

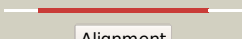






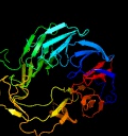






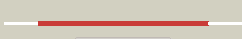







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3212_(-)_3589390_3590613
Date	Thu Aug 8 16:20:41 BST 2019
Unique Job ID	2bc0aa702801dce6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kv9A_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: type ii quinoxemoprotein alcohol dehydrogenase; PDBTitle: structure at 1.9 a resolution of a quinoxemoprotein alcohol2 dehydrogenase from pseudomonas putida hk5
2	c4pk1A_	 Alignment		100.0	14	PDB header: protein binding Chain: A: PDB Molecule: chimera protein of outer membrane protein assembly factors PDBTitle: structure of bamb fused to a bama potra domain fragment
3	c1kb0A_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: quinoxemoprotein alcohol dehydrogenase; PDBTitle: crystal structure of quinoxemoprotein alcohol dehydrogenase from2 comamonas testosteroni
4	c1yiqA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: quinoxemoprotein alcohol dehydrogenase; PDBTitle: molecular cloning and structural analysis of2 quinoxemoprotein alcohol dehydrogenase adhiig from3 pseudomonas putida hk5. compariison to the other4 quinoxemoprotein alcohol dehydrogenase adhiib found in the5 same microorganism.
5	d1kb0a2	 Alignment		100.0	15	Fold: 8-bladed beta-propeller Superfamily: Quinoxemoprotein alcohol dehydrogenase-like Family: Quinoxemoprotein alcohol dehydrogenase-like
6	c4cvcA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of quinone-dependent alcohol dehydrogenase from2 pseudogluconobacter saccharoketogenenes with zinc in the active site
7	d2ad6a1	 Alignment		100.0	14	Fold: 8-bladed beta-propeller Superfamily: Quinoxemoprotein alcohol dehydrogenase-like Family: Quinoxemoprotein alcohol dehydrogenase-like
8	c4mh1A_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: sorbose dehydrogenase; PDBTitle: crystal structure and functional studies of quinoxemoprotein I-sorbose2 dehydrogenase from ketogulonigenium vulgare y25
9	c6damA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: lanthanide-dependent methanol dehydrogenase xoxf; PDBTitle: crystal structure of lanthanide-dependent methanol dehydrogenase xoxf2 from methylmicrobium buryatense 5g
10	d1flga_	 Alignment		100.0	15	Fold: 8-bladed beta-propeller Superfamily: Quinoxemoprotein alcohol dehydrogenase-like Family: Quinoxemoprotein alcohol dehydrogenase-like
11	d1kv9a2	 Alignment		100.0	15	Fold: 8-bladed beta-propeller Superfamily: Quinoxemoprotein alcohol dehydrogenase-like Family: Quinoxemoprotein alcohol dehydrogenase-like

12	c4maeB_	Alignment		100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: methanol dehydrogenase; PDBTitle: methanol dehydrogenase from methylacidiphilum fumarolicum solv
13	d1w6sa_	Alignment		100.0	12	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
14	d1lrwa_	Alignment		100.0	14	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
15	c3p1A_	Alignment		100.0	14	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.
16	c4hdjA_	Alignment		100.0	16	PDB header: protein binding Chain: A: PDB Molecule: outer membrane protein assembly factor bamb; PDBTitle: crystal structure of bamb from pseudomonas aeruginosa
17	c3q54A_	Alignment		100.0	13	PDB header: lipid binding protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfgl; PDBTitle: crystal structure of escherichia coli bamb
18	c4immA_	Alignment		99.9	11	PDB header: chaperone Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfgl; PDBTitle: the crystal structure of bamb from moraxella catarrhalis
19	c4yzsB_	Alignment		99.9	17	PDB header: signaling protein Chain: B: PDB Molecule: eukaryotic translation initiation factor 2-alpha kinase 3; PDBTitle: crystal structures reveal transient perk luminal domain2 tetramerization in er stress signaling
20	c3hxiA_	Alignment		99.8	10	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
21	c5sv7D_	Alignment	not modelled	99.8	15	PDB header: translation Chain: D: PDB Molecule: eukaryotic translation initiation factor 2-alpha kinase 3; PDBTitle: the crystal structure of a chaperone
22	c5v1dA_	Alignment	not modelled	99.8	14	PDB header: transferase/substrate Chain: A: PDB Molecule: eif2ak3 protein; PDBTitle: complex structure of the bovine perk luminal domain and its substrate2 peptide
23	c2be1A_	Alignment	not modelled	99.7	15	PDB header: transcription Chain: A: PDB Molecule: serine/threonine-protein kinase/endoribonuclease ire1; PDBTitle: structure of the compact luminal domain of yeast ire1
24	c6rteB_	Alignment	not modelled	99.7	9	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
25	c2hz6A_	Alignment	not modelled	99.7	11	PDB header: signaling protein Chain: A: PDB Molecule: endoplasmic reticulum to nucleus signalling 1 PDBTitle: the crystal structure of human ire1-alpha luminal domain
26	c4zyzA_	Alignment	not modelled	99.7	9	PDB header: signaling protein Chain: A: PDB Molecule: eukaryotic translation initiation factor 2-alpha kinase 3; PDBTitle: crystal structures reveal transient perk luminal domain2 tetramerization in er stress signaling
27	c6cmkB_	Alignment	not modelled	99.6	14	PDB header: metal binding protein Chain: B: PDB Molecule: aztd protein; PDBTitle: crystal structure of citrobacter koseri aztd
28	c6ck1C_	Alignment	not modelled	99.6	16	PDB header: metal binding protein Chain: C: PDB Molecule: a1b2f4 protein; PDBTitle: crystal structure of paracoccus denitrificans aztd

29	c3no2A	Alignment	not modelled	99.6	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein of unknown function (baccac_01654) from <i>Bacteroides caccae</i> at 1.35 Å resolution
30	d1jmbx	Alignment	not modelled	99.5	12	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
31	d2madh	Alignment	not modelled	99.5	12	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
32	d1pbyb	Alignment	not modelled	99.4	12	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
33	c2j57J	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: x-ray reduced <i>Paracoccus denitrificans</i> methylamine dehydrogenase n-quinol in complex with amicyanin.
34	d2bbkh	Alignment	not modelled	99.2	11	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
35	c3mbrX	Alignment	not modelled	99.1	11	PDB header: transferase Chain: X: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of the glutamyl cyclase from <i>Xanthomonas campestris</i>
36	c1nnoA	Alignment	not modelled	99.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite reductase2 from <i>Pseudomonas aeruginosa</i>
37	c5f30B	Alignment	not modelled	99.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: thiocyanate dehydrogenase; PDBTitle: thiocyanate dehydrogenase from <i>Thioalkalivibrio paradoxus</i>
38	c3c75J	Alignment	not modelled	99.1	17	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: <i>Paracoccus versutus</i> methylamine dehydrogenase in complex2 with amicyanin
39	c2i0tB	Alignment	not modelled	99.1	10	PDB header: oxidoreductase Chain: B: PDB Molecule: aromatic amine dehydrogenase; PDBTitle: crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
40	d1l0qa2	Alignment	not modelled	99.0	15	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: YVTN repeat
41	c3nolA	Alignment	not modelled	99.0	9	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of <i>Zymomonas mobilis</i> glutamyl cyclase (trigonal2 form)
42	c2h47F	Alignment	not modelled	98.9	12	PDB header: oxidoreductase/electron transport Chain: F: PDB Molecule: aromatic amine dehydrogenase; PDBTitle: crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from <i>Alicyclohexium3 faecalis</i> (form 1)
43	c3dsmA	Alignment	not modelled	98.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bacuni_02894; PDBTitle: crystal structure of the surface layer protein bacuni_02894 from <i>Bacteroides uniformis</i> , northeast structural genomics consortium3 target btr193d.
44	c1gq1B	Alignment	not modelled	98.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome cd1 nitrite reductase; PDBTitle: cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
45	c1l0qC	Alignment	not modelled	98.9	13	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
46	c3vh0C	Alignment	not modelled	98.8	15	PDB header: protein binding/dna Chain: C: PDB Molecule: uncharacterized protein ynce; PDBTitle: crystal structure of <i>E. coli</i> ynce complexed with dna
47	c3nokB	Alignment	not modelled	98.6	10	PDB header: transferase Chain: B: PDB Molecule: glutamyl cyclase; PDBTitle: crystal structure of <i>Myxococcus xanthus</i> glutamyl cyclase
48	c4nlmA	Alignment	not modelled	98.6	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo1340 protein; PDBTitle: 1.18 Å resolution crystal structure of uncharacterized protein2 lmo1340 from <i>Listeria monocytogenes</i> egd-e
49	c3u4yA	Alignment	not modelled	98.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein (dtox_1751)2 from <i>Desulfotomaculum acetoxidans</i> dsm 771.
50	c5n1aB	Alignment	not modelled	98.4	9	PDB header: translation Chain: B: PDB Molecule: utp4; PDBTitle: crystal structure of utp4 from <i>Chaetomium thermophilum</i>
51	c5juyB	Alignment	not modelled	98.4	10	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
52	d1nira2	Alignment	not modelled	98.2	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
53	c2iwaA	Alignment	not modelled	98.2	11	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: unbound glutamyl cyclotransferase from <i>Carica papaya</i> .
54	c2hv6A	Alignment	not modelled	98.2	16	PDB header: cell adhesion Chain: A: PDB Molecule: type 4 fimbrial biogenesis protein pily1;

54	c31xvA	Alignment	not modelled	98.2	10	PDBTitle: crystal structure of pseudomonas aeruginosa pily1 c-terminal2 domain PDB header: oxidoreductase
55	c1fwxB	Alignment	not modelled	98.0	8	Chain: B: PDB Molecule: nitrous oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from p. denitrificans
56	c6nd4O	Alignment	not modelled	98.0	15	PDB header: ribosome Chain: O: PDB Molecule: utp1; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
57	d1k32a2	Alignment	not modelled	97.8	10	Fold: 6-bladed beta-propeller Superfamily: Tricorn protease N-terminal domain Family: Tricorn protease N-terminal domain
58	c3bwsA	Alignment	not modelled	97.8	11	PDB header: unknown function Chain: A: PDB Molecule: protein lp49; PDBTitle: crystal structure of the leptospiral antigen lp49
59	d1fwxa2	Alignment	not modelled	97.7	8	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
60	c1n6dE	Alignment	not modelled	97.7	10	PDB header: hydrolase Chain: E: PDB Molecule: tricorn protease; PDBTitle: tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
61	c1k32E	Alignment	not modelled	97.7	10	PDB header: hydrolase Chain: E: PDB Molecule: tricorn protease; PDBTitle: crystal structure of the tricorn protease
62	c5k1bB	Alignment	not modelled	97.7	9	PDB header: protein binding/hydrolase Chain: B: PDB Molecule: wd repeat-containing protein 48; PDBTitle: crystal structure of the uaf1/usp12 complex in f222 space group
63	c5dfzB	Alignment	not modelled	97.7	12	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase vps15; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
64	c3dm0A	Alignment	not modelled	97.7	10	PDB header: sugar binding protein,signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein fused with rack1; PDBTitle: maltose binding protein fusion with rack1 from a. thaliana
65	c3e5zA	Alignment	not modelled	97.6	11	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.
66	d1qksa2	Alignment	not modelled	97.5	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
67	d1qnia2	Alignment	not modelled	97.5	7	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
68	c6nd4O	Alignment	not modelled	97.4	6	PDB header: ribosome Chain: Q: PDB Molecule: utp12; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
69	c3wj9A	Alignment	not modelled	97.4	8	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2a; PDBTitle: crystal structure of the eukaryotic initiation factor
70	c1qniE	Alignment	not modelled	97.3	7	PDB header: oxidoreductase Chain: E: PDB Molecule: nitrous-oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from pseudomonas nautica_2 at 2.4a resolution
71	c4v0nH	Alignment	not modelled	97.2	12	PDB header: hydrolase/structural protein Chain: H: PDB Molecule: bardet-biedl syndrome 1 protein; PDBTitle: crystal structure of bbs1n in complex with arl6dn, soaked with mercury
72	c6nd4T	Alignment	not modelled	97.2	8	PDB header: ribosome Chain: T: PDB Molecule: utp21; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
73	c3g4hB	Alignment	not modelled	97.2	9	PDB header: hydrolase Chain: B: PDB Molecule: regucalcin; PDBTitle: crystal structure of human senescence marker protein-30 (zinc bound)
74	c2ghsA	Alignment	not modelled	97.1	12	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
75	d2ghsa1	Alignment	not modelled	97.1	12	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
76	c3pe7A	Alignment	not modelled	97.1	11	PDB header: lyase Chain: A: PDB Molecule: oligogalacturonate lyase; PDBTitle: oligogalacturonate lyase in complex with manganese
77	c5cvlA	Alignment	not modelled	96.8	9	PDB header: protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48 (uaf-1), residues 2-580
78	d1k32a3	Alignment	not modelled	96.7	12	Fold: 7-bladed beta-propeller Superfamily: Tricorn protease domain 2 Family: Tricorn protease domain 2
79	c3dr2A	Alignment	not modelled	96.7	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

80	c6nd4U	Alignment	not modelled	96.7	10	PDB header: ribosome Chain: U: PDB Molecule: sof1; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
81	c6nd4W	Alignment	not modelled	96.7	9	PDB header: ribosome Chain: W: PDB Molecule: utp7; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
82	d2p4oa1	Alignment	not modelled	96.7	9	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: All0351-like
83	c6dloA	Alignment	not modelled	96.6	10	PDB header: cytosolic protein Chain: A: PDB Molecule: leucine-rich repeat serine/threonine-protein kinase 2; PDBTitle: crystal structure of lrrk2 wd40 domain dimer
84	c6nd4N	Alignment	not modelled	96.6	9	PDB header: ribosome Chain: N: PDB Molecule: utp4; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
85	c2vz1A	Alignment	not modelled	96.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: galactose oxidase; PDBTitle: premat-galactose oxidase
86	c4wjuB	Alignment	not modelled	96.4	10	PDB header: biosynthetic protein Chain: B: PDB Molecule: ribosome assembly protein 4; PDBTitle: crystal structure of rsa4 from saccharomyces cerevisiae
87	c3lrvA	Alignment	not modelled	96.4	8	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.
88	c5a1vK	Alignment	not modelled	96.4	8	PDB header: transport protein Chain: K: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat linkage i
89	c3j65q	Alignment	not modelled	96.2	10	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l18; PDBTitle: arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
90	c5tztT	Alignment	not modelled	96.2	9	PDB header: translation Chain: T: PDB Molecule: utp21; PDBTitle: architecture of the yeast small subunit processome
91	c4czvB	Alignment	not modelled	96.2	12	PDB header: gene regulation Chain: B: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan2; PDBTitle: structure of the neurospora crassa pan2 wd40 domain
92	c4nnsxA	Alignment	not modelled	96.1	9	PDB header: protein binding Chain: A: PDB Molecule: u3 small nucleolar rna-associated protein 21; PDBTitle: crystal structure of the utp21 tandem wd domain
93	c5cvoD	Alignment	not modelled	96.1	10	PDB header: hydrolase/protein binding Chain: D: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
94	c4by2C	Alignment	not modelled	96.0	9	PDB header: structural protein Chain: C: PDB Molecule: anastral spindle 2, sas 4; PDBTitle: sas-4 (dcpap) tcp domain in complex with a proline rich motif of ana22 (dstil) of drosophila melanogaster
95	c4yhCA	Alignment	not modelled	96.0	11	PDB header: structural protein Chain: A: PDB Molecule: sterol regulatory element-binding protein cleavage- PDBTitle: crystal structure of the wd40 domain of scap from fission yeast
96	c3iytG	Alignment	not modelled	96.0	9	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
97	c1nexD	Alignment	not modelled	95.8	11	PDB header: ligase, cell cycle Chain: D: PDB Molecule: cdc4 protein; PDBTitle: crystal structure of scskp1-sccd4-cpd peptide complex
98	c5c86A	Alignment	not modelled	95.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: kelch domain-containing protein; PDBTitle: novel fungal alcohol oxidase with catalytic diversity among the aa52 family, apo form
99	c5a31R	Alignment	not modelled	95.7	10	PDB header: cell cycle Chain: R: PDB Molecule: the anaphase-promoting complex chain r; PDBTitle: structure of the human apc-cdh1-hsl1-ubch10 complex.
100	c5wbiA	Alignment	not modelled	95.6	10	PDB header: protein binding Chain: A: PDB Molecule: regulatory-associated protein of tor 1; PDBTitle: crystal structure of the arabidopsis thaliana raptor
101	c5cvoA	Alignment	not modelled	95.6	9	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
102	c2w18A	Alignment	not modelled	95.5	8	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
103	c3sbrF	Alignment	not modelled	95.5	11	PDB header: oxidoreductase Chain: F: PDB Molecule: nitrous-oxide reductase; PDBTitle: pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
104	c3fgbB	Alignment	not modelled	95.4	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein q89zh8_bactn; PDBTitle: crystal structure of the q89zh8_bactn protein from bacteroides2 thetaiotaomicron. northeast structural genomics consortium target3 btr289b.
105	c4yczA	Alignment	not modelled	95.4	12	PDB header: structural protein Chain: A: PDB Molecule: fusion protein of sec13 and nup145c; PDBTitle: y-complex hub (nup85-nup120-nup145c-sec13 complex) from m. thermophila2 (a.k.a. t. heterothallica)

106	c6nd4L_	Alignment	not modelled	95.4	7	PDB header: ribosome Chain: L: PDB Molecule: utp5; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
107	c4ui9R_	Alignment	not modelled	95.1	13	PDB header: cell cycle Chain: R: PDB Molecule: fizzy-related protein homolog; PDBTitle: atomic structure of the human anaphase-promoting complex
108	c4qriA_	Alignment	not modelled	95.0	16	PDB header: hydrolase Chain: A: PDB Molecule: putative 6-phosphogluconolactonase; PDBTitle: crystal structure of a putative 6-phosphogluconolactonase2 (bacuni_04672) from bacteroides uniformis atcc 8492 at 2.20 a3 resolution
109	c5nzvC_	Alignment	not modelled	94.7	8	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copi coat linkage iv
110	c4ui9I_	Alignment	not modelled	94.6	13	PDB header: cell cycle Chain: I: PDB Molecule: anaphase-promoting complex subunit 4; PDBTitle: atomic structure of the human anaphase-promoting complex
111	c5h64b_	Alignment	not modelled	94.6	11	PDB header: transferase Chain: B: PDB Molecule: regulatory-associated protein of mtor; PDBTitle: cryo-em structure of mtorc1
112	c5i5iA_	Alignment	not modelled	94.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrous-oxide reductase; PDBTitle: shewanella denitrificans nitrous oxide reductase, app form
113	d1mdah_	Alignment	not modelled	94.0	11	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
114	d1k3ia3	Alignment	not modelled	93.9	15	Fold: 7-bladed beta-propeller Superfamily: Galactose oxidase, central domain Family: Galactose oxidase, central domain
115	d1ospo_	Alignment	not modelled	93.8	11	Fold: open-sided beta-meander Superfamily: Outer surface protein Family: Outer surface protein
116	c5a5uB_	Alignment	not modelled	93.7	11	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: structure of mammalian eif3 in the context of the 43s preinitiation2 complex
117	c6chgD_	Alignment	not modelled	93.1	8	PDB header: transferase Chain: D: PDB Molecule: klla0a08800p; PDBTitle: crystal structure of the yeast compass catalytic module
118	c4unmB_	Alignment	not modelled	92.5	13	PDB header: metal binding protein Chain: B: PDB Molecule: secreted protein; PDBTitle: structure of galactose oxidase homologue from streptomyces lividans
119	c3hfgB_	Alignment	not modelled	92.1	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein lp_2219; PDBTitle: crystal structure of the lp_2219 protein from lactobacillus plantarum.2 northeast structural genomics consortium target lpr118.
120	c4bh6H_	Alignment	not modelled	92.1	9	PDB header: cell cycle Chain: H: PDB Molecule: apc/c activator protein cdh1; PDBTitle: insights into degron recognition by apc coactivators from2 the structure of an acm1-cdh1 complex