
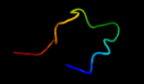




















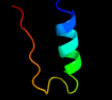
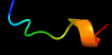
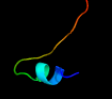
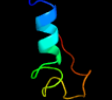




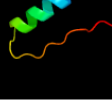


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3412_(- )_3831906_3832316
Date	Fri Aug 9 18:20:08 BST 2019
Unique Job ID	236a239471122f2d

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2jmsA_</a>	 Alignment		39.5	45	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> pheromone en-6; <b>PDBTitle:</b> nmr structure of en-6 pheromone from the antarctic ciliate2 euplotes nobilii
2	<a href="#">c6hzkB_</a>	 Alignment		26.4	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoribulokinase; <b>PDBTitle:</b> crystal structure of redox-inhibited phosphoribulokinase from2 synechococcus sp. (strain pcc 6301)
3	<a href="#">d2idob1</a>	 Alignment		24.6	27	<b>Fold:</b> DNA polymerase III theta subunit-like <b>Superfamily:</b> DNA polymerase III theta subunit-like <b>Family:</b> DNA polymerase III theta subunit-like
4	<a href="#">d1a7ja_</a>	 Alignment		21.8	9	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
5	<a href="#">c2kk1A_</a>	 Alignment		19.5	55	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrosine-protein kinase abl2; <b>PDBTitle:</b> solution structure of c-terminal domain of tyrosine-protein2 kinase abl2 from homo sapiens, northeast structural3 genomics consortium (nesg) target hr5537a
6	<a href="#">c2jp3A_</a>	 Alignment		18.3	27	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
7	<a href="#">c1zzpA_</a>	 Alignment		17.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase abl1; <b>PDBTitle:</b> solution structure of the f-actin binding domain of bcr-2 abl/c-abl
8	<a href="#">c2k5ca_</a>	 Alignment		17.0	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein pf0385; <b>PDBTitle:</b> nmr structure for pf0385
9	<a href="#">c5wc3S_</a>	 Alignment		16.3	29	<b>PDB header:</b> protein transport <b>Chain:</b> S; <b>PDB Molecule:</b> spoiiaag, stage iii sporulation engulfment assemblyprotein; <b>PDBTitle:</b> spoiiaag
10	<a href="#">d1y4oa1</a>	 Alignment		15.8	28	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
11	<a href="#">d1v7ba2</a>	 Alignment		15.6	21	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain

12	<a href="#">c3tqcB_</a>	Alignment		14.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> structure of the pantothenate kinase (coaa) from coxiella burnetii
13	<a href="#">c5ohdB_</a>	Alignment		14.7	33	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> growth hormone receptor; <b>PDBTitle:</b> putative inactive (dormant) dimeric state of ghr transmembrane domain
14	<a href="#">d2hz5a1</a>	Alignment		13.6	29	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
15	<a href="#">c3mb2_</a>	Alignment		13.4	21	<b>PDB header:</b> isomerase <b>Chain:</b> J: <b>PDB Molecule:</b> 4-oxalocrotonate tautomerase family enzyme - beta subunit; <b>PDBTitle:</b> kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the 4 tautomerase superfamily
16	<a href="#">c3n23E_</a>	Alignment		13.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the high affinity complex between ouabain and the 2 e2p form of the sodium-potassium pump
17	<a href="#">c5f34A_</a>	Alignment		12.8	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannoside acyltransferase; <b>PDBTitle:</b> crystal structure of membrane associated pata from mycobacterium 2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
18	<a href="#">c2ktIA_</a>	Alignment		12.1	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> structure of c-terminal domain from mttyrrs of a. nidulans
19	<a href="#">c4bwcA_</a>	Alignment		11.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase b-like 1; <b>PDBTitle:</b> x-ray structure of a phospholipase b like protein 1 from 2 bovine kidneys
20	<a href="#">d1sq5a_</a>	Alignment		11.7	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
21	<a href="#">d2o34a1</a>	Alignment	not modelled	11.6	33	<b>Fold:</b> T-fold <b>Superfamily:</b> ApbE-like <b>Family:</b> DVU1097-like
22	<a href="#">c6bxtB_</a>	Alignment	not modelled	11.6	55	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> mitochondrial association factor 1; <b>PDBTitle:</b> crystal structure of toxoplasma gondii mitochondrial association 2 factor 1 a (maf1a) in complex with adpribose
23	<a href="#">c3qfeB_</a>	Alignment	not modelled	11.4	29	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dihydrodipicolinate synthase family protein; <b>PDBTitle:</b> crystal structures of a putative dihydrodipicolinate synthase family 2 protein from coccidioides immitis
24	<a href="#">c2hmcA_</a>	Alignment	not modelled	11.1	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase dapa from 2 agrobacterium tumefaciens
25	<a href="#">d1cvua1</a>	Alignment	not modelled	11.1	14	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Myeloperoxidase-like
26	<a href="#">c4uzmA_</a>	Alignment	not modelled	10.9	33	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein igaa homolog; <b>PDBTitle:</b> shotgun proteolysis: a practical application
27	<a href="#">c3fgrA_</a>	Alignment	not modelled	10.8	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phospholipase b-like 2 28 kda form; <b>PDBTitle:</b> two chain form of the 66.3 kda protein at 1.8 angstrom
28	<a href="#">c5fwuA_</a>	Alignment	not modelled	10.6	50	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> kremen protein 1; <b>PDBTitle:</b> wnt modulator kremen crystal form ii at 2.8a

29	<a href="#">d1wjva1</a>	Alignment	not modelled	10.4	20	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> C2HC finger
30	<a href="#">c4dppB</a>	Alignment	not modelled	10.4	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase 2, chloroplastic; <b>PDBTitle:</b> the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana
31	<a href="#">c4cs6A</a>	Alignment	not modelled	10.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside adenylyltransferase; <b>PDBTitle:</b> crystal structure of aada - an aminoglycoside adenylyltransferase
32	<a href="#">c2rpsA</a>	Alignment	not modelled	10.0	33	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> chemokine; <b>PDBTitle:</b> solution structure of a novel insect chemokine isolated from2 integument
33	<a href="#">c2zxeG</a>	Alignment	not modelled	9.9	20	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
34	<a href="#">c3dgpB</a>	Alignment	not modelled	9.8	36	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase ii transcription factor b subunit 5; <b>PDBTitle:</b> crystal structure of the complex between tfb5 and the c-terminal2 domain of tfb2
35	<a href="#">d2gdza1</a>	Alignment	not modelled	9.8	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
36	<a href="#">c3vdoB</a>	Alignment	not modelled	9.8	38	<b>PDB header:</b> dna binding protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anti-sigma-k factor rskA; <b>PDBTitle:</b> structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
37	<a href="#">d1w6ga3</a>	Alignment	not modelled	9.8	26	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
38	<a href="#">c6ckgA</a>	Alignment	not modelled	9.5	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-glycerate 3-kinase; <b>PDBTitle:</b> d-glycerate 3-kinase from cryptococcus neoformans var. grubii serotype2 a (h99 / atcc 208821 / cbs 10515 / fgsc 9487)
39	<a href="#">d1sqwa2</a>	Alignment	not modelled	9.4	24	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Pre-PUA domain <b>Family:</b> Nip7p homolog, N-terminal domain
40	<a href="#">c3b4uB</a>	Alignment	not modelled	9.3	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
41	<a href="#">c6bxwA</a>	Alignment	not modelled	9.2	58	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial association factor 1; <b>PDBTitle:</b> crystal structure of toxoplasma gondii mitochondrial association2 factor 1 b (maf1b) in complex with adprribose
42	<a href="#">d1h9aa2</a>	Alignment	not modelled	8.7	23	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Glucose 6-phosphate dehydrogenase-like
43	<a href="#">d2gvia2</a>	Alignment	not modelled	8.6	43	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> FwdE C-terminal domain-like
44	<a href="#">d1wifa1</a>	Alignment	not modelled	8.5	38	<b>Fold:</b> Cdc48 domain 2-like <b>Superfamily:</b> Cdc48 domain 2-like <b>Family:</b> Cdc48 domain 2-like
45	<a href="#">c1wjvA</a>	Alignment	not modelled	8.2	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell growth regulating nucleolar protein lyar; <b>PDBTitle:</b> solution structure of the n-terminal zinc finger domain of2 mouse cell growth regulating nucleolar protein lyar
46	<a href="#">d1z9ha1</a>	Alignment	not modelled	8.2	50	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
47	<a href="#">c5ui3C</a>	Alignment	not modelled	8.1	18	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dhdpS from chlamydomonas reinhardtii
48	<a href="#">d1w2za2</a>	Alignment	not modelled	8.1	40	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
49	<a href="#">c6et8B</a>	Alignment	not modelled	7.9	15	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> albicidin resistance protein; <b>PDBTitle:</b> crystal structure of alba in complex with albicidin
50	<a href="#">c2gesA</a>	Alignment	not modelled	7.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
51	<a href="#">c2e2zA</a>	Alignment	not modelled	7.9	25	<b>PDB header:</b> protein transport, chaperone regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tim15; <b>PDBTitle:</b> solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70
52	<a href="#">c4lqvA</a>	Alignment	not modelled	7.8	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> x-ray crystal structure of glucose-6-phosphate 1-dehydrogenase from2 mycobacterium avium
53	<a href="#">d1qkia2</a>	Alignment	not modelled	7.8	42	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Glucose 6-phosphate dehydrogenase-like
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase;

54	<a href="#">c2bhbB</a>	Alignment	not modelled	7.7	42	<b>PDBTitle:</b> x-ray structure of human glucose-6-phosphate dehydrogenase (deletion2 variant) complexed with glucose-6-phosphate
55	<a href="#">c4ijjA</a>	Alignment	not modelled	7.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative c4-type zinc finger protein, dksa/trar family; <b>PDBTitle:</b> structure of transcription factor dksa2 from pseudomonas aeruginosa
56	<a href="#">d1ji7a</a>	Alignment	not modelled	7.6	40	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Pointed domain
57	<a href="#">c5afdA</a>	Alignment	not modelled	7.1	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminatase lyase; <b>PDBTitle:</b> native structure of n-acetylneuraminatase lyase (sialic acid aldolase)2 from allivibrio salmonicida
58	<a href="#">d1odfa</a>	Alignment	not modelled	7.1	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
59	<a href="#">c5oeoC</a>	Alignment	not modelled	7.1	44	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v <b>PDBTitle:</b> solution structure of the complex of trpv5(655-725) with a calmodulin2 e32q/e68q double mutant
60	<a href="#">c3vpbF</a>	Alignment	not modelled	6.9	33	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> alpha-aminoadipate carrier protein lysw; <b>PDBTitle:</b> argx from sulfobolus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
61	<a href="#">c3m8eA</a>	Alignment	not modelled	6.9	71	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> protein structure of type iii plasmid segregation tubr
62	<a href="#">c3w1sC</a>	Alignment	not modelled	6.8	20	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> ubiquitin-like protein atg12; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae atg12-atg5 conjugate2 bound to the n-terminal domain of atg16
63	<a href="#">c3iwcD</a>	Alignment	not modelled	6.8	31	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylmethionine decarboxylase; <b>PDBTitle:</b> t. maritima adometdc complex with s-adenosylmethionine methyl ester
64	<a href="#">c1h9aA</a>	Alignment	not modelled	6.7	25	<b>PDB header:</b> oxidoreductase (choh(d) - nad(p)) <b>Chain:</b> A: <b>PDB Molecule:</b> glucose 6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from I. mesenteroides with coenzyme nadp
65	<a href="#">d1d6za2</a>	Alignment	not modelled	6.6	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
66	<a href="#">c3eb2A</a>	Alignment	not modelled	6.6	45	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
67	<a href="#">d1xfia</a>	Alignment	not modelled	6.5	21	<b>Fold:</b> AF1104-like <b>Superfamily:</b> AF1104-like <b>Family:</b> AF1104-like
68	<a href="#">d1xkya1</a>	Alignment	not modelled	6.5	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
69	<a href="#">c5fr7B</a>	Alignment	not modelled	6.4	36	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> amyrr; <b>PDBTitle:</b> erwinia amylovora amyrr amyovorran repressor, a member of the ybjn2 protein family
70	<a href="#">c1qkiE</a>	Alignment	not modelled	6.3	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> x-ray structure of human glucose 6-phosphate dehydrogenase (variant2 canton r459l) complexed with structural nadp+
71	<a href="#">c5hy4D</a>	Alignment	not modelled	6.3	50	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> ring-opening amidohydrolase; <b>PDBTitle:</b> structure-function analysis of functionally diverse members of the2 cyclic amide hydrolase family of toberlone fold enzymes
72	<a href="#">c4e9iB</a>	Alignment	not modelled	6.2	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi
73	<a href="#">c6o58C</a>	Alignment	not modelled	6.2	29	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> calcium uniporter protein, mitochondrial; <b>PDBTitle:</b> human mcu-emre complex, dimer of channel
74	<a href="#">c2eg5C</a>	Alignment	not modelled	6.2	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> xanthosine methyltransferase; <b>PDBTitle:</b> the structure of xanthosine methyltransferase
75	<a href="#">c2k2dA</a>	Alignment	not modelled	6.2	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ring finger and chy zinc finger domain- <b>PDBTitle:</b> solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c
76	<a href="#">c2vt8B</a>	Alignment	not modelled	6.1	25	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> proteasome inhibitor pi31 subunit; <b>PDBTitle:</b> structure of a conserved dimerisation domain within fbox7 and pi31
77	<a href="#">d1uw4a</a>	Alignment	not modelled	6.1	36	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Smg-4/UPF3
78	<a href="#">c1tjID</a>	Alignment	not modelled	6.1	29	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> dnak suppressor protein; <b>PDBTitle:</b> crystal structure of transcription factor dksa from e. coli
79	<a href="#">d1za0a1</a>	Alignment	not modelled	6.1	33	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like

						<b>Family:</b> Ribonucleotide reductase-like
80	<a href="#">c2jo1A_</a>	Alignment	not modelled	6.0	18	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
81	<a href="#">c4uuzC_</a>	Alignment	not modelled	6.0	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna replication licensing factor mcm2; <b>PDBTitle:</b> mcm2-histone complex
82	<a href="#">c2kq9A_</a>	Alignment	not modelled	6.0	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dnak suppressor protein; <b>PDBTitle:</b> solution structure of dnak suppressor protein from agrobacterium2 tumefaciens c58. northeast structural genomics consortium target3 att12/ontario center for structural proteomics target atc0888
83	<a href="#">c2ox1A_</a>	Alignment	not modelled	6.0	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ymgb; <b>PDBTitle:</b> structure and function of the e. coli protein ymgb: a protein critical2 for biofilm formation and acid resistance
84	<a href="#">c1w1fA_</a>	Alignment	not modelled	5.9	38	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisome biogenesis factor 1; <b>PDBTitle:</b> structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
85	<a href="#">c2zkrf_</a>	Alignment	not modelled	5.9	14	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> rna expansion segment es7 part iii; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
86	<a href="#">c3na2C_</a>	Alignment	not modelled	5.8	47	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein of unknown function from mine drainage2 metagenome leptospirillum rubarum
87	<a href="#">d1se7a_</a>	Alignment	not modelled	5.8	38	<b>Fold:</b> DNA polymerase III theta subunit-like <b>Superfamily:</b> DNA polymerase III theta subunit-like <b>Family:</b> DNA polymerase III theta subunit-like
88	<a href="#">c2hw2A_</a>	Alignment	not modelled	5.8	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rifampin adp-ribosyl transferase; <b>PDBTitle:</b> crystal structure of rifampin adp-ribosyl transferase in complex with2 rifampin
89	<a href="#">c5ihfA_</a>	Alignment	not modelled	5.8	40	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> virg-like protein; <b>PDBTitle:</b> salmonella typhimurium virg-like (stv) protein
90	<a href="#">c2r94B_</a>	Alignment	not modelled	5.8	33	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; <b>PDBTitle:</b> crystal structure of kd(p)ga from t.tenax
91	<a href="#">d1w6ga2</a>	Alignment	not modelled	5.7	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
92	<a href="#">c6grvA_</a>	Alignment	not modelled	5.6	31	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> metallothionein; <b>PDBTitle:</b> cadmium(ii) form of full-length metallothionein from pseudomonas2 fluorescens q2-87 (pflq2 mt)
93	<a href="#">c5hy0D_</a>	Alignment	not modelled	5.6	50	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> ring-opening amidohydrolase; <b>PDBTitle:</b> orotic acid hydrolase
94	<a href="#">c5ms1A_</a>	Alignment	not modelled	5.6	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> anti-sigma-f factor fin; <b>PDBTitle:</b> solution structure of the b. subtilis anti-sigma-f factor, fin
95	<a href="#">c2elvA_</a>	Alignment	not modelled	5.6	38	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406; <b>PDBTitle:</b> solution structure of the 6th c2h2 zinc finger of human2 zinc finger protein 406
96	<a href="#">c5uujA_</a>	Alignment	not modelled	5.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkz; <b>PDBTitle:</b> streptomyces sahachiroi dna glycosylase alkz
97	<a href="#">d2ae9a1</a>	Alignment	not modelled	5.5	43	<b>Fold:</b> DNA polymerase III theta subunit-like <b>Superfamily:</b> DNA polymerase III theta subunit-like <b>Family:</b> DNA polymerase III theta subunit-like
98	<a href="#">c2ma5A_</a>	Alignment	not modelled	5.5	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific demethylase 5b; <b>PDBTitle:</b> solution nmr structure of phd type zinc finger domain of lysine-2 specific demethylase 5b (plu-1/jarid1b) from homo sapiens, northeast3 structural genomics consortium (nesg) target hr7375c
99	<a href="#">c6arhA_</a>	Alignment	not modelled	5.5	30	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuramate lyase; <b>PDBTitle:</b> crystal structure of human nal at a resolution of 1.6 angstrom