








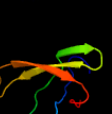














Phyre2

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Description	RVBD0611c_(-)_705964_706347
Date	Fri Jul 26 01:50:17 BST 2019
Unique Job ID	f58cce72a0f49c50

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3p8dB_	 Alignment		84.8	27	PDB header: protein binding Chain: B; PDB Molecule: medulloblastoma antigen mu-mb-50.72; PDBTitle: crystal structure of the second tudor domain of human phf20 (homodimer2 form)
2	c2ldmA_	 Alignment		82.3	23	PDB header: transcription/protein binding Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2
3	c3qiiA_	 Alignment		78.3	21	PDB header: transcription regulator Chain: A; PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 2 of human phd finger protein 20
4	c4tseA_	 Alignment		75.0	26	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase mib1; PDBTitle: crystal structure of the mib repeat domain of mind bomb 1
5	c3l2uA_	 Alignment		51.9	17	PDB header: recombination/dna Chain: A; PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv)2 intasome in complex with magnesium and gs91373 (elvitegravir)
6	c1xnll_	 Alignment		49.1	24	PDB header: cell cycle Chain: I; PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: tandem tudor domain of 53bp1
7	c2equA_	 Alignment		46.4	13	PDB header: protein binding Chain: A; PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1
8	c4uc4A_	 Alignment		42.5	22	PDB header: replication Chain: A; PDB Molecule: lysine-specific demethylase 4b; PDBTitle: crystal structure of hybrid tudor domain of human lysine demethylase2 kdm4b
9	c5ld2D_	 Alignment		41.1	21	PDB header: hydrolase Chain: D; PDB Molecule: recbcd enzyme subunit recd; PDBTitle: cryo-em structure of recbcd+dna complex revealing activated nuclease2 domain
10	c3dlmA_	 Alignment		38.1	20	PDB header: transferase Chain: A; PDB Molecule: histone-lysine n-methyltransferase setdb1; PDBTitle: crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
11	c5zwxB_	 Alignment		37.7	19	PDB header: gene regulation Chain: B; PDB Molecule: duf724 domain-containing protein 6-like; PDBTitle: crystal structure of raphanus sativus agdp1 agd12 in complex with an2 h3k9me2 peptide

12	c2oviA_	Alignment		35.4	15	PDB header: ligand binding protein, metal transport Chain: A: PDB Molecule: hypothetical protein chux; PDBTitle: structure of the heme binding protein chux
13	c1vw4G_	Alignment		33.9	35	PDB header: ribosome Chain: G: PDB Molecule: 54s ribosomal protein l50, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
14	c2qqsB_	Alignment		33.1	21	PDB header: oxidoreductase Chain: B: PDB Molecule: jmjc domain-containing histone demethylation PDBTitle: jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
15	c2xdpA_	Alignment		30.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 4c; PDBTitle: crystal structure of the tudor domain of human jmjd2c
16	d1e2wa2	Alignment		30.3	38	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
17	d2hqva1	Alignment		28.1	17	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: ChuX-like
18	c2ph0A_	Alignment		28.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q6d2t7_erwct protein from erwinia carotovora.2 nesg target ewr41.
19	d1ci3m2	Alignment		27.8	24	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
20	c5zwzA_	Alignment		27.7	18	PDB header: gene regulation Chain: A: PDB Molecule: agenet domain-containing protein; PDBTitle: crystal structure of arabidopsis thaliana agdp1 agd34
21	d1twia1	Alignment	not modelled	27.2	23	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
22	d1cqva_	Alignment	not modelled	26.3	26	Fold: Mbth/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
23	c2zfdB_	Alignment	not modelled	25.0	18	PDB header: signaling protein/transferase Chain: B: PDB Molecule: putative uncharacterized protein t20l15_90; PDBTitle: the crystal structure of plant specific calcium binding protein atcb122 in complex with the regulatory domain of atcipk14
24	c1e2vB_	Alignment	not modelled	24.6	38	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
25	c5v77B_	Alignment	not modelled	24.2	43	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from neisseria2 gonorrhoeae
26	c3pifD_	Alignment	not modelled	24.1	27	PDB header: hydrolase Chain: D: PDB Molecule: 5'->3' exoribonuclease (xrn1); PDBTitle: crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
27	c4ro6A_	Alignment	not modelled	22.9	12	PDB header: lyase Chain: A: PDB Molecule: lactoylglutathione lyase; PDBTitle: crystal structure of glyoxalase i from zea mays
28	d2gycf2	Alignment	not modelled	22.6	32	Fold: Mbth/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain

29	c1q90A_	Alignment	not modelled	22.6	38	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastoquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
30	d1twua_	Alignment	not modelled	21.4	19	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Hypothetical protein YycE
31	c3zi1A_	Alignment	not modelled	21.3	21	PDB header: isomerase Chain: A: PDB Molecule: glyoxalase domain-containing protein 4; PDBTitle: crystal structure of human glyoxalase domain-containing protein 42 (glod4)
32	d1edqa1	Alignment	not modelled	20.5	42	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
33	d2j0i2	Alignment	not modelled	19.5	42	Fold: Mbth/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
34	c5exvD_	Alignment	not modelled	18.3	19	PDB header: heme-binding protein Chain: D: PDB Molecule: hemin-degrading hems.chux domain protein; PDBTitle: crystal structure of heme binding protein hutx from vibrio cholerae
35	c4xpmB_	Alignment	not modelled	18.2	24	PDB header: protein binding Chain: B: PDB Molecule: uncharacterized protein ycr075w-a; PDBTitle: crystal structure of ego-tc
36	d2do3a1	Alignment	not modelled	17.7	19	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
37	d2diqa1	Alignment	not modelled	17.7	22	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
38	d2hqxa1	Alignment	not modelled	17.6	11	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
39	c2hqxB_	Alignment	not modelled	17.6	11	PDB header: transcription Chain: B: PDB Molecule: p100 co-activator tudor domain; PDBTitle: crystal structure of human p100 tudor domain conserved2 region
40	c2xk0A_	Alignment	not modelled	17.5	16	PDB header: transcription Chain: A: PDB Molecule: polycomb protein pcl; PDBTitle: solution structure of the tudor domain from drosophila2 polycomblike (pcl)
41	c4ce4I_	Alignment	not modelled	16.8	37	PDB header: ribosome Chain: I: PDB Molecule: mrp19; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
42	c1mg7B_	Alignment	not modelled	16.7	24	PDB header: gene regulation Chain: B: PDB Molecule: early switch protein xol-1 2.2k splice form; PDBTitle: crystal structure of xol-1
43	d2hbba1	Alignment	not modelled	16.2	26	Fold: Mbth/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
44	c1ssfA_	Alignment	not modelled	16.2	20	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
45	c2qghA_	Alignment	not modelled	16.1	25	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-hsine
46	c2ky9A_	Alignment	not modelled	15.1	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ydhk; PDBTitle: solution nmr structure of ydhk c-terminal domain from b.subtilis,2 northeast structural genomics consortium target target sr518
47	c4a4fA_	Alignment	not modelled	14.8	15	PDB header: rna binding protein Chain: A: PDB Molecule: survival of motor neuron-related-splicing factor 30; PDBTitle: solution structure of spf30 tudor domain in complex with symmetrically2 dimethylated arginine
48	c4q5wB_	Alignment	not modelled	14.7	20	PDB header: transcription Chain: B: PDB Molecule: maternal protein tudor; PDBTitle: crystal structure of extended-tudor 9 of drosophila melanogaster
49	d2d9ta1	Alignment	not modelled	14.4	22	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
50	c6dgaA_	Alignment	not modelled	14.3	16	PDB header: unknown function Chain: A: PDB Molecule: rpfr; PDBTitle: cronobacter turicensis rpfr quorum-sensing receptor rpff interaction2 domain
51	c4wyqB_	Alignment	not modelled	14.0	20	PDB header: hydrolase/protein binding Chain: B: PDB Molecule: risc-loading complex subunit tarbp2; PDBTitle: crystal structure of the dicer-trbp interface
52	c4v19I_	Alignment	not modelled	13.6	37	PDB header: ribosome Chain: I: PDB Molecule: mitoribosomal protein bl9m, mrp19; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
53	c4l0jA_	Alignment	not modelled	13.5	18	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase i; PDBTitle: structure of a translocation signal domain mediating conjugative2 transfer by type iv secretion systems
54	c2jtdA_	Alignment	not modelled	13.3	16	PDB header: cell adhesion Chain: A: PDB Molecule: myomesin-1;

						PDBTitle: skelemin immunoglobulin c2 like domain 4
55	c5nleC_	Alignment	not modelled	13.3	19	PDB header: sugar binding protein Chain: C: PDB Molecule: galectin; PDBTitle: chicken grifin (crystallisation ph: 8.0)
56	c2d9tA_	Alignment	not modelled	13.1	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tudor domain-containing protein 3; PDBTitle: solution structure of the tudor domain of tudor domain2 containing protein 3 from mouse
57	d2r5fa1	Alignment	not modelled	12.7	29	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
58	c2hfgR_	Alignment	not modelled	12.4	83	PDB header: immune system Chain: R: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of hbr3 bound to cb3s-fab
59	c1osxA_	Alignment	not modelled	12.3	55	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily PDBTitle: solution structure of the extracellular domain of blys2 receptor 3 (br3)
60	d1osxa_	Alignment	not modelled	12.3	55	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: BAFF receptor-like
61	c6mzoA_	Alignment	not modelled	12.2	44	PDB header: hydrolase Chain: A: PDB Molecule: inactive zymogen c11 protease; PDBTitle: x-ray structure of an inactive zymogen c11 protease from2 parabacteroides distasonis
62	c2kaoA_	Alignment	not modelled	12.1	31	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b1; PDBTitle: structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
63	d1oqen_	Alignment	not modelled	11.9	83	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: BAFF receptor-like
64	c1oqeN_	Alignment	not modelled	11.9	83	PDB header: immune system Chain: N: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of stall-1 with baff-r
65	c2kt7A_	Alignment	not modelled	11.9	11	PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: putative peptidoglycan bound protein (lpxtg) PDBTitle: solution nmr structure of mucin-binding domain of protein2 lmo0835 from listeria monocytogenes, northeast structural3 genomics consortium target lmr64a
66	c5ohoB_	Alignment	not modelled	11.6	20	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: crystal structure of the kowx-kow4 domain of human dsif
67	d2b2na1	Alignment	not modelled	11.4	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
68	c5o60H_	Alignment	not modelled	11.3	32	PDB header: ribosome Chain: H: PDB Molecule: 50s ribosomal protein I9; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
69	c1p0t0_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: O: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
70	c1p0tu_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: U: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
71	c1p0tR_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: R: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
72	c1p0tf_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: F: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
73	c1p0tS_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: S: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
74	c1p0tI_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: I: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
75	c1p0tL_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: L: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
76	c1p0t6_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: 6: PDB Molecule: PDB Fragment: residues 1-63; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
77	c1p0th_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: H: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
78	c1p0td_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: D: PDB Molecule: tumor necrosis factor receptor superfamily member 13c; PDBTitle: crystal structure of the baff-baff-r complex (part ii)
79	c1p0t4_	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: 4: PDB Molecule: PDBTitle: crystal structure of the baff-baff-r complex (part ii)
						PDB header: protein binding

