Phyre^2

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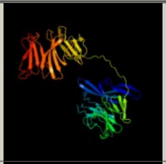
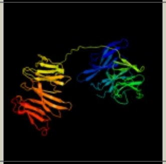
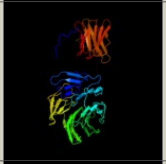
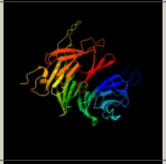
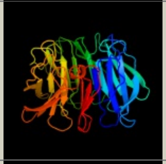
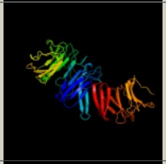
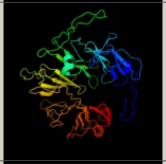
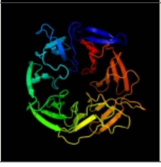
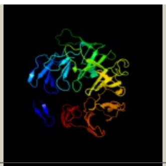
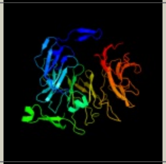
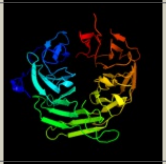
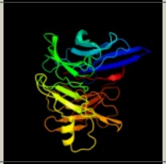
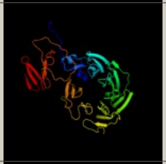
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1k32E_	Alignment		100.0	10	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** crystal structure of the tricorn protease
2	c1n6dE_	Alignment		100.0	10	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
3	c1nr0A_	Alignment		100.0	12	**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).
4	c3pe7A_	Alignment		100.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**oligogalacturonate lyase; **PDBTitle:** oligogalacturonate lyase in complex with manganese
5	c3iytG_	Alignment		100.0	16	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** structure of an apoptosome-procaspase-9 card complex
6	d1k32a3	Alignment		100.0	10	**Fold:**7-bladed beta-propeller **Superfamily:**Tricorn protease domain 2 **Family:**Tricorn protease domain 2
7	c3dm0A_	Alignment		100.0	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
8	c1pi6A_	Alignment		99.9	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** yeast actin interacting protein 1 (aip1), orthorhombic crystal form
9	d1xfda1	Alignment		99.9	11	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
10	c2w8bB_	Alignment		99.9	13	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal
11	c3c5mC_	Alignment		99.9	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

12	d1orva1	Alignment		99.9	10	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
13	c3bwsA_	Alignment		99.9	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein lp49; **PDBTitle:** crystal structure of the leptospiral antigen lp49
14	d2bgra1	Alignment		99.9	9	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
15	d1nira2	Alignment		99.9	10	**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
16	c2ivzD_	Alignment		99.9	12	**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
17	c1gq1B_	Alignment		99.9	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
18	c2oajA_	Alignment		99.9	14	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
19	c3jroA_	Alignment		99.9	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
20	d1qksa2	Alignment		99.9	10	**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
21	c3mkqA_	Alignment	not modelled	99.9	9	**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
22	c1nnoA_	Alignment	not modelled	99.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrite reductase; **PDBTitle:** conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
23	d1gxra_	Alignment	not modelled	99.9	13	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
24	d1jmxb_	Alignment	not modelled	99.9	13	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
25	c1xfdD_	Alignment	not modelled	99.9	11	**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
26	c2ecfA_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
27	c1z68A_	Alignment	not modelled	99.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fibroblast activation protein, alpha subunit; **PDBTitle:** crystal structure of human fibroblast activation protein alpha
28	c2pm9A_	Alignment	not modelled	99.9	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec31;

28	c2pm9A_	Alignment	not modelled	99.9	15	**PDBTitle:** crystal structure of yeast sec13/31 vertex element of the2 copii vesicular coat
29	c2qtbB_	Alignment	not modelled	99.9	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl peptidase 4; **PDBTitle:** human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
30	c2g5tA_	Alignment	not modelled	99.9	8	**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
31	c3fgbB_	Alignment	not modelled	99.9	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.
32	c1r5mA_	Alignment	not modelled	99.9	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sir4-interacting protein sif2; **PDBTitle:** crystal structure of the c-terminal wd40 domain of sif2
33	c2eepA_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl aminopeptidase iv, putative; **PDBTitle:** prolyl tripeptidyl aminopeptidase complexed with an inhibitor
34	c3ei4D_	Alignment	not modelled	99.9	15	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-hsddb2 complex
35	d1k32a2	Alignment	not modelled	99.9	14	**Fold:**6-bladed beta-propeller **Superfamily:**Tricorn protease N-terminal domain **Family:**Tricorn protease N-terminal domain
36	c2j04B_	Alignment	not modelled	99.9	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ydr362cp; **PDBTitle:** the tau60-tau91 subcomplex of yeast transcription factor2 iiic
37	c2j57J_	Alignment	not modelled	99.9	13	**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.
38	c2i0tB_	Alignment	not modelled	99.9	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
39	d2hqsa1	Alignment	not modelled	99.9	9	**Fold:**6-bladed beta-propeller **Superfamily:**TolB, C-terminal domain **Family:**TolB, C-terminal domain
40	c2h47F_	Alignment	not modelled	99.9	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)
41	c3dw8B_	Alignment	not modelled	99.8	11	**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
42	c2gopB_	Alignment	not modelled	99.8	9	**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
43	d1fwxa2	Alignment	not modelled	99.8	7	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
44	d1erja_	Alignment	not modelled	99.8	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
45	c3ei3B_	Alignment	not modelled	99.8	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-drddb2 complex
46	d1yfqa_	Alignment	not modelled	99.8	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**Cell cycle arrest protein BUB3
47	c2ojhA_	Alignment	not modelled	99.8	18	**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
48	c2pbiB_	Alignment	not modelled	99.8	14	**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
49	d2madh_	Alignment	not modelled	99.8	12	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
50	d2bbkh_	Alignment	not modelled	99.8	12	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
51	c3c75J_	Alignment	not modelled	99.8	10	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
52	c3acpA_	Alignment	not modelled	99.8	11	**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
53	c2w18A_	Alignment	not modelled	99.8	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
54	c1qniE_		Alignment	not modelled	99.8	12	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from2 pseudomonas nautica, at 2.4a resolution
55	c3fm0A_	Alignment	not modelled	99.8	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**protein ciao1; **PDBTitle:** crystal structure of wd40 protein ciao1
56	d1nr0a1	Alignment	not modelled	99.8	15	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
57	c3i2nA_	Alignment	not modelled	99.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd repeat-containing protein 92; **PDBTitle:** crystal structure of wd40 repeats protein wdr92
58	d1ospo_	Alignment	not modelled	99.8	6	**Fold:**open-sided beta-meander **Superfamily:**Outer surface protein **Family:**Outer surface protein
59	d1tbga_	Alignment	not modelled	99.8	11	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
60	d1qnia2	Alignment	not modelled	99.8	11	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
61	c3jzhA_	Alignment	not modelled	99.8	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb protein eed; **PDBTitle:** eed-h3k79me3
62	d1l0qa2	Alignment	not modelled	99.8	13	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**YVTN repeat
63	c2xznR_	Alignment	not modelled	99.8	12	**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
64	d1nexb2	Alignment	not modelled	99.8	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
65	c3u4yA_	Alignment	not modelled	99.8	15	**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.
66	c3hfqB_	Alignment	not modelled	99.8	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.
67	c2gnqA_	Alignment	not modelled	99.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd-repeat protein 5; **PDBTitle:** structure of wdr5
68	c3mmyE_	Alignment	not modelled	99.8	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
69	c2qxvA_	Alignment	not modelled	99.8	12	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**embryonic ectoderm development; **PDBTitle:** structural basis of ezh2 recognition by eed
70	c3iz6a_	Alignment	not modelled	99.8	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
71	c4a11B_	Alignment	not modelled	99.8	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna excision repair protein ercc-8; **PDBTitle:** structure of the hsddb1-hscsa complex
72	c3frxB_	Alignment	not modelled	99.8	13	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein subunit beta- **PDBTitle:** crystal structure of the yeast orthologue of rack1, asc1.
73	c3jrpA_	Alignment	not modelled	99.8	7	**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
74	d1pgua1	Alignment	not modelled	99.8	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
75	d2ovrb2	Alignment	not modelled	99.8	8	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
76	d1vyhc1	Alignment	not modelled	99.7	7	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
77	c3eg6A_	Alignment	not modelled	99.7	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**wd repeat-containing protein 5; **PDBTitle:** structure of wdr5 bound to mll1 peptide
78	c1fwxB_	Alignment	not modelled	99.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrous oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from p. denitrificans
79	c1vyhT_	Alignment	not modelled	99.7	7	**PDB header:**hydrolase **Chain:** T: **PDB Molecule:**platelet-activating factor acetylhydrolase ib **PDBTitle:** paf-ah holoenzyme: lis1/alfa2

80	c1nexD_	Alignment	not modelled	99.7	11	**PDB header:**ligase, cell cycle **Chain:** D: **PDB Molecule:**cdc4 protein; **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
81	d1k8kc_	Alignment	not modelled	99.7	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
82	d1sq9a_	Alignment	not modelled	99.7	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
83	c2ovqB_	Alignment	not modelled	99.7	12	**PDB header:**transcription/cell cycle **Chain:** B: **PDB Molecule:**f-box/wd repeat protein 7; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
84	c3dwlH_	Alignment	not modelled	99.7	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
85	d1pbyb_	Alignment	not modelled	99.7	12	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
86	c2vduB_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase- **PDBTitle:** structure of trm8-trm82, the yeast trna m7g methylation2 complex
87	d1ri6a_	Alignment	not modelled	99.7	12	**Fold:**7-bladed beta-propeller **Superfamily:**Putative isomerase YbhE **Family:**Putative isomerase YbhE
88	c3fhcA_	Alignment	not modelled	99.7	12	**PDB header:**transport protein/hydrolase **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup214; **PDBTitle:** crystal structure of human dbp5 in complex with nup214
89	c3vh0C_	Alignment	not modelled	99.7	13	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce; **PDBTitle:** crystal structure of e. coli ynce complexed with dna
90	d1tl2a_	Alignment	not modelled	99.7	12	**Fold:**5-bladed beta-propeller **Superfamily:**Tachylectin-2 **Family:**Tachylectin-2
91	c3ow8A_	Alignment	not modelled	99.7	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd repeat-containing protein 61; **PDBTitle:** crystal structure of the wd repeat-containing protein 61
92	d1qfma1	Alignment	not modelled	99.7	12	**Fold:**7-bladed beta-propeller **Superfamily:**Peptidase/esterase 'gauge' domain **Family:**Prolyl oligopeptidase, N-terminal domain
93	c3g4hB_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**regucalcin; **PDBTitle:** crystal structure of human senescence marker protein-30 (zinc bound)
94	d1nr0a2	Alignment	not modelled	99.7	8	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
95	c3greA_	Alignment	not modelled	99.7	13	**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
96	c3lrvA_	Alignment	not modelled	99.7	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.
97	c2hu7A_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
98	c1yr2A_	Alignment	not modelled	99.6	13	**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
99	c2aq5A_	Alignment	not modelled	99.6	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of murine coronin-1
100	c3odtB_	Alignment	not modelled	99.6	7	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of wd40 beta propeller domain of doa1
101	c2bklB_	Alignment	not modelled	99.6	13	**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
102	c3sbrF_	Alignment	not modelled	99.6	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
103	c1qfmA_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
104	c3e5zA_	Alignment	not modelled	99.5	13	**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.
105	c2g8sB_	Alignment	not modelled	99.5	11	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**glucose/sorbosone dehydrogenases; **PDBTitle:** crystal structure of the soluble aldose sugar dehydrogenase2 (asd) from escherichia coli in the apo-form

106	c2hesX_	Alignment	not modelled	99.5	11	**PDB header:**biosynthetic protein **Chain:** X: **PDB Molecule:**ydr267cp; **PDBTitle:** cytosolic iron-sulphur assembly protein- 1
107	c3cfvA_	Alignment	not modelled	99.5	14	**PDB header:**histone/chaperone **Chain:** A: **PDB Molecule:**histone-binding protein rbbp7; **PDBTitle:** structural basis of the interaction of rbap46/rbap48 with2 histone h4
108	c2pm7B_	Alignment	not modelled	99.5	14	**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
109	c2zkqa_	Alignment	not modelled	99.5	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
110	c3bg1E_	Alignment	not modelled	99.5	10	**PDB header:**protein transport, hydrolase **Chain:** E: **PDB Molecule:**protein sec13 homolog; **PDBTitle:** architecture of a coat for the nuclear pore membrane
111	c1p22A_	Alignment	not modelled	99.4	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**f-box/wd-repeat protein 1a; **PDBTitle:** structure of a beta-trcp1-skp1-beta-catenin complex:2 destruction motif binding and lysine specificity on the3 scfbeta-trcp1 ubiquitin ligase
112	c2oitA_	Alignment	not modelled	99.4	15	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**nucleoporin 214kda; **PDBTitle:** crystal structure of the n-terminal domain of the human2 proto-oncogene nup214/can
113	d2dg1a1	Alignment	not modelled	99.4	9	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
114	c3azqA_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
115	c3eweC_	Alignment	not modelled	99.4	9	**PDB header:**protein transport,structural protein **Chain:** C: **PDB Molecule:**nucleoporin seh1; **PDBTitle:** crystal structure of the nup85/seh1 complex
116	c3iumA_	Alignment	not modelled	99.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** appep_wtx opened state
117	c3dr2A_	Alignment	not modelled	99.4	13	**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
118	d1pgua2	Alignment	not modelled	99.3	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
119	d2p4oa1	Alignment	not modelled	99.3	10	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**All0351-like
120	d1pjxa_	Alignment	not modelled	99.3	11	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like