Phyre2

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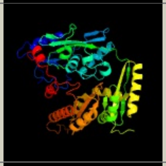
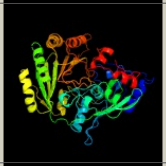
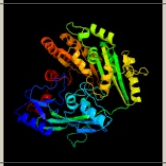
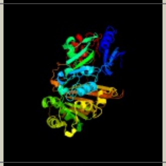
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vfvA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xylitol oxidase; **PDBTitle:** alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
2	c4ml8C_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytokinin oxidase 2; **PDBTitle:** structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
3	c4fdoA_	Alignment		100.0	17	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**oxidoreductase dpre1; **PDBTitle:** mycobacterium tuberculosis dpre1 in complex with ct319
4	c3bw7A_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 1; **PDBTitle:** maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
5	c4oalB_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytokinin dehydrogenase 4; **PDBTitle:** crystal structure of maize cytokinin oxidase/dehydrogenase 4 (zmcko4)2 in complex with phenylurea inhibitor cppu in alternative spacegroup
6	c6c80B_	Alignment		100.0	20	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cytokinin oxidase luckx1.1; **PDBTitle:** crystal structure of a flax cytokinin oxidase
7	c4bc9C_	Alignment		100.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase, peroxisomal; **PDBTitle:** mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl
8	c3pm9A_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
9	c2exrA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 7; **PDBTitle:** x-ray structure of cytokinin oxidase/dehydrogenase (ckx) from2 arabidopsis thaliana at5g21482
10	c2bvfA_	Alignment		100.0	15	**PDB header:**oxidase **Chain:** A: **PDB Molecule:**6-hydroxy-d-nicotine oxidase; **PDBTitle:** crystal structure of 6-hydoxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
11	c4ud8B_	Alignment		100.0	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fad-binding and bbe domain-containing protein; **PDBTitle:** atbbe15

12	c3vteA_	Alignment		100.0	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tetrahydrocannabinolic acid synthase; **PDBTitle:** crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
13	c5l6fA_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad linked oxidase-like protein; **PDBTitle:** xylooligosaccharide oxidase from myceliophthora thermophila c1 in2 complex with xylobiose
14	c1wveB_	Alignment		100.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-cresol dehydrogenase [hydroxylating] **PDBTitle:** p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
15	c6f74B_	Alignment		100.0	12	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**alcohol oxidase; **PDBTitle:** crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1
16	c3w8wA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative fad-dependent oxygenase encm; **PDBTitle:** the crystal structure of encm
17	c6eo5A_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ppbbe-like 1 d396n; **PDBTitle:** physcomitrella patens bbe-like 1 variant d396n
18	c3tsjA_	Alignment		100.0	13	**PDB header:**allergen, oxidoreductase **Chain:** A: **PDB Molecule:**pollen allergen phl p 4; **PDBTitle:** crystal structure of phl p 4, a grass pollen allergen with glucose2 dehydrogenase activity
19	c1zr6A_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase; **PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
20	c3rjaA_	Alignment		100.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbohydrate oxidase; **PDBTitle:** crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue
21	c5d79B_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**berberine bridge enzyme-like protein; **PDBTitle:** structure of bbe-like #28 from arabidopsis thaliana
22	c6f73B_	Alignment	not modelled	100.0	16	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**mtvao615; **PDBTitle:** crystal structure of vao-type flavoprotein mtvao615 at ph 5.0 from2 myceliophthora thermophila c1
23	c3fwaA_	Alignment	not modelled	100.0	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**reticuline oxidase; **PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
24	c1i19B_	Alignment	not modelled	100.0	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** crystal structure of cholesterol oxidase from b.sterolicum
25	c5fxpA_	Alignment	not modelled	100.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol oxidase; **PDBTitle:** crystal structure of eugenol oxidase in complex with2 vanillin
26	c3d2hA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**berberine bridge-forming enzyme; **PDBTitle:** structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
27	c5i1wD_	Alignment	not modelled	100.0	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**crmk; **PDBTitle:** crystal structure of crmk, a flavoenzyme involved in the shunt product2 recycling mechanism in caerulomycin biosynthesis
28	c3popD_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gilr oxidase; **PDBTitle:** the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
						PDB header:oxidoreductase

29	c2ipiD_	Alignment	not modelled	100.0	13	**Chain:** D: **PDB Molecule:**aclacinomycin oxidoreductase (aknox); **PDBTitle:** crystal structure of aclacinomycin oxidoreductase
30	c1ahuB_	Alignment	not modelled	100.0	13	**PDB header:**flavoenzyme **Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase; **PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
31	c3js8A_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** solvent-stable cholesterol oxidase
32	c2wdwB_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative hexose oxidase; **PDBTitle:** the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
33	c2y3rC_	Alignment	not modelled	100.0	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**taml; **PDBTitle:** structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 taml in p21 space group
34	c2uuvC_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase; **PDBTitle:** alkyldihydroxyacetonephosphate synthase in p1
35	c1f0xA_	Alignment	not modelled	100.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme.
36	d1w1oa2	Alignment	not modelled	100.0	26	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
37	d1wvfa2	Alignment	not modelled	100.0	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
38	d1e8ga2	Alignment	not modelled	100.0	18	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
39	d2i0ka2	Alignment	not modelled	100.0	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
40	c2yvsA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycolate oxidase subunit glce; **PDBTitle:** crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
41	d1f0xa2	Alignment	not modelled	100.0	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
42	d1uxya1	Alignment	not modelled	99.9	11	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
43	d1hska1	Alignment	not modelled	99.9	14	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
44	c4pytA_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of a murb family ep-udp-n-acetylglucosamine2 reductase
45	c4jayC_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of p. aeruginosa murb in complex with nadp+
46	c1hskA_	Alignment	not modelled	99.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of s. aureus murb
47	c1mbbA_	Alignment	not modelled	99.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uridine diphospho-n-acetylenolpyruvylglucosamine **PDBTitle:** oxidoreductase
48	c5jzxB_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of udp-n-acetylenolpyruvoylglucosamine reductase2 (murb) from mycobacterium tuberculosis
49	c3i99A_	Alignment	not modelled	99.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** the crystal structure of the udp-n-acetylenolpyruvoylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
50	c2gquA_	Alignment	not modelled	99.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvylglucosamine reductase; **PDBTitle:** crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
51	d1w1oa1	Alignment	not modelled	99.5	14	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Cytokinin dehydrogenase 1
52	d2i0ka1	Alignment	not modelled	99.3	11	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Cholesterol oxidase
53	d1e8ga1	Alignment	not modelled	98.2	9	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Vanillyl-alcohol oxidase-like
						Fold: Ferredoxin-like

54	d1f0xa1	Alignment	not modelled	97.7	11	**Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**D-lactate dehydrogenase
55	d1wvfa1	Alignment	not modelled	97.4	12	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Vanillyl-alcohol oxidase-like
56	d1ffvc2	Alignment	not modelled	94.7	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
57	d1n62c2	Alignment	not modelled	94.0	18	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
58	c5y6qB_	Alignment	not modelled	93.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde oxidase medium subunit; **PDBTitle:** crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
59	d1t3qc2	Alignment	not modelled	92.3	20	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
60	c3hrdC_	Alignment	not modelled	87.8	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
61	d1v97a6	Alignment	not modelled	86.9	8	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
62	c1n62C_	Alignment	not modelled	86.7	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbon monoxide dehydrogenase medium chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
63	c1ffuF_	Alignment	not modelled	86.7	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cutm, flavoprotein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
64	d3b9jb2	Alignment	not modelled	86.6	7	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
65	c2w3rG_	Alignment	not modelled	86.4	14	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
66	c2gvsA_	Alignment	not modelled	86.2	20	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**chemosensory protein csp-sg4; **PDBTitle:** nmr solution structure of cspsg4
67	c4zohB_	Alignment	not modelled	85.3	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase fad-binding subunit; **PDBTitle:** crystal structure of glyceraldehyde oxidoreductase
68	d1kx9b_	Alignment	not modelled	85.3	17	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
69	d1n8va_	Alignment	not modelled	84.5	18	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
70	c1t3qF_	Alignment	not modelled	84.0	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**quinoline 2-oxidoreductase medium subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
71	d1jroa4	Alignment	not modelled	83.4	9	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
72	c3etrM_	Alignment	not modelled	82.5	7	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of xanthine oxidase in complex with lumazine
73	c3b9jJ_	Alignment	not modelled	82.5	7	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
74	c5g5hB_	Alignment	not modelled	72.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative xanthine dehydrogenase yags fad-binding subunit; **PDBTitle:** escherichia coli periplasmic aldehyde oxidase r440h mutant
75	c1wygA_	Alignment	not modelled	70.2	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
76	d1rm6b2	Alignment	not modelled	56.2	22	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
77	c1rm6E_	Alignment	not modelled	55.2	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**4-hydroxybenzoyl-coa reductase beta subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
78	d1qupa2	Alignment	not modelled	47.2	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
79	c3zyvA_	Alignment	not modelled	46.4	2	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aox3; **PDBTitle:** crystal structure of the mouse liver aldehyde oxidase 3 (maox3)

80	c1qupA_	Alignment	not modelled	43.7	7	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide dismutase
81	d1fe0a_	Alignment	not modelled	42.0	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
82	c4ru3A_	Alignment	not modelled	40.2	20	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**puncturing protein gp41; **PDBTitle:** crystal structure of the cell puncturing protein gp41 from pseudomonas2 phage sn
83	c1jk9D_	Alignment	not modelled	33.8	7	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
84	d1bf2a1	Alignment	not modelled	31.6	39	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
85	d1poib_	Alignment	not modelled	30.1	11	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
86	c4y2iA_	Alignment	not modelled	28.4	29	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative metal-binding transport protein; **PDBTitle:** gold ion bound to golb
87	c4uhxA_	Alignment	not modelled	26.0	4	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidase; **PDBTitle:** human aldehyde oxidase in complex with phthalazine and thioridazine
88	d2o1ra1	Alignment	not modelled	25.4	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
89	c2crlA_	Alignment	not modelled	24.8	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** the apo form of hma domain of copper chaperone for2 superoxide dismutase
90	c2k2pA_	Alignment	not modelled	23.5	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
91	c5jbfB_	Alignment	not modelled	22.9	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inactive glucansucrase; **PDBTitle:** 4,6-alpha-glucanotransferase gtfb (d1015n mutant) from lactobacillus2 reuteri 121 complexed with maltopentaose
92	c2hldH_	Alignment	not modelled	19.8	18	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**atp synthase delta chain, mitochondrial; **PDBTitle:** crystal structure of yeast mitochondrial f1-atpase
93	c3aicC_	Alignment	not modelled	19.7	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucosyltransferase-si; **PDBTitle:** crystal structure of glucansucrase from streptococcus mutans
94	c6fp6X_	Alignment	not modelled	19.4	13	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** complex of human cu,zn sod1 with the human copper chaperone for sod12 in a compact conformation
95	c3pqiA_	Alignment	not modelled	18.8	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gene product 138; **PDBTitle:** crystal structure of the bacteriophage phi92 membrane-piercing protein2 gp138
96	d1t47a2	Alignment	not modelled	18.6	23	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
97	c3ttoD_	Alignment	not modelled	17.5	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dextransucrase; **PDBTitle:** crystal structure of leuconostoc mesenteroides nrrl b-1299 n-2 terminally truncated dextransucrase dsr-e in triclinic form
98	c2mzqA_	Alignment	not modelled	17.4	7	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**single-strand telomeric dna-binding protein gbp2; **PDBTitle:** nmr structure of the rrm3 domain of gbp2
99	d1sb6a_	Alignment	not modelled	16.8	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain