






















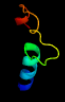









Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1653_(argj)_1866638_1867852
 Date Fri Aug 2 13:30:25 BST 2019
 Unique Job ID 2238ec346c49a61b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vz6a_	 Alignment		100.0	33	Fold: DmpA/Argj-like Superfamily: DmpA/Argj-like Family: Argj-like
2	c1vraB_	 Alignment		100.0	35	PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
3	c3it4B_	 Alignment		100.0	100	PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj PDBTitle: the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
4	c2vzkD_	 Alignment		100.0	32	PDB header: transferase Chain: D: PDB Molecule: glutamate n-acetyltransferase 2 beta chain; PDBTitle: structure of the acyl-enzyme complex of an n-terminal nucleophile2 (ntn) hydrolase, oat2
5	c3it4C_	 Alignment		100.0	100	PDB header: transferase Chain: C: PDB Molecule: arginine biosynthesis bifunctional protein argj PDBTitle: the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
6	c1vraA_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
7	c2v4iA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: glutamate n-acetyltransferase 2 alpha chain; PDBTitle: structure of a novel n-acyl-enzyme intermediate of an n-2 terminal nucleophile (ntn) hydrolase, oat2
8	d1ohua_	 Alignment		89.6	15	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
9	c3s3uB_	 Alignment		82.9	24	PDB header: transferase Chain: B: PDB Molecule: cysteine transferase; PDBTitle: crystal structure of uncleaved thnt t282c
10	d2ponb1	 Alignment		80.5	19	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
11	d1k3ka_	 Alignment		80.3	38	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death

12	c3n5iC_	Alignment		78.4	23	PDB header: hydrolase Chain: C: PDB Molecule: beta-peptidyl aminopeptidase; PDBTitle: crystal structure of the precursor (s250a mutant) of the n-terminal2 beta-aminopeptidase bapa
13	c2vm6A_	Alignment		77.8	29	PDB header: immune system Chain: A: PDB Molecule: bcl-2-related protein a1; PDBTitle: human bcl2-a1 in complex with bim-bh3 peptide
14	d2jm6b1	Alignment		75.0	40	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
15	c2vofA_	Alignment		74.2	24	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-related protein a1; PDBTitle: structure of mouse a1 bound to the puma bh3-domain
16	c5wddA_	Alignment		73.0	24	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-related ovarian killer protein; PDBTitle: crystal structure of chicken bok
17	c2yv6A_	Alignment		72.2	33	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2 homologous antagonist/killer; PDBTitle: crystal structure of human bcl-2 family protein bak
18	c3axgN_	Alignment		71.8	9	PDB header: hydrolase Chain: N: PDB Molecule: endotype 6-aminohexanoat-oligomer hydrolase; PDBTitle: structure of 6-aminohexanoate-oligomer hydrolase
19	d1b65a_	Alignment		71.8	25	Fold: DmpA/ArgJ-like Superfamily: DmpA/ArgJ-like Family: DmpA-like
20	c5tzba_	Alignment		71.0	23	PDB header: hydrolase Chain: A: PDB Molecule: d-aminopeptidase; PDBTitle: burkholderia sp. beta-aminopeptidase
21	d1pq1a_	Alignment	not modelled	70.4	54	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
22	c2kuaA_	Alignment	not modelled	69.6	16	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 10; PDBTitle: solution structure of a divergent bcl-2 protein
23	d1ysga1	Alignment	not modelled	69.4	47	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
24	c2drhD_	Alignment	not modelled	69.2	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: 361aa long hypothetical d-aminopeptidase; PDBTitle: crystal structure of the ph0078 protein from pyrococcus horikoshii ot3
25	d1bxa_	Alignment	not modelled	69.1	47	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
26	c4b4sA_	Alignment	not modelled	68.9	27	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 10; PDBTitle: crystal structure of a pro-survival bcl-2:bim bh3 complex
27	c2xa0A_	Alignment	not modelled	68.8	47	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator bcl-2; PDBTitle: crystal structure of bcl-2 in complex with a bax bh32 peptide
28	d1q59a_	Alignment	not modelled	68.6	47	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
						PDB header: apoptosis

29	c2a5yA	Alignment	not modelled	67.6	23	Chain: A: PDB Molecule: apoptosis regulator ced-9; PDBTitle: structure of a ced-4/ced-9 complex
30	c3qbrA	Alignment	not modelled	67.4	44	PDB header: apoptosis Chain: A: PDB Molecule: sjchgc06286 protein; PDBTitle: bakbh3 in complex with sja
31	c2jvfA	Alignment	not modelled	66.0	33	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein
32	c5wosA	Alignment	not modelled	65.6	24	PDB header: viral protein Chain: A: PDB Molecule: cnpv058 bcl-2 like protein; PDBTitle: structural and functional insights into canarypox virus cnp0582 regulation of apoptosis
33	d1f16a	Alignment	not modelled	62.9	54	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
34	c5ua4A	Alignment	not modelled	62.0	47	PDB header: apoptosis Chain: A: PDB Molecule: 5-hl; PDBTitle: crystal structure of a179l:bid bh3 complex
35	c2o2fA	Alignment	not modelled	61.6	47	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator bcl-2; PDBTitle: solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
36	d1g5ma	Alignment	not modelled	61.3	47	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
37	d1o0la	Alignment	not modelled	61.3	53	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
38	c3pk1A	Alignment	not modelled	60.4	38	PDB header: apoptosis/apoptosis regulator Chain: A: PDB Molecule: induced myeloid leukemia cell differentiation protein mcl- PDBTitle: crystal structure of mcl-1 in complex with the baxbh3 domain
39	c5tzipA	Alignment	not modelled	59.9	29	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein fpv039; PDBTitle: crystal structure of fpv039:bik bh3 complex
40	c6h1nA	Alignment	not modelled	59.4	47	PDB header: apoptosis Chain: A: PDB Molecule: bcl2-like 10 (apoptosis facilitator); PDBTitle: crystal structure of a zebra-fish pro-survival protein nrz- apo
41	d1zy3a1	Alignment	not modelled	58.2	53	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
42	c1qysA	Alignment	not modelled	57.1	33	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
43	c4bduC	Alignment	not modelled	56.3	86	PDB header: apoptosis Chain: C: PDB Molecule: green fluorescent protein, apoptosis regulator bax; PDBTitle: bax bh3-in-groove dimer (gfp)
44	c4wgiA	Alignment	not modelled	53.2	38	PDB header: apoptosis/inhibitor Chain: A: PDB Molecule: maltose-binding periplasmic protein,induced myeloid PDBTitle: a single diastereomer of a macrolactam core binds specifically to2 myeloid cell leukemia 1 (mcl1)
45	c2du4B	Alignment	not modelled	48.8	22	PDB header: ligase/rna Chain: B: PDB Molecule: o-phosphoseryl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys
46	c5w63A	Alignment	not modelled	46.5	54	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator bax; PDBTitle: crystal structure of channel catfish bax
47	c1eiyA	Alignment	not modelled	43.4	33	PDB header: ligase/rna Chain: A: PDB Molecule: phenylalanyl-trna synthetase; PDBTitle: the crystal structure of phenylalanyl-trna synthetase from thermus2 thermophilus complexed with cognate trnaphe
48	c3v7nA	Alignment	not modelled	43.3	24	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase (thrc) from from burkholderia2 thailandensis
49	d1qnaa1	Alignment	not modelled	38.7	45	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
50	c2odrD	Alignment	not modelled	38.1	22	PDB header: ligase Chain: D: PDB Molecule: phosphoseryl-trna synthetase; PDBTitle: methanococcus maripaludis phosphoseryl-trna synthetase
51	c2du3A	Alignment	not modelled	37.6	22	PDB header: ligase/rna Chain: A: PDB Molecule: o-phosphoseryl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys and o-phosphoserine
52	d1aisa1	Alignment	not modelled	36.6	35	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
53	d1cdwa2	Alignment	not modelled	36.2	30	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
54	c5twaA	Alignment	not modelled	36.0	41	PDB header: apoptosis Chain: A: PDB Molecule: bcl-x homologous protein, bhp2; PDBTitle: crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2
						Fold: TBP-like

55	d1cdwa1	Alignment	not modelled	35.8	40	Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
56	d1nh2a1	Alignment	not modelled	34.9	50	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
57	c5wcoC	Alignment	not modelled	34.6	56	PDB header: viral protein Chain: C: PDB Molecule: ns2; PDBTitle: matrix protein (m1) of infectious salmon anaemia virus
58	c2odrC	Alignment	not modelled	34.1	22	PDB header: ligase Chain: C: PDB Molecule: phosphoseryl-trna synthetase; PDBTitle: methanococcus maripaludis phosphoseryl-trna synthetase
59	d1kl7a	Alignment	not modelled	33.6	28	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
60	c4b0aA	Alignment	not modelled	31.8	52	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 1, linker, PDBTitle: the high-resolution structure of ytbp-ytaf1 identifies2 conserved and competing interaction surfaces in3 transcriptional activation
61	c2du7C	Alignment	not modelled	31.7	13	PDB header: ligase Chain: C: PDB Molecule: o-phosphoseryl-trna synthetase; PDBTitle: crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
62	d1aisa2	Alignment	not modelled	31.4	35	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
63	c2odrA	Alignment	not modelled	29.7	13	PDB header: ligase Chain: A: PDB Molecule: phosphoseryl-trna synthetase; PDBTitle: methanococcus maripaludis phosphoseryl-trna synthetase
64	c5vmnA	Alignment	not modelled	29.7	40	PDB header: viral protein Chain: A: PDB Molecule: bak protein; PDBTitle: crystal structure of grouper iridovirus giv66
65	d2fiqa1	Alignment	not modelled	28.6	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
66	d1nh2a2	Alignment	not modelled	27.7	25	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
67	c3pcoC	Alignment	not modelled	27.5	27	PDB header: ligase Chain: C: PDB Molecule: phenylalanyl-trna synthetase, alpha subunit; PDBTitle: crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
68	d1mp9a2	Alignment	not modelled	26.9	35	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
69	d1mp9a1	Alignment	not modelled	26.5	35	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
70	c3l4gl	Alignment	not modelled	24.5	22	PDB header: ligase Chain: I: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
71	c4onxB	Alignment	not modelled	24.1	15	PDB header: transferase Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: 2.8 angstrom crystal structure of sensor domain of histidine kinase2 from clostridium perfringens.
72	c1mp9B	Alignment	not modelled	23.2	33	PDB header: dna binding protein Chain: B: PDB Molecule: tata-binding protein; PDBTitle: tbp from a mesothermophilic archaeon, sulfolobus acidocaldarius
73	d1vb3a1	Alignment	not modelled	23.0	33	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
74	d1qnaa2	Alignment	not modelled	22.2	30	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
75	d1gnta	Alignment	not modelled	22.0	16	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Hybrid cluster protein (prismane protein)
76	d2i5ua1	Alignment	not modelled	20.5	22	Fold: DnaD domain-like Superfamily: DnaD domain-like Family: DnaD domain
77	c5aca1	Alignment	not modelled	20.5	33	PDB header: virus Chain: 1: PDB Molecule: vp1; PDBTitle: structure-based energetics of protein interfaces guide foot-and-mouth2 disease virus vaccine design
78	d1osya	Alignment	not modelled	20.3	60	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fungal immunomodulatory protein, FIP Family: Fungal immunomodulatory protein, FIP
79	c3f3hA	Alignment	not modelled	19.8	53	PDB header: antitumor protein Chain: A: PDB Molecule: immunomodulatory protein ling zhi-8; PDBTitle: crystal structure and anti-tumor activity of lz-8 from the fungus2 ganoderma lucidum
80	c5t58N	Alignment	not modelled	18.9	11	PDB header: cell cycle Chain: N: PDB Molecule: klla0c15939p; PDBTitle: structure of the mind complex shows a regulatory focus

						of yeast2 kinetochore assembly
81	c6pi9A_	Alignment	not modelled	18.8	20	PDB header: transferase Chain: A: PDB Molecule: 16s rrna (guanine(1405)-n(7))-methyltransferase; PDBTitle: crystal structure of 16s rrna methylase rmtf in complex with s-2 adenosyl-l-homocysteine
82	c3l4gC_	Alignment	not modelled	18.8	13	PDB header: ligase Chain: C: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
83	c5xyiB_	Alignment	not modelled	18.8	7	PDB header: ribosome Chain: B: PDB Molecule: ribosomal protein s3ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
84	c1b70A_	Alignment	not modelled	18.3	33	PDB header: ligase Chain: A: PDB Molecule: phenylalanyl-trna synthetase; PDBTitle: phenylalanyl trna synthetase complexed with phenylalanine
85	c3eikB_	Alignment	not modelled	18.2	33	PDB header: transcription Chain: B: PDB Molecule: tata-box-binding protein; PDBTitle: double stranded dna binding protein
86	c4guaB_	Alignment	not modelled	17.2	9	PDB header: hydrolase Chain: B: PDB Molecule: non-structural polyprotein; PDBTitle: alphavirus p23pro-zbd
87	d1yzha1	Alignment	not modelled	17.0	28	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TrmB-like
88	c2z8uQ_	Alignment	not modelled	16.4	33	PDB header: transcription Chain: Q: PDB Molecule: tata-box-binding protein; PDBTitle: methanococcus jannaschii tbp
89	d1r4qa_	Alignment	not modelled	15.8	21	Fold: Ribosome inactivating proteins (RIP) Superfamily: Ribosome inactivating proteins (RIP) Family: Shiga toxin, A-chain
90	d1s4ka_	Alignment	not modelled	15.7	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdiL-like
91	c2odrB_	Alignment	not modelled	15.4	13	PDB header: ligase Chain: B: PDB Molecule: phosphoseryl-trna synthetase; PDBTitle: methanococcus maripaludis phosphoseryl-trna synthetase
92	c5fg3A_	Alignment	not modelled	15.2	30	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor if-2; PDBTitle: crystal structure of gdp-bound aif5b from aeropyrum pernix
93	c2r9qD_	Alignment	not modelled	15.1	9	PDB header: hydrolase Chain: D: PDB Molecule: 2'-deoxycytidine 5'-triphosphate deaminase; PDBTitle: crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
94	c2mvaA_	Alignment	not modelled	15.1	43	PDB header: toxin Chain: A: PDB Molecule: rhtx toxin; PDBTitle: solution structure of the toxin, rhtx
95	c3q5xA_	Alignment	not modelled	15.0	29	PDB header: cell cycle Chain: A: PDB Molecule: protein cut8; PDBTitle: structure of proteasome tether
96	c1xc0A_	Alignment	not modelled	15.0	42	PDB header: signaling protein Chain: A: PDB Molecule: pardaxin p-4; PDBTitle: twenty lowest energy structures of pa4 by solution nmr
97	c4f9dA_	Alignment	not modelled	15.0	10	PDB header: hydrolase Chain: A: PDB Molecule: poly-beta-1,6-n-acetyl-d-glucosamine n-deacetylase; PDBTitle: structure of escherichia coli pgab 42-655 in complex with nickel
98	d1fmd1_	Alignment	not modelled	14.6	33	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
99	c2wd5B_	Alignment	not modelled	14.3	27	PDB header: cell cycle Chain: B: PDB Molecule: structural maintenance of chromosomes protein 3; PDBTitle: smc hinge heterodimer (mouse)