

Putative targets of Swi4 found in YEASTRACT (<http://www.yeasttract.com/formfindregulated.php>)
sorted by regulated process in GO slim mapper (<https://www.yeastgenome.org/goSlimMapper>).

We highlighted in "lipid metabolic process" the genes related to sphingolipid synthesis.

GO Terms from the biological process Ontology			
GO Term (GO ID)	Genes Annotated to the GO Term	GO Term Usage in Gene List	Genome Frequency of Use

<p>Response to chemical (GO:0042221)</p>	<p>ADR1, AFB1, AGA1, AGA2, AMF1, APE1, ASK10, ATX1, BAR1, BOP3, CAD1, CCP1, CDC14, CLN2, CTT1, CUZ1, DAK1, DDR2, DIC1, DSE1, ECM38, EDC3, ERT1, ERV1, ETT1, FAP7, FAR1, FES1, FKH1, FRT1, FUS3, GAD1, GLN1, GPA1, GPX1, GRE3, HAP5, HCM1, HSP104, HSP12, HSP26, HSP30, HSP42, ITC1, IXR1, MCK1, MCR1, MF(ALPHA)1, MFA1, MFA2, MHR1, MOT3, MRK1, MSB2, MSN2, NCE103, NCL1, NQM1, NRG2, NRT1, NTH1, ODC1, ODC2, ORM2, PDR1, PDR15, PDR18, PDR5, PRX1, PSR1, PTR3, QDR2, RDR1, RDS2, ROG3, ROQ1, ROX1, SCH9, SIS1, SKS1, SKY1, SRX1, SSA4, SST2, STE18, STE6, STF2, SVF1, SWI1, THI7, THI72, TMC1, TPO2, TPO3, TPO4, UGA2, UME6, URM1, USV1,</p>	<p>114 of 1023 genes, 11.14%</p>	<p>607 of 6439 annotated genes, 9.43%</p>
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<p>Transcription by RNA polymerase II (GO:0006366)</p>	<p>ABF2, ACE2, ADR1, AFT1, ARP9, ASF1, CAD1, DAT1, DOT6, ELP3, EMI2, ERT1, ETT1, FCP1, FKH1, FKH2, FMS1, GTS1, HAL1, HAP5, HCM1, HHF1, HHF2, HIR2, HMO1, HOS3, HTA1, HTB1, HTL1, IKI3, IME1, ITC1, IXR1, JHD1, MED1, MET32, MKS1, MOT3, MSN2, NAB3, NDD1, NHP10, NRG2, PDC2, PDP3, PDR1, PHD1, POP2, PSR1, PUT3, RAD2, RAP1, RDR1, RDS2, REF2, RFX1, RME1, RNT1, ROX1, RPB9, RPH1, RPT1, RRD1, RSC3, RSC58, RTR1, RTT109, RVB1, SCH9, SDD4, SKS1, SNF2, SOK2, SPT21, SSU72, STB1, SWI1, SWI4, TAF6, TBF1, TEC1, TFA2, TFB2, TFG2, THP2, TOA2, TYE7, UME6, USV1, WHI2, XBP1, YCR106W, YHP1, YKE2, YLL054C, YLR321C, YOR338W, YOX1, YPR009W</p>	<p>99 of 1023 genes, 9.68%</p>	<p>549 of 6439 annotated genes, 8.53%</p>
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<p>Mitotic cell cycle (GO:0000278)</p>	<p>ACE2, AFT1, ALK1, AMN1, APC2, APC5, ASE1, BUD4, BUD9, CBF2, CDC14, CDC45, CDC5, CDC6, CHL1, CHS2, CLB1, CLB2, CLB5, CLB6, CLN1, CLN2, CLN3, CTF18, CYK3, DAM1, DMA2, DSL1, DSN1, DUO1, FAR1, FKH1, FKH2, GIC2, GIN4, HIR2, HOS3, HSL1, IBD2, INN1, IRC15, MCD1, MCK1, MCM22, MCM3, MET32, MLC1, MSA1, MSB2, MUS81, NDD1, NET1, NIS1, NRM1, PEF1, PIN4, POL1, POL30, PSE1, RAX2, REF2, RME1, ROM2, RRD1, SDS23, SDS24, SFG1, SKG6, SMC4, SPC98, SPO12, SPR28, SRL3, STB1, STU2, SWI4, TOM1, TOS2, VHS1, WHI3, XBP1, YBL031W, YHP1, YOX1, ZDS2, ZPR1</p>	<p>86 of 1023 genes, 8.41%</p>	<p>392 of 6439 annotated genes, 6.09%</p>
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<p>Transmembrane transport (GO:0055085)</p>	<p>ADY2, AGP1, ALP1, AMF1, ATG22, ATP20, CYT1, DAL5, DIC1, ENB1, ERV1, FCY2, FEX1, FTR1, GLK1, HOT13, HSP30, HXK1, HXK2, HXT10, HXT11, HXT17, HXT2, HXT4, HXT7, MDH2, MEP1, MPH2, NCA3, NRT1, ODC1, ODC2, OPT2, PAM16, PAM18, PDR15, PDR18, PDR5, PEX14, PEX25, PHM7, PHO89, PHO90, PIC2, PNS1, PTR2, PUT4, QDR2, RCF1, RSN1, SBH2, SEC72, SIA1, SIT1, SKS1, SMF3, SSA4, SSU1, STE6, TAT1, TAT2, THI7, THI72, TIM12, TIM21, TIM50, TPO2, TPO3, TPO4, VPS73, XDJ1, YBR219C, YBR220C, YBR287W, YCR028C, YEA6, YIL170W, YIL171W, YLR152C, YPQ2, YRO2, ZRT1, ZRT2</p>	<p>83 of 1023 genes, 8.11%</p>	<p>456 of 6439 annotated genes, 7.08%</p>
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<p>Cell wall organization or biogenesis (GO:0071554)</p>	<p>BAR1, CHS1, CHS2, CHS6, CIS3, CRH1, CTS1, CWH41, CWP1, CWP2, DSE1, DSE2, ECM19, ECM23, ECM9, EXG1, FKS1, GAS2, GAS3, GAS4, GFA1, GSC2, HPF1, HSP150, INA1, IRS4, KTR2, LDS2, LOH1, MSB2, NCA3, NCE102, NCW2, OSW2, PAU21, PIR1, PIR3, PIR5, PSA1, PST1, PUN1, RCR1, RDS2, RNT1, ROM2, SBE2, SCW4, SED1, SHC1, SIM1, SPI1, SRL1, SSP2, SUN4, SUR7, TIR3, TIR4, UTH1, WSC3, YBR067C, YGP1, YHR030C, YMR084W, YPK2, YPS1, YPS3</p>	<p>66 of 1023 genes, 6.45%</p>	<p>298 of 6439 annotated genes, 4.63%</p>
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Meiotic cell cycle (GO:0051321)	ADY2, AFT1, CDC14, CDC5, CLB1, CLB5, CLB6, CWP1, DSN1, EMI2, GAS2, GAS4, GSC2, HHF1, HHF2, HHT1, HHT2, HOP2, IME1, IRC15, LDS2, LOH1, MCK1, MCM22, MSC1, MSC6, MSH2, MSH6, MUS81, NKP1, OSW2, PAP2, POL1, POL30, RAD17, RDH54, RFA3, RIM4, RME1, RMR1, SHC1, SKI8, SMA1, SMA2, SMC4, SPC98, SPO12, SPO16, SPO20, SPR28, SPR6, SPS4, SSO2, SSP2, SUR7, TGS1, UME6, XRS2, YOR338W, YSW1, ZIP2	61 of 1023 genes, 5.96%	321 of 6439 annotated genes, 4.99%
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<p>Chromatin organization (GO:0006325)</p>	<p>ADR1, APC5, ARP9, ASA1, ASF1, BDF1, BRE2, CDC45, CDC6, DIA2, DOT6, ESC8, FKH1, FKH2, HAT1, HEK2, HHF1, HHF2, HHO1, HHT1, HHT2, HIR2, HMO1, HOS3, HST2, HTA1, HTA2, HTB1, HTL1, IRS4, ITC1, JHD1, MCM3, MCM5, MCM7, MSH2, MSN2, NET1, NHP10, NNT1, ORC4, POL30, RAP1, RNT1, RPH1, RSC3, RSC58, RTT109, RVB1, SCS2, SNF2, SPT21, SWC5, SWI1, TAF6, TBF1, UAF30, UME6, YLR321C, YOR338W, ZDS2</p>	<p>61 of 1023 genes, 5.96%</p>	<p>308 of 6439 annotated genes, 4.78%</p>
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<p>Carbohydrate metabolic process (GO:0005975)</p>	<p>AMS1, ATG11, CIT1, CIT2, CRH1, CTS1, CWH41, DAK1, DSF1, EMI2, ENO1, ERR1, ERT1, EXG1, FKS1, GAL10, GAS2, GAS3, GAS4, GLK1, GND2, GPM2, GPP2, GRE3, GSC2, GSY2, GUT2, HXK1, HXK2, ICL1, IGD1, IMA5, IPK1, MAL12, MAL32, MDH2, NQM1, OPI10, PDC2, PFK27, PGM2, PIB1, PIG1, PKP1, PYC1, SCW4, SGA1, SIM1, SOL4, SUC2, SUN4, TDH3, TYE7, UTH1, XKS1, XYL2, YBR056W, YIL167W, YJR096W, YNR071C, ZWF1</p>	<p>61 of 1023 genes, 5.96%</p>	<p>248 of 6439 annotated genes, 3.85%</p>
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rRNA processing (GO:0006364)	BCD1, BMT5, BRX1, CIC1, DBP3, DBP6, DBP8, DIP2, E MG1, ENP1, FAF1, FAP7, FCF1, HCR1, IMP3, IMP4, IPI1, IPI3, LOC1, LSM7, LSM8, MAK5, MRT4, MTR3, NIP7, NOC3, NOC4, NOG1, NOP16, NOP56, NOP8, NOP9, POP4, POP7, PRP43, REX2, RNT1, RPL35A, RPL7A, RPL7B, RPL8A, RPL8B, RPS1A, RPS20, RPS7B, RPS9A, RPS9B, RRB1, RRP45, RRP5, RRP6, RRP7, RTC3, SRD1, TOM1, UTP15, UTP23, YDL229W, YTM1, ZUO1	60 of 1023 genes, 5.87%	356 of 6439 annotated genes, 5.53%
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<p>Ion transport (GO:0006811)</p>	<p>ADY2, AFT1, AMF1, ATP20, ATX1, CSR1, CYT1, DAL5, DIC1, EMP70, ENB1, FAA4, FEX1, FIT2, FRE3, FRE4, FRE5, FTR1, HSP30, HXT10, HXT11, HXT17, HXT2, HXT4, HXT7, MDM10, MDM35, MEP1, MPH2, NCA3, NCE102, OPT2, PHM7, PHO89, PHO90, PIC2, PRY1, PRY2, PTR2, QDR2, RCF1, RCH1, RSB1, RSN1, SFK1, SIA1, SIT1, SMF3, SSU1, TDH3, TPO2, TPO3, TPO4, VPS20, YBR219C, YBR220C, YCR028C, YRO2, ZRT1, ZRT2</p>	<p>60 of 1023 genes, 5.87%</p>	<p>349 of 6439 annotated genes, 5.42%</p>
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<p>Regulation of cell cycle (GO:0051726)</p>	<p>AMN1, APC2, APC5, CDC14, CDC33, CDC45, CDC5, CDC6, CIP1, CLB1, CLB2, CLB5, CLB6, CLN1, CLN2, CLN3, DAM1, DBF2, DMA2, DSL1, DUO1, FAR1, FKH1, FKH2, FUS3, GIC2, GIN4, HSL1, HUG1, IBD2, IME1, IRC15, MET32, MSA1, MUS81, NET1, PCL1, PCL2, PCL5, PIN4, PSE1, RAD17, REF2, RME1, ROM2, RSC3, RTT107, SDS23, SDS24, SKG6, SPO12, SPO16, TOS2, WHI2, WHI3, YHR030C, YLR321C, ZDS2</p>	<p>58 of 1023 genes, 5.67%</p>	<p>309 of 6439 annotated genes, 4.80%</p>
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Lipid metabolic process (GO:0006629)	ACH1, AFT1, AIM45, ALG14, ARE2, AUR1 , CLD1, CSH1 , CSR1, DCI1, EEB1, ELO1, ERG28, ERG3, ERG5, ERG9, FAA4, FMP30, GAB1, GPC1, GPI15, GPI18, GTS1, IPT1 , KAP95, LAC1 , LPX1, LRO1, MCR1, MOT3, OPI10, ORM2, OSH6, PLB1, PLB2, PLB3, SCH9, SCS2, SFK1, SUR1 , SUR2 , TCB2, TGL5, TLG2, TML25, TSC10 , UME6, URA7, VAC7, YDC1 , YJU3, YPC1	52 of 1023 genes, 5.08%	340 of 6439 annotated genes, 5.28%
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DNA repair (GO:0006281)	BDF1, BLM10, CDC45, CHL1, CTF18, DDR48, DIN7, HAT1, HHT1, HHT2, HTA1, HTA2, HTB1, HUG1, IXR1, KRE29, MCD1, MCK1, MCM3, MCM5, MCM7, MPH1, MSH2, MSH6, MUS81, NHP10, PAP2, POL1, POL30, POL4, PSF3, PSO2, RAD17, RAD2, RAD27, RDH54, REV7, RFA3, RPB9, RRD1, RRM3, RTT107, RTT109, RVB1, SXLX5, SNF2, SRS2, TFB2, UNG1, XRS2, YLR321C, YRA1	52 of 1023 genes, 5.08%	303 of 6439 annotated genes, 4.71%
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<p>Organelle fission (GO:0048285)</p>	<p>AFT1, AMN1, APC2, APC5, ASE1, CBF2, CDC14, CDC 5, CHL1, CLB1, CLB2, CLB 5, CTF18, DAM1, DBF2, D MA2, DSL1, DSN1, GIC2, H IR2, HOP2, IBD2, IME1, IR C15, MCD1, MCK1, MCM2 2, MSC1, MSC6, MUS81, N ET1, NIS1, PEX25, POL30, PSE1, RAD17, RDH54, RFA 3, RIM4, RME1, RMR1, SD S23, SDS24, SKI8, SMC4, S PO12, SPO16, YBL031W, ZI P2</p>	<p>49 of 1023 genes, 4.79%</p>	<p>271 of 6439 annotated genes, 4.21%</p>
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<p>Nucleobase-containing small molecule metabolic process (GO:0055086)</p>	<p>ADE13, ADE17, ATP20, BNA1, BNA4, CAB5, CDC21, CDC8, CIT1, CPA1, CPA2, CYT1, DAS2, EMI2, ENO1, ERR1, FAA4, FAP7, GFA1, GLK1, GPM2, HXK1, HXK2, ISN1, NCA3, NMA1, NNR1, NNR2, PFK27, PGM2, PHM8, PSA1, RNR1, RNR2, RNR3, RNR4, SNZ2, SNZ3, SPE2, TDH3, TYE7, URA1, URA3, URA4, URA6, URA7, YGK1, YMR084W, YOR111W</p>	<p>49 of 1023 genes, 4.79%</p>	<p>223 of 6439 annotated genes, 3.46%</p>
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<p>Regulation of organelle organization (GO:0033043)</p>	<p>ADR1, AMN1, APC2, APC5, ASF1, ATG11, BDF1, CDC14, CDC45, CDC5, CDC6, CLB1, CLB2, CLB5, DAM1, DMA2, DSL1, DUO1, ENO1, EST1, FKH1, FKH2, GIC2, GYP7, HHO1, HIR2, HSP82, HST2, IBD2, IME1, MCM5, NET1, OPT2, PEF1, PKP1, PSE1, RAP1, REF2, RME1, ROM2, SDS23, SDS24, SLA1, SPO12, SPO16, TBF1, TGS1, XBP1, YOR338W</p>	<p>49 of 1023 genes, 4.79%</p>	<p>342 of 6439 annotated genes, 5.31%</p>
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Cellular amino acid metabolic process (GO:0006520)	AAT1, ADI1, ALD2, ALD3, ALT1, ARG1, ARG7, ASP3-3, BNA1, BNA4, CAR1, CHA1, CPA1, CPA2, GAD1, GDH3, GFA1, GLN1, ILV5, IRC7, LEU1, LYS2, LYS5, MAE1, MET13, MET3, MET32, MMF1, MSE1, MSY1, PUT1, PUT3, SCH9, SER2, SNO3, SNZ1, SNZ2, SNZ3, SRY1, STR3, THR1, UGA1, UGA2, URA7, YHR033W, YIL167W, YMR084W	47 of 1023 genes, 4.59%	222 of 6439 annotated genes, 3.45%
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<p>DNA recombination (GO:0006310)</p>	<p>CDC45, CDC5, CTF18, DIN7, HHO1, HO, HOP2, HST2, IRC15, KRE29, MCD1, MCM3, MCM5, MCM7, MHR1, MPH1, MSC1, MSC6, MSH2, MSH6, MUS81, NHP10, PAP2, PSF3, RAD17, RAD27, RDH54, RFA3, RIM4, RMR1, RTT109, SKI8, SNF2, SPO16, SRS2, THP2, TLC1, XRS2, YLR035C-A, YRF1-2, YRF1-4, YRF1-5, YRF1-7, ZIP2</p>	<p>44 of 1023 genes, 4.30%</p>	<p>252 of 6439 annotated genes, 3.91%</p>
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<p>Cytoskeleton organization (GO:0007010)</p>	<p>AFR1, APC2, ARP9, ASE1, BBP1, BNI5, BUD4, CBF2, CDC14, CDC5, CHS2, CIN1, CLB1, CLB2, CLB5, CTF13, DAM1, DMA2, DUO1, GIC2, GIN4, HCM1, HSP42, IRC15, LIA1, MLC1, NET1, PCL1, PCL2, REF2, ROM2, RRD1, SFK1, SLA1, SLM1, SPC29, SPC42, SPC98, SPR28, STU2, SUR7, WHI2, YBL031W, YTA6</p>	<p>44 of 1023 genes, 4.30%</p>	<p>275 of 6439 annotated genes, 4.27%</p>
<p>Cellular response to DNA damage stimulus (GO:0006974)</p>	<p>ALK1, BDF1, BLM10, DDR2, DIN7, HAT1, HSP30, HTA1, HTA2, HTL1, HUG1, KRE29, MCD1, MCK1, MPH1, MSH2, MSH6, MUS81, PIN4, PLM2, POL30, POL4, PSO2, RAD17, RAD2, RAD27, RAP1, RDH54, REV7, RPB9, RRM3, RTT107, RTT109, RVB1, SLX5, SML1, SRS2, TFB2, TOS4, UNG1, XRS2, YIM1</p>	<p>42 of 1023 genes, 4.11%</p>	<p>238 of 6439 annotated genes, 3.70%</p>

<p>Mitochondrion organization (GO:0007005)</p>	<p>ABF2, ATG11, ATG12, ATG3, ATG33, ATG41, ATG8, ATP20, CDC14, ERV1, FMC1, HCM1, HOT13, HSP82, ILV5, MDM1, MDM10, MDM35, MHR1, MIC12, MIC27, NGR1, PAM16, PAM18, PET117, PET191, PKP1, PUF3, RCF1, REX2, RRM3, SED1, SML1, STI1, SUN4, TIM12, TIM21, TIM50, UTH1, WHI2, XDJ1, YOR019W</p>	<p>42 of 1023 genes, 4.11%</p>	<p>284 of 6439 annotated genes, 4.41%</p>
<p>Monocarboxylic acid metabolic process (GO:0032787)</p>	<p>ACH1, AIM45, ALD2, ALD3, ALD5, ASP3-3, BNA1, BNA4, CSR1, DCI1, EEB1, ELO1, EMI2, ENO1, ERR1, FAA4, FDH1, FMS1, GLK1, GND2, GOR1, GPM2, HSP32, HSP33, HXK1, HXK2, ICL1, IRC7, MAE1, PFK27, PYC1, SPE2, SPE3, SPE4, SRY1, TDH3, TML25, TYE7, UGA1, UGA2</p>	<p>40 of 1023 genes, 3.91%</p>	<p>170 of 6439 annotated genes, 2.64%</p>

<p>Peptidyl-amino acid modification (GO:0018193)</p>	<p>ALK1, ARD1, ASF1, BRE2, CPR8, DBF2, EFM4, EFM5, EFM6, ELP3, FPR2, HAT1, HHF1, HHF2, HSL1, KAP95, KRE29, LIA1, MCK1, NNT1, PFA5, PKP1, PSE1, RKM4, RRD1, RTT109, RVB1, SCH9, SFM1, SKY1, SLX5, SPO16, TAF6, VHS1, YCK1, YIR042C, YOR338W, YPK2, YPK3, ZIP2</p>	<p>40 of 1023 genes, 3.91%</p>	<p>250 of 6439 annotated genes, 3.88%</p>
<p>Protein phosphorylation (GO:0006468)</p>	<p>ALK1, ASF1, ATG11, CDC5, CIP1, CLB1, CLB2, CLB5, CLB6, CLN1, CLN2, CLN3, CRP1, DBF2, FAR1, FMP48, FUS3, GIN4, HSL1, ISR1, MCK1, MRK1, NCE102, PCL1, PCL2, PCL5, PKP1, SCH9, SKS1, SKY1, SPL2, SSP2, TFB2, VHS1, YCK1, YHR030C, YPK2, YPK3, YPL150W</p>	<p>39 of 1023 genes, 3.81%</p>	<p>247 of 6439 annotated genes, 3.84%</p>

Chromosome segregation (GO:0007059)	AFT1, APC2, APC5, ASE1, CBF2, CDC14, CDC5, CHL1, CLB1, CLB2, CLB5, CTF18, DAM1, DMA2, DSL1, DSN1, DUO1, ESC8, GIP4, HIR2, HOP2, IBD2, IRC15, MCD1, MCK1, MCM22, MUS81, NNF1, POL30, RDH54, SDS23, SDS24, SMC4, SPO16, YBL031W, YLR321C, ZIP2	37 of 1023 genes, 3.62%	219 of 6439 annotated genes, 3.40%
Response to oxidative stress (GO:0006979)	ASK10, ATX1, CCP1, CTT1, DDR2, ERV1, FAP7, FCP1, GAD1, GPX1, GRE3, HCM1, HSP104, HSP12, HSP30, HSP42, MCR1, MHR1, MSN2, NCE103, NCL1, NQM1, PIN4, PRX1, SCH9, SNF2, SRX1, SVF1, UGA2, URM1, XBP1, YDL124W, YDR222W, YHB1, YJR096W, ZWF1	36 of 1023 genes, 3.52%	131 of 6439 annotated genes, 2.03%

DNA replication (GO:0006260)	CDC45, CDC6, CLB5, CLB6, CTF18, DIA2, FKH1, FKH2, IPI1, IPI3, MCM3, MCM5, MCM7, MHR1, MPH1, MSH2, MSH6, NOC3, ORC4, POL1, POL30, PSF3, RAD27, RFA3, RIM4, RNR1, RNR2, RNR3, RNR4, RRM3, RSC3, SLD7, SML1, SNF2, SWI1, YLR321C	36 of 1023 genes, 3.52%	151 of 6439 annotated genes, 2.35%
Sporulation (GO:0043934)	BDF1, CWP1, EMI2, GAS2, GAS4, GSC2, HHH1, HHH2, HHT1, HHT2, IME1, LDS2, LOH1, MCK1, OSW2, PRB1, RIM4, SGA1, SHC1, SMA1, SMA2, SPO12, SPO16, SPO20, SPR28, SPR6, SPS4, SSO2, SSP2, SUR7, TGL5, UBX6, XRS2, YOR338W, YSW1	35 of 1023 genes, 3.42%	169 of 6439 annotated genes, 2.62%

Protein targeting (GO:0006605)	APE1, ATG11, ATG12, ATG3, ATG41, ATG8, COG2, ERV1, HOT13, HSP82, KAP95, MDH2, MDM10, MRS6, PAM16, PAM18, PEP12, PEP4, PEX14, PEX25, PFA5, SBH2, SEC72, SPL2, SRP68, SRP72, SSA4, STI1, TIM12, TIM21, TIM50, TLG2, TRS130, VPS73, XDJ1	35 of 1023 genes, 3.42%	259 of 6439 annotated genes, 4.02%
Generation of precursor metabolites and energy (GO:0006091)	AIM45, ATF1, ATG11, CYT1, DAK1, EMI2, ENO1, ERR1, GLK1, GND2, GPM2, GSY2, HXK1, HXK2, IGD1, IRC15, MFA2, NCA3, NDE1, NQM1, PDC2, PFK27, PGM2, PIG1, RGI1, RGI2, SGA1, SOL4, TDH3, TKL1, TYE7, YMR315W, ZWF1	33 of 1023 genes, 3.23%	139 of 6439 annotated genes, 2.16%

<p>Proteolysis involved in cellular protein catabolic process (GO:0051603)</p>	<p>AMN1, APC2, APC5, ATG42, BLM10, COS1, COS2, COS3, COS4, COS6, COS8, CP S1, CUZ1, DIA2, DMA2, FE S1, GGA2, LUG1, MGR3, MUB1, PEP4, PUP3, ROQ1, RPN10, RPT1, RQC2, SIS1, SLX5, SSE2, TOM1, UBX6, VPS20, YUH1</p>	<p>33 of 1023 genes, 3.23%</p>	<p>264 of 6439 annotated genes, 4.10%</p>
<p>Cofactor metabolic process (GO:0051186)</p>	<p>ALD2, ALD3, ARA2, BNA1, BNA4, BUD17, CAB5, CCP1, CIT1, COQ11, CTT1, ECM38, FAA4, FMS1, FOL1, FOL2, HEM13, MET13, NMA1, NNR1, NNR2, PUF3, SNO3, SNZ1, SNZ2, SNZ3, SPE2, SPE3, SPE4, THI11, THI12</p>	<p>31 of 1023 genes, 3.03%</p>	<p>196 of 6439 annotated genes, 3.04%</p>

<p>Cytoplasmic translation (GO:0002181)</p>	<p>CDC33, GCD1, GCD11, GIS2, HCR1, PRT1, RPL11B, RPL13A, RPL22A, RPL22B, RPL28, RPL32, RPL35A, RPL43A, RPL5, RPL7A, RPL7B, RPL8A, RPL8B, RPL9B, RPS1A, RPS20, RPS26A, RPS7B, RPS9A, TIF34, TIF5, TRM7, YDL229W</p>	<p>29 of 1023 genes, 2.83%</p>	<p>205 of 6439 annotated genes, 3.18%</p>
<p>Regulation of protein modification process (GO:0031399)</p>	<p>ACM1, ASF1, ATG11, CIP1, CLB1, CLB2, CLB5, CLB6, CLN1, CLN2, CLN3, FAR1, FUS3, GIP4, KAP95, NCE102, NET1, PCL1, PCL2, PCL5, FIG1, PSE1, RRD1, SPL2, SPO16, SSP2, XBP1, YOR338W, ZIP2</p>	<p>29 of 1023 genes, 2.83%</p>	<p>220 of 6439 annotated genes, 3.42%</p>

RNA catabolic process (GO:0006401)	CDC33, DBR1, DCS1, EDC2, EDC3, HEK2, IPK1, LSM7, MRT4, MTR3, NAB3, NGL1, NGR1, PAP2, PIN4, POP2, POP4, POP7, PUB1, PUF3, RAD27, RNT1, RRP45, RRP6, SKI8, TRF5, VTS1, WHI3	28 of 1023 genes, 2.74%	161 of 6439 annotated genes, 2.50%
Ribosomal large subunit biogenesis (GO:0042273)	BCD1, BRX1, CIC1, DBP3, DBP6, IPI1, IPI3, LOC1, MAK5, MRT4, NIP7, NOC2, NOC3, NOG1, NOP16, NOP8, P RP43, RPL11B, RPL35A, RPL5, RPL7A, RPL7B, RPL8A, RPL8B, RRP5, SYO1, TOM1, YTM1	28 of 1023 genes, 2.74%	124 of 6439 annotated genes, 1.93%
Response to osmotic stress (GO:0006970)	APE1, CDC14, CTT1, EDC3, FRT1, GLN1, GPP2, GRE3, HAL1, HSP104, HSP12, HSP26, HSP30, HSP42, HSP82, MCK1, MOT3, MRK1, MSB2, MSN2, NRG2, PSR1, ROX1, RRD1, SCH9, SIS1, USV1	27 of 1023 genes, 2.64%	98 of 6439 annotated genes, 1.52%

Regulation of DNA metabolic process (GO:0051052)	CDC6, EST1, FKH1, FKH2, HHO1, HSP82, HST2, IPI1, IPI3, IXR1, MCM5, MPH1, MSH2, MSH6, PAP2, POL30, RRM3, RTT107, RTT109, SLD7, SPO16, SRS2, TBF1, TGS1, VTS1	25 of 1023 genes, 2.44%	96 of 6439 annotated genes, 1.49%
Golgi vesicle transport (GO:0048193)	ARF1, ATG8, BET5, CHS6, COG2, CSR1, DSL1, ERP3, GGA2, GOT1, GRH1, GTS1, MRS6, MUK1, PEF1, PEP12, SEC16, SFB2, SNC2, SSO2, TLG2, TRS130, TRS23, UFE1, YET3	25 of 1023 genes, 2.44%	204 of 6439 annotated genes, 3.17%
Cytokinesis (GO:0000910)	APC2, BUD4, BUD9, CDC14, CDC5, CHS2, CYK3, DBF2, DMA2, INN1, MLC1, MSB2, NET1, NIS1, PEF1, RAX2, REF2, RGL1, ROM2, SKG6, SPR28, SUN4, TOS2, UTH1, YHR030C	25 of 1023 genes, 2.44%	106 of 6439 annotated genes, 1.65%

Ribosomal small subunit biogenesis (GO:0042274)	DBP8, DIP2, EMG1, ENP1, FAF1, FAP7, FCF1, HCR1, IMP3, IMP4, LOC1, LSM7, NOC4, NOP9, PRP43, RPS1A, RPS20, RPS7B, RPS9A, RPS9B, RRP5, RRP7, TOM1, UTP15, UTP23	25 of 1023 genes, 2.44%	148 of 6439 annotated genes, 2.30%
tRNA processing (GO:0008033)	DUS4, ELP3, GCD10, IKI3, LSM7, LSM8, MSS1, NAB3, NCL1, PAP2, POP4, POP7, RPC11, RPR2, TAD3, TAN1, TGS1, THG1, TRM1, TRM2, TRM44, TRM7, TRM8, URM1	24 of 1023 genes, 2.35%	132 of 6439 annotated genes, 2.05%
Regulation of translation (GO:0006417)	AEP1, CDC33, EDC2, ETT1, FES1, GCD1, GCD11, GCD2, GCD6, GIS2, HEK2, LOC1, NCL1, NGR1, POP2, PUF3, RPS9A, RPS9B, RQC2, TIF5, VTS1, WHI3, YOR302W	23 of 1023 genes, 2.25%	194 of 6439 annotated genes, 3.01%

Response to starvation (GO:0042594)	AFT1, ASP3-3, ATG11, ATG8, DCS1, DDR2, ERT1, GCD1, IRS4, MSN2, PEP4, PHM8, PHO5, PRB1, SDS23, SDS24, SEA4, SNF2, SWI1, YDL229W, YOR062C, ZPR1	22 of 1023 genes, 2.15%	78 of 6439 annotated genes, 1.21%
Protein folding (GO:0006457)	ACL4, AHA1, BTN2, CIN1, CIN2, CPR8, FMO1, HSP104, HSP26, HSP32, HSP33, HSP42, HSP82, SIS1, SSA4, SSE2, STI1, TCP1, XDJ1, YDL229W, YKE2, ZUO1	22 of 1023 genes, 2.15%	121 of 6439 annotated genes, 1.88%
Conjugation (GO:0000746)	AFB1, AFR1, AGA1, AGA2, ASG7, BAR1, CLN2, DSE1, FAR1, FUS1, FUS2, FUS3, GPA1, HBT1, MF(ALPHA)1, MFA1, MFA2, ROG3, SCW4, SST2, STE18, YPS1	22 of 1023 genes, 2.15%	118 of 6439 annotated genes, 1.83%

Protein modification by small protein conjugation or removal (GO:0070647)	ACM1, AMN1, APC2, APC5, ASF1, DIA2, DMA2, KAP95, KRE29, LUG1, MPE1, PIB1, PSE1, RFA3, SLX5, SPO16, TOM1, ULA1, URM1, YUH1, ZIP2	21 of 1023 genes, 2.05%	221 of 6439 annotated genes, 3.43%
DNA-templated transcription, elongation (GO:0006354)	ARP9, ASF1, FKH1, FKH2, HIR2, HTL1, JHD1, MTF1, PDP3, POP2, RPA49, RPB9, RPH1, RSC3, RSC58, SSU72, TFG2, THP2, TYE7, YKE2, YLR321C	21 of 1023 genes, 2.05%	107 of 6439 annotated genes, 1.66%
mRNA processing (GO:0006397)	CUS2, DBR1, DRN1, EDC2, FKH1, GTS1, LSM7, LSM8, MPE1, MTF2, NAB3, NGR1, PRP43, PRP9, REF2, SKY1, SMB1, SMD2, SNT309, SSU72	20 of 1023 genes, 1.96%	227 of 6439 annotated genes, 3.53%
Vitamin metabolic process (GO:0006766)	ALD2, ALD3, BNA1, BNA4, BUD17, FMS1, FOL1, FOL2, PDC2, PHO3, RIB4, SNO3, SNZ1, SNZ2, SNZ3, SPE2, SPE3, SPE4, THI11, THI12	20 of 1023 genes, 1.96%	60 of 6439 annotated genes, 0.93%

RNA modification (GO:0009451)	BMT5, DUS4, ELP3, EMG1, GCD10, IKI3, MSS1, NCL1, NOP56, PAP2, TAD3, TAN1, TGS1, THG1, TRM1, TRM2, TRM44, TRM7, TRM8, URM1	20 of 1023 genes, 1.96%	180 of 6439 annotated genes, 2.80%
Organelle assembly (GO:0070925)	ASE1, ATG11, ATG12, ATG3, ATG41, ATG8, BNI5, CBF2, CDC14, CDC5, CLB1, CLB2, CLB5, CTF13, DMA2, EDC3, GIN4, PUB1, SPC98, THP2	20 of 1023 genes, 1.96%	120 of 6439 annotated genes, 1.86%
Mitochondrial translation (GO:0032543)	AEP3, IMG2, MHR1, MMF1, MRP4, MRPL20, MRPL25, MRPL28, MRPL40, MRPL44, MRPL50, MRPL8, MRPS16, MRPS8, MSD1, MSE1, MSY1, MTF2, PTH4, YLR139C	20 of 1023 genes, 1.96%	176 of 6439 annotated genes, 2.73%
Regulation of transport (GO:0051049)	AFT1, ASK10, FKS1, FUS3, GPA1, KAP95, NCE102, OPT2, PEF1, PHO90, RCF1, ROG3, ROM2, SCS2, SEC16, SFK1, SKS1, SKY1, YHR030C	19 of 1023 genes, 1.86%	110 of 6439 annotated genes, 1.71%

Telomere organization (GO:0032200)	BRE2, EST1, HEK2, HSP82, NHP10, PSO2, RAP1, RFA3, RRM3, SLX5, TBF1, TGS1, THP2, TLC1, XRS2, YRF1-2, YRF1-4, YRF1-5, YRF1-7	19 of 1023 genes, 1.86%	84 of 6439 annotated genes, 1.30%
Nucleobase-containing compound transport (GO:0015931)	ENP1, FCY2, HEK2, KAP95, LOC1, NIC96, NRT1, NUP100, PIN4, PSE1, RPS26A, SIS1, THP2, TOM1, VPS20, YBR219C, YBR220C, YEA6, YRA1	19 of 1023 genes, 1.86%	178 of 6439 annotated genes, 2.76%
Response to heat (GO:0009408)	AHA1, DDR2, HSP104, HSP12, HSP26, HSP30, HSP42, HSP82, MCK1, MRK1, MSN2, NUP100, PSR1, SSA4, SWI4, WHI2, WSC3	17 of 1023 genes, 1.66%	79 of 6439 annotated genes, 1.23%
Cellular ion homeostasis (GO:0006873)	AFT1, ATX1, COS3, DBF2, EMP70, ENB1, ERV1, FRE3, FRE4, FRE5, PDR5, PGM2, PIC2, RCH1, SIT1, SKY1, SMF3	17 of 1023 genes, 1.66%	160 of 6439 annotated genes, 2.48%

Histone modification (GO:0016570)	ALK1, ARD1, ASF1, BRE2, ELP3, FMS1, HAT1, HHF1, HHF2, HOS3, JHD1, RPH1, RTT109, RVB1, TAF6, XBP1, YOR338W	17 of 1023 genes, 1.66%	143 of 6439 annotated genes, 2.22%
Pseudohyphal growth (GO:0007124)	DBR1, DSE2, ECM23, EMP70, FKH1, FKH2, FLO11, IME1, MKS1, NRG2, PHD1, SFG1, SKS1, SOK2, TEC1, UME6, WHI3	17 of 1023 genes, 1.66%	75 of 6439 annotated genes, 1.16%
Vacuole organization (GO:0007033)	ATG11, ATG12, ATG3, ATG41, ATG8, CDC14, CLN3, ENO1, GYP7, OPT2, PBI2, PEP12, SFK1, VAC17, VAC7, VTC2	16 of 1023 genes, 1.56%	106 of 6439 annotated genes, 1.65%
Endocytosis (GO:0006897)	FKS1, GTS1, OSH6, ROG3, ROM2, SDS24, SLA1, SNC2, SUR7, SVL3, SWH1, TLG2, WHI2, YCK1, YCR028C	15 of 1023 genes, 1.47%	124 of 6439 annotated genes, 1.93%
Vesicle organization (GO:0016050)	MST28, PEF1, PEP12, PRM8, SEC16, SFB2, SNC2, SPO20, SSO2, TLG2, UFE1, UIP3, VPS20, YAR028W, YCR007C	15 of 1023 genes, 1.47%	104 of 6439 annotated genes, 1.62%

Organelle fusion (GO:0048284)	CLN3, ENO1, FUS2, GPA1, GYP7, OPT2, PBI2, PEP12, SNC2, SPO20, SSO2, TLG2, UFE1, VTC2	14 of 1023 genes, 1.37%	105 of 6439 annotated genes, 1.63%
Endosomal transport (GO:0016197)	BTN2, COS1, COS2, COS3, COS4, COS6, COS8, EMP70, GGA2, GOT1, MUK1, SLM1, SNA2, TRS130	14 of 1023 genes, 1.37%	104 of 6439 annotated genes, 1.62%
Carbohydrate transport (GO:0008643)	ASK10, GLK1, HXK1, HXK2, HXT10, HXT11, HXT17, HXT2, HXT4, HXT7, MPH2, SKS1, YIL170W, YIL171W	14 of 1023 genes, 1.37%	49 of 6439 annotated genes, 0.76%
Protein dephosphorylation (GO:0006470)	CDC14, CLB2, FCP1, GIP4, NET1, PIG1, PSR1, REF2, RRD1, RTR1, SIA1, SSU72, TIM50, WHI2	14 of 1023 genes, 1.37%	95 of 6439 annotated genes, 1.48%
Lipid transport (GO:0006869)	CSR1, FAA4, MDM10, MDM35, NCE102, OPT2, OSH6, PRY1, PRY2, RSB1, SCS2, SFK1, SWH1, TCB2	14 of 1023 genes, 1.37%	72 of 6439 annotated genes, 1.12%
Cellular respiration (GO:0045333)	CIT1, CIT2, CYT1, GDS1, HAP5, ICL1, MDH2, ODC1, ODC2, PUF3, SDH4, YLR139C	12 of 1023 genes, 1.17%	111 of 6439 annotated genes, 1.72%

RNA splicing (GO:0008380)	CUS2, DBR1, DRN1, GTS1, LSM7, LSM8, PRP43, PRP9, SKY1, SMB1, SMD2, SNT309	12 of 1023 genes, 1.17%	156 of 6439 annotated genes, 2.42%
Cell morphogenesis (GO:0000902)	AFR1, CIN2, FKS1, FUS1, FUS2, GIC2, GSC2, HBT1, OPT2, RAX2, YCK1, YPK2	12 of 1023 genes, 1.17%	49 of 6439 annotated genes, 0.76%
Translational initiation (GO:0006413)	AEP3, CDC33, GCD1, GCD11, GCD2, GCD6, HCR1, PR T1, SIS1, TIF34, TIF5	11 of 1023 genes, 1.08%	70 of 6439 annotated genes, 1.09%
Protein acylation (GO:0043543)	AKR2, ARD1, ASF1, ELP3, HAT1, PFA5, RTT109, RVB1, TAF6, YIR042C, YOR338W	11 of 1023 genes, 1.08%	80 of 6439 annotated genes, 1.24%
Ribosome assembly (GO:0042255)	BRX1, IPI1, IPI3, MRT4, NIP7, RPL11B, RPL5, RPS26A, RRP5, RRP7, TIF5	11 of 1023 genes, 1.08%	80 of 6439 annotated genes, 1.24%
SnoRNA processing (GO:0043144)	MTR3, NAB3, PAP2, POP4, POP7, REF2, RNT1, RPR2, RRP45, RRP6, TRF5	11 of 1023 genes, 1.08%	45 of 6439 annotated genes, 0.70%
Oligosaccharide metabolic process (GO:0009311)	AMS1, CWH41, HSP104, IM A5, MAL12, MAL32, MPH2, NTH1, PGM2, SUC2, YML100W	11 of 1023 genes, 1.08%	30 of 6439 annotated genes, 0.47%

Amino acid transport (GO:0006865)	AGP1, ALP1, ATG22, BTN2, ODC1, ODC2, PUT4, TAT1, TAT2, YPQ2	10 of 1023 genes, 0.98%	57 of 6439 annotated genes, 0.89%
Invasive growth in response to glucose limitation (GO:0001403)	DIA2, DSE1, EMP70, FLO11, FUS3, GPG1, SNF2, TEC1, URM1, WHI3	10 of 1023 genes, 0.98%	54 of 6439 annotated genes, 0.84%
Protein maturation (GO:0051604)	ARD1, ATG42, HO, HSP82, KEX2, LIA1, MAP1, PEP4, YIR042C, YPS1	10 of 1023 genes, 0.98%	95 of 6439 annotated genes, 1.48%
DNA-templated transcription, initiation (GO:0006352)	HMO1, MTF1, RPA49, RPB9, RPT1, SSU72, TAF6, TFA2, TFG2, TOA2	10 of 1023 genes, 0.98%	82 of 6439 annotated genes, 1.27%
Nucleus organization (GO:0006997)	CDC5, FUS2, GPA1, KAP95, MDM1, NET1, NIC96, SYH1, TGS1, TOM1	10 of 1023 genes, 0.98%	70 of 6439 annotated genes, 1.09%
Protein glycosylation (GO:0006486)	ALG14, CWH41, GFA1, KTR2, MNN1, OCH1, OST4, OST5, PSA1, YMR084W	10 of 1023 genes, 0.98%	77 of 6439 annotated genes, 1.20%
Protein alkylation (GO:0008213)	BRE2, EFM4, EFM5, EFM6, HHF1, HHF2, NNT1, RKM4, SFM1	9 of 1023 genes, 0.88%	59 of 6439 annotated genes, 0.92%
Ribosomal subunit export from nucleus (GO:0000054)	ARB1, LOC1, MRT4, NIC96, NOG1, NOP9, YDL229W, ZUO1	8 of 1023 genes, 0.78%	53 of 6439 annotated genes, 0.82%

Protein lipidation (GO:0006497)	AKR2, ATG12, ATG3, GAB1, GPI15, GPI18, PFA5	7 of 1023 genes, 0.68%	49 of 6439 annotated genes, 0.76%
Membrane fusion (GO:0061025)	ATG8, PEP12, SNC2, SPO20, SSO2, TLG2, UFE1	7 of 1023 genes, 0.68%	54 of 6439 annotated genes, 0.84%
Organelle inheritance (GO:0048308)	ABF2, INP2, MDM1, PEP12, SCS2, VAC17, VAC7	7 of 1023 genes, 0.68%	56 of 6439 annotated genes, 0.87%
Peroxisome organization (GO:0007031)	ADR1, DSL1, GPX1, INP2, MDH2, PEX14, PEX25	7 of 1023 genes, 0.68%	51 of 6439 annotated genes, 0.79%
Transposition (GO:0032196)	DBR1, FUS3, RTT107, RTT109, TEC1, YLR035C-A	6 of 1023 genes, 0.59%	114 of 6439 annotated genes, 1.77%
Transcription by RNA polymerase I (GO:0006360)	HMO1, RPA43, RPA49, SCH9, UAF30, UTP15	6 of 1023 genes, 0.59%	69 of 6439 annotated genes, 1.07%
DNA-templated transcription, termination (GO:0006353)	FKH1, NAB3, REF2, RNT1, RPC11, SSU72	6 of 1023 genes, 0.59%	42 of 6439 annotated genes, 0.65%
Cell budding (GO:0007114)	BUD4, GIN4, NIS1, PEF1, RAX2, URM1	6 of 1023 genes, 0.59%	59 of 6439 annotated genes, 0.92%
Exocytosis (GO:0006887)	OSH6, SNC2, SPO20, SSO2, SWH1	5 of 1023 genes, 0.49%	54 of 6439 annotated genes, 0.84%
tRNA aminoacylation for protein translation (GO:0006418)	MSD1, MSE1, MSY1, VAS1, WRS1	5 of 1023 genes, 0.49%	37 of 6439 annotated genes, 0.57%
Translational elongation (GO:0006414)	RQC2, YDL229W, ZUO1	3 of 1023 genes, 0.29%	338 of 6439 annotated genes, 5.25%

Transcription by RNA polymerase III (GO:0006383)	RPC11, SCH9	2 of 1023 genes, 0.20%	42 of 6439 annotated genes, 0.65%
Membrane invagination (GO:0010324)	ATG8	1 of 1023 genes, 0.10%	1 of 6439 annotated genes, 0.02%