Phyre^2

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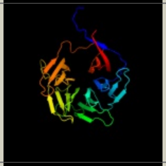
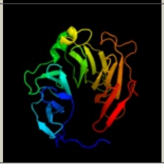
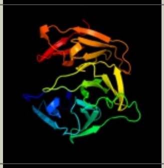
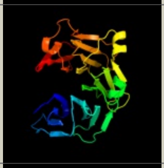
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qqzA_	Alignment		100.0	98	**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
2	c3fw0A_	Alignment		99.9	13	**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)
3	c3hrpA_	Alignment		99.9	10	**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
4	c2ghsA_	Alignment		99.9	11	**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
5	d2ghsa1	Alignment		99.9	11	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
6	d2p4oa1	Alignment		99.9	16	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**All0351-like
7	c3dr2A_	Alignment		99.8	12	**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
8	c2qc5A_	Alignment		99.8	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**streptogramin b lactonase; **PDBTitle:** streptogramin b lyase structure
9	c2z2pA_	Alignment		99.8	11	**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
10	c3kyaA_	Alignment		99.8	9	**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
11	d2dg1a1	Alignment		99.8	12	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like

12	c3tc9B_	Alignment		99.8	11	**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
13	c3u4yA_	Alignment		99.8	9	**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.
14	c3e5zA_	Alignment		99.8	8	**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.
15	d1npea_	Alignment		99.8	12	**Fold:**6-bladed beta-propeller **Superfamily:**YWTD domain **Family:**YWTD domain
16	c3s8vA_	Alignment		99.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor-related protein 6; **PDBTitle:** crystal structure of lrp6-dkk1 complex
17	c3g4hB_	Alignment		99.8	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**regucalcin; **PDBTitle:** crystal structure of human senescence marker protein-30 (zinc bound)
18	c3soqA_	Alignment		99.8	10	**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
19	d1pjxa_	Alignment		99.8	12	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
20	c3bwsA_	Alignment		99.8	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein lp49; **PDBTitle:** crystal structure of the leptospiral antigen lp49
21	d1q7fa_	Alignment	not modelled	99.8	15	**Fold:**6-bladed beta-propeller **Superfamily:**NHL repeat **Family:**NHL repeat
22	c1n7dA_	Alignment	not modelled	99.8	7	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** extracellular domain of the ldl receptor
23	c2p9wA_	Alignment	not modelled	99.8	15	**PDB header:**allergen **Chain:** A: **PDB Molecule:**mal s 1 allergenic protein; **PDBTitle:** crystal structure of the major malassezia sympodialis allergen mala s2 1
24	c2qe8B_	Alignment	not modelled	99.7	12	**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
25	d1rwia_	Alignment	not modelled	99.7	14	**Fold:**6-bladed beta-propeller **Superfamily:**NHL repeat **Family:**NHL repeat
26	c3vh0C_	Alignment	not modelled	99.7	15	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce; **PDBTitle:** crystal structure of e. coli ynce complexed with dna
27	c1ijqA_	Alignment	not modelled	99.7	7	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** crystal structure of the ldl receptor ywtd-egf domain pair
28	c3s94A_	Alignment	not modelled	99.7	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor-related protein 6; **PDBTitle:** crystal structure of lrp6-e1e2
29	c3pelA	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase;

29	c3nofA_	Alignment	not modelled	99.7	15	**PDBTitle:** crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
30	d1jofa_	Alignment	not modelled	99.7	9	**Fold:**7-bladed beta-propeller **Superfamily:**3-carboxy-cis,cis-mucoante lactonizing enzyme **Family:**3-carboxy-cis,cis-mucoante lactonizing enzyme
31	d1ijqa1	Alignment	not modelled	99.7	7	**Fold:**6-bladed beta-propeller **Superfamily:**YWTD domain **Family:**YWTD domain
32	c2iwaA_	Alignment	not modelled	99.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** unbound glutaminyl cyclotransferase from carica papaya.
33	c3hfqB_	Alignment	not modelled	99.7	11	**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.
34	d1v04a_	Alignment	not modelled	99.6	14	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**Serum paraoxonase/arylesterase 1, PON1
35	c3mbrX_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** crystal structure of the glutaminyl cyclase from xanthomonas2 campestris
36	c3a9gA_	Alignment	not modelled	99.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pqq-dependent sugar dehydrogenase apo-form
37	c1qniE_	Alignment	not modelled	99.6	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
38	c3fgbB_	Alignment	not modelled	99.6	11	**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.
39	c3dsmA_	Alignment	not modelled	99.6	13	**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.
40	c3dm0A_	Alignment	not modelled	99.6	11	**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
41	c2oajA_	Alignment	not modelled	99.6	10	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
42	d1jmxb_	Alignment	not modelled	99.6	17	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
43	c2fp8A_	Alignment	not modelled	99.6	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**strictosidine synthase; **PDBTitle:** structure of strictosidine synthase, the biosynthetic entry to the2 monoterpenoid indole alkaloid family
44	c3mkqA_	Alignment	not modelled	99.6	11	**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
45	d1crua_	Alignment	not modelled	99.6	15	**Fold:**6-bladed beta-propeller **Superfamily:**Soluble quinoprotein glucose dehydrogenase **Family:**Soluble quinoprotein glucose dehydrogenase
46	c1fwxB_	Alignment	not modelled	99.6	5	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrous oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from p. denitrificans
47	c1gq1B_	Alignment	not modelled	99.6	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
48	d1qnia2	Alignment	not modelled	99.5	10	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
49	c2g8sB_	Alignment	not modelled	99.5	16	**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
50	c3sbrF_	Alignment	not modelled	99.5	8	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
51	d1qksa2	Alignment	not modelled	99.5	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
52	c1nnoA_	Alignment	not modelled	99.5	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrite reductase; **PDBTitle:** conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
53	c2ismA_	Alignment	not modelled	99.5	11	**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
						PDB header:transferase

54	c3nokB_	Alignment	not modelled	99.5	10	**Chain:** B: **PDB Molecule:**glutaminyl cyclase; **PDBTitle:** crystal structure of myxococcus xanthus glutaminyl cyclase
55	d1pbyb_	Alignment	not modelled	99.5	17	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
56	d1ri6a_	Alignment	not modelled	99.4	7	**Fold:**7-bladed beta-propeller **Superfamily:**Putative isomerase YbhE **Family:**Putative isomerase YbhE
57	c1l0qC_	Alignment	not modelled	99.4	14	**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
58	d1fwxa2	Alignment	not modelled	99.4	10	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
59	c2j57J_	Alignment	not modelled	99.4	10	**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.
60	d2madh_	Alignment	not modelled	99.4	8	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
61	c3lrvA_	Alignment	not modelled	99.4	9	**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.
62	c1nr0A_	Alignment	not modelled	99.4	6	**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).
63	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
64	c3dasA_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the pqq-bound form of aldose sugar2 dehydrogenase (adh) from streptomyces coelicolor
65	d1nira2	Alignment	not modelled	99.3	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
66	c3jroA_	Alignment	not modelled	99.3	13	**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
67	c1pi6A_	Alignment	not modelled	99.3	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** yeast actin interacting protein 1 (aip1), orthorhombic crystal form
68	c1k32E_	Alignment	not modelled	99.3	10	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** crystal structure of the tricorn protease
69	c1n6dE_	Alignment	not modelled	99.3	10	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
70	c2h47F_	Alignment	not modelled	99.3	9	**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)
71	d1k32a3	Alignment	not modelled	99.2	10	**Fold:**7-bladed beta-propeller **Superfamily:**Tricorn protease domain 2 **Family:**Tricorn protease domain 2
72	c3c75J_	Alignment	not modelled	99.2	12	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
73	c2aq5A_	Alignment	not modelled	99.2	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of murine coronin-1
74	d1tl2a_	Alignment	not modelled	99.2	10	**Fold:**5-bladed beta-propeller **Superfamily:**Tachylectin-2 **Family:**Tachylectin-2
75	d1l0qa2	Alignment	not modelled	99.2	13	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**YVTN repeat
76	c2vduB_	Alignment	not modelled	99.2	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase- **PDBTitle:** structure of trm8-trm82, the yeast trna m7g methylation2 complex
77	c2w8bB_	Alignment	not modelled	99.2	12	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal
78	c3q6kA_	Alignment	not modelled	99.2	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**43.2 kda salivary protein; **PDBTitle:** salivary protein from lutzomyia longipalpis
79	c2i0tB_	Alignment	not modelled	99.1	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase

80	d2bbkh_	Alignment	not modelled	99.1	10	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
81	d1nr0a1	Alignment	not modelled	99.1	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
82	c3dw8B_	Alignment	not modelled	99.1	9	**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
83	c2w18A_	Alignment	not modelled	99.0	12	**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	c3no2A_	Alignment	not modelled	99.0	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein of unknown function (baccac_01654) from2 bacteroides caccae at 1.35 a resolution
85	c2ivzD_	Alignment	not modelled	99.0	10	**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
86	d1h6la_	Alignment	not modelled	99.0	14	**Fold:**6-bladed beta-propeller **Superfamily:**Thermostable phytase (3-phytase) **Family:**Thermostable phytase (3-phytase)
87	c3frxB_	Alignment	not modelled	99.0	15	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein subunit beta- **PDBTitle:** crystal structure of the yeast orthologue of rack1, asc1.
88	c2j04B_	Alignment	not modelled	99.0	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ydr362cp; **PDBTitle:** the tau60-tau91 subcomplex of yeast transcription factor2 iiic
89	d1ospo_	Alignment	not modelled	98.9	9	**Fold:**open-sided beta-meander **Superfamily:**Outer surface protein **Family:**Outer surface protein
90	d1gxra_	Alignment	not modelled	98.9	14	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
91	c3ei4D_	Alignment	not modelled	98.9	12	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-hsddb2 complex
92	c3acpA_	Alignment	not modelled	98.9	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
93	d1xfda1	Alignment	not modelled	98.9	10	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
94	c2iwkB_	Alignment	not modelled	98.9	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
95	c1r5mA_	Alignment	not modelled	98.9	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sir4-interacting protein sif2; **PDBTitle:** crystal structure of the c-terminal wd40 domain of sif2
96	c3dwlH_	Alignment	not modelled	98.8	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
97	d2bgra1	Alignment	not modelled	98.8	9	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
98	c3fhcA_	Alignment	not modelled	98.8	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
99	c2pm9A_	Alignment	not modelled	98.8	16	**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
100	c2pbiB_	Alignment	not modelled	98.8	12	**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
101	d1orva1	Alignment	not modelled	98.8	12	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
102	c3iz6a_	Alignment	not modelled	98.8	16	**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
103	c2oitA_	Alignment	not modelled	98.7	9	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**nucleoporin 214kda; **PDBTitle:** crystal structure of the n-terminal domain of the human2 proto-oncogene nup214/can
104	d1yfqa_	Alignment	not modelled	98.7	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**Cell cycle arrest protein BUB3
105	c2wg3C_	Alignment	not modelled	98.7	14	**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
106	c3i2nA_	Alignment	not modelled	98.7	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd repeat-containing protein 92; **PDBTitle:** crystal structure of wd40 repeats protein wdr92
107	d1k8kc_	Alignment	not modelled	98.6	11	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
108	d1k32a2	Alignment	not modelled	98.6	8	**Fold:**6-bladed beta-propeller **Superfamily:**Tricorn protease N-terminal domain **Family:**Tricorn protease N-terminal domain
109	c3pe7A_	Alignment	not modelled	98.6	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**oligogalacturonate lyase; **PDBTitle:** oligogalacturonate lyase in complex with manganese
110	c2gnqA_	Alignment	not modelled	98.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd-repeat protein 5; **PDBTitle:** structure of wdr5
111	c3greA_	Alignment	not modelled	98.6	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
112	c3ei3B_	Alignment	not modelled	98.6	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-drddb2 complex
113	d1tbga_	Alignment	not modelled	98.6	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
114	d1vyhc1	Alignment	not modelled	98.5	13	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
115	c1vyhT_	Alignment	not modelled	98.5	13	**PDB header:**hydrolase **Chain:** T: **PDB Molecule:**platelet-activating factor acetylhydrolase ib **PDBTitle:** paf-ah holoenzyme: lis1/alfa2
116	d1nr0a2	Alignment	not modelled	98.5	13	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
117	c1xfdD_	Alignment	not modelled	98.5	8	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**dipeptidyl aminopeptidase-like protein 6; **PDBTitle:** structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family
118	c3mmyE_	Alignment	not modelled	98.4	11	**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
119	c3eg6A_	Alignment	not modelled	98.4	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**wd repeat-containing protein 5; **PDBTitle:** structure of wdr5 bound to mll1 peptide
120	d1nexb2	Alignment	not modelled	98.4	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat