf in i form at 4 a resolution
60	c5d0nA_	Alignment	not modelled	16.1	75	PDB header: transferase Chain: A: PDB Molecule: pyruvate, phosphate dikinase regulatory protein, PDBTitle: crystal structure of maize pdrp bound with amp
61	c1vddC_	Alignment	not modelled	15.1	20	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
62	c4goxA_	Alignment	not modelled	14.9	36	PDB header: transferase Chain: A: PDB Molecule: polyketide synthase; PDBTitle: sulfotransferase domain from the synechococcus pcc 7002 olefin2 synthase
63	c3ap3A_	Alignment	not modelled	14.4	43	PDB header: transferase Chain: A: PDB Molecule: protein-tyrosine sulfotransferase 2; PDBTitle: crystal structure of human tyrosylprotein sulfotransferase-2 complexed2 with pap
64	c1oheA_	Alignment	not modelled	11.7	16	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
65	c1b9qA_	Alignment	not modelled	10.0	80	PDB header: collagen facit xiv Chain: A: PDB Molecule: protein (collagen alpha 1); PDBTitle: nmr structure of heparin binding site of non collagenous2 domain i (nc1) of collagen facit xiv
66	c1b9pA_	Alignment	not modelled	10.0	80	PDB header: collagen facit xiv Chain: A: PDB Molecule: protein (collagen alpha 1); PDBTitle: nmr structure of heparin binding site of non collagenous2 domain i (nc1) of collagen facit xiv
67	c3u88M_	Alignment	not modelled	10.0	44	PDB header: transcription Chain: M: PDB Molecule: histone-lysine n-methyltransferase 2a; PDBTitle: crystal structure of human menin in complex with ml1 and ledgf
68	c3aqpB_	Alignment	not modelled	8.6	13	PDB header: membrane protein Chain: B: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
69	c6csxA_	Alignment	not modelled	8.5	19	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb; PDBTitle: single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom
70	c3u4gA_	Alignment	not modelled	8.4	42	PDB header: transferase Chain: A: PDB Molecule: namn:dmb phosphoribosyltransferase; PDBTitle: the structure of cobt from pyrococcus horikoshii
71	c2zq5A_	Alignment	not modelled	8.0	36	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)
72	c6f2dJ_	Alignment	not modelled	7.7	15	PDB header: protein transport Chain: J: PDB Molecule: flagellar biosynthetic protein fliq; PDBTitle: a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
73	c6f2dI_	Alignment	not modelled	7.7	15	PDB header: protein transport Chain: I: PDB Molecule: flagellar biosynthetic protein fliq; PDBTitle: a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
74	c2v50A_	Alignment	not modelled	7.6	18	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
75	c3k3gA_	Alignment	not modelled	7.6	12	PDB header: transport protein Chain: A: PDB Molecule: urea transporter; PDBTitle: crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
76	c6r6bI_	Alignment	not modelled	7.6	8	PDB header: protein transport Chain: I: PDB Molecule: surface presentation of antigens protein spaq; PDBTitle: structure of the core shigella flexneri type iii secretion system2 export gate complex sctrst (spa24/spa9/spa29).
77	c2micB_	Alignment	not modelled	7.3	20	PDB header: membrane protein Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
78	c2micA_	Alignment	not modelled	7.3	20	PDB header: membrane protein Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
79	c2z6vA_	Alignment	not modelled	6.7	36	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein;

79	c2z0vA_	Alignment	not modelled	6.7	30	PDBTitle: crystal structure of sulfotransferase stf9 from2 mycobacterium avium
80	c4cdiC_	Alignment	not modelled	6.0	33	PDB header: membrane protein Chain: C: PDB Molecule: predicted protein; PDBTitle: crystal structure of acrb-acrz complex
81	c5zvqA_	Alignment	not modelled	5.9	14	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr