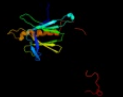
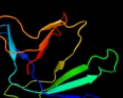
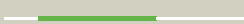
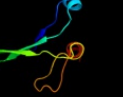
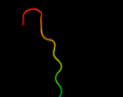
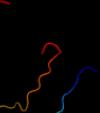


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kr0A_	 Alignment		100.0	24	PDB header: protein binding Chain: A: PDB Molecule: proteasomal ubiquitin receptor adrm1; PDBTitle: a proteasome protein
2	c2z59A_	 Alignment		100.0	29	PDB header: protein transport Chain: A: PDB Molecule: protein adrm1; PDBTitle: complex structures of mouse rpn13 (22-130aa) and ubiquitin
3	c2r2yA_	 Alignment		100.0	29	PDB header: protein binding Chain: A: PDB Molecule: protein adrm1; PDBTitle: crystal structure of the proteasomal rpn13 pru-domain
4	c2z4dA_	 Alignment		100.0	100	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn13; PDBTitle: nmr structures of yeast proteasome component rpn13
5	d2aj7a1	 Alignment		81.0	18	Fold: BH3618-like Superfamily: BH3618-like Family: BH3618-like
6	d1ddwa_	 Alignment		51.3	15	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
7	d1evha_	 Alignment		50.3	13	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
8	c2l23A_	 Alignment		35.3	20	PDB header: transcription Chain: A: PDB Molecule: mediator of rna polymerase ii transcription subunit 25; PDBTitle: nmr structure of the acid (activator interacting domain) of the human2 mediator med25 protein
9	c2kc8B_	 Alignment		29.4	32	PDB header: toxin/toxin repressor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: structure of e. coli toxin rele (r81a/r83a) mutant in2 complex with antitoxin relbc (k47-l79) peptide
10	d2hx0a1	 Alignment		22.0	19	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: AF0104-like
11	c3fkeB_	 Alignment		19.7	16	PDB header: rna binding protein Chain: B: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of the ebola vp35 interferon inhibitory domain

12	d2h6la1	Alignment		19.1	16	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: AF0104-like
13	d2ns0a1	Alignment		18.8	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
14	d1qqga2	Alignment		18.0	33	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)
15	d1egxa_	Alignment		17.3	19	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
16	c1bcra_	Alignment		14.9	31	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine carboxypeptidase ii; PDBTitle: complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature
17	c2dt4A_	Alignment		14.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph0802; PDBTitle: crystal structure of pyrococcus horikoshii a plant- and prokaryote-2 conserved (ppc) protein at 1.60 resolution
18	c3isyA_	Alignment		13.5	14	PDB header: protein binding Chain: A: PDB Molecule: intracellular proteinase inhibitor; PDBTitle: crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
19	c3apaA_	Alignment		13.5	18	PDB header: sugar binding protein Chain: A: PDB Molecule: zymogen granule membrane protein 16; PDBTitle: crystal structure of human pancreatic secretory protein zg16p
20	d1olma2	Alignment		12.3	23	Fold: Supernatant protein factor (SPF), C-terminal domain Superfamily: Supernatant protein factor (SPF), C-terminal domain Family: Supernatant protein factor (SPF), C-terminal domain
21	c3egbA_	Alignment	not modelled	12.1	18	PDB header: protein binding Chain: A: PDB Molecule: protein pellino homolog 2; PDBTitle: structure of pellino2 fha domain at 3.3 angstroms resolution.
22	c1z8rA_	Alignment	not modelled	11.9	16	PDB header: hydrolase Chain: A: PDB Molecule: coxsackievirus b4 polyprotein; PDBTitle: 2a cysteine proteinase from human coxsackievirus b4 (strain2 jvb / benschoten / new york / 51)
23	c3hwuA_	Alignment	not modelled	11.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of putative dna-binding protein (yp_299413.1) from2 ralstonia eutropha jmp134 at 1.30 a resolution
24	d2hrva_	Alignment	not modelled	10.8	8	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
25	c1qqgA_	Alignment	not modelled	9.3	33	PDB header: signal transduction Chain: A: PDB Molecule: insulin receptor substrate 1; PDBTitle: crystal structure of the ph-ptb targeting region of irs-1
26	c1gxsc_	Alignment	not modelled	9.0	20	PDB header: lyase Chain: C: PDB Molecule: p-(s)-hydroxymandelonitrile lyase chain a; PDBTitle: crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme
27	d1xoub_	Alignment	not modelled	8.6	35	Fold: EspA/CesA-like Superfamily: EspA/CesA-like Family: EspA chaperone CesA
						Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc

28	d1zaka2	Alignment	not modelled	8.6	40	finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
29	d1i2ha	Alignment	not modelled	8.5	11	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
30	d2a6sa1	Alignment	not modelled	7.7	19	Fold: RelE-like Superfamily: RelE-like Family: YoeB/Txe-like
31	d1xr0b	Alignment	not modelled	7.2	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)
32	d2gdtal	Alignment	not modelled	7.2	24	Fold: SARS Nsp1-like Superfamily: SARS Nsp1-like Family: SARS Nsp1-like
33	d1usma	Alignment	not modelled	7.1	24	Fold: DcoH-like Superfamily: PCD-like Family: PCD-like
34	c1jmuD	Alignment	not modelled	7.0	19	PDB header: viral protein Chain: D: PDB Molecule: protein mu-1; PDBTitle: crystal structure of the reovirus mu1/sigma3 complex
35	c3htnA	Alignment	not modelled	6.9	14	PDB header: metal binding protein Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: crystal structure of a putative dna binding protein (bt_1116) from2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution
36	d1r9wa	Alignment	not modelled	6.7	11	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Replication initiation protein E1
37	d1oqka	Alignment	not modelled	6.6	13	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: RNase P subunit p29-like
38	d1gpca	Alignment	not modelled	6.5	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Phage ssDNA-binding proteins
39	d1bqua2	Alignment	not modelled	6.4	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
40	c3oeiH	Alignment	not modelled	6.4	10	PDB header: toxin, protein binding Chain: H: PDB Molecule: relk (toxin rv3358); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
41	c2odxA	Alignment	not modelled	6.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c oxidase polypeptide iv; PDBTitle: solution structure of zn(ii)cox4
42	d3bwuc1	Alignment	not modelled	6.2	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
43	c3ewgA	Alignment	not modelled	6.1	8	PDB header: transcription Chain: A: PDB Molecule: putative transcription antitermination protein nusg; PDBTitle: crystal structure of the n-terminal domain of nusg (ngn) from2 methanocaldococcus jannaschii
44	c2zkro	Alignment	not modelled	6.0	15	PDB header: ribosomal protein/rna Chain: O: PDB Molecule: rna expansion segment es30; PDBTitle: 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
45	d2hg6a1	Alignment	not modelled	6.0	33	Fold: PA1123-like Superfamily: PA1123-like Family: PA1123-like
46	d1jl1a	Alignment	not modelled	5.9	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
47	c3pjyB	Alignment	not modelled	5.9	8	PDB header: transcription regulator Chain: B: PDB Molecule: hypothetical signal peptide protein; PDBTitle: crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
48	c2ktrA	Alignment	not modelled	5.7	18	PDB header: signaling protein, transport protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: nmr structure of p62 pb1 dimer determined based on pcs
49	c2cseB	Alignment	not modelled	5.4	19	PDB header: virus Chain: B: PDB Molecule: major outer-capsid protein mu1; PDBTitle: features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
50	d1eeta1	Alignment	not modelled	5.4	24	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
51	c2lhkB	Alignment	not modelled	5.3	30	PDB header: chaperone Chain: B: PDB Molecule: I0052; PDBTitle: structural analysis of a chaperone in type iii secretion system
52	d1mu2a1	Alignment	not modelled	5.3	24	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
53	c3ddcB	Alignment	not modelled	5.2	18	PDB header: hydrolase/apoptosis Chain: B: PDB Molecule: ras association domain-containing family protein 5; PDBTitle: crystal structure of nore1a in complex with ras PDB header: heme binding protein

54	c3u22B_	Alignment	not modelled	5.2	6	Chain: B: PDB Molecule: putative hmuy_like heme binding protein; PDBTitle: crystal structure of a putative hmuy_like heme binding protein2 (bvu_2192) from bacteroides vulgatus atcc 8482 at 2.12 a resolution
55	d1qc6a_	Alignment	not modelled	5.2	18	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
56	d1f08a_	Alignment	not modelled	5.2	22	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Replication initiation protein E1
57	c3ks8D_	Alignment	not modelled	5.2	12	PDB header: viral protein/rna Chain: D: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of reston ebolavirus vp35 rna binding2 domain in complex with 18bp dsrna
58	c3iz5D_	Alignment	not modelled	5.1	15	PDB header: ribosome Chain: D: PDB Molecule: 60s ribosomal protein l4 (l4p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
59	c3dwvB_	Alignment	not modelled	5.1	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione peroxidase-like protein; PDBTitle: glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
60	d1fltx_	Alignment	not modelled	5.1	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: l set domains
61	d2r4qa1	Alignment	not modelled	5.1	13	Fold: Phosphotyrosine protein phosphatases l-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
62	c3q6kA_	Alignment	not modelled	5.0	12	PDB header: protein binding Chain: A: PDB Molecule: 43.2 kda salivary protein; PDBTitle: salivary protein from lutzomyia longipalpis