Phyre2

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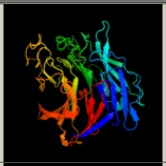
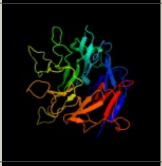
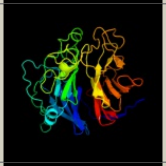
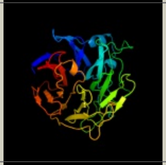
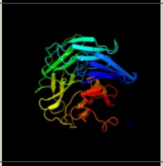
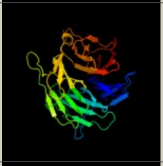
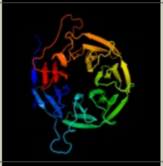
Description	P75804
Date	Thu Jan 5 12:14:23 GMT 2012
Unique Job ID	fb0d198ee716e1c4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g8sB_	Alignment		100.0	98	**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
2	d1crua_	Alignment		100.0	28	**Fold:**6-bladed beta-propeller **Superfamily:**Soluble quinoprotein glucose dehydrogenase **Family:**Soluble quinoprotein glucose dehydrogenase
3	c3a9gA_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pqq-dependent sugar dehydrogenase apo-form
4	c2wg3C_	Alignment		100.0	17	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**hedgehog-interacting protein; **PDBTitle:** crystal structure of the complex between human hedgehog-2 interacting protein hip and desert hedgehog without calcium
5	c2ismA_	Alignment		100.0	35	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of the putative oxidoreductase (glucose2 dehydrogenase) (ttha0570) from thermus theromophilus hb8
6	c3dasA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the pqq-bound form of aldose sugar2 dehydrogenase (adh) from streptomyces coelicolor
7	c2qe8B_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative hydrolase (ava_4197) from anabaena2 variabilis atcc 29413 at 1.35 a resolution
8	d1pjxa_	Alignment		99.9	12	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
9	d2dg1a1	Alignment		99.9	15	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
10	c3dr2A_	Alignment		99.8	9	**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
11	c3g4hB_	Alignment		99.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**regucalcin; **PDBTitle:** crystal structure of human senescence marker protein-30 (zinc bound)

12	c3bwsA_	Alignment		99.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein lp49; **PDBTitle:** crystal structure of the leptospiral antigen lp49
13	c3hrpA_	Alignment		99.8	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
14	c3fw0A_	Alignment		99.8	17	**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)
15	c3qqzA_	Alignment		99.8	13	**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
16	c3dm0A_	Alignment		99.8	13	**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
17	c2qc5A_	Alignment		99.8	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**streptogramin b lactonase; **PDBTitle:** streptogramin b lyase structure
18	d2p4oa1	Alignment		99.8	13	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**All0351-like
19	c3e5zA_	Alignment		99.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative gluconolactonase; **PDBTitle:** crystal structure of the putative gluconolactonase in protein family2 pf08450. northeast structural genomics consortium target drr130.
20	c2z2pA_	Alignment		99.7	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
21	c2ghsA_	Alignment	not modelled	99.7	13	**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
22	d2ghsa1	Alignment	not modelled	99.7	13	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
23	c3kyaA_	Alignment	not modelled	99.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphatase; **PDBTitle:** crystal structure of putative phosphatase (np_812416.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.77 a resolution
24	c3tc9B_	Alignment	not modelled	99.7	12	**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
25	c3hfqB_	Alignment	not modelled	99.7	13	**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.
26	c1gq1B_	Alignment	not modelled	99.7	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
27	c1nnoA_	Alignment	not modelled	99.7	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrite reductase; **PDBTitle:** conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
28	c1r5mA_	Alignment	not modelled	99.6	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sir4-interacting protein sif2;

						PDBTitle: crystal structure of the c-terminal wd40 domain of sif2
29	c3jroA_	Alignment	not modelled	99.6	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
30	d1rwia_	Alignment	not modelled	99.6	17	**Fold:**6-bladed beta-propeller **Superfamily:**NHL repeat **Family:**NHL repeat
31	d1nira2	Alignment	not modelled	99.6	9	**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
32	c3fgbB_	Alignment	not modelled	99.6	10	**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.
33	c2fp8A_	Alignment	not modelled	99.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**strictosidine synthase; **PDBTitle:** structure of strictosidine synthase, the biosynthetic entry to the2 monoterpenoid indole alkaloid family
34	c3ei4D_	Alignment	not modelled	99.6	12	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-hsddb2 complex
35	c3vh0C_	Alignment	not modelled	99.6	9	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce; **PDBTitle:** crystal structure of e. coli ynce complexed with dna
36	c1nr0A_	Alignment	not modelled	99.6	13	**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).
37	d1qksa2	Alignment	not modelled	99.6	8	**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
38	d1ri6a_	Alignment	not modelled	99.5	10	**Fold:**7-bladed beta-propeller **Superfamily:**Putative isomerase YbhE **Family:**Putative isomerase YbhE
39	d1v04a_	Alignment	not modelled	99.5	12	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**Serum paraoxonase/arylesterase 1, PON1
40	c3u4yA_	Alignment	not modelled	99.5	11	**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.
41	d1q7fa_	Alignment	not modelled	99.5	10	**Fold:**6-bladed beta-propeller **Superfamily:**NHL repeat **Family:**NHL repeat
42	c3fm0A_	Alignment	not modelled	99.5	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**protein ciao1; **PDBTitle:** crystal structure of wd40 protein ciao1
43	c1n6dE_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
44	c3iz6a_	Alignment	not modelled	99.5	11	**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
45	c2i0tB_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
46	c3jzhA_	Alignment	not modelled	99.5	7	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb protein eed; **PDBTitle:** eed-h3k79me3
47	c2iwaA_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** unbound glutaminyl cyclotransferase from carica papaya.
48	d2madh_	Alignment	not modelled	99.5	10	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
49	c2pbiB_	Alignment	not modelled	99.5	13	**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
50	d1jmxb_	Alignment	not modelled	99.4	10	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
51	c3frxB_	Alignment	not modelled	99.4	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein subunit beta- **PDBTitle:** crystal structure of the yeast orthologue of rack1, asc1.
52	c3dw8B_	Alignment	not modelled	99.4	8	**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
53	c3ei3B_	Alignment	not modelled	99.4	8	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage-binding protein 2;

						PDBTitle: structure of the hsddb1-drddb2 complex
54	c3iytG_	Alignment	not modelled	99.4	13	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** structure of an apoptosome-procaspase-9 card complex
55	c3i2nA_	Alignment	not modelled	99.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd repeat-containing protein 92; **PDBTitle:** crystal structure of wd40 repeats protein wdr92
56	d2bbkh_	Alignment	not modelled	99.4	9	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
57	d1fwxa2	Alignment	not modelled	99.4	8	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
58	d2ovrb2	Alignment	not modelled	99.4	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
59	d1tbga_	Alignment	not modelled	99.4	13	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
60	d1k32a3	Alignment	not modelled	99.4	12	**Fold:**7-bladed beta-propeller **Superfamily:**Tricorn protease domain 2 **Family:**Tricorn protease domain 2
61	c2h47F_	Alignment	not modelled	99.4	10	**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)
62	c4a11B_	Alignment	not modelled	99.4	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna excision repair protein ercc-8; **PDBTitle:** structure of the hsddb1-hscsa complex
63	c1k32E_	Alignment	not modelled	99.4	12	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** crystal structure of the tricorn protease
64	c2j57J_	Alignment	not modelled	99.4	8	**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.
65	d1xfda1	Alignment	not modelled	99.4	8	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
66	c2qxvA_	Alignment	not modelled	99.4	8	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**embryonic ectoderm development; **PDBTitle:** structural basis of ezh2 recognition by eed
67	c1qniE_	Alignment	not modelled	99.4	10	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from2 pseudomonas nautica, at 2.4a resolution
68	c2pm9A_	Alignment	not modelled	99.4	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
69	c2oajA_	Alignment	not modelled	99.4	11	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
70	c1vyhT_	Alignment	not modelled	99.4	11	**PDB header:**hydrolase **Chain:** T: **PDB Molecule:**platelet-activating factor acetylhydrolase ib **PDBTitle:** paf-ah holoenzyme: lis1/alfa2
71	d1vyhc1	Alignment	not modelled	99.4	11	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
72	c3mmyE_	Alignment	not modelled	99.4	9	**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
73	c3s94A_	Alignment	not modelled	99.4	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor-related protein 6; **PDBTitle:** crystal structure of lrp6-e1e2
74	c2zkqa_	Alignment	not modelled	99.3	12	**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
75	d1yfqa_	Alignment	not modelled	99.3	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**Cell cycle arrest protein BUB3
76	c3eg6A_	Alignment	not modelled	99.3	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**wd repeat-containing protein 5; **PDBTitle:** structure of wdr5 bound to mll1 peptide
77	d1gxra_	Alignment	not modelled	99.3	8	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
78	c3mkqA_	Alignment	not modelled	99.3	12	**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
79	c2gnqA_	Alignment	not modelled	99.3	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd-repeat protein 5; **PDBTitle:** structure of wdr5

80	d1qnia2	Alignment	not modelled	99.3	9	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
81	d1nr0a1	Alignment	not modelled	99.3	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
82	c3jrpA_	Alignment	not modelled	99.3	9	**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
83	c2w18A_	Alignment	not modelled	99.3	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
84	c1fwxB_	Alignment	not modelled	99.2	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrous oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from p. denitrificans
85	c3c75J_	Alignment	not modelled	99.2	11	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
86	c3soqA_	Alignment	not modelled	99.2	22	**PDB header:**protein binding/antagonist **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor-related protein 6; **PDBTitle:** the structure of the first ywtd beta propeller domain of lrp6 in2 complex with a dkk1 peptide
87	c3bg1E_	Alignment	not modelled	99.2	11	**PDB header:**protein transport, hydrolase **Chain:** E: **PDB Molecule:**protein sec13 homolog; **PDBTitle:** architecture of a coat for the nuclear pore membrane
88	c2xznR_	Alignment	not modelled	99.2	11	**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
89	c3cfvA_	Alignment	not modelled	99.2	11	**PDB header:**histone/chaperone **Chain:** A: **PDB Molecule:**histone-binding protein rbbp7; **PDBTitle:** structural basis of the interaction of rbap46/rbap48 with2 histone h4
90	c2j04B_	Alignment	not modelled	99.2	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ydr362cp; **PDBTitle:** the tau60-tau91 subcomplex of yeast transcription factor2 iiic
91	d2bgra1	Alignment	not modelled	99.2	8	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
92	d1k8kc_	Alignment	not modelled	99.2	7	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
93	d1l0qa2	Alignment	not modelled	99.2	10	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**YVTN repeat
94	c3ow8A_	Alignment	not modelled	99.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd repeat-containing protein 61; **PDBTitle:** crystal structure of the wd repeat-containing protein 61
95	c3pe7A_	Alignment	not modelled	99.2	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**oligogalacturonate lyase; **PDBTitle:** oligogalacturonate lyase in complex with manganese
96	d1tl2a_	Alignment	not modelled	99.1	12	**Fold:**5-bladed beta-propeller **Superfamily:**Tachylectin-2 **Family:**Tachylectin-2
97	d1pgua1	Alignment	not modelled	99.1	11	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
98	c3acpA_	Alignment	not modelled	99.1	9	**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
99	d1nr0a2	Alignment	not modelled	99.1	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
100	c2hesX_	Alignment	not modelled	99.1	8	**PDB header:**biosynthetic protein **Chain:** X: **PDB Molecule:**ydr267cp; **PDBTitle:** cytosolic iron-sulphur assembly protein- 1
101	c2w8bB_	Alignment	not modelled	99.1	14	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal
102	c3c5mC_	Alignment	not modelled	99.1	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**oligogalacturonate lyase; **PDBTitle:** crystal structure of oligogalacturonate lyase (vpa0088)2 from vibrio parahaemolyticus. northeast structural3 genomics consortium target vpr199
103	d1orva1	Alignment	not modelled	99.1	10	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
104	d1pbyb_	Alignment	not modelled	99.1	12	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
105	c3sbrF_	Alignment	not modelled	99.1	9	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
						PDB header:signaling protein,protein binding

106	c3greA_	Alignment	not modelled	99.1	11	**Chain:** A: **PDB Molecule:**serine/threonine-protein kinase vps15; **PDBTitle:** crystal structure of saccharomyces cerevisiae vps15 wd2 repeat domain
107	c3s8vA_	Alignment	not modelled	99.1	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor-related protein 6; **PDBTitle:** crystal structure of lrp6-dkk1 complex
108	c3fhcA_	Alignment	not modelled	99.1	10	**PDB header:**transport protein/hydrolase **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup214; **PDBTitle:** crystal structure of human dbp5 in complex with nup214
109	c3dsmA_	Alignment	not modelled	99.0	12	**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.
110	d1npea_	Alignment	not modelled	99.0	17	**Fold:**6-bladed beta-propeller **Superfamily:**YWTD domain **Family:**YWTD domain
111	c2ojhA_	Alignment	not modelled	99.0	19	**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
112	c1n7dA_	Alignment	not modelled	99.0	17	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** extracellular domain of the ldl receptor
113	c2aq5A_	Alignment	not modelled	99.0	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of murine coronin-1
114	d1nexb2	Alignment	not modelled	99.0	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
115	c2ovqB_	Alignment	not modelled	99.0	11	**PDB header:**transcription/cell cycle **Chain:** B: **PDB Molecule:**f-box/wd repeat protein 7; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
116	c1pi6A_	Alignment	not modelled	99.0	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** yeast actin interacting protein 1 (aip1), orthorhombic crystal form
117	c2pm7B_	Alignment	not modelled	99.0	8	**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
118	d1erja_	Alignment	not modelled	99.0	11	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
119	d1ijqa1	Alignment	not modelled	98.9	15	**Fold:**6-bladed beta-propeller **Superfamily:**YWTD domain **Family:**YWTD domain
120	c2p9wA_	Alignment	not modelled	98.9	12	**PDB header:**allergen **Chain:** A: **PDB Molecule:**mal s 1 allergenic protein; **PDBTitle:** crystal structure of the major malassezia sympodialis allergen mala s2 1