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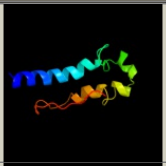
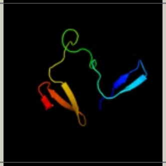
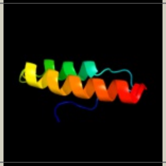
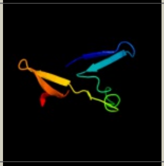
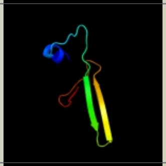
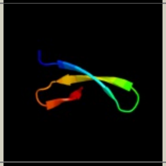
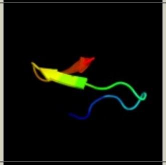
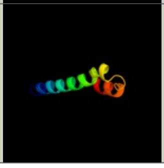
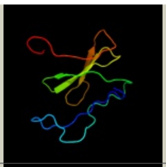
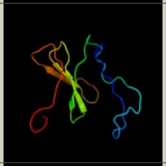
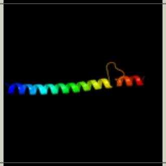
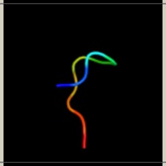
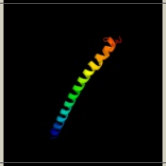
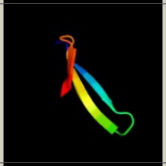
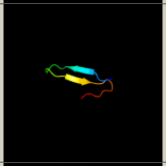
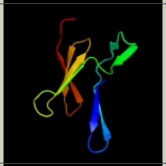
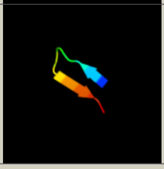
Description	P09153
Date	Thu Jan 5 11:02:01 GMT 2012
Unique Job ID	30ff869a82790588

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kz6A_	Alignment		97.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2
2	c2jxwA_	Alignment		69.3	34	**PDB header:**formin binding protein **Chain:** A: **PDB Molecule:**ww domain-binding protein 4; **PDBTitle:** solution structure of the tandem ww domains of fbp21
3	c2kt9A_	Alignment		61.6	28	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**probable 30s ribosomal protein psrp-3; **PDBTitle:** solution nmr structure of probable 30s ribosomal protein2 psrp-3 (ycf65-like protein) from synechocystis sp. (strain3 pcc 6803), northeast structural genomics consortium target4 target sgr46
4	c1tk7A_	Alignment		27.5	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cg4244-pb; **PDBTitle:** nmr structure of ww domains (ww3-4) from suppressor of2 deltex
5	c2c7hA_	Alignment		26.2	24	**PDB header:**ubiquitin-like protein **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 6, isoform 3; **PDBTitle:** solution nmr structure of the dwnn domain from human rbbp6
6	c1w18A_	Alignment		23.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**levansucrase; **PDBTitle:** crystal structure of levansucrase from gluconacetobacter2 diazotrophicus
7	d1o6wa1	Alignment		23.1	35	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
8	c2ov2O_	Alignment		22.6	10	**PDB header:**protein binding/transferase **Chain:** O: **PDB Molecule:**serine/threonine-protein kinase pak 4; **PDBTitle:** the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
9	c1rfoC_	Alignment		20.9	25	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**whisker antigen control protein; **PDBTitle:** trimeric foldon of the t4 phagehead fibritin
10	c2odbB_	Alignment		20.5	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 6; **PDBTitle:** the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
11	d1x4ta1	Alignment		19.3	27	**Fold:**Long alpha-hairpin **Superfamily:**ISY1 domain-like **Family:**ISY1 N-terminal domain-like

12	d2ghsa1	Alignment		17.2	16	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
13	c2ghsA_	Alignment		17.2	16	**PDB header:**calcium-binding protein **Chain:** A: **PDB Molecule:**agr_c_1268p; **PDBTitle:** crystal structure of a calcium-binding protein, regucalcin2 (agr_c_1268) from agrobacterium tumefaciens str. c58 at 1.55 a3 resolution
14	c2xv5A_	Alignment		16.1	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-a/c; **PDBTitle:** human lamin a coil 2b fragment
15	c1e0aB_	Alignment		14.7	30	**PDB header:**signalling protein **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** cdc42 complexed with the gtpase binding domain of p212 activated kinase
16	c1gk6B_	Alignment		14.4	14	**PDB header:**vimentin **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
17	c1zr7A_	Alignment		14.2	39	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**huntingtin-interacting protein hypa/fbp11; **PDBTitle:** solution structure of the first ww domain of fbp11
18	c2dk7A_	Alignment		14.1	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation regulator 1; **PDBTitle:** solution structure of ww domain in transcription elongation2 regulator 1
19	c2h47F_	Alignment		13.6	19	**PDB header:**oxidoreductase/electron transport **Chain:** F: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of an electron transfer complex between2 aromatic amine dephydrogenase and azurin from alcaligenes3 faecalis (form 1)
20	d1ll7a2	Alignment		13.4	50	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
21	c1gq1B_	Alignment	not modelled	13.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
22	d1ln1a_	Alignment	not modelled	12.3	19	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**STAR domain
23	d2rm0w1	Alignment	not modelled	12.3	33	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
24	c1f3mB_	Alignment	not modelled	11.5	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** crystal structure of human serine/threonine kinase pak1
25	d1w9pa2	Alignment	not modelled	11.4	42	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
26	c2diiA_	Alignment	not modelled	11.0	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
27	c1v1hB_	Alignment	not modelled	10.6	25	**PDB header:**adenovirus **Chain:** B: **PDB Molecule:**fibritin, fiber protein; **PDBTitle:** adenovirus fibre shaft sequence n-terminally fused to the2 bacteriophage t4 fibritin foldon trimerisation motif with3 a short linker
28	d2diia1	Alignment	not modelled	10.6	7	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain

29	c3o0rC_	Alignment	not modelled	10.5	16	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
30	d1jofa_	Alignment	not modelled	10.3	16	**Fold:**7-bladed beta-propeller **Superfamily:**3-carboxy-cis,cis-mucoante lactonizing enzyme **Family:**3-carboxy-cis,cis-mucoante lactonizing enzyme
31	d2dk1a1	Alignment	not modelled	9.9	26	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
32	c1ox3A_	Alignment	not modelled	9.9	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** crystal structure of mini-fibritin
33	d1q67a_	Alignment	not modelled	9.6	12	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Dcp1
34	c1x8yA_	Alignment	not modelled	9.2	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
35	d1pcna1	Alignment	not modelled	9.0	47	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Colipase-like **Family:**Colipase-like
36	d2e45a1	Alignment	not modelled	8.7	27	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
37	c1avyA_	Alignment	not modelled	8.7	25	**PDB header:**coiled coil **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** fibritin deletion mutant m (bacteriophage t4)
38	d2paja1	Alignment	not modelled	8.7	12	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
39	c2qkmG_	Alignment	not modelled	8.6	35	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**spbc3b9.21 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
40	c2dk1A_	Alignment	not modelled	8.1	26	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**ww domain-binding protein 4; **PDBTitle:** solution structure of ww domain in ww domain binding2 protein 4 (wbp-4)
41	c1gk4A_	Alignment	not modelled	8.1	10	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
42	c1ymzA_	Alignment	not modelled	7.8	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
43	c2jz8A_	Alignment	not modelled	7.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bh09830; **PDBTitle:** solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
44	d2hqxa1	Alignment	not modelled	7.7	20	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
45	c2hqxB_	Alignment	not modelled	7.7	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**p100 co-activator tudor domain; **PDBTitle:** crystal structure of human p100 tudor domain conserved2 region
46	d1pina1	Alignment	not modelled	7.6	27	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
47	c2b9nZ_	Alignment	not modelled	7.2	17	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein ctc; **PDBTitle:** 50s ribosomal subunit from a crystal structure of release factor rf2,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400.
48	c1nwdC_	Alignment	not modelled	7.0	7	**PDB header:**binding protein/hydrolase **Chain:** C: **PDB Molecule:**glutamate decarboxylase; **PDBTitle:** solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
49	c1nwdB_	Alignment	not modelled	7.0	7	**PDB header:**binding protein/hydrolase **Chain:** B: **PDB Molecule:**glutamate decarboxylase; **PDBTitle:** solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
50	c1q67B_	Alignment	not modelled	6.8	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**decapping protein involved in mrna degradation- **PDBTitle:** crystal structure of dcp1p
51	c3movB_	Alignment	not modelled	6.7	13	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
52	c2v43A_	Alignment	not modelled	6.4	24	**PDB header:**regulator **Chain:** A: **PDB Molecule:**sigma-e factor regulatory protein rseb; **PDBTitle:** crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
53	c2lawA_	Alignment	not modelled	6.4	27	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**yorkie homolog; **PDBTitle:** structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
54	d1f8ab1	Alignment	not modelled	6.4	27	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain

55	d1o6wa2	Alignment	not modelled	6.4	27	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
56	c1o6wA_	Alignment	not modelled	6.3	35	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**pre-mrna processing protein prp40; **PDBTitle:** solution structure of the prp40 ww domain pair of the yeast2 splicing factor prp40
57	c2ysiA_	Alignment	not modelled	6.3	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**transcription elongation regulator 1; **PDBTitle:** solution structure of the first ww domain from the mouse2 transcription elongation regulator 1, transcription factor3 ca150
58	c3gf8A_	Alignment	not modelled	6.2	19	**PDB header:**carbohydrate binding protein **Chain:** A: **PDB Molecule:**putative polysaccharide binding proteins (duf1812); **PDBTitle:** crystal structure of putative polysaccharide binding proteins2 (duf1812) (np_809975.1) from bacteroides thetaiotaomicron vpi-5482 at3 2.20 a resolution
59	c1yiuA_	Alignment	not modelled	6.2	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy e3 ubiquitin protein ligase; **PDBTitle:** itch e3 ubiquitin ligase ww3 domain
60	d2madh_	Alignment	not modelled	5.8	10	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
61	d1eysh1	Alignment	not modelled	5.7	27	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**Photosynthetic reaction centre, H-chain, cytoplasmic domain
62	c2i5nH_	Alignment	not modelled	5.5	23	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**reaction center protein h chain; **PDBTitle:** 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
63	c2kykA_	Alignment	not modelled	5.4	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** the sandwich region between two lmp2a py motif regulates the2 interaction between aip4ww2domain and py motif
64	c1eysH_	Alignment	not modelled	5.4	27	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
65	c2djyA_	Alignment	not modelled	5.4	14	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**smad ubiquitination regulatory factor 2; **PDBTitle:** solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
66	c2l5fA_	Alignment	not modelled	5.2	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pre-mrna-processing factor 40 homolog a; **PDBTitle:** solution structure of the tandem ww domains from hypa/fbp11
67	d1d7qa_	Alignment	not modelled	5.1	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
68	d2oa5a1	Alignment	not modelled	5.0	21	**Fold:**BLRF2-like **Superfamily:**BLRF2-like **Family:**BLRF2-like
69	d1zr7a1	Alignment	not modelled	5.0	38	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
70	c3ok8A_	Alignment	not modelled	5.0	0	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**brain-specific angiogenesis inhibitor 1-associated protein **PDBTitle:** i-bar of pinkbar
71	d1ywia1	Alignment	not modelled	5.0	35	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain