



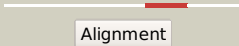



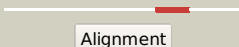



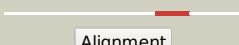

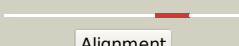

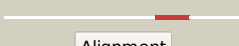

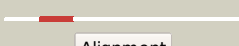




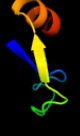
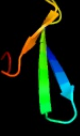

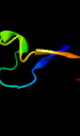
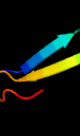





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0336 (-)_400192_401703
Date	Tue Jul 23 14:50:40 BST 2019
Unique Job ID	d34e8c0366203d13

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qgpA_</a>	 Alignment		99.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease; <b>PDBTitle:</b> x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium target3 gmr87.
2	<a href="#">c5mkwA_</a>	 Alignment		98.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna annealing helicase and endonuclease zranb3; <b>PDBTitle:</b> crystal structure of the human zranb3 hnh domain
3	<a href="#">c6ghcA_</a>	 Alignment		98.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methylcytosine-specific restriction enzyme a; <b>PDBTitle:</b> modification dependent eokmcra restriction endonuclease
4	<a href="#">c5x1hS_</a>	 Alignment		98.4	21	<b>PDB header:</b> protein transport <b>Chain:</b> S: <b>PDB Molecule:</b> icmj (dotn); <b>PDBTitle:</b> structure of legionella pneumophila dotn
5	<a href="#">c5h0mA_</a>	 Alignment		98.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease; <b>PDBTitle:</b> crystal structure of deep-sea thermophilic bacteriophage gve2 hnh2 endonuclease with zinc ion
6	<a href="#">c5vgbA_</a>	 Alignment		97.8	13	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9; <b>PDBTitle:</b> crystal structure of nmecas9 hnh domain bound to anti-crispr acric1
7	<a href="#">c5zmmD_</a>	 Alignment		97.5	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein mcra; <b>PDBTitle:</b> structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra
8	<a href="#">c4ogeA_</a>	 Alignment		96.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease domain protein; <b>PDBTitle:</b> crystal structure of the type ii-c cas9 enzyme from actinomyces2 naeslundii
9	<a href="#">c5axwA_</a>	 Alignment		96.2	19	<b>PDB header:</b> hydrolase/rna/dna <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9; <b>PDBTitle:</b> crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam)
10	<a href="#">d1vz0a1</a>	 Alignment		91.3	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
11	<a href="#">c6ghsA_</a>	 Alignment		90.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tagi restriction endonuclease; <b>PDBTitle:</b> modification dependent tagi restriction endonuclease

12	<a href="#">c4cmqB_</a>	Alignment		82.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> crispr-associated endonuclease cas9/csn1; <b>PDBTitle:</b> crystal structure of mn-bound s.pyogenes cas9
13	<a href="#">d2gykb1</a>	Alignment		80.6	21	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif
14	<a href="#">d2ho2a1</a>	Alignment		79.3	37	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
15	<a href="#">c3mkyP_</a>	Alignment		79.1	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> P: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-323)-18mer dna complex, i23 form
16	<a href="#">d2jb0b1</a>	Alignment		76.9	27	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif
17	<a href="#">d2ysca1</a>	Alignment		75.6	41	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
18	<a href="#">c3mkzU_</a>	Alignment		75.3	16	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> U: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-272)-18mer complex, p21 form
19	<a href="#">d1r71a_</a>	Alignment		67.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
20	<a href="#">c1r71B_</a>	Alignment		66.3	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor protein korb; <b>PDBTitle:</b> crystal structure of the dna binding domain of korb in complex with2 the operator dna
21	<a href="#">d2e45a1</a>	Alignment	not modelled	61.4	36	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
22	<a href="#">c4uhpA_</a>	Alignment	not modelled	52.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> large component of pyocin ap41; <b>PDBTitle:</b> crystal structure of the pyocin ap41 dnase-immunity complex
23	<a href="#">c4qkoH_</a>	Alignment	not modelled	51.7	26	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> H: <b>PDB Molecule:</b> pyocin-s2; <b>PDBTitle:</b> the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
24	<a href="#">c5ew5C_</a>	Alignment	not modelled	50.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin-e9; <b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9
25	<a href="#">c4bxB_</a>	Alignment	not modelled	49.0	19	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cpap; <b>PDBTitle:</b> structure of the wild-type tcp10 domain of danio rerio cpap in complex2 with a peptide of danio rerio stil
26	<a href="#">c7ceiB_</a>	Alignment	not modelled	48.3	26	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> protein (colicin e7 immunity protein); <b>PDBTitle:</b> the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
27	<a href="#">c4by2C_</a>	Alignment	not modelled	46.9	22	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> anastral spindle 2, sas 4; <b>PDBTitle:</b> sas-4 (dcpap) tcp domain in complex with a proline rich motif of ana22 (dstil) of drosophila melanogaster
28	<a href="#">d2dlka1</a>	Alignment	not modelled	42.7	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2 <b>PDB header:</b> structural protein, protein binding

29	<a href="#">c4ld3A_</a>	Alignment	not modelled	42.2	16	<b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structural analysis of the microcephaly protein cpap g-box domain2 suggests a role in centriole elongation.
30	<a href="#">c3plwA_</a>	Alignment	not modelled	39.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> recombination enhancement function protein; <b>PDBTitle:</b> ref protein from p1 bacteriophage
31	<a href="#">c3t0yA_</a>	Alignment	not modelled	35.8	25	<b>PDB header:</b> transcription regulator/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
32	<a href="#">c5g2xC_</a>	Alignment	not modelled	35.3	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> group ii intron-encoded protein ltra; <b>PDBTitle:</b> structure a of group ii intron complexed with its reverse2 transcriptase
33	<a href="#">c4go1A_</a>	Alignment	not modelled	33.6	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lsrr; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsrr from e.2 coli.
34	<a href="#">c1va1A_</a>	Alignment	not modelled	30.9	38	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor sp1; <b>PDBTitle:</b> solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
35	<a href="#">d1zfdA_</a>	Alignment	not modelled	29.4	63	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
36	<a href="#">d1a1a1</a>	Alignment	not modelled	29.4	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
37	<a href="#">c2w48D_</a>	Alignment	not modelled	29.4	26	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
38	<a href="#">c1nbwA_</a>	Alignment	not modelled	29.2	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydratase reactivase alpha subunit; <b>PDBTitle:</b> glycerol dehydratase reactivase
39	<a href="#">d2glia4</a>	Alignment	not modelled	29.1	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
40	<a href="#">d1ncsa_</a>	Alignment	not modelled	29.0	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
41	<a href="#">d1w6ga1</a>	Alignment	not modelled	27.6	31	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Amine oxidase catalytic domain <b>Family:</b> Amine oxidase catalytic domain
42	<a href="#">d1a1ga1</a>	Alignment	not modelled	26.5	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
43	<a href="#">c5jhfA_</a>	Alignment	not modelled	26.0	29	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> kth0d11660p; <b>PDBTitle:</b> crystal structure of atg13(17br)-atg13(17lr)-atg17-atg29-atg31 complex
44	<a href="#">d1ejga_</a>	Alignment	not modelled	25.5	45	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
45	<a href="#">d1bhia_</a>	Alignment	not modelled	25.1	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
46	<a href="#">d1u86a1</a>	Alignment	not modelled	23.9	63	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
47	<a href="#">d1a1ha1</a>	Alignment	not modelled	23.6	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
48	<a href="#">d1jmna_</a>	Alignment	not modelled	23.3	30	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
49	<a href="#">d1tf3a2</a>	Alignment	not modelled	22.3	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
50	<a href="#">c2b8tA_</a>	Alignment	not modelled	21.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
51	<a href="#">d1f2ig1</a>	Alignment	not modelled	21.5	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
52	<a href="#">d1ubdc3</a>	Alignment	not modelled	21.2	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
53	<a href="#">d1aaya1</a>	Alignment	not modelled	21.1	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
54	<a href="#">d2glia3</a>	Alignment	not modelled	20.7	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
55	<a href="#">d1pt4a_</a>	Alignment	not modelled	20.7	56	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Cyclotides <b>Family:</b> Kalata B1
						<b>PDB header:</b> plant protein

56	<a href="#">c4ttnA</a>	Alignment	not modelled	20.5	56	<b>Chain:</b> A; <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> quasi-racemic structure of [g6a]kalata b1
57	<a href="#">d1n1ua</a>	Alignment	not modelled	20.5	44	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Cyclotides <b>Family:</b> Kalata B1
58	<a href="#">c1n1ua</a>	Alignment	not modelled	20.5	44	<b>PDB header:</b> antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> kalata b1; <b>PDBTitle:</b> nmr structure of [ala1,15]kalata b1
59	<a href="#">c1pxeA</a>	Alignment	not modelled	20.4	55	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> neural zinc finger transcription factor 1; <b>PDBTitle:</b> solution structure of a cchhc domain of neural zinc finger2 factor-1
60	<a href="#">c2khaA</a>	Alignment	not modelled	20.4	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> solution structure of linear kalata b1 (loop 6)
61	<a href="#">c4ttoA</a>	Alignment	not modelled	20.3	56	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> quasi-racemic structure of [v25a] kalata b1
62	<a href="#">c2mn1A</a>	Alignment	not modelled	20.3	56	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> kalata b1[w23ww]; <b>PDBTitle:</b> solution structure of kalata b1[w23ww]
63	<a href="#">c2f2iA</a>	Alignment	not modelled	20.3	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> solution structure of [p20d,v21k]-kalata b1
64	<a href="#">c4ttmA</a>	Alignment	not modelled	20.3	56	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> racemic structure of kalata b1 (kb1)
65	<a href="#">c5xe7A</a>	Alignment	not modelled	20.0	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigj; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
66	<a href="#">c4umkA</a>	Alignment	not modelled	19.8	8	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A; <b>PDB Molecule:</b> probable chromosome-partitioning protein parb; <b>PDBTitle:</b> the complex of spo0j and pars dna in chromosomal partition system
67	<a href="#">d1sp2a</a>	Alignment	not modelled	19.3	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
68	<a href="#">d2dika2</a>	Alignment	not modelled	19.2	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
69	<a href="#">c1orxA</a>	Alignment	not modelled	19.1	40	<b>PDB header:</b> antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> kalata b1; <b>PDBTitle:</b> solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
70	<a href="#">d1w2za1</a>	Alignment	not modelled	19.0	28	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Amine oxidase catalytic domain <b>Family:</b> Amine oxidase catalytic domain
71	<a href="#">c2pncB</a>	Alignment	not modelled	19.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> copper amine oxidase, liver isozyme; <b>PDBTitle:</b> crystal structure of bovine plasma copper-containing amine oxidase in2 complex with clonidine
72	<a href="#">c5fgmA</a>	Alignment	not modelled	18.6	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigr; <b>PDBTitle:</b> streptomyces coelicolor sigr region 4
73	<a href="#">c6dhrA</a>	Alignment	not modelled	18.5	44	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> rivi3; <b>PDBTitle:</b> nmr solution structure of rivi3
74	<a href="#">c2lamA</a>	Alignment	not modelled	18.5	44	<b>PDB header:</b> antiviral protein <b>Chain:</b> A; <b>PDB Molecule:</b> cyclotide cter m; <b>PDBTitle:</b> three-dimensional structure of the cyclotide cter m
75	<a href="#">c1nb1A</a>	Alignment	not modelled	18.3	56	<b>PDB header:</b> antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> kalata b1; <b>PDBTitle:</b> high resolution solution structure of kalata b1
76	<a href="#">d1nb1a</a>	Alignment	not modelled	18.3	56	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Cyclotides <b>Family:</b> Kalata B1
77	<a href="#">d2glia5</a>	Alignment	not modelled	18.3	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
78	<a href="#">d1s7oa</a>	Alignment	not modelled	17.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
79	<a href="#">c6j0eB</a>	Alignment	not modelled	17.3	16	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> arsenic responsive repressor arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
80	<a href="#">c3e4hA</a>	Alignment	not modelled	17.1	44	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> varv peptide f; <b>PDBTitle:</b> crystal structure of the cyclotide varv f
81	<a href="#">d1ttya</a>	Alignment	not modelled	17.0	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
82	<a href="#">c3vepA</a>	Alignment	not modelled	16.8	26	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> A; <b>PDB Molecule:</b> probable rna polymerase sigma-d factor; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda

83	<a href="#">d1nbla_</a>	Alignment	not modelled	16.5	40	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
84	<a href="#">c1ui7A_</a>	Alignment	not modelled	16.4	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylethylamine oxidase; <b>PDBTitle:</b> site-directed mutagenesis of his433 involved in binding of2 copper ion in arthrobacter globiformis amine oxidase
85	<a href="#">c4v30A_</a>	Alignment	not modelled	16.2	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cereblon isoform 4; <b>PDBTitle:</b> cereblon isoform 4 from magnetospirillum gryphiswaldense in2 complex with lenalidomide
86	<a href="#">c2f2jA_</a>	Alignment	not modelled	16.0	40	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> solution structure of [w19k, p20n, v21k]-kalata b1
87	<a href="#">c3hslX_</a>	Alignment	not modelled	16.0	36	<b>PDB header:</b> replication <b>Chain:</b> X: <b>PDB Molecule:</b> orf59; <b>PDBTitle:</b> the crystal structure of pf-8, the dna polymerase accessory subunit2 from kaposi's sarcoma-associated herpesvirus
88	<a href="#">d1d6za1</a>	Alignment	not modelled	15.9	25	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Amine oxidase catalytic domain <b>Family:</b> Amine oxidase catalytic domain
89	<a href="#">c1kalA_</a>	Alignment	not modelled	15.9	56	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> kalata b1; <b>PDBTitle:</b> elucidation of the primary and three-dimensional structure2 of the uterotonic polypeptide kalata b1
90	<a href="#">d1okha_</a>	Alignment	not modelled	15.7	40	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
91	<a href="#">d2oqea1</a>	Alignment	not modelled	15.5	31	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Amine oxidase catalytic domain <b>Family:</b> Amine oxidase catalytic domain
92	<a href="#">c2lurA_</a>	Alignment	not modelled	15.4	56	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> kalata; <b>PDBTitle:</b> nmr solution structure of kb1[ghrw;23-28]
93	<a href="#">c2c10D_</a>	Alignment	not modelled	15.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> membrane copper amine oxidase; <b>PDBTitle:</b> the structure of a truncated, soluble version of semicarbazide-2 sensitive amine oxidase
94	<a href="#">c2z0IA_</a>	Alignment	not modelled	15.2	36	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> early antigen protein d; <b>PDBTitle:</b> crystal structure of ebv-dna polymerase accessory protein2 bmrfl
95	<a href="#">c2o8xA_</a>	Alignment	not modelled	15.1	35	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
96	<a href="#">c2k7gA_</a>	Alignment	not modelled	15.1	44	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> varv peptide f; <b>PDBTitle:</b> solution structure of varv f
97	<a href="#">c3sztB_</a>	Alignment	not modelled	14.8	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
98	<a href="#">d1orla_</a>	Alignment	not modelled	14.7	30	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
99	<a href="#">c2lfwA_</a>	Alignment	not modelled	14.7	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> phyr sigma-like domain; <b>PDBTitle:</b> nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1