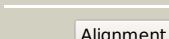
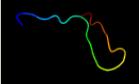
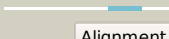

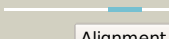
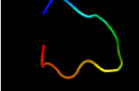
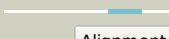

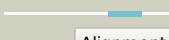













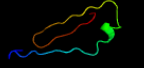


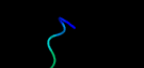
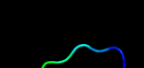


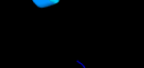



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2307B (-) _2579514_2579945
Date	Mon Aug 5 13:25:45 BST 2019
Unique Job ID	cb084d6e67c89c12

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xnwA_</a>	 Alignment		37.5	32	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate cyclase exoxy; <b>PDBTitle:</b> crystal structure of exoxy, a unique nucleotidyl cyclase toxin from2 pseudomonas aeruginosa
2	<a href="#">c3zoqA_</a>	 Alignment		35.1	57	<b>PDB header:</b> hydrolase/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> structure of bsudg-p56 complex
3	<a href="#">c5x3hA_</a>	 Alignment		34.7	64	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> the y81g mutant of the ung crystal structure from nitratifactor2 salsuginis
4	<a href="#">d1laue_</a>	 Alignment		32.9	57	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
5	<a href="#">c3tr7A_</a>	 Alignment		31.3	64	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> structure of a uracil-dna glycosylase (ung) from coxiella burnetii
6	<a href="#">d2hxma1</a>	 Alignment		30.7	71	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
7	<a href="#">c2zhxG_</a>	 Alignment		29.9	50	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> G: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> crystal structure of uracil-dna glycosylase from mycobacterium2 tuberculosis in complex with a proteinaceous inhibitor
8	<a href="#">d3euga_</a>	 Alignment		29.7	57	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
9	<a href="#">d1okba_</a>	 Alignment		29.2	71	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
10	<a href="#">c3cxmA_</a>	 Alignment		29.0	57	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil
11	<a href="#">c2booA_</a>	 Alignment		28.8	64	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> the crystal structure of uracil-dna n-glycosylase (ung) from2 deinococcus radiodurans.

12	<a href="#">c2uurA_</a>	Alignment		26.1	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(ix) chain; <b>PDBTitle:</b> n-terminal nc4 domain of collagen ix
13	<a href="#">d1hn0a1</a>	Alignment		24.2	50	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Chondroitin AC/alginate lyase <b>Family:</b> Hyaluronate lyase-like catalytic, N-terminal domain
14	<a href="#">c5uj6A_</a>	Alignment		24.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolases family 2, sugar binding domain protein; <b>PDBTitle:</b> crystal structure of bacteroides uniformis beta-glucuronidase
15	<a href="#">c1u5mA_</a>	Alignment		20.7	43	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha 1 type ii collagen isoform 1; <b>PDBTitle:</b> structure of a chordin-like cysteine-rich repeat (vwc2 module) from collagen iia
16	<a href="#">d1u5ma_</a>	Alignment		20.7	43	<b>Fold:</b> Fnl-like domain <b>Superfamily:</b> Fnl-like domain <b>Family:</b> VWC domain
17	<a href="#">c2ahmG_</a>	Alignment		19.2	14	<b>PDB header:</b> viral protein, replication <b>Chain:</b> G: <b>PDB Molecule:</b> replicase polyprotein 1ab, heavy chain; <b>PDBTitle:</b> crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
18	<a href="#">d2ahme1</a>	Alignment		18.9	14	<b>Fold:</b> Coronavirus NSP8-like <b>Superfamily:</b> Coronavirus NSP8-like <b>Family:</b> Coronavirus NSP8-like
19	<a href="#">c3g7dA_</a>	Alignment		18.4	50	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> phpd; <b>PDBTitle:</b> native phpd with cadmium atoms
20	<a href="#">d2fc6a1</a>	Alignment		18.4	60	<b>Fold:</b> CCCH zinc finger <b>Superfamily:</b> CCCH zinc finger <b>Family:</b> CCCH zinc finger
21	<a href="#">c4v19S_</a>	Alignment	not modelled	18.3	24	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> mitoribosomal protein ul18m, mrpl18; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
22	<a href="#">c3ub0D_</a>	Alignment	not modelled	18.2	21	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> non-structural protein 6, nsp6,; <b>PDBTitle:</b> crystal structure of the nonstructural protein 7 and 8 complex of2 feline coronavirus
23	<a href="#">d2j8xa1</a>	Alignment	not modelled	16.4	54	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
24	<a href="#">d1fjra_</a>	Alignment	not modelled	16.2	27	<b>Fold:</b> Methuselah ectodomain <b>Superfamily:</b> Methuselah ectodomain <b>Family:</b> Methuselah ectodomain
25	<a href="#">d1uzdc1</a>	Alignment	not modelled	16.0	56	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
26	<a href="#">c1hn0A_</a>	Alignment	not modelled	16.0	50	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> chondroitin abc lyase i; <b>PDBTitle:</b> crystal structure of chondroitin abc lyase i from proteus vulgaris at2 1.9 angstroms resolution
27	<a href="#">d1cwva5</a>	Alignment	not modelled	15.8	55	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> Invasin/intimin cell-adhesion fragment, C-terminal domain
28	<a href="#">c5nn7A_</a>	Alignment	not modelled	15.6	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> kshv uracil-dna glycosylase, apo form
						<b>Fold:</b> Knottins (small inhibitors, toxins, lectins)

29	<a href="#">d1ehda2</a>	Alignment	not modelled	15.4	50	<b>Superfamily:</b> Plant lectins/antimicrobial peptides <b>Family:</b> Hevein-like agglutinin (lectin) domain
30	<a href="#">c2fc6A</a>	Alignment	not modelled	15.1	60	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> target of egr1, member 1; <b>PDBTitle:</b> solution structure of the zf-ccch domain of target of egr1,2 member 1 (nuclear)
31	<a href="#">c2owrD</a>	Alignment	not modelled	14.8	38	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> crystal structure of vaccinia virus uracil-dna glycosylase
32	<a href="#">d8rucj</a>	Alignment	not modelled	14.1	56	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
33	<a href="#">d2erfa1</a>	Alignment	not modelled	13.5	16	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
34	<a href="#">c2q1fA</a>	Alignment	not modelled	13.4	38	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> chondroitinase; <b>PDBTitle:</b> crystal structure of chondroitin sulfate lyase abc from bacteroides2 thetaiotaomicron wal2926
35	<a href="#">d1ej7s</a>	Alignment	not modelled	12.4	56	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
36	<a href="#">c2mfsA</a>	Alignment	not modelled	11.8	40	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> ep-amp1; <b>PDBTitle:</b> solution nmr structure of the cactus-derived antimicrobial peptide ep-2 amp1
37	<a href="#">d1en2a2</a>	Alignment	not modelled	11.4	56	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant lectins/antimicrobial peptides <b>Family:</b> Hevein-like agglutinin (lectin) domain
38	<a href="#">c3asiA</a>	Alignment	not modelled	11.4	33	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> neurexin-1-alpha; <b>PDBTitle:</b> alpha-neurexin-1 ectodomain fragment; Ins5-egf3-Ins6
39	<a href="#">c2qieA</a>	Alignment	not modelled	11.3	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2; <b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex with precursor2 z
40	<a href="#">d1t1ra3</a>	Alignment	not modelled	11.2	70	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	<a href="#">d1vcaa1</a>	Alignment	not modelled	11.0	30	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
42	<a href="#">d1pgsa2</a>	Alignment	not modelled	10.8	16	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> PHM/PNGase F <b>Family:</b> Glycosyl-asparaginase
43	<a href="#">d1vfsa1</a>	Alignment	not modelled	10.6	23	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Alanine racemase
44	<a href="#">d1a0ia1</a>	Alignment	not modelled	10.3	50	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
45	<a href="#">c6hq8B</a>	Alignment	not modelled	9.8	67	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-1,3-oligosaccharide phosphorylase; <b>PDBTitle:</b> bacterial beta-1,3-oligosaccharide phosphorylase from gh149 with2 laminarihexaose bound at a surface site
46	<a href="#">c5x55A</a>	Alignment	not modelled	9.2	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable uracil-dna glycosylase; <b>PDBTitle:</b> crystal structure of mimivirus uracil-dna glycosylase
47	<a href="#">d1ddza2</a>	Alignment	not modelled	8.7	25	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
48	<a href="#">d1x4ka2</a>	Alignment	not modelled	8.7	44	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
49	<a href="#">d1f60b</a>	Alignment	not modelled	8.1	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eEF-1beta-like <b>Family:</b> eEF-1beta-like
50	<a href="#">c1cb8A</a>	Alignment	not modelled	7.8	38	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (chondroitinase ac); <b>PDBTitle:</b> chondroitinase ac lyase from flavobacterium heparinum
51	<a href="#">d1fm0e</a>	Alignment	not modelled	7.7	33	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Molybdopterin synthase subunit MoaE <b>Family:</b> Molybdopterin synthase subunit MoaE
52	<a href="#">d1j83a</a>	Alignment	not modelled	7.6	29	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 17 carbohydrate binding module, CBM17
53	<a href="#">c1oigA</a>	Alignment	not modelled	7.5	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> dumpy, isoform y; <b>PDBTitle:</b> the solution structure of the dpy module from the dumpy protein
54	<a href="#">d1ir1s</a>	Alignment	not modelled	7.5	56	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
55	<a href="#">c4e4fD</a>	Alignment	not modelled	7.4	50	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> mannonate dehydratase; <b>PDBTitle:</b> crystal structure of enolase pc1_0802 (target efi-502240) from2 pectobacterium carotovorum subsp. carotovorum pc1
56	<a href="#">d1rcqa1</a>	Alignment	not modelled	7.3	30	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like

						<b>Family:</b> Alanine racemase
57	<a href="#">d1q3ja_</a>	Alignment	not modelled	7.3	43	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Gurmarin-like <b>Family:</b> Antifungal peptide
58	<a href="#">c1q3jA_</a>	Alignment	not modelled	7.3	43	<b>PDB header:</b> antifungal protein <b>Chain:</b> A: <b>PDB Molecule:</b> alo3; <b>PDBTitle:</b> solution structure of alo3: a new knottin-type antifungal peptide from2 the insect acrocinus longimanus
59	<a href="#">d1ddza1</a>	Alignment	not modelled	7.1	25	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
60	<a href="#">c5wb5B_</a>	Alignment	not modelled	7.0	27	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> leishmania if4e-1 bound to leishmania 4e-ip1
61	<a href="#">d1gh8a_</a>	Alignment	not modelled	6.9	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eEF-1beta-like <b>Family:</b> eEF-1beta-like
62	<a href="#">c3kw3B_</a>	Alignment	not modelled	6.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
63	<a href="#">c3v3wA_</a>	Alignment	not modelled	6.7	56	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> starvation sensing protein rspa; <b>PDBTitle:</b> crystal structure of an enolase from the soil bacterium cellvibrio2 japonicus (target efi-502161) with bound mg and glycerol
64	<a href="#">d1prtb1</a>	Alignment	not modelled	6.5	63	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
65	<a href="#">c3imkA_</a>	Alignment	not modelled	6.4	38	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative molybdenum carrier protein; <b>PDBTitle:</b> crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
66	<a href="#">d2cupa3</a>	Alignment	not modelled	6.4	29	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
67	<a href="#">c6rdu9_</a>	Alignment	not modelled	6.3	33	<b>PDB header:</b> proton transport <b>Chain:</b> 9: <b>PDB Molecule:</b> asa-9: polytomella f-atp synthase associated subunit 9; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
68	<a href="#">c3tenD_</a>	Alignment	not modelled	6.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cs2 hydrolase; <b>PDBTitle:</b> holo form of carbon disulfide hydrolase
69	<a href="#">c3aaiB_</a>	Alignment	not modelled	6.1	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> copper homeostasis operon regulatory protein; <b>PDBTitle:</b> x-ray crystal structure of csor from thermus thermophilus hb8
70	<a href="#">c1iq5B_</a>	Alignment	not modelled	6.0	67	<b>PDB header:</b> metal binding protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ca2+/calmodulin dependent kinase kinase; <b>PDBTitle:</b> calmodulin/nematode ca2+/calmodulin dependent kinase kinase2 fragment
71	<a href="#">c5g23A_</a>	Alignment	not modelled	6.0	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> type-iv like pilin ttha1219; <b>PDBTitle:</b> type iv-like pilin ttha1219 from thermus thermophilus
72	<a href="#">c1zuvA_</a>	Alignment	not modelled	5.9	53	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> amaranthus caudatus antimicrobial peptide 2; <b>PDBTitle:</b> 24 nmr structures of acamp2-like peptide with phenylalanine2 18 mutated to tryptophan
73	<a href="#">c6jbcC_</a>	Alignment	not modelled	5.9	33	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> molybdenum cofactor biosynthesis protein e; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
74	<a href="#">c2mijA_</a>	Alignment	not modelled	5.8	83	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> spbc2 prophage-derived bacteriocin sublancin-168; <b>PDBTitle:</b> nmr structure of the s-linked glycopeptide sublancin 168
75	<a href="#">d1v58a2</a>	Alignment	not modelled	5.7	35	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> DsbC/DsbG N-terminal domain-like <b>Family:</b> DsbC/DsbG N-terminal domain-like
76	<a href="#">c2mniA_</a>	Alignment	not modelled	5.6	35	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hp_q4d059; <b>PDBTitle:</b> chemical shift assignments and structure of q4d059, a hypothetical2 protein from trypanosoma cruzi
77	<a href="#">c2c5dA_</a>	Alignment	not modelled	5.6	29	<b>PDB header:</b> signaling protein/receptor <b>Chain:</b> A: <b>PDB Molecule:</b> growth-arrest-specific protein 6 precursor; <b>PDBTitle:</b> structure of a minimal gas6-axl complex
78	<a href="#">d2cupa1</a>	Alignment	not modelled	5.4	30	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
79	<a href="#">c2wjsA_</a>	Alignment	not modelled	5.4	40	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> laminin subunit alpha-2; <b>PDBTitle:</b> crystal structure of the lg1-3 region of the laminin alpha22 chain
80	<a href="#">d2fiya1</a>	Alignment	not modelled	5.4	19	<b>Fold:</b> FdhE-like <b>Superfamily:</b> FdhE-like <b>Family:</b> FdhE-like
81	<a href="#">d2ixoa1</a>	Alignment	not modelled	5.3	27	<b>Fold:</b> PTPA-like <b>Superfamily:</b> PTPA-like <b>Family:</b> PTPA-like
						<b>PDB header:</b> protein binding

82	<a href="#">c3oiqB_</a>	Alignment	not modelled	5.3	34	<b>Chain:</b> B; <b>PDB Molecule:</b> dna polymerase alpha catalytic subunit a; <b>PDBTitle:</b> crystal structure of yeast telomere protein cdc13 ob1 and the2 catalytic subunit of dna polymerase alpha pol1
83	<a href="#">c4o1kA_</a>	Alignment	not modelled	5.2	28	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
84	<a href="#">d1ic1a1</a>	Alignment	not modelled	5.2	43	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
85	<a href="#">c5efvC_</a>	Alignment	not modelled	5.1	27	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> phi eta orf 56-like protein; <b>PDBTitle:</b> the host-recognition device of staphylococcus aureus phage phi11
86	<a href="#">c3pmmA_</a>	Alignment	not modelled	5.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578