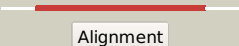



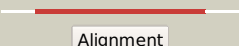





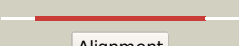






















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3641c_fic_4080104_4080739
 Date Fri Aug 9 18:20:32 BST 2019
 Unique Job ID 06c08dc3c57e2345

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vzaD_	 Alignment		100.0	27	PDB header: cell adhesion Chain: D: PDB Molecule: cell filamentation protein; PDBTitle: type iv secretion system effector protein bepa
2	c4npsA_	 Alignment		100.0	25	PDB header: cell adhesion Chain: A: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of bep1 protein (virb-translocated bartonella2 effector protein) from bartonella clarridgeiae
3	c4m16A_	 Alignment		100.0	26	PDB header: cell adhesion Chain: A: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the n-terminal fic domain of bartonella effector2 protein (bep); substrate of virb t4ss (virb-translocated bep effector3 protein) from bartonella sp. ar 15-3
4	c4lu4A_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: putative cell filamentation protein; PDBTitle: crystal structure of the n-terminal fic domain of a putative cell2 filamentation protein (virb-translocated bep effector protein) from3 bartonella quintana
5	c4xi8B_	 Alignment		100.0	22	PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the fic domain of bep5 protein (virb-translocated2 bartonella effector protein) from bartonella clarridgeiae
6	c4py3B_	 Alignment		100.0	23	PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the n-terminal fic domain of bep8 protein (virb-2 translocated bartonella effector protein) from bartonella sp. 1-1c
7	c3shgA_	 Alignment		100.0	28	PDB header: transferase/protein binding Chain: A: PDB Molecule: vbht; PDBTitle: vbht fic protein from bartonella schoenbuchensis in complex with vbha2 antitoxin
8	c5jffC_	 Alignment		100.0	30	PDB header: transferase Chain: C: PDB Molecule: probable adenosine monophosphate-protein transferase fic; PDBTitle: e. coli ecfict mutant g55r in complex with ecfica
9	c5nwfB_	 Alignment		100.0	27	PDB header: toxin Chain: B: PDB Molecule: fic family protein; PDBTitle: enterococcus faecalis fic protein (h111a).
10	c2f6sA_	 Alignment		100.0	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cell filamentation protein, putative; PDBTitle: structure of cell filamentation protein (fic) from helicobacter pylori
11	d2f6sa1	 Alignment		100.0	25	Fold: Fic-like Superfamily: Fic-like Family: Fic-like

12	d2g03a1	Alignment		100.0	25	Fold: Fic-like Superfamily: Fic-like Family: Fic-like
13	c4u0zH_	Alignment		100.0	17	PDB header: transferase Chain: H: PDB Molecule: adenosine monophosphate-protein transferase ficd; PDBTitle: eukaryotic fic domain containing protein with bound apcpp
14	c3cucB_	Alignment		99.9	14	PDB header: signaling protein Chain: B: PDB Molecule: protein of unknown function with a fic domain; PDBTitle: crystal structure of a fic domain containing signaling protein2 (bt_2513) from bacteroides thetaiotaomicron vpi-5482 at 2.71 a3 resolution
15	c4rglA_	Alignment		99.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution
16	c5jj6A_	Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: adenosine monophosphate-protein transferase ficd homolog; PDBTitle: fic-1 (aa134 - 508) from c. elegans
17	c3eqxB_	Alignment		99.9	13	PDB header: dna binding protein Chain: B: PDB Molecule: fic domain containing transcriptional regulator; PDBTitle: crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
18	c4x2eA_	Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: fic family protein putative filamentation induced by camp PDBTitle: clostridium difficile wild type fic protein
19	c3n3vA_	Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: adenosine monophosphate-protein transferase ibpa; PDBTitle: crystal structure of ibpafic2-h3717a in complex with adenylated2 cdc42
20	c3dd7A_	Alignment		99.0	16	PDB header: ribosome inhibitor Chain: A: PDB Molecule: death on curing protein; PDBTitle: structure of doch66y in complex with the c-terminal domain of phd
21	c3letB_	Alignment	not modelled	98.3	17	PDB header: transferase Chain: B: PDB Molecule: adenosine monophosphate-protein transferase vops; PDBTitle: crystal structure of fic domain containing ampylator, vops
22	d1s0pa_	Alignment	not modelled	42.4	13	Fold: N-terminal domain of adenylcyclase associated protein, CAP Superfamily: N-terminal domain of adenylcyclase associated protein, CAP Family: N-terminal domain of adenylcyclase associated protein, CAP
23	c3n0aA_	Alignment	not modelled	40.3	10	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase auxilin; PDBTitle: crystal structure of auxilin (40-400)
24	d3etja2	Alignment	not modelled	40.3	39	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
25	c2c46B_	Alignment	not modelled	37.1	9	PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and 5'-2 phosphatase
26	c3awfC_	Alignment	not modelled	34.4	14	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: voltage-sensor containing phosphatase; PDBTitle: crystal structure of pten-like domain of ci-vsp (236-576)
27	c2imgA_	Alignment	not modelled	30.6	29	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
28	c3rgqA_	Alignment	not modelled	29.3	18	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptprt1 in complex with pi(5)p

29	d1yl7a1	Alignment	not modelled	28.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
30	c2ee7A	Alignment	not modelled	28.5	7	PDB header: structural protein Chain: A: PDB Molecule: sperm flagellar protein 1; PDBTitle: solution structure of the ch domain from human sperm2 flagellar protein 1
31	c1yn9B	Alignment	not modelled	28.3	17	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
32	d1ohea2	Alignment	not modelled	27.2	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
33	c1d5rA	Alignment	not modelled	25.2	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphoinositide phosphatase pten; PDBTitle: crystal structure of the pten tumor suppressor
34	d1mkpa	Alignment	not modelled	24.8	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
35	c4nyhB	Alignment	not modelled	24.5	21	PDB header: hydrolase Chain: B: PDB Molecule: rna/rnp complex-1-interacting phosphatase; PDBTitle: orthorhombic crystal form of pir1 dual specificity phosphatase core
36	c2lcyA	Alignment	not modelled	24.0	41	PDB header: viral protein Chain: A: PDB Molecule: virion spike glycoprotein; PDBTitle: nmr structure of the complete internal fusion loop from ebolavirus gp22 at ph 5.5
37	c6i28A	Alignment	not modelled	22.7	15	PDB header: viral protein Chain: A: PDB Molecule: orf98 ptp-2; PDBTitle: crystal structure of cydia pomonella ptp-2 phosphatase
38	c3s4eA	Alignment	not modelled	22.3	13	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 19; PDBTitle: crystal structure of a novel mitogen-activated protein kinase2 phosphatase, skrp1
39	c2htfA	Alignment	not modelled	22.0	35	PDB header: transferase Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain
40	c1zzwA	Alignment	not modelled	21.7	17	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of catalytic domain of human map kinase2 phosphatase 5
41	c2wgpA	Alignment	not modelled	20.8	22	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 14; PDBTitle: crystal structure of human dual specificity phosphatase 14
42	c2y96A	Alignment	not modelled	20.2	21	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27
43	c2gwoC	Alignment	not modelled	19.8	21	PDB header: hydrolase Chain: C: PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmdp
44	c2i6oA	Alignment	not modelled	19.3	23	PDB header: hydrolase Chain: A: PDB Molecule: sulfolobus solfataricus protein tyrosine PDBTitle: crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
45	c2nt2C	Alignment	not modelled	19.0	29	PDB header: hydrolase Chain: C: PDB Molecule: protein phosphatase slingshot homolog 2; PDBTitle: crystal structure of slingshot phosphatase 2
46	c2e0tA	Alignment	not modelled	18.4	22	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
47	d1s2xa	Alignment	not modelled	18.1	21	Fold: STAT-like Superfamily: Cag-Z Family: Cag-Z
48	c1s2xA	Alignment	not modelled	18.1	21	PDB header: unknown function Chain: A: PDB Molecule: cag-z; PDBTitle: crystal structure of cag-z from helicobacter pylori
49	c3emuA	Alignment	not modelled	17.9	9	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
50	c1wrmA	Alignment	not modelled	17.9	17	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 22; PDBTitle: crystal structure of jsp-1
51	c1yl7F	Alignment	not modelled	17.8	14	PDB header: oxidoreductase Chain: F: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c)
52	d1dih1	Alignment	not modelled	17.7	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
53	c4ki9A	Alignment	not modelled	17.6	17	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
54	c5jnmA	Alignment	not modelled	17.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: mannitol-1-phosphate 5-dehydrogenase; PDBTitle: crystal structure of mtdl from staphylococcus aureus at

					1.7-angstrom2 resolution
55	c2r0bA	Alignment	not modelled	17.5	17 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
56	c2m3vA	Alignment	not modelled	16.8	18 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
57	c2oudA	Alignment	not modelled	16.1	17 PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
58	c5kt0A	Alignment	not modelled	15.8	24 PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
59	c4kyrA	Alignment	not modelled	15.4	18 PDB header: hydrolase, sugar binding protein Chain: A: PDB Molecule: phosphoglucan phosphatase lsf2, chloroplastic; PDBTitle: structure of a product bound plant phosphatase
60	c3jipA	Alignment	not modelled	15.3	33 PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
61	d1u8fo1	Alignment	not modelled	14.9	18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
62	c4r30C	Alignment	not modelled	14.8	33 PDB header: hydrolase Chain: C: PDB Molecule: laforin; PDBTitle: structure of human laforin dual specificity phosphatase domain
63	c2g6zB	Alignment	not modelled	14.7	22 PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 5; PDBTitle: crystal structure of human dusp5
64	c4iqzD	Alignment	not modelled	14.4	31 PDB header: unknown function Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: the crystal structure of a large insert in rna polymerase (rpsc)2 subunit from e. coli
65	d1vm6a3	Alignment	not modelled	14.4	40 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	d1j0xo1	Alignment	not modelled	14.3	18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
67	d1i9sa	Alignment	not modelled	14.2	13 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
68	c4jmkA	Alignment	not modelled	14.0	21 PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 8; PDBTitle: structure of dusp8
69	c2aucC	Alignment	not modelled	14.0	7 PDB header: membrane protein Chain: C: PDB Molecule: myosin a tail interacting protein; PDBTitle: structure of the plasmodium mtip-myoa complex, a key component of the2 parasite invasion motor
70	d1hdgo1	Alignment	not modelled	13.9	14 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
71	d2b5id2	Alignment	not modelled	13.6	33 Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
72	c2hcmA	Alignment	not modelled	13.6	30 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
73	c5xjvA	Alignment	not modelled	13.5	21 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
74	d1ggaa1	Alignment	not modelled	13.4	26 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	d1yq2a2	Alignment	not modelled	13.4	17 Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
76	c2vfwB	Alignment	not modelled	13.1	44 PDB header: transferase Chain: B: PDB Molecule: short-chain z-isoprenyl diphosphate synthetase; PDBTitle: rv1086 native
77	c3ihtB	Alignment	not modelled	13.1	80 PDB header: transferase Chain: B: PDB Molecule: s-adenosyl-l-methionine methyl transferase; PDBTitle: crystal structure of s-adenosyl-l-methionine methyl transferase2 (yp_165822.1) from silicibacter pomeroyi dss-3 at 1.80 a resolution
78	d1d5ra2	Alignment	not modelled	13.1	24 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
					PDB header: hydrolase

79	c1yz4A_	Alignment	not modelled	13.0	25	Chain: A: PDB Molecule: dual specificity phosphatase-like 15 isoform a; PDBTitle: crystal structure of dusp15
80	d1i32a1	Alignment	not modelled	13.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
81	c5wo1A_	Alignment	not modelled	12.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase dapb from <i>coxiella2 burnetii</i>
82	c4hd5A_	Alignment	not modelled	12.9	0	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of bc0361, a polysaccharide deacetylase from <i>2 bacillus cereus</i>
83	d1vpda1	Alignment	not modelled	12.8	13	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
84	d3gpdg1	Alignment	not modelled	12.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
85	d1m3ga_	Alignment	not modelled	12.5	26	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
86	c1yx7A_	Alignment	not modelled	12.4	12	PDB header: metal binding protein Chain: A: PDB Molecule: calsensin; PDBTitle: nmr structure of calsensin, energy minimized average2 structure.
87	c6dzpg_	Alignment	not modelled	12.0	57	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: cryo-em structure of mycobacterium smegmatis c(minus) 50s ribosomal2 subunit
88	c5eesA_	Alignment	not modelled	12.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dapb in complex with nadp+ from <i>corynebacterium2 glutamicum</i>
89	c2vg2C_	Alignment	not modelled	11.9	50	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
90	c1drwA_	Alignment	not modelled	11.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
91	c3h2zA_	Alignment	not modelled	11.8	28	PDB header: oxidoreductase Chain: A: PDB Molecule: mannitol-1-phosphate 5-dehydrogenase; PDBTitle: the crystal structure of mannitol-1-phosphate dehydrogenase from <i>2 shigella flexneri</i>
92	d1vhra_	Alignment	not modelled	11.4	26	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
93	d1k3ta1	Alignment	not modelled	11.3	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
94	d2cvza1	Alignment	not modelled	11.2	9	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
95	c5xw4A_	Alignment	not modelled	10.7	25	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
96	c2j034_	Alignment	not modelled	10.7	56	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
97	d2j0141	Alignment	not modelled	10.7	56	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
98	c4q2uM_	Alignment	not modelled	10.4	11	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
99	c5xk9F_	Alignment	not modelled	10.4	25	PDB header: transferase Chain: F: PDB Molecule: undecaprenyl diphosphate synthase; PDBTitle: crystal structure of isosesquilandulyl diphosphate synthase from <i>2 streptomyces sp. strain cnh-189</i> in complex with gssp and dmapp