
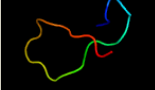

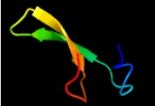
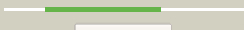












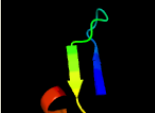
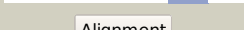



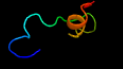

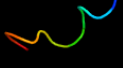
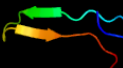
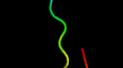
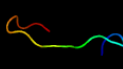





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1590_(-)_1791341_1791580
Date	Fri Aug 2 13:30:18 BST 2019
Unique Job ID	e7a682b0f8441212

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6o3pA_	 Alignment		81.4	30	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
2	c2gb5B_	 Alignment		80.9	22	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
3	c5y06A_	 Alignment		59.8	15	PDB header: unknown function Chain: A: PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis
4	d1wj0a_	 Alignment		37.8	75	Fold: SBT domain Superfamily: SBT domain Family: SBT domain
5	d1ul4a_	 Alignment		34.6	60	Fold: SBT domain Superfamily: SBT domain Family: SBT domain
6	c2l9zA_	 Alignment		33.8	35	PDB header: transcription Chain: A: PDB Molecule: pr domain zinc finger protein 4; PDBTitle: zinc knuckle in prdm4
7	c5l9wC_	 Alignment		32.6	29	PDB header: ligase Chain: C: PDB Molecule: acetophenone carboxylase beta subunit; PDBTitle: crystal structure of the apc core complex
8	d1ul5a_	 Alignment		28.0	63	Fold: SBT domain Superfamily: SBT domain Family: SBT domain
9	d1pn0a2	 Alignment		22.1	35	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
10	c2l4jA_	 Alignment		21.8	27	PDB header: transcription Chain: A: PDB Molecule: yes-associated protein 2 (yap2); PDBTitle: yap ww2
11	c5m45l_	 Alignment		21.6	28	PDB header: ligase Chain: I: PDB Molecule: acetone carboxylase gamma subunit; PDBTitle: structure of acetone carboxylase purified from xanthobacter2 autotrophicus

12	c4gndC_	Alignment		19.7	26	PDB header: transferase Chain: C: PDB Molecule: histone-lysine n-methyltransferase nsd3; PDBTitle: crystal structure of nsd3 tandem phd5-c5hch domains
13	d1tk7a2	Alignment		19.5	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
14	d1nqa2	Alignment		19.3	45	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
15	c5d5hA_	Alignment		18.9	24	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of mycobacterium tuberculosis topoisomerase i
16	c2lawA_	Alignment		18.7	33	PDB header: signaling protein/transcription Chain: A: PDB Molecule: yorkie homolog; PDBTitle: structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
17	c2kq0A_	Alignment		18.4	31	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide ilptappeynea
18	c2jmfA_	Alignment		18.2	33	PDB header: ligase/signaling protein Chain: A: PDB Molecule: e3 ubiquitin-protein ligase suppressor of deltex; PDBTitle: solution structure of the su(dx) ww4- notch py peptide2 complex
19	c1dvbA_	Alignment		17.2	33	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
20	c2zajA_	Alignment		17.0	20	PDB header: protein binding Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz PDBTitle: solution structure of the short-isoform of the second ww2 domain from the human membrane-associated guanylate kinase,3 ww and pdz domain-containing protein 1 (magi-1)
21	d1yuza2	Alignment	not modelled	16.7	36	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
22	c2hr5B_	Alignment	not modelled	16.4	50	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
23	c3cngC_	Alignment	not modelled	16.2	21	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
24	c2mdwA_	Alignment	not modelled	15.9	56	PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of a strand-swapped dimer of the ww domain
25	c2lvuA_	Alignment	not modelled	15.8	50	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 10
26	c3g5rA_	Alignment	not modelled	15.4	38	PDB header: transferase Chain: A: PDB Molecule: methylenetetrahydrofolate--trna-(uracil-5-)- PDBTitle: crystal structure of thermus thermophilus trmf0 in complex with2 tetrahydrofolate
27	c5fja_	Alignment	not modelled	14.5	22	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase iii subunit rpc10; PDBTitle: cryo-em structure of yeast rna polymerase iii at 4.7 a
28	c4c2mX_	Alignment	not modelled	14.3	21	PDB header: transcription Chain: X: PDB Molecule: dna-directed rna polymerase i subunit rpa12; PDBTitle: structure of rna polymerase i at 2.8 a resolution

29	c2xhqA	Alignment	not modelled	12.9	33	PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
30	c4kisA	Alignment	not modelled	12.8	29	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex
31	c3lmcA	Alignment	not modelled	12.8	25	PDB header: hydrolase Chain: A: PDB Molecule: peptidase, zinc-dependent; PDBTitle: crystal structure of zinc-dependent peptidase from methanocorpusculum2 labreanum (strain z), northeast structural genomics consortium target3 mur16
32	d1lkoa2	Alignment	not modelled	12.8	33	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
33	c2n8tA	Alignment	not modelled	12.0	27	PDB header: ligase/peptide Chain: A: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: solution structure of the rnedd4 ww2 domain-cx43ct peptide complex by2 nmr
34	c2lb0A	Alignment	not modelled	11.9	40	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
35	c1wr4A	Alignment	not modelled	11.9	33	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-protein ligase nedd4-2; PDBTitle: solution structure of the second ww domain of nedd4-2
36	c2lazA	Alignment	not modelled	11.9	40	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
37	c1ymzA	Alignment	not modelled	11.7	40	PDB header: unknown function Chain: A: PDB Molecule: cc45; PDBTitle: cc45, an artificial ww domain designed using statistical2 coupling analysis
38	c2ysfA	Alignment	not modelled	11.7	33	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: solution structure of the fourth ww domain from the human2 e3 ubiquitin-protein ligase itchy homolog, itch
39	d2jmfa1	Alignment	not modelled	11.6	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
40	c1wr7A	Alignment	not modelled	11.5	33	PDB header: ligase Chain: A: PDB Molecule: nedd4-2; PDBTitle: solution structure of the third ww domain of nedd4-2
41	c4iloA	Alignment	not modelled	11.4	44	PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
42	c2yshA	Alignment	not modelled	11.2	33	PDB header: protein binding Chain: A: PDB Molecule: growth-arrest-specific protein 7; PDBTitle: solution structure of the ww domain from the human growth-2 arrest-specific protein 7, gas-7
43	c2kykA	Alignment	not modelled	11.0	33	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: the sandwich region between two lmp2a py motif regulates the2 interaction between arp4ww2domain and py motif
44	d1tk7a1	Alignment	not modelled	10.9	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
45	d1dgsa1	Alignment	not modelled	10.8	43	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
46	c5ydyA	Alignment	not modelled	10.7	33	PDB header: signaling protein Chain: A: PDB Molecule: ww2 domain and ppxy motif complex; PDBTitle: nmr structure of yap1-2 ww2 domain with lats1 ppxy motif complex
47	c2ysqA	Alignment	not modelled	10.7	27	PDB header: protein binding Chain: A: PDB Molecule: syntaxin-binding protein 4; PDBTitle: solution structure of the ww domain from the human syntaxin-2 binding protein 4
48	c2mkdA	Alignment	not modelled	10.3	33	PDB header: dna binding protein Chain: A: PDB Molecule: zinc finger protein 346; PDBTitle: human jaz zf3 residues 168-227
49	c2x7mA	Alignment	not modelled	10.2	33	PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
50	c6j69A	Alignment	not modelled	10.0	33	PDB header: cell cycle Chain: A: PDB Molecule: protein kibra; PDBTitle: structure of kibra and dendrin complex
51	c1u5kA	Alignment	not modelled	10.0	29	PDB header: recombination,replication Chain: A: PDB Molecule: hypothetical protein; PDBTitle: recombinational repair protein reco
52	c6n2oB	Alignment	not modelled	9.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: pyruvate ferredoxin/ferredoxin oxidoreductase, beta PDBTitle: 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound
53	d1dsva	Alignment	not modelled	9.6	40	Fold: Retrovirus zinc finger-like domains Superfamily: Retrovirus zinc finger-like domains Family: Retrovirus zinc finger-like domains
54	c2nb9A	Alignment	not modelled	9.5	41	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein;

						PDBTitle: solution structure of zitp zinc finger
55	c3hkzP_	Alignment	not modelled	9.2	31	PDB header: transferase Chain: P; PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
56	d1fftb1	Alignment	not modelled	9.1	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
57	c5h4uB_	Alignment	not modelled	8.8	47	PDB header: hydrolase Chain: B; PDB Molecule: endo-beta-1,4-glucanase; PDBTitle: crystal structure of cellulase from antarctic springtail, cryptopygus2 antarcticus
58	c2dmvA_	Alignment	not modelled	8.5	47	PDB header: ligase Chain: A; PDB Molecule: itchy homolog e3 ubiquitin protein ligase; PDBTitle: solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itich)
59	c3d5d6_	Alignment	not modelled	8.3	33	PDB header: ribosome Chain: 6; PDB Molecule: 50s ribosomal protein l33; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of the second 70s ribosome. the entire3 crystal structure contains two 70s ribosomes as described in remark4 400.
60	d2f21a1	Alignment	not modelled	8.2	47	Fold: WW domain-like Superfamily: WW domain Family: WW domain
61	c3gh1A_	Alignment	not modelled	8.2	40	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: predicted nucleotide-binding protein; PDBTitle: crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
62	c1e0mA_	Alignment	not modelled	8.0	27	PDB header: de novo protein Chain: A; PDB Molecule: wwprototype; PDBTitle: prototype ww domain
63	c4rulA_	Alignment	not modelled	8.0	27	PDB header: isomerase/dna Chain: A; PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
64	c5flmI_	Alignment	not modelled	7.9	24	PDB header: transcription Chain: I; PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
65	c2c6bA_	Alignment	not modelled	7.8	43	PDB header: ligase Chain: A; PDB Molecule: ubiquitin-protein ligase e3 mdm2; PDBTitle: solution structure of the c4 zinc-finger domain of hdm2
66	d1k9ra_	Alignment	not modelled	7.7	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
67	c2dvwB_	Alignment	not modelled	7.7	27	PDB header: protein binding Chain: B; PDB Molecule: salvador homolog 1 protein; PDBTitle: solution structure of the second ww domain from mouse2 salvador homolog 1 protein (mww45)
68	c2mzjA_	Alignment	not modelled	7.7	14	PDB header: rna binding protein Chain: A; PDB Molecule: nucleolar protein 6; PDBTitle: nmr-structure of the nop6-rbd from s. cerevisiae
69	d1d1la_	Alignment	not modelled	7.6	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
70	d4croa_	Alignment	not modelled	7.4	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
71	c2pijB_	Alignment	not modelled	7.4	29	PDB header: transcription Chain: B; PDB Molecule: prophage pfl 6 cro; PDBTitle: structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
72	d1i5hw_	Alignment	not modelled	7.2	40	Fold: WW domain-like Superfamily: WW domain Family: WW domain
73	c4uxjB_	Alignment	not modelled	7.2	13	PDB header: transferase Chain: B; PDB Molecule: thymidine kinase; PDBTitle: leishmania major thymidine kinase in complex with dttp
74	c1zr9A_	Alignment	not modelled	7.1	30	PDB header: transcription Chain: A; PDB Molecule: zinc finger protein 593; PDBTitle: solution structure of a human c2h2-type zinc finger protein
75	d1zr9a1	Alignment	not modelled	7.1	30	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
76	c2cr8A_	Alignment	not modelled	6.8	43	PDB header: cell cycle Chain: A; PDB Molecule: mdm4 protein; PDBTitle: solution structure of the zf-ranbp domain of p53-binding2 protein mdm4
77	d1f8ab1	Alignment	not modelled	6.7	53	Fold: WW domain-like Superfamily: WW domain Family: WW domain
78	c3na7A_	Alignment	not modelled	6.7	24	PDB header: gene regulation, chaperone Chain: A; PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
79	d1l8fa_	Alignment	not modelled	6.4	40	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: Eng V-like
80	c1i3ql_	Alignment	not modelled	6.4	21	PDB header: transcription Chain: I; PDB Molecule: dna-directed rna polymerase ii 14.2kd PDBTitle: rna polymerase ii crystal form i at 3.1 a resolution

81	c1yiuA_	Alignment	not modelled	6.4	40	PDB header: ligase Chain: A: PDB Molecule: itchy e3 ubiquitin protein ligase; PDBTitle: itch e3 ubiquitin ligase ww3 domain
82	c2djiyA_	Alignment	not modelled	6.3	40	PDB header: ligase/signaling protein Chain: A: PDB Molecule: smad ubiquitination regulatory factor 2; PDBTitle: solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
83	c5zb8B_	Alignment	not modelled	6.3	38	PDB header: dna binding protein Chain: B: PDB Molecule: pfluendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfluendoq2 from pyrococcus furiosus
84	c5m45K_	Alignment	not modelled	6.1	31	PDB header: ligase Chain: K: PDB Molecule: acetone carboxylase beta subunit; PDBTitle: structure of acetone carboxylase purified from xanthobacter2 autotrophicus
85	d1zu1a2	Alignment	not modelled	6.0	15	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
86	d1pina1	Alignment	not modelled	5.9	53	Fold: WW domain-like Superfamily: WW domain Family: WW domain
87	c1x31D_	Alignment	not modelled	5.8	57	PDB header: oxidoreductase Chain: D: PDB Molecule: sarcosine oxidase delta subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
88	c6cxoB_	Alignment	not modelled	5.8	17	PDB header: immune system Chain: B: PDB Molecule: complement component c9; PDBTitle: complement component-9
89	c3l4hA_	Alignment	not modelled	5.8	27	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase hecw1; PDBTitle: helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
90	c2ez5W_	Alignment	not modelled	5.7	20	PDB header: signalling protein,ligase Chain: W: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: solution structure of the dnedd4 ww3* domain- comm lpsy2 peptide complex
91	d1i8gb_	Alignment	not modelled	5.7	53	Fold: WW domain-like Superfamily: WW domain Family: WW domain
92	c4rdmB_	Alignment	not modelled	5.7	20	PDB header: hydrolase/dna Chain: B: PDB Molecule: restriction endonuclease r.ngovii; PDBTitle: crystal structure of r.ngoavii restriction endonuclease b3 domain with2 cognate dna
93	c2lcqA_	Alignment	not modelled	5.7	27	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
94	c2jrrA_	Alignment	not modelled	5.7	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of q5lls5 from silicibacter2 pomeroyi. northeast structural genomics consortium target3 sir90
95	d1isua_	Alignment	not modelled	5.6	43	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
96	c6hu9n_	Alignment	not modelled	5.6	25	PDB header: oxidoreductase/electron transport Chain: N: PDB Molecule: cytochrome b; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
97	c1cl4A_	Alignment	not modelled	5.5	44	PDB header: viral protein Chain: A: PDB Molecule: protein (gag polyprotein); PDBTitle: nucleocapsid protein from mason-pfizer monkey virus (mpmv)
98	d2itka1	Alignment	not modelled	5.4	40	Fold: WW domain-like Superfamily: WW domain Family: WW domain
99	d2cona1	Alignment	not modelled	5.3	36	Fold: Rubredoxin-like Superfamily: NOB1 zinc finger-like Family: NOB1 zinc finger-like