Phyre^2

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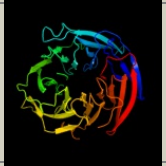
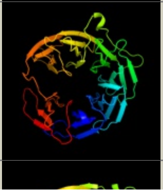
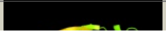
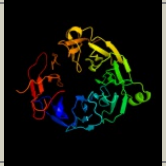
Description	P52697
Date	Thu Jan 5 12:06:01 GMT 2012
Unique Job ID	995d0d5d59bb31ed

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ri6a_	Alignment		100.0	99	**Fold:**7-bladed beta-propeller **Superfamily:**Putative isomerase YbhE **Family:**Putative isomerase YbhE
2	c3hfqB_	Alignment		100.0	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein lp_2219; **PDBTitle:** crystal structure of the lp_2219 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr118.
3	d1jofa_	Alignment		100.0	13	**Fold:**7-bladed beta-propeller **Superfamily:**3-carboxy-cis,cis-mucoante lactonizing enzyme **Family:**3-carboxy-cis,cis-mucoante lactonizing enzyme
4	c3fgbB_	Alignment		100.0	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein q89zh8_bactn; **PDBTitle:** crystal structure of the q89zh8_bactn protein from2 bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr289b.
5	d1l0qa2	Alignment		100.0	19	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**YVTN repeat
6	c3u4yA_	Alignment		99.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein (dtox_1751)2 from desulfotomaculum acetoxidans dsm 771.
7	c3bwsA_	Alignment		99.9	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein lp49; **PDBTitle:** crystal structure of the leptospiral antigen lp49
8	c3dm0A_	Alignment		99.9	12	**PDB header:**sugar binding protein,signaling protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein fused with **PDBTitle:** maltose binding protein fusion with rack1 from a. thaliana
9	c1nnoA_	Alignment		99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrite reductase; **PDBTitle:** conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
10	d2madh_	Alignment		99.9	11	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
11	c1gq1B_	Alignment		99.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
						

12	d1nira2	Alignment		99.9	13	**Fold:**8-bladed beta-propeller **Superfamily:**C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase **Family:**C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase
13	d1qksa2	Alignment		99.9	12	**Fold:**8-bladed beta-propeller **Superfamily:**C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase **Family:**C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase
14	c2i0tB_	Alignment		99.9	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
15	d1pbyb_	Alignment		99.9	11	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
16	c1l0qC_	Alignment		99.9	19	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**surface layer protein; **PDBTitle:** tandem yvtn beta-propeller and pkd domains from an archaeal surface2 layer protein
17	c2h47F_	Alignment		99.9	12	**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)
18	d1jmxb_	Alignment		99.9	11	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
19	c2j57J_	Alignment		99.9	14	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** x-ray reduced paraccocus denitrificans methylamine2 dehydrogenase n-quinol in complex with amicyanin.
20	c3c75J_	Alignment		99.9	14	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
21	c3sbrF_	Alignment	not modelled	99.9	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
22	d1qnia2	Alignment	not modelled	99.9	14	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
23	d1fwxa2	Alignment	not modelled	99.9	12	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
24	c3jroA_	Alignment	not modelled	99.9	11	**PDB header:**transport protein, structural protein **Chain:** A: **PDB Molecule:**fusion protein of protein transport protein sec13 **PDBTitle:** nup84-nup145c-sec13 edge element of the npc lattice
25	c1qniE_	Alignment	not modelled	99.9	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from2 pseudomonas nautica, at 2.4a resolution
26	c2pm9A_	Alignment	not modelled	99.9	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec31; **PDBTitle:** crystal structure of yeast sec13/31 vertex element of the2 copii vesicular coat
27	d2bbkh_	Alignment	not modelled	99.8	13	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
28	c3dsmA_	Alignment	not modelled	99.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bacuni_02894; **PDBTitle:** crystal structure of the surface layer protein bacuni_02894 from2 bacteroides uniformis, northeast structural genomics consortium3 target btr193d.
						PDB header:oxidoreductase

29	c1fwxB_	Alignment	not modelled	99.8	12	**Chain:** B: **PDB Molecule:**nitrous oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from p. denitrificans
30	c2w18A_	Alignment	not modelled	99.8	10	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**partner and localizer of brca2; **PDBTitle:** crystal structure of the c-terminal wd40 domain of human2 palb2
31	c1nr0A_	Alignment	not modelled	99.8	8	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** two seven-bladed beta-propeller domains revealed by the2 structure of a c. elegans homologue of yeast actin3 interacting protein 1 (aip1).
32	c3vh0C_	Alignment	not modelled	99.8	11	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce; **PDBTitle:** crystal structure of e. coli ynce complexed with dna
33	d1gxra_	Alignment	not modelled	99.8	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
34	c3mmyE_	Alignment	not modelled	99.8	12	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**mrna export factor; **PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
35	c2aq5A_	Alignment	not modelled	99.8	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of murine coronin-1
36	d1yfqa_	Alignment	not modelled	99.8	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**Cell cycle arrest protein BUB3
37	d1k8kc_	Alignment	not modelled	99.8	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
38	c3mkqA_	Alignment	not modelled	99.8	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**coatomer beta'-subunit; **PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
39	c3jzhA_	Alignment	not modelled	99.8	7	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb protein eed; **PDBTitle:** eed-h3k79me3
40	c3i2nA_	Alignment	not modelled	99.8	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd repeat-containing protein 92; **PDBTitle:** crystal structure of wd40 repeats protein wdr92
41	c3iytG_	Alignment	not modelled	99.8	15	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** structure of an apoptosome-procaspase-9 card complex
42	c2j04B_	Alignment	not modelled	99.8	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ydr362cp; **PDBTitle:** the tau60-tau91 subcomplex of yeast transcription factor2 iiic
43	c3ei3B_	Alignment	not modelled	99.8	8	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-drddb2 complex
44	c3frxB_	Alignment	not modelled	99.8	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein subunit beta- **PDBTitle:** crystal structure of the yeast orthologue of rack1, asc1.
45	c3cfvA_	Alignment	not modelled	99.8	10	**PDB header:**histone/chaperone **Chain:** A: **PDB Molecule:**histone-binding protein rbbp7; **PDBTitle:** structural basis of the interaction of rbap46/rbap48 with2 histone h4
46	d1nr0a1	Alignment	not modelled	99.8	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
47	c4a11B_	Alignment	not modelled	99.8	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna excision repair protein ercc-8; **PDBTitle:** structure of the hsddb1-hscsa complex
48	c1r5mA_	Alignment	not modelled	99.8	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sir4-interacting protein sif2; **PDBTitle:** crystal structure of the c-terminal wd40 domain of sif2
49	c1pi6A_	Alignment	not modelled	99.8	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** yeast actin interacting protein 1 (aip1), orthorhombic crystal form
50	c3ei4D_	Alignment	not modelled	99.7	12	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-hsddb2 complex
51	c2xznR_	Alignment	not modelled	99.7	10	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**rack1; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
52	c2pm7B_	Alignment	not modelled	99.7	9	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec13; **PDBTitle:** crystal structure of yeast sec13/31 edge element of the2 copii vesicular coat, selenomethionine version
53	c3jrpA_	Alignment	not modelled	99.7	8	**PDB header:**transport protein, structural protein **Chain:** A: **PDB Molecule:**fusion protein of protein transport protein sec13 **PDBTitle:** sec13 with nup145c (aa109-179) insertion blade
54	c2oajA_	Alignment	not modelled	99.7	10	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
55	c2qxvA_	Alignment	not modelled	99.7	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**embryonic ectoderm development;

						PDBTitle: structural basis of ezh2 recognition by eed
56	c3ow8A_	Alignment	not modelled	99.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd repeat-containing protein 61; **PDBTitle:** crystal structure of the wd repeat-containing protein 61
57	d1nexb2	Alignment	not modelled	99.7	13	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
58	d1erja_	Alignment	not modelled	99.7	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
59	d1tbga_	Alignment	not modelled	99.7	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
60	c2ojhA_	Alignment	not modelled	99.7	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1656/agr_c_3050; **PDBTitle:** the structure of putative tolb from agrobacterium tumefaciens
61	c2ovqB_	Alignment	not modelled	99.7	9	**PDB header:**transcription/cell cycle **Chain:** B: **PDB Molecule:**f-box/wd repeat protein 7; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
62	d1sq9a_	Alignment	not modelled	99.7	11	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
63	d2ovrb2	Alignment	not modelled	99.7	6	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
64	c3dw8B_	Alignment	not modelled	99.7	7	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase 2a 55 kda regulatory **PDBTitle:** structure of a protein phosphatase 2a holoenzyme with b55 subunit
65	c3acpA_	Alignment	not modelled	99.7	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**wd repeat-containing protein ygl004c; **PDBTitle:** crystal structure of yeast rpn14, a chaperone of the 19s regulatory2 particle of the proteasome
66	c3fm0A_	Alignment	not modelled	99.7	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**protein ciao1; **PDBTitle:** crystal structure of wd40 protein ciao1
67	c2vduB_	Alignment	not modelled	99.7	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase- **PDBTitle:** structure of trm8-trm82, the yeast trna m7g methylation2 complex
68	c3greA_	Alignment	not modelled	99.7	11	**PDB header:**signaling protein,protein binding **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase vps15; **PDBTitle:** crystal structure of saccharomyces cerevisiae vps15 wd2 repeat domain
69	c3eg6A_	Alignment	not modelled	99.7	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**wd repeat-containing protein 5; **PDBTitle:** structure of wdr5 bound to mll1 peptide
70	c2gnqA_	Alignment	not modelled	99.7	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd-repeat protein 5; **PDBTitle:** structure of wdr5
71	d1k32a3	Alignment	not modelled	99.7	7	**Fold:**7-bladed beta-propeller **Superfamily:**Tricorn protease domain 2 **Family:**Tricorn protease domain 2
72	c3iz6a_	Alignment	not modelled	99.7	14	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
73	c2iwaA_	Alignment	not modelled	99.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** unbound glutaminyl cyclotransferase from carica papaya.
74	c2pbiB_	Alignment	not modelled	99.6	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein subunit beta 5; **PDBTitle:** the multifunctional nature of gbeta5/rgs9 revealed from its crystal2 structure
75	d1vyhc1	Alignment	not modelled	99.6	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
76	d2p4oa1	Alignment	not modelled	99.6	11	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**All0351-like
77	c1nexD_	Alignment	not modelled	99.6	10	**PDB header:**ligase, cell cycle **Chain:** D: **PDB Molecule:**cdc4 protein; **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
78	c3bg1E_	Alignment	not modelled	99.6	8	**PDB header:**protein transport, hydrolase **Chain:** E: **PDB Molecule:**protein sec13 homolog; **PDBTitle:** architecture of a coat for the nuclear pore membrane
79	c1vyhT_	Alignment	not modelled	99.6	9	**PDB header:**hydrolase **Chain:** T: **PDB Molecule:**platelet-activating factor acetylhydrolase ib **PDBTitle:** paf-ah holoenzyme: lis1/alfa2
80	c3lrvA_	Alignment	not modelled	99.6	14	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor 19; **PDBTitle:** the prp19 wd40 domain contains a conserved protein interaction region2 essential for its function.
81	d1xfda1	Alignment	not modelled	99.6	7	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like

82	d2dg1a1	Alignment	not modelled	99.6	9	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
83	d1pgua1	Alignment	not modelled	99.6	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
84	c2w8bB_	Alignment	not modelled	99.6	12	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal
85	c3g4hB_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**regucalcin; **PDBTitle:** crystal structure of human senescence marker protein-30 (zinc bound)
86	c3dr2A_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exported gluconolactonase; **PDBTitle:** structural and functional analyses of xc5397 from2 xanthomonas campestris: a gluconolactonase important in3 glucose secondary metabolic pathways
87	c3dwlH_	Alignment	not modelled	99.6	8	**PDB header:**structural protein **Chain:** H: **PDB Molecule:**actin-related protein 2/3 complex subunit 1; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
88	d2bgra1	Alignment	not modelled	99.6	11	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
89	c2ivzD_	Alignment	not modelled	99.6	11	**PDB header:**protein transport/hydrolase **Chain:** D: **PDB Molecule:**protein tolb; **PDBTitle:** structure of tolb in complex with a peptide of the colicin2 e9 t-domain
90	c3odtB_	Alignment	not modelled	99.6	9	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of wd40 beta propeller domain of doa1
91	d1nr0a2	Alignment	not modelled	99.5	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
92	d1pjxa_	Alignment	not modelled	99.5	10	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
93	c2hesX_	Alignment	not modelled	99.5	9	**PDB header:**biosynthetic protein **Chain:** X: **PDB Molecule:**ydr267cp; **PDBTitle:** cytosolic iron-sulphur assembly protein- 1
94	c2zkqa_	Alignment	not modelled	99.5	11	**PDB header:**ribosomal protein/rna **Chain:** A: **PDB Molecule:**18s ribosomal rna; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
95	d1v04a_	Alignment	not modelled	99.5	19	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**Serum paraoxonase/arylesterase 1, PON1
96	d2hqsa1	Alignment	not modelled	99.5	12	**Fold:**6-bladed beta-propeller **Superfamily:**TolB, C-terminal domain **Family:**TolB, C-terminal domain
97	c3eweC_	Alignment	not modelled	99.5	10	**PDB header:**protein transport,structural protein **Chain:** C: **PDB Molecule:**nucleoporin seh1; **PDBTitle:** crystal structure of the nup85/seh1 complex
98	c3qqzA_	Alignment	not modelled	99.5	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein yjik; **PDBTitle:** crystal structure of the c-terminal domain of the yjik protein from2 escherichia coli cft073
99	c1p22A_	Alignment	not modelled	99.5	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**f-box/wd-repeat protein 1a; **PDBTitle:** structure of a beta-trcp1-skp1-beta-catenin complex:2 destruction motif binding and lysine specificity on the3 scfbeta-trcp1 ubiquitin ligase
100	d1q7fa_	Alignment	not modelled	99.5	10	**Fold:**6-bladed beta-propeller **Superfamily:**NHL repeat **Family:**NHL repeat
101	c3fhcA_	Alignment	not modelled	99.5	8	**PDB header:**transport protein/hydrolase **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup214; **PDBTitle:** crystal structure of human dbp5 in complex with nup214
102	c3nolA_	Alignment	not modelled	99.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
103	c3hrpA_	Alignment	not modelled	99.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of structural genomics protein of unknown function2 (np_812590.1) from bacteroides thetaiotaomicron vpi-5482 at 1.70 a3 resolution
104	c3fw0A_	Alignment	not modelled	99.4	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**peptidyl-glycine alpha-amidating monooxygenase; **PDBTitle:** structure of peptidyl-alpha-hydroxyglycine alpha-amidating2 lyase (pal) bound to alpha-hydroxyhippuric acid (non-3 peptidic substrate)
105	c1k32E_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** crystal structure of the tricorn protease
106	c1n6dE_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative

107	c2oitA_	Alignment	not modelled	99.4	10	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**nucleoporin 214kda; **PDBTitle:** crystal structure of the n-terminal domain of the human2 proto-oncogene nup214/can
108	c3nokB_	Alignment	not modelled	99.4	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutaminyl cyclase; **PDBTitle:** crystal structure of myxococcus xanthus glutaminyl cyclase
109	c2g8sB_	Alignment	not modelled	99.4	11	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**glucose/sorbosone dehydrogenases; **PDBTitle:** crystal structure of the soluble aldose sugar dehydrogenase2 (asd) from escherichia coli in the apo-form
110	d1orva1	Alignment	not modelled	99.4	12	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
111	c3mbrX_	Alignment	not modelled	99.3	13	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** crystal structure of the glutaminyl cyclase from xanthomonas2 campestris
112	c2z2pA_	Alignment	not modelled	99.3	8	**PDB header:**lyase/antibiotic **Chain:** A: **PDB Molecule:**virginiamycin b lyase; **PDBTitle:** crystal structure of catalytically inactive h270a virginiamycin b2 lyase from staphylococcus aureus with quinupristin
113	c3pe7A_	Alignment	not modelled	99.3	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**oligogalacturonate lyase; **PDBTitle:** oligogalacturonate lyase in complex with manganese
114	c3e5zA_	Alignment	not modelled	99.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative gluconolactonase; **PDBTitle:** x-ray structure of the putative gluconolactonase in protein family2 pf08450. northeast structural genomics consortium target drr130.
115	d1ospo_	Alignment	not modelled	99.3	11	**Fold:**open-sided beta-meander **Superfamily:**Outer surface protein **Family:**Outer surface protein
116	c2iwkB_	Alignment	not modelled	99.3	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrous oxide reductase; **PDBTitle:** inhibitor-bound form of nitrous oxide reductase from2 achromobacter cycloclastes at 1.7 angstrom resolution
117	d1k32a2	Alignment	not modelled	99.3	11	**Fold:**6-bladed beta-propeller **Superfamily:**Tricorn protease N-terminal domain **Family:**Tricorn protease N-terminal domain
118	c3tc9B_	Alignment	not modelled	99.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical hydrolase; **PDBTitle:** crystal structure of a hypothetical hydrolase (bt_3476) from2 bacteroides thetaiotaomicron vpi-5482 at 2.23 a resolution
119	c2ghsA_	Alignment	not modelled	99.2	15	**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
120	d2ghsa1	Alignment	not modelled	99.2	15	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like