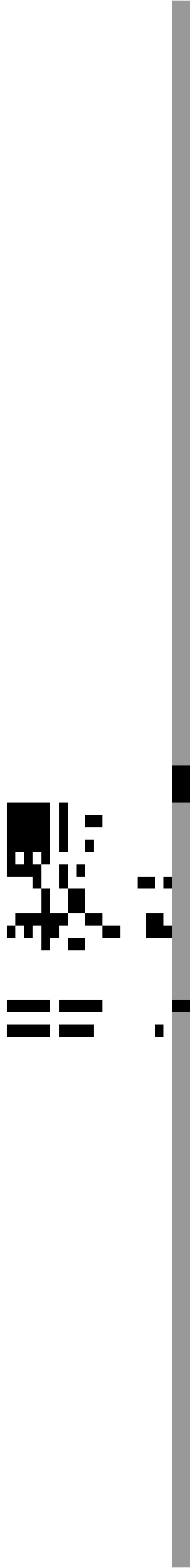
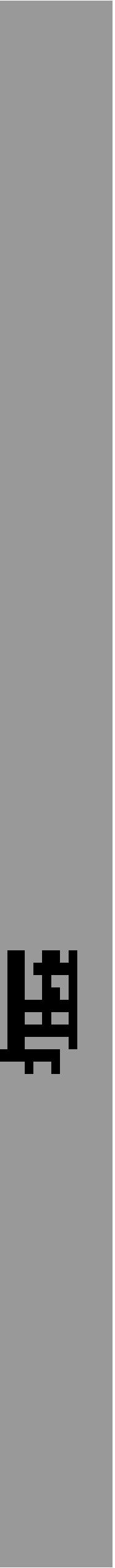
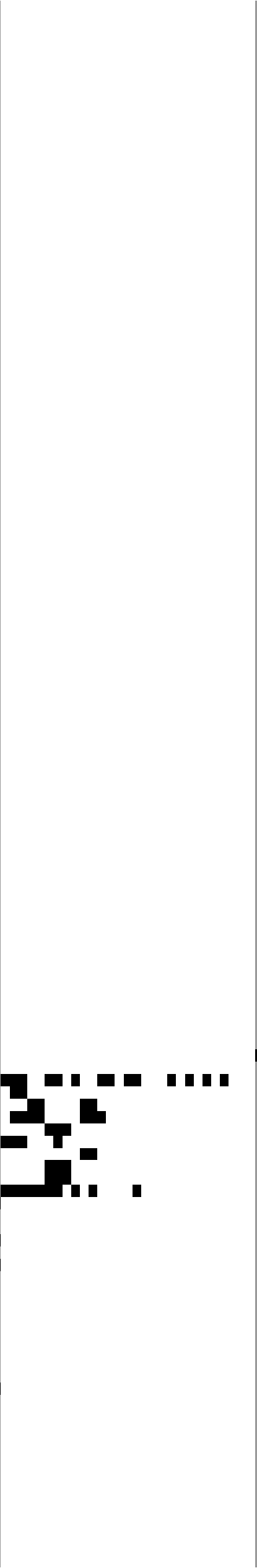
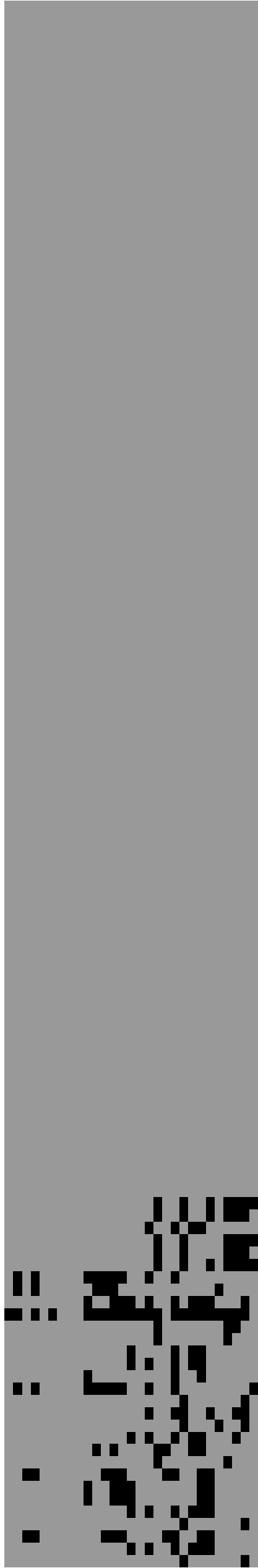


dolichol-linked oligosaccharide biosynthetic process (GO:0006488)
transferase activity, transferring hexosyl groups (GO:0016758)
monovalent inorganic cation transmembrane transporter activity (GO:0015077)
electron transport chain (GO:0022900)
phosphorylation (GO:0016310)
phosphorus metabolic process (GO:0006793)
cation transmembrane transporter activity (GO:0008324)
mitochondrion (GO:0005739)
mitochondrial envelope (GO:0005740)
mitochondrial respiratory chain complex III (GO:0005750)
mitochondrial inner membrane (GO:0005743)
cytoplasm (GO:0005737)
mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
envelope (GO:0031975)
oxidoreductase activity, acting on heme group of donors (GO:0016675)
substrate-specific transmembrane transporter activity (GO:0022891)
oxidoreductase activity, acting on diphenols and related substances as donors (GO:0016679)
ATP synthesis coupled electron transport (GO:0042773)
mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
proton-transporting ATP synthase complex, catalytic core F(1) (GO:0045261)
oxidation reduction (GO:0055114)
glutamate biosynthetic process (GO:0006537)
energy derivation by oxidation of organic compounds (GO:0015980)
mitochondrial proton-transporting ATP synthase complex (GO:0005753)
generation of precursor metabolites and energy (GO:0006091)
hydrogen ion transporting ATP synthase activity, rotational mechanism (GO:0046933)
transporter activity (GO:005215)
aerobic respiration (GO:0009060)
ATP synthesis coupled proton transport (GO:0015986)
intracellular (GO:0005622)
purine nucleotide biosynthetic process (GO:0006164)
organelle membrane (GO:0031090)
proton transport (GO:0015992)
cofactor metabolic process (GO:0051186)
nucleotide metabolic process (GO:0009117)
oxidoreductase activity (GO:0016491)
cell death (GO:0008219)
proton-transporting two-sector ATPase complex (GO:0016469)
transmembrane ion transport (GO:0034220)
purine ribonucleotide metabolic process (GO:0009150)
ATP metabolic process (GO:0046034)
purine ribonucleoside triphosphate biosynthetic process (GO:0009206)
tricarboxylic acid cycle (GO:0006099)
nucleobase, nucleoside and nucleotide metabolic process (GO:0055086)
ribonucleotide biosynthetic process (GO:0009260)
purine nucleoside triphosphate metabolic process (GO:0009144)
FAD binding (GO:0050660)
ribonucleoside triphosphate metabolic process (GO:0009199)
nucleoside triphosphate biosynthetic process (GO:0009142)
metal ion binding (GO:0046872)
proton-transporting ATPase activity, rotational mechanism (GO:0046961)
coenzyme catabolic process (GO:0009109)
mitochondrial respiratory chain complex IV (GO:0005751)
mitochondrial nucleoid (GO:0042645)
mitochondrial proton-transporting ATP synthase, catalytic core (GO:0005754)
isoleucine-tRNA ligase activity (GO:0004822)
metal cluster binding (GO:0051540)
iron ion binding (GO:0005506)
NADH dehydrogenase (ubiquinone) activity (GO:0008137)
mitochondrial proton-transporting ATP synthase, central stalk (GO:0005756)
mitochondrial respiratory chain complex II (GO:0005749)
succinate dehydrogenase complex (GO:0045281)
nitrogen compound catabolic process (GO:0044270)
cellular amine metabolic process (GO:0009308)
carboxylic acid metabolic process (GO:0019752)
arginine biosynthetic process (GO:0006526)
nitrogen compound biosynthetic process (GO:0044271)
glutamine family amino acid metabolic process (GO:0009064)
amino acid biosynthetic process (GO:0008652)
ornithine biosynthetic process (GO:0006592)
cellular aromatic compound metabolic process (GO:0006725)
ligase activity (GO:0016874)
pyridoxal phosphate binding (GO:0030170)
steroid binding (GO:0005496)
biosynthetic process (GO:0009058)
membrane-enclosed lumen (GO:0031974)
vitamin binding (GO:0019842)
methionine biosynthetic process (GO:0009086)
amine biosynthetic process (GO:0009309)
cysteine biosynthetic process (GO:0019344)
sulfur compound biosynthetic process (GO:0044272)
nitrogen compound metabolic process (GO:0006807)
serine family amino acid metabolic process (GO:0009069)
organic acid metabolic process (GO:0006082)
sulfate assimilation (GO:000103)
transferase activity (GO:0016740)
O-acetyltransferase activity (GO:0008374)
catalytic activity (GO:0003824)
L-lditol 2-dehydrogenase activity (GO:0003939)
hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553)
cellular carbohydrate metabolic process (GO:0044262)
purine nucleoside monophosphate metabolic process (GO:0009126)
oxidoreductase activity, acting on CH-OH group of donors (GO:0016614)
glycogen catabolic process (GO:0005980)
ribonucleoside monophosphate metabolic process (GO:0009161)
nucleoside monophosphate biosynthetic process (GO:0009124)
cation binding (GO:0043169)
regulation of transferase activity (GO:0051338)
regulation of cyclin-dependent protein kinase activity (GO:0000079)
nuclear cohesin complex (GO:0000798)
kinase regulator activity (GO:0019207)
cyclin-dependent protein kinase regulator activity (GO:0016538)
regulation of molecular function (GO:0065009)
cellular response to DNA damage stimulus (GO:0034984)
DNA-dependent DNA replication (GO:0006261)
M phase (GO:0000279)
nucleus (GO:0005634)
cyclin-dependent protein kinase holoenzyme complex (GO:0000307)
protein kinase binding (GO:0019901)
mitotic sister chromatid cohesion (GO:0007064)
sister chromatid segregation (GO:0000819)
double-stranded DNA binding (GO:0003690)
cellular response to stimulus (GO:0051716)
regulation of S phase of mitotic cell cycle (GO:0007090)
cell division (GO:0051301)
S phase (GO:0051320)
mitotic cell cycle (GO:0000278)
reproductive cellular process (GO:0048610)
regulation of establishment or maintenance of cell polarity (GO:0032878)
ATP binding (GO:0005524)
meiosis (GO:0007126)
meiotic cell cycle (GO:0051321)
mitosis (GO:0007067)
positive regulation of DNA replication (GO:0045740)
adenyl nucleotide binding (GO:0030554)
organelle fission (GO:0048285)
premeiotic DNA synthesis (GO:0006279)



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