



B GO biological process complete

	FC	p-value
positive regulation of RNA polymerase II transcriptional preinitiation	23.72	2.3·10 ⁻⁵
complex assembly	22.14	1.2·10 ⁻¹²
proteasomal ubiquitin-independent protein catabolic process	18.98	0.00028
protein N-linked glycosylation via asparagine	18.98	0.00028
oxaloacetate metabolic process	18.98	0.00028
NADH metabolic process	18.98	0.00028
posttranslational protein targeting to endoplasmic reticulum membrane	18.98	0.00028
proteasome assembly	18.64	1.1·10 ⁻⁹
mitochondrial electron transport, succinate to ubiquinone	17.79	0.00204
signal peptide processing	16.94	6.7·10 ⁻⁵
glycolipid biosynthetic process	9.82	4.6·10 ⁻⁸
cotranslational protein targeting to membrane	13.84	5.6·10 ⁻⁶
poly(A) ⁺ mRNA export from nucleus	13.55	0.00070
protein prenylation	13.55	0.00070
peptide catabolic process	11.86	0.00101
tricarboxylic acid cycle	9.66	1.9·10 ⁻⁷
glucose 6-phosphate metabolic process	9.49	0.00192
glycolytic process	9.49	1·10 ⁻⁵
NADP metabolic process	9.12	0.00059
retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	9.04	1.4·10 ⁻⁵
mannosylation	8.37	0.00024
glucose metabolic process	7.91	0.00099
endoplasmic reticulum to Golgi vesicle-mediated transport	7.39	2.9·10 ⁻¹⁰
ATP-dependent chromatin remodeling	6.98	0.00158
cellular aldehyde metabolic process	6.78	0.00061
negative regulation of cellular amide metabolic process	6.59	0.00195
Golgi organization	6.59	0.00195
polyol biosynthetic process	6.24	0.00238
nucleotide-sugar metabolic process	6.24	0.00238
proteasome-mediated ubiquitin-dependent protein catabolic process	6.2	2.5·10 ⁻¹³
protein peptidyl-prolyl isomerization	5.27	0.00186
cell redox homeostasis	4.41	0.00093
response to endoplasmic reticulum stress	4.13	0.00137
transcription by RNA polymerase II	3.54	0.00019
negative regulation of gene expression	2.58	0.00065
mRNA processing	2.52	0.00084

C

abnC, acbd6, aco2, acp1, act17, act18, act21, adm1-2, agnD, alg1, alg3, alyA, ap2a1-2, aplQ, apm2, argJ, arpA, arpD, arpE, arpF, arpH, arsA, atox1, bloc1s1, cdc73, cdk7, chcA, chid1, clc, clybl, cniB, cnr1, cnxX, copA, copB, copB2, copE, crtA, cstf1, cttnbl1, culD, cxdA, cxfA, cxgE, cycC, cyp508A4, cypE, DG1122, dgtA, dgtB, dhx16, dicA, dlcA, dnpep, dpm2-2, dpoA, dpp3-2, dr1, drnA-2, dynC, dync1li1, dynD, echs1, eco1, empA, empB, empC, empD, enoA, ergic3, erh, esd, etfa, etfb, etfdh, fntA, fntB, gabT, gcvH1, gemA, gemin1, ggtA, glk, glnA2, gloA, gloB1, gmd, gmppA, gnd, gpaI, gpdA, gpmA, gtaT, gtaW, gtf2h3, gxcL, H2Av2, hcpA, helC, hemB, hspL, idhM, ints7, ipkA1, ippB, isw, itpk1, iunH, lap, ldhd, lkhA, lsm4, lsm8, masA, mcee, mcft, mdhA, mdhB, mdhC, med10, med15, med16, med18, med27, med4, med7, med9, mgm101, mlkA, mmgt, mtpn, myoC, nagB, ndkM, nif3, nup107, nup93, oplah, ost1, ost2, ost3, ost4, ostc, paf1, pcbd, pccA, pccB, pdhA, pdi1, pemtB, pex19, pex2, pfkA, pfp1, pggt1b, pgkA, pgmA, phbA, phbB, pigB, pigS, pigT, pigW, pigX, pksB, pmmA, ppa1, ppiA, ppp2r4, prdx5, prlA, prsB, psaA, psaB, psmA1, psmA2, psmA3, psmA4, psmA5, psmA6, psmA7, psmB1, psmB2, psmB3, psmB4-2, psmB5, psmB6, psmB7, psmC1, psmC2, psmC3, psmC4, psmC5, psmC6, psmD1, psmD10, psmD11, psmD12, psmD13, psmD14, psmD2, psmD3, psmD4, psmD6, psmD7, psmD8-2, psmG1, psmG2, psmG3, pter, rabF1-2, rabgta, rae1, rbbD, repE, rer1, rnu1b, rnu2c, rpb11, rpb4, rpiA, sae1, sarB, scfd2, scsB, sdhA, sdhB, sdhC, sdhD, sec11, sec13, sec20, sec24, sec31, sec61a, sec61b, sec61g, sf3b5, sgtA, sir2C, slc35b4, smlA, smp3, smu1, snd1, snrpA1, snrpD3, sod2, spc1, spc2, spc3, sr, srp14-2, srp19, srp68, srp72, srpA, srpB, ssr1, ssr2, ssr3, ssu72, stt3, swp1, thyB, tkt-2, trappc2, trappc4, tRNA-Met-CAU-2, tsn, tubA, tubA2, uba2, uba5, ubr7, uch2, ufc1, ufd1, ugt1, usp14, usp39, vatP, vps36, wbp1, xpnpep1, xpo7, zmpste24

