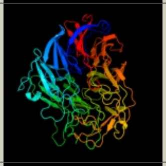
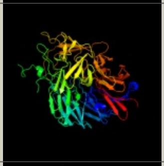
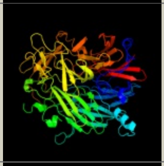
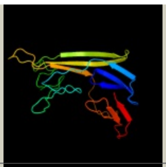
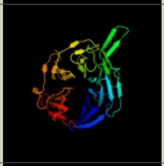
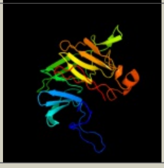
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P15877
Date	Thu Jan 5 11:34:57 GMT 2012
Unique Job ID	45f667485f99845a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kb0A_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein alcohol dehydrogenase; **PDBTitle:** crystal structure of quinohemoprotein alcohol dehydrogenase from2 comamonas testosteroni
2	c1yiqA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein alcohol dehydrogenase; **PDBTitle:** molecular cloning and structural analysis of2 quinohemoprotein alcohol dehydrogenase adhiig from3 pseudomonas putida hk5. compariison to the other4 quinohemoprotein alcohol dehydrogenase adhiib found in the5 same microorganism.
3	c1kv9A_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type ii quinohemoprotein alcohol dehydrogenase; **PDBTitle:** structure at 1.9 a resolution of a quinohemoprotein alcohol2 dehydrogenase from pseudomonas putida hk5
4	d1kb0a2	Alignment		100.0	29	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
5	d1flga_	Alignment		100.0	25	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
6	d2ad6a1	Alignment		100.0	30	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
7	d1w6sa_	Alignment		100.0	28	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
8	d1kv9a2	Alignment		100.0	31	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
9	d1lrwa_	Alignment		100.0	28	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
10	c2be1A_	Alignment		100.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase/endoribonuclease ire1; **PDBTitle:** structure of the compact lumenal domain of yeast ire1
11	c3p1lA_	Alignment		100.0	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**lipoprotein yfgl; **PDBTitle:** crystal structure of escherichia coli bamb, a lipoprotein component of2 the beta-barrel assembly machinery complex, native crystals.

12	c2hz6A_	Alignment		99.8	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**endoplasmic reticulum to nucleus signalling 1 **PDBTitle:** the crystal structure of human ire1-alpha luminal domain
13	c3no2A_	Alignment		99.6	12	**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
14	c3hxjA_	Alignment		99.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrrolo-quinoline quinone; **PDBTitle:** crystal structure of pyrrolo-quinoline quinone (pqq_dh) from2 methanococcus maripaludis, northeast structural genomics consortium3 target mrr86
15	c2j57J_	Alignment		99.2	16	**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.
16	d1jmxb_	Alignment		99.2	18	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
17	d2madh_	Alignment		99.2	11	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
18	c1nnoA_	Alignment		99.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrite reductase; **PDBTitle:** conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
19	d1pbyb_	Alignment		99.1	17	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
20	c3mbrX_	Alignment		99.1	14	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** crystal structure of the glutaminyl cyclase from xanthomonas2 campestris
21	c1gq1B_	Alignment	not modelled	99.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
22	c3nolA_	Alignment	not modelled	99.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
23	c3hx6A_	Alignment	not modelled	99.0	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**type 4 fimbrial biogenesis protein pily1; **PDBTitle:** crystal structure of pseudomonas aeruginosa pily1 c-terminal2 domain
24	c3vh0C_	Alignment	not modelled	98.9	15	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce; **PDBTitle:** crystal structure of e. coli ynce complexed with dna
25	c3c75J_	Alignment	not modelled	98.7	15	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
26	d2bbkh_	Alignment	not modelled	98.7	15	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
27	c2h47F_	Alignment	not modelled	98.6	14	**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)
28	c1l0qC_	Alignment	not modelled	98.6	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

29	c3u4yA_	Alignment	not modelled	98.5	16	**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.
30	c3nokB_	Alignment	not modelled	98.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutaminyl cyclase; **PDBTitle:** crystal structure of myxococcus xanthus glutaminyl cyclase
31	c3dsmA_	Alignment	not modelled	98.2	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.
32	c2iwaA_	Alignment	not modelled	98.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** unbound glutaminyl cyclotransferase from carica papaya.
33	c2i0tB_	Alignment	not modelled	98.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
34	d1l0qa2	Alignment	not modelled	98.0	18	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**YVTN repeat
35	d1qksa2	Alignment	not modelled	97.9	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
36	d1nira2	Alignment	not modelled	97.8	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
37	d1fwxa2	Alignment	not modelled	97.7	18	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
38	c1fwxB_	Alignment	not modelled	97.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrous oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from p. denitrificans
39	c3bwsA_	Alignment	not modelled	97.6	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein lp49; **PDBTitle:** crystal structure of the leptospiral antigen lp49
40	c3elqA_	Alignment	not modelled	97.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfate sulfotransferase; **PDBTitle:** crystal structure of a bacterial arylsulfate2 sulfotransferase
41	c1qniE_	Alignment	not modelled	97.1	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
42	c3fgbB_	Alignment	not modelled	96.7	15	**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.
43	d1pjxa_	Alignment	not modelled	96.6	11	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
44	c2w18A_	Alignment	not modelled	96.1	11	**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
45	c2fp8A_	Alignment	not modelled	95.5	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**strictosidine synthase; **PDBTitle:** structure of strictosidine synthase, the biosynthetic entry to the2 monoterpenoid indole alkaloid family
46	c3g4hB_	Alignment	not modelled	94.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**regucalcin; **PDBTitle:** crystal structure of human senescence marker protein-30 (zinc bound)
47	c3hfqB_	Alignment	not modelled	94.4	12	**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.
48	c3dm0A_	Alignment	not modelled	94.2	14	**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
49	c2oajA_	Alignment	not modelled	93.4	11	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
50	d2ghsa1	Alignment	not modelled	92.7	15	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
51	c2ghsA_	Alignment	not modelled	92.7	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
52	c2zuxA_	Alignment	not modelled	92.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yesw protein; **PDBTitle:** crystal structure of rhamnogalacturonan lyase yesw2 complexed with rhamnose
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**exported gluconolactonase;

53	c3dr2A_	Alignment	not modelled	92.0	20	**PDBTitle:** structural and functional analyses of xc5397 from2 xanthomonas campestris: a gluconolactonase important in3 glucose secondary metabolic pathways
54	c3sbrF_	Alignment	not modelled	90.8	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
55	c3fw0A_	Alignment	not modelled	90.7	15	**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)
56	c3mmyE_	Alignment	not modelled	90.2	13	**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
57	c1n7dA_	Alignment	not modelled	90.2	19	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** extracellular domain of the ldl receptor
58	d1nr0a1	Alignment	not modelled	90.1	16	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
59	d1yfqa_	Alignment	not modelled	89.6	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**Cell cycle arrest protein BUB3
60	d1k32a2	Alignment	not modelled	87.9	11	**Fold:**6-bladed beta-propeller **Superfamily:**Tricorn protease N-terminal domain **Family:**Tricorn protease N-terminal domain
61	d1mdah_	Alignment	not modelled	87.0	13	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
62	c2wg3C_	Alignment	not modelled	85.5	11	**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
63	c3iytG_	Alignment	not modelled	83.2	12	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** structure of an apoptosome-procaspase-9 card complex
64	d2p4oa1	Alignment	not modelled	82.6	11	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**All0351-like
65	c3s25A_	Alignment	not modelled	79.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical 7-bladed beta-propeller-like protein; **PDBTitle:** crystal structure of a hypothetical 7-bladed beta-propeller-like2 protein (eubrec_1955) from eubacterium rectale atcc 33656 at 1.88 a3 resolution
66	c3c5mC_	Alignment	not modelled	79.3	8	**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
67	c3ei4D_	Alignment	not modelled	78.7	12	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-hsddb2 complex
68	d1qnia2	Alignment	not modelled	72.9	11	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
69	d2dg1a1	Alignment	not modelled	71.8	16	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
70	d1jofa_	Alignment	not modelled	71.3	13	**Fold:**7-bladed beta-propeller **Superfamily:**3-carboxy-cis,cis-mucoante lactonizing enzyme **Family:**3-carboxy-cis,cis-mucoante lactonizing enzyme
71	d1s1da_	Alignment	not modelled	70.0	15	**Fold:**5-bladed beta-propeller **Superfamily:**Apyrase **Family:**Apyrase
72	d1npea_	Alignment	not modelled	69.1	15	**Fold:**6-bladed beta-propeller **Superfamily:**YWTD domain **Family:**YWTD domain
73	c3npeA_	Alignment	not modelled	67.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; **PDBTitle:** structure of vp14 in complex with oxygen
74	c2uvkB_	Alignment	not modelled	67.4	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**yjht; **PDBTitle:** structure of yjht
75	c3s94A_	Alignment	not modelled	66.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor-related protein 6; **PDBTitle:** crystal structure of lrp6-e1e2
76	d2bgra1	Alignment	not modelled	65.1	12	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
77	c3pe7A_	Alignment	not modelled	64.3	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**oligogalacturonate lyase; **PDBTitle:** oligogalacturonate lyase in complex with manganese
78	c3qqzA_	Alignment	not modelled	62.8	10	**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
79	c3lrvA_	Alignment	not modelled	57.9	11	**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.
80	c2ifsA_	Alignment	not modelled	54.9	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wiskott-aldrich syndrome protien ineracting **PDBTitle:** structure of the n-wasp evh1 domain in complex with an2 extended wip peptide
81	c2vz1A_	Alignment	not modelled	54.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**galactose oxidase; **PDBTitle:** premat-galactose oxidase
82	d1gxra_	Alignment	not modelled	54.3	20	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
83	c2g8sB_	Alignment	not modelled	52.1	13	**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
84	c3q6kA_	Alignment	not modelled	50.9	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**43.2 kda salivary protein; **PDBTitle:** salivary protein from lutzomyia longipalpis
85	c1c9lA_	Alignment	not modelled	49.7	17	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**clathrin; **PDBTitle:** peptide-in-groove interactions link target proteins to the2 b-propeller of clathrin
86	d1ijqa1	Alignment	not modelled	49.0	16	**Fold:**6-bladed beta-propeller **Superfamily:**YWTD domain **Family:**YWTD domain
87	d1nlna_	Alignment	not modelled	46.0	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
88	c2pbiB_	Alignment	not modelled	45.6	17	**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
89	d1utca2	Alignment	not modelled	44.3	27	**Fold:**7-bladed beta-propeller **Superfamily:**Clathrin heavy-chain terminal domain **Family:**Clathrin heavy-chain terminal domain
90	d1ri6a_	Alignment	not modelled	42.5	15	**Fold:**7-bladed beta-propeller **Superfamily:**Putative isomerase YbhE **Family:**Putative isomerase YbhE
91	c2xtsD_	Alignment	not modelled	42.4	24	**PDB header:**oxidoreductase/electron transport **Chain:** D: **PDB Molecule:**cytochrome; **PDBTitle:** crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
92	c2iwkB_	Alignment	not modelled	42.1	10	**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
93	d1kshb_	Alignment	not modelled	41.7	42	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
94	d2r6gf1	Alignment	not modelled	39.8	20	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
95	c3e5zA_	Alignment	not modelled	39.5	18	**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.
96	c1bpoA_	Alignment	not modelled	36.4	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein (clathrin); **PDBTitle:** clathrin heavy-chain terminal domain and linker
97	c1ijqA_	Alignment	not modelled	35.9	18	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** crystal structure of the ldl receptor ywtd-egf domain pair
98	c2oitA_	Alignment	not modelled	35.9	12	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**nucleoporin 214kda; **PDBTitle:** crystal structure of the n-terminal domain of the human2 proto-oncogene nup214/can
99	d1orva1	Alignment	not modelled	35.8	12	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
100	c1xi4D_	Alignment	not modelled	35.6	21	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**clathrin heavy chain; **PDBTitle:** clathrin d6 coat
101	d1h6la_	Alignment	not modelled	34.3	24	**Fold:**6-bladed beta-propeller **Superfamily:**Thermostable phytase (3-phytase) **Family:**Thermostable phytase (3-phytase)
102	c2biwC_	Alignment	not modelled	32.5	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**apocarotenoid-cleaving oxygenase; **PDBTitle:** crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme
103	c3tekA_	Alignment	not modelled	32.1	32	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**thermodbp-single stranded dna binding protein; **PDBTitle:** thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
104	d1es5a_	Alignment	not modelled	32.0	8	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like

						Family:beta-Lactamase/D-ala carboxypeptidase
105	d1tbga_	Alignment	not modelled	31.9	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
106	c2v20A_	Alignment	not modelled	31.7	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase tem; **PDBTitle:** structure of a tem-1 beta-lactamase insertant2 allosterically regulated by kanamycin and anions. complex3 with sulfate.
107	d1mkea1	Alignment	not modelled	31.4	33	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Enabled/VASP homology 1 domain (EVH1 domain)
108	d1g2914	Alignment	not modelled	31.3	16	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
109	c2qe8B_	Alignment	not modelled	31.0	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
110	d1qfma1	Alignment	not modelled	30.7	13	**Fold:**7-bladed beta-propeller **Superfamily:**Peptidase/esterase 'gauge' domain **Family:**Prolyl oligopeptidase, N-terminal domain
111	d1pgua1	Alignment	not modelled	28.9	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
112	d1y9qa2	Alignment	not modelled	28.1	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
113	c2gnqA_	Alignment	not modelled	27.7	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd-repeat protein 5; **PDBTitle:** structure of wdr5
114	c3ei3B_	Alignment	not modelled	27.7	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-drddb2 complex
115	c2zuyA_	Alignment	not modelled	27.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yesx protein; **PDBTitle:** crystal structure of exotype rhamnogalacturonan lyase yesx
116	c3pjzA_	Alignment	not modelled	27.0	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**potassium uptake protein trkh; **PDBTitle:** crystal structure of the potassium transporter trkh from vibrio2 parahaemolyticus
117	d1zgka1	Alignment	not modelled	25.8	37	**Fold:**6-bladed beta-propeller **Superfamily:**Kelch motif **Family:**Kelch motif
118	c3odtB_	Alignment	not modelled	25.6	17	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of wd40 beta propeller domain of doa1
119	c3eg6A_	Alignment	not modelled	25.3	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**wd repeat-containing protein 5; **PDBTitle:** structure of wdr5 bound to mll1 peptide
120	c3of6D_	Alignment	not modelled	24.9	33	**PDB header:**immune system **Chain:** D: **PDB Molecule:**pre t-cell antigen receptor alpha; **PDBTitle:** human pre-t cell receptor crystal structure