Phyre2

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Description	P0A855
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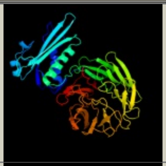
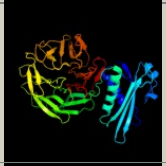
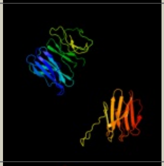
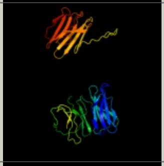
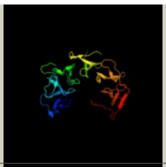
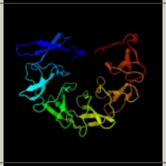
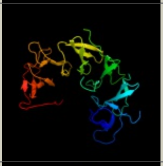
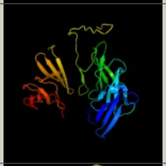
Unique Job ID	6b37b73bed2f7f2b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w8bB_	Alignment		100.0	100	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal
2	c2ivzD_	Alignment		100.0	100	**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
3	d2hqsa1	Alignment		100.0	100	**Fold:**6-bladed beta-propeller **Superfamily:**TolB, C-terminal domain **Family:**TolB, C-terminal domain
4	c1k32E_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** crystal structure of the tricorn protease
5	c1n6dE_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
6	d1k32a2	Alignment		100.0	16	**Fold:**6-bladed beta-propeller **Superfamily:**Tricorn protease N-terminal domain **Family:**Tricorn protease N-terminal domain
7	c3pe7A_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**oligogalacturonate lyase; **PDBTitle:** oligogalacturonate lyase in complex with manganese
8	c2gopB_	Alignment		100.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trilobed protease; **PDBTitle:** the beta-propeller domain of the trilobed protease from pyrococcus2 furiosus reveals an open velcro topology
9	c2ojhA_	Alignment		99.9	22	**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
10	c3c5mC_	Alignment		99.9	15	**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
11	d1k32a3	Alignment		99.9	19	**Fold:**7-bladed beta-propeller **Superfamily:**Tricorn protease domain 2 **Family:**Tricorn protease domain 2

12	d1orva1	Alignment		99.9	19	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
13	c2eepA_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl aminopeptidase iv, putative; **PDBTitle:** prolyl tripeptidyl aminopeptidase complexed with an inhibitor
14	d2bgra1	Alignment		99.9	15	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
15	d1xfda1	Alignment		99.9	21	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
16	c1xfdD_	Alignment		99.9	17	**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
17	c1z68A_	Alignment		99.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fibroblast activation protein, alpha subunit; **PDBTitle:** crystal structure of human fibroblast activation protein alpha
18	c2g5tA_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase 4; **PDBTitle:** crystal structure of human dipeptidyl peptidase iv (dppiv)2 complexed with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
19	c2ecfA_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
20	d2hqsa2	Alignment		99.9	100	**Fold:**Anticodon-binding domain-like **Superfamily:**TolB, N-terminal domain **Family:**TolB, N-terminal domain
21	c2qtbB_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl peptidase 4; **PDBTitle:** human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
22	c3bwsA_	Alignment	not modelled	99.9	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein lp49; **PDBTitle:** crystal structure of the leptospiral antigen lp49
23	c2hu7A_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
24	c3dm0A_	Alignment	not modelled	99.9	16	**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
25	c3fgbB_	Alignment	not modelled	99.9	18	**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.
26	c2i0tB_	Alignment	not modelled	99.8	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
27	c1gq1B_	Alignment	not modelled	99.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
28	c3u4yA_	Alignment	not modelled	99.8	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.
29	d1l0qa2	Alignment	not modelled	99.8	17	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**YVTN repeat
30	d1qfma1	Alignment	not modelled	99.8	15	**Fold:**7-bladed beta-propeller **Superfamily:**Peptidase/esterase 'gauge' domain **Family:**Prolyl oligopeptidase, N-terminal domain
31	c2j57J_	Alignment	not modelled	99.8	15	**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.
32	c2h47F_	Alignment	not modelled	99.8	13	**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)
33	c3mkqA_	Alignment	not modelled	99.8	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
34	c1nr0A_	Alignment	not modelled	99.8	11	**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).
35	c3jroA_	Alignment	not modelled	99.8	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
36	c1yr2A_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
37	c2bklB_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
38	c1nnoA_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrite reductase; **PDBTitle:** conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
39	c3c75J_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
40	c2oajA_	Alignment	not modelled	99.8	12	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
41	c1l0qC_	Alignment	not modelled	99.8	17	**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
42	c1qfmA_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
43	c3iytG_	Alignment	not modelled	99.8	13	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** structure of an apoptosome-procaspase-9 card complex
44	d1ri6a_	Alignment	not modelled	99.8	13	**Fold:**7-bladed beta-propeller **Superfamily:**Putative isomerase YbhE **Family:**Putative isomerase YbhE
45	d2bbkh_	Alignment	not modelled	99.8	16	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
46	c3azqA_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
47	c2j04B_	Alignment	not modelled	99.8	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ydr362cp; **PDBTitle:** the tau60-tau91 subcomplex of yeast transcription factor2 iiic
48	d1qnia2	Alignment	not modelled	99.8	9	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
49	d1ospo_	Alignment	not modelled	99.8	14	**Fold:**open-sided beta-meander **Superfamily:**Outer surface protein **Family:**Outer surface protein
50	d2madh_	Alignment	not modelled	99.7	14	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
51	d1jmxb_	Alignment	not modelled	99.7	16	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
52	d1fwxa2	Alignment	not modelled	99.7	8	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
53	c3iumA_	Alignment	not modelled	99.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** appep_wtx opened state
						PDB header:structural protein

54	c2aq5A_	Alignment	not modelled	99.7	14	**Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of murine coronin-1
55	c1r5mA_	Alignment	not modelled	99.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sir4-interacting protein sif2; **PDBTitle:** crystal structure of the c-terminal wd40 domain of sif2
56	c3hfqB_	Alignment	not modelled	99.7	15	**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.
57	d1pbyb_	Alignment	not modelled	99.7	19	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
58	d1qksa2	Alignment	not modelled	99.7	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
59	c2pbiB_	Alignment	not modelled	99.7	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
60	c3jrpA_	Alignment	not modelled	99.7	13	**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
61	d1nira2	Alignment	not modelled	99.7	15	**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
62	d1tbga_	Alignment	not modelled	99.7	14	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
63	c3g4hB_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**regucalcin; **PDBTitle:** crystal structure of human senescence marker protein-30 (zinc bound)
64	c2xe4A_	Alignment	not modelled	99.7	14	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**oligopeptidase b; **PDBTitle:** structure of oligopeptidase b from leishmania major
65	c2w18A_	Alignment	not modelled	99.7	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
66	d1gxra_	Alignment	not modelled	99.7	11	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
67	c1qniE_	Alignment	not modelled	99.6	6	**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	c1fwxB_	Alignment	not modelled	99.6	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrous oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from p. denitrificans
69	c2gnqA_	Alignment	not modelled	99.6	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd-repeat protein 5; **PDBTitle:** structure of wdr5
70	c3iz6a_	Alignment	not modelled	99.6	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
71	c1pi6A_	Alignment	not modelled	99.6	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** yeast actin interacting protein 1 (aip1), orthorhombic crystal form
72	d1yfqa_	Alignment	not modelled	99.6	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**Cell cycle arrest protein BUB3
73	c2vduB_	Alignment	not modelled	99.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase- **PDBTitle:** structure of trm8-trm82, the yeast trna m7g methylation2 complex
74	c3lrvA_	Alignment	not modelled	99.6	13	**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.
75	d1vyhc1	Alignment	not modelled	99.6	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
76	c3ei3B_	Alignment	not modelled	99.6	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-drddb2 complex
77	d2ovrb2	Alignment	not modelled	99.6	13	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
78	c3ei4D_	Alignment	not modelled	99.6	9	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-hsddb2 complex
79	d1nr0a1	Alignment	not modelled	99.6	13	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat

80	c1vyhT_	Alignment	not modelled	99.6	10	**PDB header:**hydrolase **Chain:** T: **PDB Molecule:**platelet-activating factor acetylhydrolase ib **PDBTitle:** paf-ah holoenzyme: lis1/alfa2
81	c3vh0C_	Alignment	not modelled	99.6	15	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce; **PDBTitle:** crystal structure of e. coli ynce complexed with dna
82	c3eg6A_	Alignment	not modelled	99.6	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**wd repeat-containing protein 5; **PDBTitle:** structure of wdr5 bound to mll1 peptide
83	c2xznR_	Alignment	not modelled	99.6	19	**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
84	c3fm0A_	Alignment	not modelled	99.6	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**protein ciao1; **PDBTitle:** crystal structure of wd40 protein ciao1
85	d2dg1a1	Alignment	not modelled	99.6	13	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
86	c2pm9A_	Alignment	not modelled	99.5	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
87	c3mmyE_	Alignment	not modelled	99.5	10	**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
88	c3acpA_	Alignment	not modelled	99.5	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
89	d1nr0a2	Alignment	not modelled	99.5	14	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
90	d1erja_	Alignment	not modelled	99.5	17	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
91	d1jofa_	Alignment	not modelled	99.5	12	**Fold:**7-bladed beta-propeller **Superfamily:**3-carboxy-cis,cis-mucoante lactonizing enzyme **Family:**3-carboxy-cis,cis-mucoante lactonizing enzyme
92	c2iwaA_	Alignment	not modelled	99.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** unbound glutaminyl cyclotransferase from carica papaya.
93	c4a11B_	Alignment	not modelled	99.5	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna excision repair protein ercc-8; **PDBTitle:** structure of the hsddb1-hscsa complex
94	c3dwlH_	Alignment	not modelled	99.5	12	**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
95	d1tl2a_	Alignment	not modelled	99.5	15	**Fold:**5-bladed beta-propeller **Superfamily:**Tachylectin-2 **Family:**Tachylectin-2
96	d1nexb2	Alignment	not modelled	99.5	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
97	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
98	c3frxB_	Alignment	not modelled	99.5	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.
99	c3qqzA_	Alignment	not modelled	99.5	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
100	c3ow8A_	Alignment	not modelled	99.4	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd repeat-containing protein 61; **PDBTitle:** crystal structure of the wd repeat-containing protein 61
101	c3bg1E_	Alignment	not modelled	99.4	11	**PDB header:**protein transport, hydrolase **Chain:** E: **PDB Molecule:**protein sec13 homolog; **PDBTitle:** architecture of a coat for the nuclear pore membrane
102	c2pm7B_	Alignment	not modelled	99.4	12	**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
103	c3cfvA_	Alignment	not modelled	99.4	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
104	d1sq9a_	Alignment	not modelled	99.4	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
105	c3dr2A_	Alignment	not modelled	99.4	14	**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

106	c3i2nA_	Alignment	not modelled	99.4	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd repeat-containing protein 92; **PDBTitle:** crystal structure of wd40 repeats protein wdr92
107	d2ghsa1	Alignment	not modelled	99.4	20	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
108	c2ghsA_	Alignment	not modelled	99.4	20	**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
109	c3s25A_	Alignment	not modelled	99.4	14	**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
110	c3greA_	Alignment	not modelled	99.4	15	**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
111	c3dw8B_	Alignment	not modelled	99.4	13	**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
112	c2qxvA_	Alignment	not modelled	99.4	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**embryonic ectoderm development; **PDBTitle:** structural basis of ezh2 recognition by eed
113	c3e5zA_	Alignment	not modelled	99.4	12	**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.
114	c3eweC_	Alignment	not modelled	99.4	11	**PDB header:**protein transport,structural protein **Chain:** C: **PDB Molecule:**nucleoporin seh1; **PDBTitle:** crystal structure of the nup85/seh1 complex
115	c3odtB_	Alignment	not modelled	99.4	13	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of wd40 beta propeller domain of doa1
116	d1pgua1	Alignment	not modelled	99.3	9	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
117	c3jzhA_	Alignment	not modelled	99.3	12	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb protein eed; **PDBTitle:** eed-h3k79me3
118	c2zkqa_	Alignment	not modelled	99.3	13	**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
119	d1k8kc_	Alignment	not modelled	99.3	11	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
120	c3dsmA_	Alignment	not modelled	99.3	7	**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.