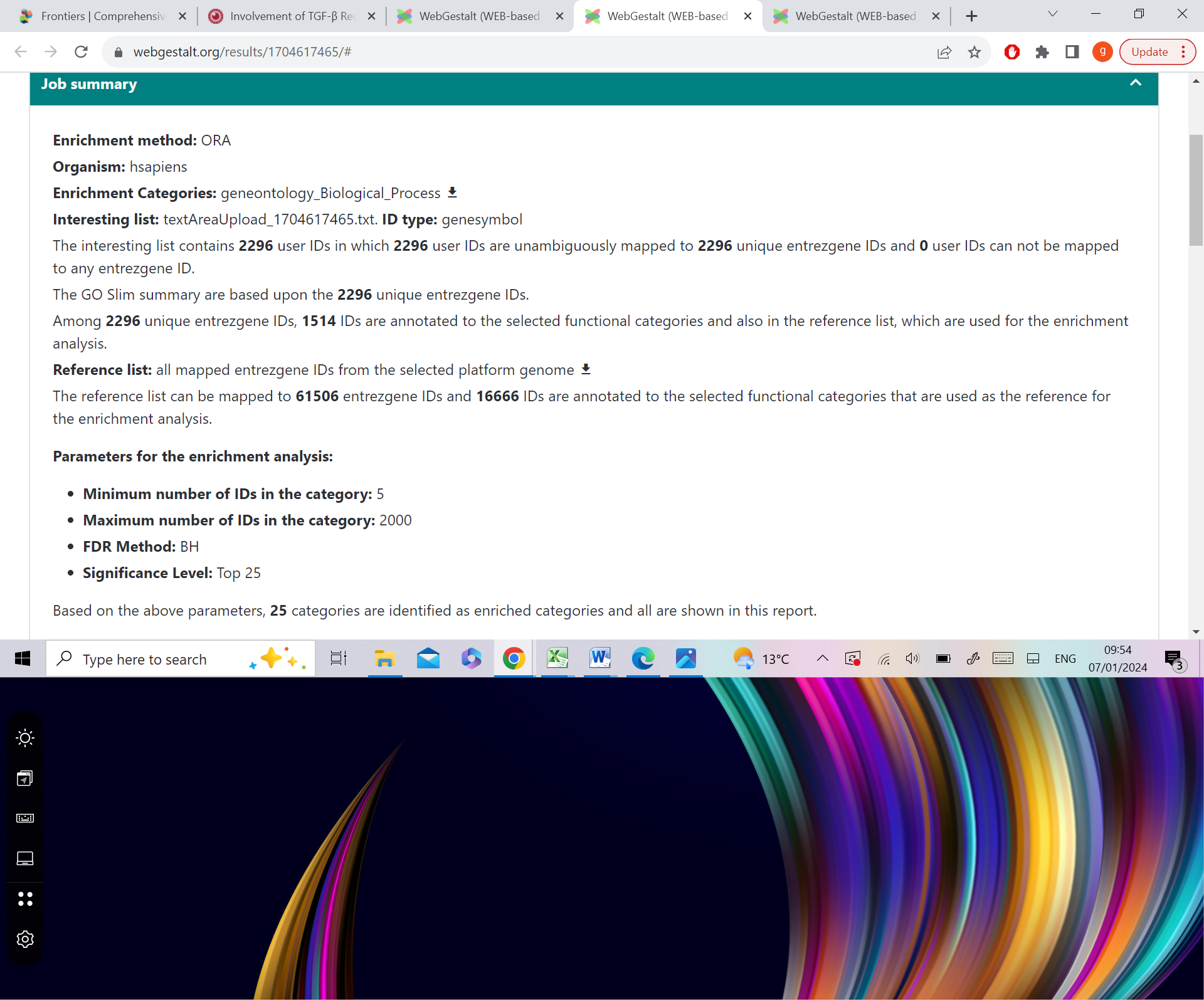
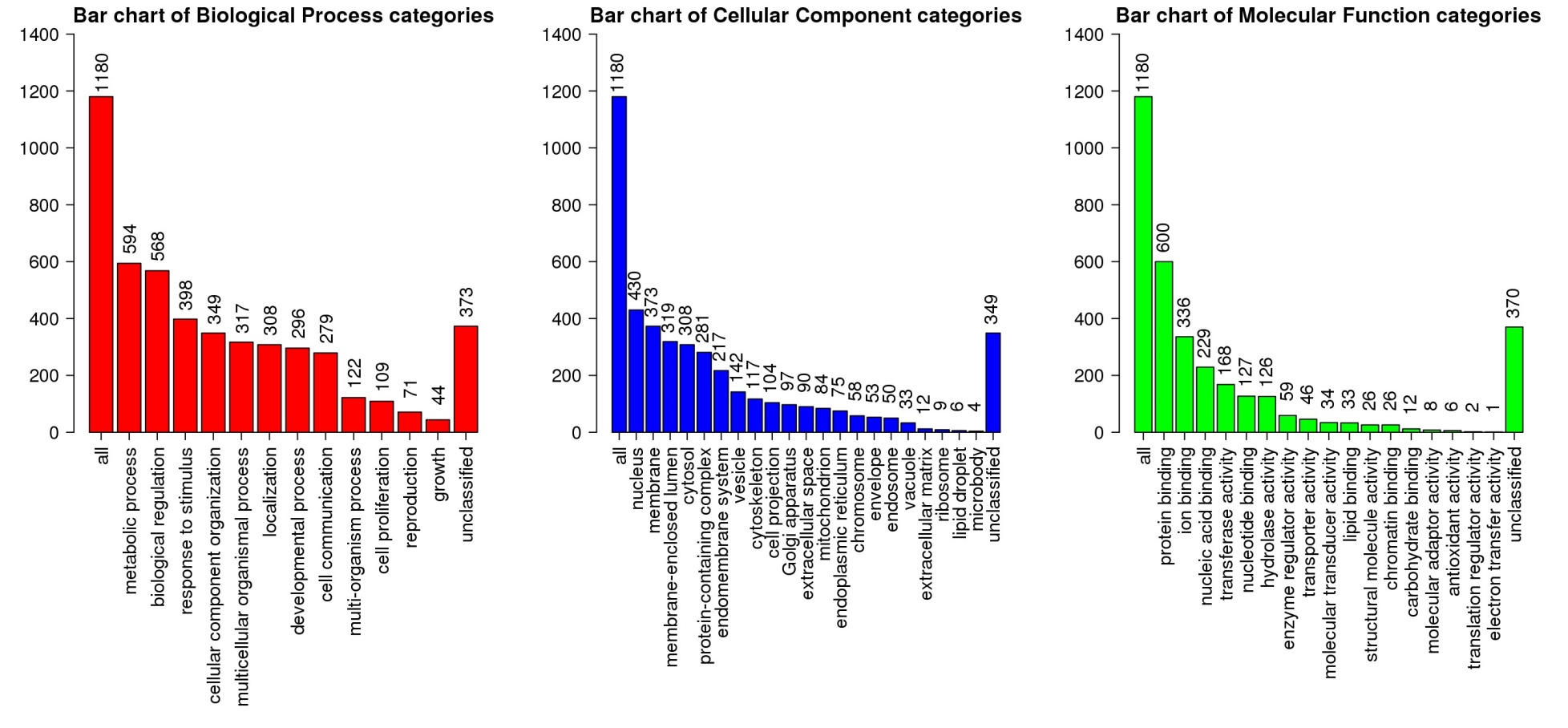
# ORA analysis of DE genes

Job summary example:



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# KD 123 VS Control (Downregulated genes)



## 1

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| **Gene Set** | **GO Biological process description** | **Overlap** | **Enrichment Ratio** | **P Value** | **Gene ID** |
| GO:0033554 | cellular response to stress | 136 | 1.552456 | 8.37E-08 | DDX39B;GNGT1;MSH5;SPDYA;ATRIP;ERCC5;FANCL;SLC39A5;OMG;NABP1;EDEM2;PARPBP;PRKAA2;RTEL1;IL6;EIF2AK3;RRAGD;RORA;WIPI1;MRNIP;HELB;FBXO4;FNIP1;NAMPT;ATM;HSPA14;EID3;EEF1E1;RAD17;GPX3;CREBRF;CEBPB;JMY;HERPUD1;TDG;CTH;PDCD4;MBIP;UVSSA;RMI2;RPAIN;SUV39H2;SNAI1;CBX8;ERCC6L2;ZNF277;BRIP1;IL1B;SESN1;ATR;SGK1;TAF9;PPM1D;YOD1;RRM2B;UPP1;FNIP2;MDM4;CCNK;GABARAPL2;OXR1;DHX36;UFM1;DLG1;ERRFI1;MAP3K20;FANCC;ZRANB3;UIMC1;ATF3;SIRT1;TSC1;XIAP;JAK2;MAP3K12;PDCD10;STK3;PDK1;FEM1B;SH3RF2;CDK7;WRN;FAN1;MAP4K3;PYROXD1;TXNRD2;BNIP3;ADNP2;MAPK12;PMAIP1;WDR48;WDR59;USP47;PTGER4;HP1BP3;TAF1;MBTPS1;RBBP5;BACH1;CFLAR;RNF168;MAPK8;IL1A;PSME4;FANCE;ITCH;SMYD2;ANKZF1;RBBP6;SPAG9;ZFYVE1;ERP44;HIPK1;MET;POLH;SETD2;TPM1;EDEM3;TAB2;SMG1;RNF169;SLU7;TFDP2;RIPK1;CEBPG;INO80D;PTPRK;UBE2D3;ATF4;CAMKK2;ERN1;BCL2L1;HK2;KDM1A;INTS3;GIGYF2 |
| GO:1901796 | regulation of signal transduction by p53 class mediator | 22 | 3.634608 | 1.36E-07 | BOP1;ATM;EEF1E1;JMY;RFFL;SNAI1;TAF13;ATR;TAF4B;TAF9;RRM2B;MDM4;TAF11;PAK1IP1;SIRT1;RRN3;PMAIP1;TAF1;SMYD2;HIPK1;TP53BP2;KDM1A |
| GO:2001020 | regulation of response to DNA damage stimulus | 28 | 2.939589 | 2.99E-07 | DDX39B;PARPBP;RTEL1;MRNIP;HELB;FBXO4;ATM;EID3;EEF1E1;RMI2;SNAI1;CBX8;ATR;TAF9;UIMC1;SIRT1;FEM1B;PMAIP1;USP47;RNF168;SMYD2;POLH;SETD2;SMG1;RNF169;CEBPG;BCL2L1;KDM1A |
| GO:0006974 | cellular response to DNA damage stimulus | 68 | 1.798036 | 1.81E-06 | DDX39B;MSH5;SPDYA;ATRIP;ERCC5;FANCL;NABP1;PARPBP;RTEL1;MRNIP;HELB;FBXO4;ATM;EID3;EEF1E1;RAD17;JMY;TDG;UVSSA;RMI2;RPAIN;SNAI1;CBX8;ERCC6L2;BRIP1;ATR;SGK1;TAF9;PPM1D;RRM2B;FNIP2;MDM4;CCNK;MAP3K20;FANCC;ZRANB3;UIMC1;SIRT1;XIAP;FEM1B;CDK7;WRN;FAN1;MAPK12;PMAIP1;WDR48;USP47;TAF1;RBBP5;BACH1;RNF168;PSME4;FANCE;SMYD2;RBBP6;HIPK1;POLH;SETD2;SMG1;RNF169;TFDP2;CEBPG;INO80D;UBE2D3;BCL2L1;KDM1A;INTS3;GIGYF2 |
| GO:0007049 | cell cycle | 123 | 1.507406 | 1.83E-06 | DDX39B;SETDB2;MSH5;BOP1;SPDYA;ATRIP;SLC39A5;CEP126;CGRRF1;ESCO1;FBXO43;NABP1;PRKAA2;RTEL1;EFHC1;CEP135;NEDD9;RRAGD;MRNIP;E2F5;FBXO4;SYCE1L;ATM;PAX6;WEE1;HERC5;RAD17;SIAH1;HBP1;JMY;TUBD1;BORA;PDCD4;CEP68;DMTF1;CCNL1;RMI2;APPL2;SUV39H2;LSM11;CSPP1;BRIP1;IL1B;ATR;CDK17;CENPC;PPM1D;HACE1;CEP120;MDM4;CCNG1;DBF4;VPS4B;CCNK;DLG1;MAP3K20;UBR2;CCNL2;GPSM2;UIMC1;BIN3;AGO4;SIRT1;TUBE1;TTC19;TSC1;TTK;KIF14;NCAPG2;FEM1B;WTAP;OFD1;CDK7;TUSC2;INHBA;PCM1;TBRG1;BUB1;KIF15;CEP192;PDGFB;ORC3;LPIN1;ARL8B;PPM1A;CDK8;HMMR;CCSAP;MAPK12;MIS12;TUBGCP4;CENPF;USP47;STMN1;STAG2;CHMP2B;TAF1;CDC23;PARD6B;AKAP9;BACH1;WRAP73;IL1A;ECD;SIAH2;UHMK1;C2CD3;SETD2;IST1;VCPIP1;TP53BP2;GDPD5;TFDP2;CLIP1;PTPRK;YY1AP1;ERN1;IPO5;CENPV;BCL2L1;INTS3;GIGYF2;NUP214 |
| GO:0016577 | histone demethylation | 9 | 6.187361 | 8.35E-06 | KDM3A;KDM5B;KDM6A;UTY;KDM5A;JMJD1C;KDM5D;JARID2;KDM1A |
| GO:0006482 | protein demethylation | 9 | 5.812369 | 1.47E-05 | KDM3A;KDM5B;KDM6A;UTY;KDM5A;JMJD1C;KDM5D;JARID2;KDM1A |
| GO:0008214 | protein dealkylation | 9 | 5.812369 | 1.47E-05 | KDM3A;KDM5B;KDM6A;UTY;KDM5A;JMJD1C;KDM5D;JARID2;KDM1A |
| GO:0070076 | histone lysine demethylation | 8 | 6.314673 | 2.27E-05 | KDM3A;KDM5B;KDM6A;UTY;KDM5A;JMJD1C;KDM5D;KDM1A |
| GO:1905515 | non-motile cilium assembly | 11 | 4.262404 | 4.08E-05 | IFT80;CEP126;CEP135;GORAB;CEP89;TOGARAM1;MAK;CC2D2A;PCM1;WRAP73;C2CD3 |
| GO:0018105 | peptidyl-serine phosphorylation | 29 | 2.191662 | 6.40E-05 | IL24;PRKAA2;IL6;EIF2AK3;CLK1;FNIP1;ATM;TBK1;RICTOR;ATR;SGK1;FNIP2;MARK3;TTK;MAP3K12;PDCD10;PDGFB;MAPK12;BCAR3;TAF1;AKAP9;MAPK8;INPP5K;UHMK1;CAPRIN2;SMG1;RIPK1;HCLS1;ERN1 |
| GO:0051726 | regulation of cell cycle | 80 | 1.541557 | 6.72E-05 | DDX39B;BOP1;SPDYA;ATRIP;CGRRF1;FBXO43;NABP1;PRKAA2;CEP135;RRAGD;MRNIP;E2F5;FBXO4;ATM;WEE1;HERC5;RAD17;HBP1;JMY;BORA;PDCD4;CCNL1;RMI2;LSM11;CSPP1;BRIP1;IL1B;ATR;CDK17;CEP120;MDM4;CCNG1;VPS4B;CCNK;DLG1;MAP3K20;CCNL2;GPSM2;UIMC1;SIRT1;TSC1;TTK;KIF14;FEM1B;OFD1;CDK7;INHBA;PCM1;TBRG1;BUB1;CEP192;PDGFB;PPM1A;CDK8;HMMR;CCSAP;MAPK12;CENPF;USP47;STAG2;CHMP2B;TAF1;CDC23;AKAP9;IL1A;ECD;UHMK1;SETD2;TP53BP2;GDPD5;TFDP2;PTPRK;YY1AP1;ERN1;IPO5;CENPV;BCL2L1;INTS3;GIGYF2;NUP214 |
| GO:0006281 | DNA repair | 44 | 1.835086 | 7.78E-05 | MSH5;ATRIP;ERCC5;FANCL;NABP1;PARPBP;RTEL1;MRNIP;HELB;ATM;EID3;RAD17;JMY;TDG;UVSSA;RMI2;RPAIN;CBX8;ERCC6L2;BRIP1;ATR;RRM2B;FANCC;ZRANB3;UIMC1;SIRT1;CDK7;WRN;FAN1;WDR48;USP47;BACH1;RNF168;PSME4;FANCE;POLH;SETD2;SMG1;RNF169;CEBPG;INO80D;UBE2D3;KDM1A;INTS3 |
| GO:0043516 | regulation of DNA damage response, signal transduction by p53 class mediator | 8 | 5.328005 | 8.73E-05 | ATM;EEF1E1;SNAI1;ATR;SIRT1;PMAIP1;SMYD2;KDM1A |
| GO:0072331 | signal transduction by p53 class mediator | 24 | 2.346277 | 9.37E-05 | BOP1;ATM;EEF1E1;JMY;RFFL;SNAI1;TAF13;ATR;TAF4B;TAF9;PPM1D;RRM2B;MDM4;TAF11;PAK1IP1;SIRT1;RRN3;PMAIP1;TAF1;SMYD2;HIPK1;TP53BP2;TFDP2;KDM1A |
| GO:0042795 | snRNA transcription by RNA polymerase II | 12 | 3.602032 | 1.04E-04 | NABP1;TAF13;TAF9;ICE2;TAF11;CCNK;CDK7;ICE1;GTF2E1;ELL2;RPRD1A;INTS3 |
| GO:0009301 | snRNA transcription | 12 | 3.552003 | 1.20E-04 | NABP1;TAF13;TAF9;ICE2;TAF11;CCNK;CDK7;ICE1;GTF2E1;ELL2;RPRD1A;INTS3 |
| GO:0044087 | regulation of cellular component biogenesis | 69 | 1.564393 | 1.41E-04 | MTPN;SEC22B;ERCC5;PRKAA2;RTEL1;CEP135;FNIP1;ATM;SCFD1;AVIL;WDPCP;IFT20;JMY;FARP2;SNAI1;RICTOR;TBC1D15;ATR;TOGARAM1;MAK;CEP120;RAB17;FNIP2;PAN3;PHLDB2;RHOQ;VPS4B;PIKFYVE;GMFB;MMP1;DHX36;DLG1;GPSM2;SH3YL1;BIN3;TRABD2A;TSC1;KIF14;SAMD8;SPTY2D1;TAPT1;RRN3;PPM1A;ZNF451;CCSAP;BCAS3;ICE1;PMAIP1;MACF1;STMN1;STAG2;HEATR1;PTGER4;CHMP2B;AKAP13;RAB5A;TAF1;AKAP9;INPP5K;WRAP73;MET;TPM1;RIOK3;CLIP1;TBC1D20;RAP1B;ARFGEF1;HCLS1;LCP1 |
| GO:0034720 | histone H3-K4 demethylation | 4 | 12.1783 | 1.50E-04 | KDM5B;KDM5A;KDM5D;KDM1A |
| GO:0070925 | organelle assembly | 64 | 1.589708 | 1.58E-04 | IFT80;SEC22B;BOP1;CFAP53;CEP126;FAM161A;PRKAA2;CEP135;GORAB;WIPI1;TTC26;SCFD1;ATG12;AVIL;WDPCP;IFT20;AHI1;VMP1;BBIP1;FARP2;CEP89;RPS10;TBC1D15;TOGARAM1;MAK;CENPC;CEP120;RAB17;PAN3;VPS4B;PIKFYVE;GABARAPL2;GPSM2;RSL24D1;IFT43;ATG2A;DNAH5;CC2D2A;OFD1;PCM1;WDR11;CEP192;TAPT1;TMF1;CCSAP;MIS12;TUBGCP4;CENPF;STAG2;CHMP2B;AKAP13;RAB5A;EFL1;AKAP9;CFLAR;WRAP73;KIAA0586;C2CD3;TPM1;IST1;RC3H1;TBC1D20;RPL12;LCP1 |
| GO:0071496 | cellular response to external stimulus | 31 | 2.002038 | 1.94E-04 | MTPN;P2RY11;SCX;CASTOR2;SLC39A5;PRKAA2;EIF2AK3;RRAGD;WIPI1;FNIP1;NAMPT;CD40;BRIP1;IL1B;SESN1;PPM1D;UPP1;GABARAPL2;ATF3;SIRT1;TSC1;WRN;BCL10;BNIP3;PMAIP1;WDR59;PTGER4;TAF1;MAPK8;ZFYVE1;ATF4 |
| GO:0009267 | cellular response to starvation | 18 | 2.592002 | 2.00E-04 | SLC39A5;PRKAA2;EIF2AK3;RRAGD;WIPI1;FNIP1;SESN1;PPM1D;UPP1;GABARAPL2;ATF3;SIRT1;WRN;PMAIP1;WDR59;MAPK8;ZFYVE1;ATF4 |
| GO:0007030 | Golgi organization | 17 | 2.664003 | 2.14E-04 | VMP1;ATP8B2;GOLPH3L;HACE1;GCC2;ATL2;ARL1;DYM;PDCD10;GOLGA5;BCAS3;RBSN;AKAP9;VCPIP1;TBC1D20;ARFGEF1;ARHGAP21 |
| GO:0031669 | cellular response to nutrient levels | 24 | 2.223863 | 2.14E-04 | P2RY11;CASTOR2;SLC39A5;PRKAA2;EIF2AK3;RRAGD;WIPI1;FNIP1;NAMPT;BRIP1;SESN1;PPM1D;UPP1;GABARAPL2;ATF3;SIRT1;TSC1;WRN;PMAIP1;WDR59;TAF1;MAPK8;ZFYVE1;ATF4 |
| GO:0018209 | peptidyl-serine modification | 29 | 2.026389 | 2.51E-04 | IL24;PRKAA2;IL6;EIF2AK3;CLK1;FNIP1;ATM;TBK1;RICTOR;ATR;SGK1;FNIP2;MARK3;TTK;MAP3K12;PDCD10;PDGFB;MAPK12;BCAR3;TAF1;AKAP9;MAPK8;INPP5K;UHMK1;CAPRIN2;SMG1;RIPK1;HCLS1;ERN1 |

## 2

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| **Gene Set** | **GO Molecular function description** | **Overlap** | **Enrichment Ratio** | **P Value** | **Gene ID** |
| GO:0016772 | transferase activity, transferring phosphorus-containing groups | 76 | 1.757476 | 1.03E-06 | IRAK3;NMNAT3;PRKAA2;EIF2AK3;CLK1;AATK;N4BP2;ATM;WEE1;GAB1;PIGN;ETNK1;MMD;NME7;TBK1;UAP1L1;CAMK1G;ATR;ACVR2A;CDK17;SGK1;MAK;PPM1D;YRDC;PAN3;GALK2;CCNG1;UAP1;CCNK;RYK;PIKFYVE;MTPAP;TRNT1;DLG1;MAP3K20;MARK3;LIMK2;TTK;STK17A;JAK2;MAP3K12;STK3;PDK1;DGKH;PRPSAP2;PANK3;CDK7;TRPM7;SAMD8;PPIP5K2;BUB1;MAP4K3;PDGFB;COQ8B;CDK8;PIK3C2A;MAPK12;AKAP13;TAF1;UGP2;MAPK8;UHMK1;HIPK1;MET;POLH;GK5;SMG1;CLK2;RIOK3;RIPK1;CAMKK2;ERN1;HMGXB3;HK2;PIP5K1A;JAK1 |
| GO:0032452 | histone demethylase activity | 9 | 7.126389 | 2.45E-06 | KDM3A;KDM5B;KDM6A;UTY;KDM5A;JMJD1C;KDM5D;JARID2;KDM1A |
| GO:0140030 | modification-dependent protein binding | 20 | 3.234199 | 3.49E-06 | ATRIP;CBX8;MBTD1;KDM5B;EPS15;ZRANB3;UIMC1;AGL;NCAPG2;FAN1;KDM5A;TAF1;RBBP5;ZRANB1;RNF168;PSME4;KDM5D;TAB2;RNF169;JARID2 |
| GO:0016301 | kinase activity | 65 | 1.76637 | 5.54E-06 | IRAK3;PRKAA2;EIF2AK3;CLK1;AATK;N4BP2;ATM;WEE1;GAB1;ETNK1;MMD;NME7;TBK1;CAMK1G;ATR;ACVR2A;CDK17;SGK1;MAK;PPM1D;PAN3;GALK2;CCNG1;CCNK;RYK;PIKFYVE;DLG1;MAP3K20;MARK3;LIMK2;TTK;STK17A;JAK2;MAP3K12;STK3;PDK1;DGKH;PANK3;CDK7;TRPM7;PPIP5K2;BUB1;MAP4K3;PDGFB;COQ8B;CDK8;PIK3C2A;MAPK12;AKAP13;TAF1;MAPK8;UHMK1;HIPK1;MET;GK5;SMG1;CLK2;RIOK3;RIPK1;CAMKK2;ERN1;HMGXB3;HK2;PIP5K1A;JAK1 |
| GO:0016773 | phosphotransferase activity, alcohol group as acceptor | 61 | 1.788929 | 7.36E-06 | IRAK3;PRKAA2;EIF2AK3;CLK1;AATK;N4BP2;ATM;WEE1;GAB1;ETNK1;MMD;TBK1;CAMK1G;ATR;ACVR2A;CDK17;SGK1;MAK;PPM1D;PAN3;GALK2;CCNG1;CCNK;RYK;PIKFYVE;MAP3K20;MARK3;LIMK2;TTK;STK17A;JAK2;MAP3K12;STK3;PDK1;DGKH;PANK3;CDK7;TRPM7;BUB1;MAP4K3;PDGFB;COQ8B;CDK8;PIK3C2A;MAPK12;AKAP13;TAF1;MAPK8;UHMK1;HIPK1;MET;GK5;SMG1;CLK2;RIOK3;RIPK1;CAMKK2;ERN1;HK2;PIP5K1A;JAK1 |
| GO:0005524 | ATP binding | 97 | 1.532961 | 1.29E-05 | DDX39B;EIF4A1;MSH5;DQX1;IRAK3;NMNAT3;CBWD6;PRKAA2;RTEL1;EIF2AK3;CLK1;HELB;AATK;N4BP2;SLFNL1;ATM;WEE1;HSPA14;RAD17;ABCA5;TDG;ETNK1;TRMU;NME7;ATP8B2;SLC22A5;TBK1;ACSL4;ERCC6L2;CAMK1G;BRIP1;ATR;ACVR2A;CDK17;SGK1;MAK;PAN3;GALK2;VPS4B;RYK;PIKFYVE;ATP13A3;MTPAP;BTAF1;TRNT1;DHX36;MAP3K20;ZRANB3;NLRC5;ATP7B;EIF4A2;RARS2;MARK3;LIMK2;NLRP1;TTK;STK17A;KIF14;JAK2;DNAH5;MAP3K12;MYO5C;QRSL1;STK3;PDK1;DGKH;PANK3;CDK7;WRN;TRPM7;PPIP5K2;BUB1;KIF15;MAP4K3;COQ8B;CDK8;PIK3C2A;MAPK12;TAF1;MAPK8;CLPX;ATP6V1B2;UHMK1;HIPK1;MET;TARS2;GK5;SMG1;CLK2;RIOK3;RIPK1;UBE2D3;CAMKK2;ERN1;HK2;PIP5K1A;JAK1 |
| GO:0035639 | purine ribonucleoside triphosphate binding | 114 | 1.465711 | 1.59E-05 | DDX39B;EIF4A1;MSH5;DQX1;IRAK3;NMNAT3;CBWD6;PRKAA2;RTEL1;EIF2AK3;RRAGD;CLK1;HELB;AATK;N4BP2;SLFNL1;ATM;WEE1;HSPA14;RAD17;ABCA5;TUBD1;TDG;ARL5B;ETNK1;RND3;TRMU;NME7;ATP8B2;SLC22A5;TBK1;ACSL4;RAB28;ERCC6L2;CAMK1G;BRIP1;ATR;ACVR2A;CDK17;SGK1;MAK;RAB17;PAN3;GALK2;RHOQ;VPS4B;RYK;PIKFYVE;ATP13A3;MTPAP;BTAF1;TRNT1;DHX36;MAP3K20;ZRANB3;NLRC5;ATP7B;EIF4A2;RARS2;ATL2;ARL1;MARK3;TUBE1;LIMK2;NLRP1;TTK;STK17A;KIF14;JAK2;DNAH5;MAP3K12;MYO5C;QRSL1;STK3;PDK1;DGKH;PANK3;CDK7;WRN;TRPM7;PPIP5K2;BUB1;KIF15;MAP4K3;COQ8B;SRP54;HBS1L;ARL8B;CDK8;PIK3C2A;MAPK12;RAB5A;EFL1;TAF1;MAPK8;ARHGAP5;CLPX;ATP6V1B2;UHMK1;HIPK1;MET;TARS2;GK5;SMG1;CLK2;RIOK3;RAP1B;RIPK1;UBE2D3;CAMKK2;ERN1;HK2;PIP5K1A;JAK1 |
| GO:0030554 | adenyl nucleotide binding | 100 | 1.508726 | 1.80E-05 | DDX39B;EIF4A1;MSH5;DQX1;IRAK3;NMNAT3;CNGB1;CBWD6;PRKAA2;RTEL1;EIF2AK3;ACBD7;CLK1;HELB;AATK;N4BP2;SLFNL1;ATM;WEE1;HSPA14;RAD17;ABCA5;TDG;ETNK1;TRMU;NME7;ATP8B2;SLC22A5;TBK1;ACSL4;ERCC6L2;CAMK1G;BRIP1;ATR;ACVR2A;CDK17;GRPEL2;SGK1;MAK;PAN3;GALK2;VPS4B;RYK;PIKFYVE;ATP13A3;MTPAP;BTAF1;TRNT1;DHX36;MAP3K20;ZRANB3;NLRC5;ATP7B;EIF4A2;RARS2;MARK3;LIMK2;NLRP1;TTK;STK17A;KIF14;JAK2;DNAH5;MAP3K12;MYO5C;QRSL1;STK3;PDK1;DGKH;PANK3;CDK7;WRN;TRPM7;PPIP5K2;BUB1;KIF15;MAP4K3;COQ8B;CDK8;PIK3C2A;MAPK12;TAF1;MAPK8;CLPX;ATP6V1B2;UHMK1;HIPK1;MET;TARS2;GK5;SMG1;CLK2;RIOK3;RIPK1;UBE2D3;CAMKK2;ERN1;HK2;PIP5K1A;JAK1 |
| GO:0032559 | adenyl ribonucleotide binding | 99 | 1.506506 | 2.12E-05 | DDX39B;EIF4A1;MSH5;DQX1;IRAK3;NMNAT3;CNGB1;CBWD6;PRKAA2;RTEL1;EIF2AK3;ACBD7;CLK1;HELB;AATK;N4BP2;SLFNL1;ATM;WEE1;HSPA14;RAD17;ABCA5;TDG;ETNK1;TRMU;NME7;ATP8B2;SLC22A5;TBK1;ACSL4;ERCC6L2;CAMK1G;BRIP1;ATR;ACVR2A;CDK17;SGK1;MAK;PAN3;GALK2;VPS4B;RYK;PIKFYVE;ATP13A3;MTPAP;BTAF1;TRNT1;DHX36;MAP3K20;ZRANB3;NLRC5;ATP7B;EIF4A2;RARS2;MARK3;LIMK2;NLRP1;TTK;STK17A;KIF14;JAK2;DNAH5;MAP3K12;MYO5C;QRSL1;STK3;PDK1;DGKH;PANK3;CDK7;WRN;TRPM7;PPIP5K2;BUB1;KIF15;MAP4K3;COQ8B;CDK8;PIK3C2A;MAPK12;TAF1;MAPK8;CLPX;ATP6V1B2;UHMK1;HIPK1;MET;TARS2;GK5;SMG1;CLK2;RIOK3;RIPK1;UBE2D3;CAMKK2;ERN1;HK2;PIP5K1A;JAK1 |
| GO:0017076 | purine nucleotide binding | 117 | 1.440562 | 2.63E-05 | DDX39B;EIF4A1;MSH5;DQX1;IRAK3;NMNAT3;CNGB1;CBWD6;PRKAA2;RTEL1;EIF2AK3;ACBD7;RRAGD;CLK1;HELB;AATK;N4BP2;SLFNL1;ATM;WEE1;HSPA14;RAD17;ABCA5;TUBD1;TDG;ARL5B;ETNK1;RND3;TRMU;NME7;ATP8B2;SLC22A5;TBK1;ACSL4;RAB28;ERCC6L2;CAMK1G;BRIP1;ATR;ACVR2A;CDK17;GRPEL2;SGK1;MAK;RAB17;PAN3;GALK2;RHOQ;VPS4B;RYK;PIKFYVE;ATP13A3;MTPAP;BTAF1;TRNT1;DHX36;MAP3K20;ZRANB3;NLRC5;ATP7B;EIF4A2;RARS2;ATL2;ARL1;MARK3;TUBE1;LIMK2;NLRP1;TTK;STK17A;KIF14;JAK2;DNAH5;MAP3K12;MYO5C;QRSL1;STK3;PDK1;DGKH;PANK3;CDK7;WRN;TRPM7;PPIP5K2;BUB1;KIF15;MAP4K3;COQ8B;SRP54;HBS1L;ARL8B;CDK8;PIK3C2A;MAPK12;RAB5A;EFL1;TAF1;MAPK8;ARHGAP5;CLPX;ATP6V1B2;UHMK1;HIPK1;MET;TARS2;GK5;SMG1;CLK2;RIOK3;RAP1B;RIPK1;UBE2D3;CAMKK2;ERN1;HK2;PIP5K1A;JAK1 |
| GO:0032553 | ribonucleotide binding | 117 | 1.440562 | 2.63E-05 | DDX39B;EIF4A1;MSH5;DQX1;IRAK3;NMNAT3;CNGB1;CBWD6;PRKAA2;RTEL1;EIF2AK3;ACBD7;RRAGD;CLK1;HELB;AATK;N4BP2;SLFNL1;ATM;WEE1;HSPA14;RAD17;ABCA5;TUBD1;TDG;ARL5B;ETNK1;RND3;TRMU;NME7;ATP8B2;SLC22A5;TBK1;ACSL4;RAB28;ERCC6L2;CAMK1G;BRIP1;ATR;ACVR2A;CDK17;SGK1;MAK;RAB17;PAN3;GALK2;RHOQ;VPS4B;RYK;PIKFYVE;ATP13A3;MTPAP;BTAF1;TRNT1;DHX36;MAP3K20;ZRANB3;NLRC5;ATP7B;EIF4A2;RARS2;ATL2;ARL1;MARK3;TUBE1;LIMK2;NLRP1;TTK;STK17A;KIF14;JAK2;DNAH5;MAP3K12;MYO5C;QRSL1;STK3;PDK1;DGKH;PANK3;CDK7;WRN;TRPM7;PPIP5K2;BUB1;KIF15;MAP4K3;COQ8B;SRP54;HBS1L;ARL8B;CDK8;PIK3C2A;MAPK12;RAB5A;EFL1;TAF1;UGP2;MAPK8;ARHGAP5;CLPX;ATP6V1B2;UHMK1;HIPK1;MET;TARS2;GK5;SMG1;CLK2;RIOK3;RAP1B;RIPK1;UBE2D3;CAMKK2;ERN1;HK2;PIP5K1A;JAK1 |
| GO:0070530 | K63-linked polyubiquitin modification-dependent protein binding | 7 | 7.306349 | 2.77E-05 | ATRIP;ZRANB3;UIMC1;ZRANB1;RNF168;TAB2;RNF169 |
| GO:0032555 | purine ribonucleotide binding | 116 | 1.43983 | 2.93E-05 | DDX39B;EIF4A1;MSH5;DQX1;IRAK3;NMNAT3;CNGB1;CBWD6;PRKAA2;RTEL1;EIF2AK3;ACBD7;RRAGD;CLK1;HELB;AATK;N4BP2;SLFNL1;ATM;WEE1;HSPA14;RAD17;ABCA5;TUBD1;TDG;ARL5B;ETNK1;RND3;TRMU;NME7;ATP8B2;SLC22A5;TBK1;ACSL4;RAB28;ERCC6L2;CAMK1G;BRIP1;ATR;ACVR2A;CDK17;SGK1;MAK;RAB17;PAN3;GALK2;RHOQ;VPS4B;RYK;PIKFYVE;ATP13A3;MTPAP;BTAF1;TRNT1;DHX36;MAP3K20;ZRANB3;NLRC5;ATP7B;EIF4A2;RARS2;ATL2;ARL1;MARK3;TUBE1;LIMK2;NLRP1;TTK;STK17A;KIF14;JAK2;DNAH5;MAP3K12;MYO5C;QRSL1;STK3;PDK1;DGKH;PANK3;CDK7;WRN;TRPM7;PPIP5K2;BUB1;KIF15;MAP4K3;COQ8B;SRP54;HBS1L;ARL8B;CDK8;PIK3C2A;MAPK12;RAB5A;EFL1;TAF1;MAPK8;ARHGAP5;CLPX;ATP6V1B2;UHMK1;HIPK1;MET;TARS2;GK5;SMG1;CLK2;RIOK3;RAP1B;RIPK1;UBE2D3;CAMKK2;ERN1;HK2;PIP5K1A;JAK1 |
| GO:0004674 | protein serine/threonine kinase activity | 39 | 1.994543 | 3.35E-05 | IRAK3;PRKAA2;EIF2AK3;CLK1;AATK;ATM;TBK1;CAMK1G;ATR;ACVR2A;CDK17;SGK1;MAK;PPM1D;CCNK;MAP3K20;MARK3;LIMK2;TTK;STK17A;MAP3K12;STK3;CDK7;TRPM7;BUB1;MAP4K3;CDK8;MAPK12;AKAP13;TAF1;MAPK8;UHMK1;HIPK1;SMG1;CLK2;RIOK3;RIPK1;CAMKK2;ERN1 |
| GO:0032451 | demethylase activity | 9 | 5.29911 | 3.50E-05 | KDM3A;KDM5B;KDM6A;UTY;KDM5A;JMJD1C;KDM5D;JARID2;KDM1A |
| GO:0008144 | drug binding | 108 | 1.452832 | 3.99E-05 | DDX39B;EIF4A1;MSH5;DQX1;IRAK3;NMNAT3;CBWD6;PRKAA2;RTEL1;EIF2AK3;CLK1;HELB;AATK;N4BP2;NAMPT;SLFNL1;ATM;WEE1;HSPA14;RAD17;ABCA5;TDG;ETNK1;CTH;TRMU;NME7;ATP8B2;SLC22A5;SUV39H2;TBK1;PPWD1;ACSL4;ERCC6L2;CAMK1G;KYAT3;BRIP1;CWC27;ATR;ACVR2A;CDK17;SGK1;MAK;NKTR;PAN3;GALK2;VPS4B;RYK;PIKFYVE;ATP13A3;MTPAP;BTAF1;TRNT1;DHX36;MAP3K20;ZRANB3;NLRC5;ATP7B;EIF4A2;RARS2;MARK3;LIMK2;NLRP1;TTK;STK17A;KIF14;PHYKPL;JAK2;DNAH5;MAP3K12;MYO5C;QRSL1;STK3;PDK1;DGKH;PANK3;CDK7;WRN;TRPM7;PPIP5K2;BUB1;KIF15;MAP4K3;COQ8B;PPIG;SRP54;CDK8;PIK3C2A;MAPK12;TAF1;MAPK8;CLPX;ATP6V1B2;UHMK1;HIPK1;MET;TARS2;GK5;SMG1;CLK2;RIOK3;RIPK1;UBE2D3;CAMKK2;ERN1;OAT;HK2;PIP5K1A;JAK1 |
| GO:0016846 | carbon-sulfur lyase activity | 5 | 9.567837 | 9.48E-05 | SCLY;MGST2;CTH;KYAT3;CENPV |
| GO:0004571 | mannosyl-oligosaccharide 1,2-alpha-mannosidase activity | 4 | 13.12161 | 1.12E-04 | MAN1C1;EDEM2;MAN1A1;EDEM3 |
| GO:0032453 | histone demethylase activity (H3-K4 specific) | 4 | 13.12161 | 1.12E-04 | KDM5B;KDM5A;KDM5D;KDM1A |
| GO:0034593 | phosphatidylinositol bisphosphate phosphatase activity | 7 | 5.953321 | 1.19E-04 | MTMR7;SACM1L;PIKFYVE;MTMR9;MTMR6;INPP5K;MTMR1 |
| GO:0004672 | protein kinase activity | 49 | 1.73371 | 1.28E-04 | IRAK3;PRKAA2;EIF2AK3;CLK1;AATK;ATM;WEE1;MMD;TBK1;CAMK1G;ATR;ACVR2A;CDK17;SGK1;MAK;PPM1D;PAN3;CCNG1;CCNK;RYK;MAP3K20;MARK3;LIMK2;TTK;STK17A;JAK2;MAP3K12;STK3;PDK1;CDK7;TRPM7;BUB1;MAP4K3;COQ8B;CDK8;MAPK12;AKAP13;TAF1;MAPK8;UHMK1;HIPK1;MET;SMG1;CLK2;RIOK3;RIPK1;CAMKK2;ERN1;JAK1 |
| GO:0031593 | polyubiquitin modification-dependent protein binding | 9 | 4.492724 | 1.39E-04 | ATRIP;EPS15;ZRANB3;UIMC1;AGL;ZRANB1;RNF168;TAB2;RNF169 |
| GO:0004559 | alpha-mannosidase activity | 5 | 8.201004 | 2.23E-04 | MAN1C1;EDEM2;MAN1A1;MAN2C1;EDEM3 |
| GO:0052866 | phosphatidylinositol phosphate phosphatase activity | 7 | 5.357989 | 2.44E-04 | MTMR7;SACM1L;PIKFYVE;MTMR9;MTMR6;INPP5K;MTMR1 |
| GO:0015923 | mannosidase activity | 5 | 7.65427 | 3.22E-04 | MAN1C1;EDEM2;MAN1A1;MAN2C1;EDEM3 |

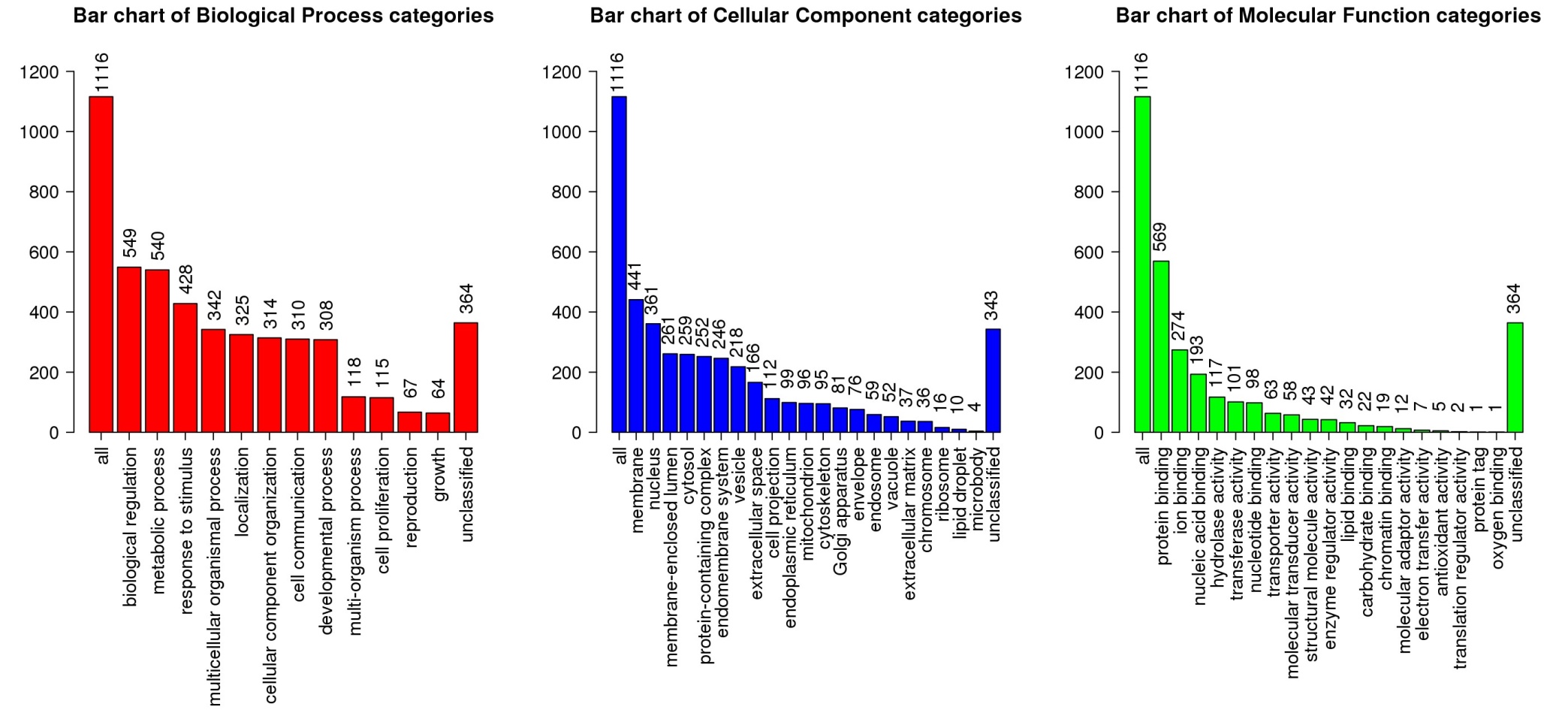
## 3

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| **Gene Set** | **KEGG pathway description** | **Overlap** | **Enrichment Ratio** | **P Value** | **Gene ID** |
| hsa03460 | Fanconi anemia pathway | 10 | 3.951852 | 1.70E-04 | ATRIP;FANCL;RMI2;BRIP1;ATR;FANCC;FAN1;WDR48;FANCE;POLH |
| hsa04140 | Autophagy | 16 | 2.6675 | 2.95E-04 | PRKAA2;EIF2AK3;RRAGD;WIPI1;ATG12;VMP1;GABARAPL2;TSC1;ATG2A;BNIP3;CFLAR;MAPK8;ZFYVE1;CAMKK2;ERN1;BCL2L1 |
| hsa04144 | Endocytosis | 24 | 2.099016 | 4.39E-04 | CHMP3;DNAJC6;SH3GL2;WASHC2A;DAB2;VPS4B;NEDD4L;WASHC4;SNX5;EPS15;SPART;RBSN;CHMP2B;RAB5A;PARD6B;ITCH;EEA1;IST1;CYTH1;ZFYVE27;ARFGEF1;ARFGEF2;PIP5K1A;ARFGAP2 |
| hsa04115 | p53 signaling pathway | 11 | 3.260278 | 4.72E-04 | GORAB;ATM;SIAH1;SESN1;ATR;PPM1D;RRM2B;MDM4;CCNG1;PMAIP1;BCL2L1 |
| hsa03013 | RNA transport | 18 | 2.246316 | 0.001038 | DDX39B;EIF4A1;SNORD3B-2;SNORD3B-1;SNORD3C;RPP14;EIF3CL;RGPD5;SNORD3A;NUP58;TRNT1;EIF4A2;XPOT;EIF1AY;THOC2;NXT1;NUP85;NUP214 |
| hsa03022 | Basal transcription factors | 7 | 3.319556 | 0.004548 | TAF13;TAF4B;TAF9;TAF11;CDK7;GTF2E1;TAF1 |
| hsa04621 | NOD-like receptor signaling pathway | 16 | 2.032381 | 0.005303 | IL6;NAMPT;ATG12;TBK1;IL1B;GABARAPL2;NLRP1;XIAP;TRPM7;STAT2;MAPK12;MAPK8;TAB2;RIPK1;BCL2L1;JAK1 |
| hsa00450 | Selenocompound metabolism | 4 | 5.021176 | 0.00694 | SCLY;CTH;KYAT3;TXNRD2 |
| hsa04068 | FoxO signaling pathway | 13 | 2.101667 | 0.008724 | SGK3;CSNK1E;FBXO32;PRKAA2;IL6;ATM;ATG12;SGK1;GABARAPL2;SIRT1;BNIP3;MAPK12;MAPK8 |
| hsa04137 | Mitophagy | 8 | 2.626462 | 0.010491 | EIF2AK3;TBK1;TBC1D15;GABARAPL2;BNIP3;MAPK8;ATF4;BCL2L1 |
| hsa04657 | IL-17 signaling pathway | 10 | 2.294624 | 0.01138 | S100A8;IL6;CEBPB;TBK1;S100A9;IL1B;MMP1;MAPK12;MAPK8;TAB2 |
| hsa04064 | NF-kappa B signaling pathway | 10 | 2.246316 | 0.013111 | ATM;CD40;IL1B;XIAP;BCL10;MALT1;CFLAR;TAB2;RIPK1;BCL2L1 |
| hsa04110 | Cell cycle | 12 | 2.065161 | 0.013123 | E2F5;ATM;WEE1;ATR;DBF4;TTK;CDK7;BUB1;ORC3;STAG2;CDC23;TFDP2 |
| hsa00564 | Glycerophospholipid metabolism | 10 | 2.2 | 0.015034 | JMJD7-PLA2G4B;ETNK1;TAZ;GPCPD1;GNPAT;DGKH;PLB1;LPIN1;AGPAT5;PISD |
| hsa04070 | Phosphatidylinositol signaling system | 10 | 2.155556 | 0.01716 | MTMR7;SACM1L;PIKFYVE;DGKH;PPIP5K2;PIK3C2A;MTMR6;INPP5K;MTMR1;PIP5K1A |
| hsa04217 | Necroptosis | 14 | 1.844198 | 0.019504 | JMJD7-PLA2G4B;CHMP3;IL1B;VPS4B;XIAP;JAK2;TRPM7;STAT2;CHMP2B;CFLAR;MAPK8;IL1A;RIPK1;JAK1 |
| hsa01524 | Platinum drug resistance | 8 | 2.33863 | 0.020257 | MGST2;GSTO2;ATM;ATP7B;XIAP;PMAIP1;POLH;BCL2L1 |
| hsa00562 | Inositol phosphate metabolism | 8 | 2.307027 | 0.02182 | MTMR7;SACM1L;PIKFYVE;PIK3C2A;MTMR6;INPP5K;MTMR1;PIP5K1A |
| hsa00520 | Amino sugar and nucleotide sugar metabolism | 6 | 2.6675 | 0.023634 | UAP1L1;PGM3;UAP1;CYB5R4;UGP2;HK2 |
| hsa04150 | mTOR signaling pathway | 13 | 1.837219 | 0.02456 | TBC1D7;ATP6V1C2;PRKAA2;RRAGD;FNIP1;RICTOR;SGK1;FNIP2;TSC1;LPIN1;WDR59;ATP6V1B2;CLIP1 |
| hsa04668 | TNF signaling pathway | 10 | 1.94 | 0.032982 | IL6;CEBPB;IL1B;MAPK12;CFLAR;MAPK8;ITCH;TAB2;RIPK1;ATF4 |
| hsa04744 | Phototransduction | 4 | 3.048571 | 0.039891 | GNGT1;RGS9;CNGB1;SLC24A1 |
| hsa05152 | Tuberculosis | 14 | 1.66905 | 0.041082 | IL23A;IL6;CEBPB;IL1B;JAK2;BCL10;MAPK12;RAB5A;MALT1;MAPK8;IL1A;EEA1;CEBPG;JAK1 |
| hsa05134 | Legionellosis | 6 | 2.328 | 0.042605 | SEC22B;IL6;CLK1;IL1B;HBS1L;BNIP3 |
| hsa04210 | Apoptosis | 11 | 1.726029 | 0.053828 | CTSK;EIF2AK3;ATM;XIAP;PMAIP1;CFLAR;MAPK8;RIPK1;ATF4;ERN1;BCL2L1 |

## 4

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| **Gene Set** | **Reactome pathway description** | **Overlap** | **Enrichment Ratio** | **P Value** | **User ID** |
| R-HSA-5633007 | Regulation of TP53 Activity | 22 | 2.758888 | 1.38E-05 | ATRIP;PRKAA2;ATM;RAD17;JMY;RFFL;RMI2;TAF13;RICTOR;BRIP1;ATR;SGK1;TAF4B;TAF9;MDM4;CCNG1;TAF11;WRN;TAF1;SMYD2;HIPK1;TP53BP2 |
| R-HSA-6804756 | Regulation of TP53 Activity through Phosphorylation | 15 | 3.271408 | 4.45E-05 | ATRIP;PRKAA2;ATM;RAD17;RMI2;TAF13;BRIP1;ATR;TAF4B;TAF9;MDM4;TAF11;WRN;TAF1;HIPK1 |
| R-HSA-74160 | Gene expression (Transcription) | 103 | 1.445215 | 4.92E-05 | DDX39B;ZNF197;ZNF26;ATRIP;ZNF761;BMI1;ZNF670;NABP1;PRKAA2;CTSK;KCTD6;ZKSCAN4;RRAGD;ZNF195;RORA;E2F5;ZNF615;PABPN1;RABGGTB;ATM;NFIA;RAD17;ZNF519;ZNF224;TAF1D;JMY;TDG;ZNF627;RFFL;ZNF124;RMI2;ZNF354B;NUP58;MED23;RNMT;LSM11;CBX8;PSMB7;TAF13;RICTOR;BRIP1;SESN1;TET1;ATR;SGK1;ZNF394;ZNF485;TAF4B;TAF9;PPM1D;ZNF506;RRM2B;ZNF200;MDM4;ICE2;CCNG1;TAF11;CCNK;ZNF484;NEDD4L;CDC40;ZNF483;KDM5B;FANCC;ARID4B;PCF11;AGO4;SIRT1;ZNF212;TSC1;ZNF266;ZKSCAN8;SOCS4;CDK7;WRN;ELF2;ZNF12;RRN3;PPM1A;NR1D2;CDK8;ICE1;PMAIP1;THOC2;GTF2E1;TAF1;RBBP5;ELL2;PSME4;RPRD1A;ITCH;SMYD2;NUP85;HIPK1;MET;TP53BP2;SLU7;JARID2;TFDP2;UBE2D3;ZNF398;INTS3;NUP214 |
| R-HSA-6807505 | RNA polymerase II transcribes snRNA genes | 13 | 3.524869 | 6.43E-05 | NABP1;TAF13;TAF9;ICE2;TAF11;CCNK;PCF11;CDK7;ICE1;GTF2E1;ELL2;RPRD1A;INTS3 |
| R-HSA-73857 | RNA Polymerase II Transcription | 92 | 1.428751 | 2.04E-04 | DDX39B;ZNF197;ZNF26;ATRIP;ZNF761;BMI1;ZNF670;NABP1;PRKAA2;CTSK;KCTD6;ZKSCAN4;RRAGD;ZNF195;RORA;E2F5;ZNF615;PABPN1;RABGGTB;ATM;RAD17;ZNF519;ZNF224;JMY;ZNF627;RFFL;ZNF124;RMI2;ZNF354B;MED23;RNMT;LSM11;CBX8;PSMB7;TAF13;RICTOR;BRIP1;SESN1;ATR;SGK1;ZNF394;ZNF485;TAF4B;TAF9;PPM1D;ZNF506;RRM2B;ZNF200;MDM4;ICE2;CCNG1;TAF11;CCNK;ZNF484;NEDD4L;CDC40;ZNF483;KDM5B;FANCC;PCF11;AGO4;ZNF212;TSC1;ZNF266;ZKSCAN8;SOCS4;CDK7;WRN;ELF2;ZNF12;PPM1A;NR1D2;CDK8;ICE1;PMAIP1;THOC2;GTF2E1;TAF1;RBBP5;ELL2;PSME4;RPRD1A;ITCH;SMYD2;HIPK1;MET;TP53BP2;SLU7;TFDP2;UBE2D3;ZNF398;INTS3 |
| R-HSA-1483255 | PI Metabolism | 13 | 3.105242 | 2.44E-04 | MTMR7;SBF2;SACM1L;TNFAIP8L3;PIKFYVE;MTMR9;PIK3C2A;MTMR6;RAB5A;INPP5K;MTMR1;GDPD5;PIP5K1A |
| R-HSA-162599 | Late Phase of HIV Life Cycle | 17 | 2.471731 | 4.92E-04 | CHMP3;NUP58;RNMT;TAF13;TAF4B;TAF9;TAF11;VPS4B;CCNK;NEDD4L;CDK7;CHMP2B;GTF2E1;TAF1;NUP85;NMT2;NUP214 |
| R-HSA-3700989 | Transcriptional Regulation by TP53 | 33 | 1.814063 | 6.57E-04 | ATRIP;PRKAA2;RRAGD;RABGGTB;ATM;RAD17;JMY;RFFL;RMI2;TAF13;RICTOR;BRIP1;SESN1;ATR;SGK1;TAF4B;TAF9;RRM2B;MDM4;CCNG1;TAF11;CCNK;FANCC;AGO4;TSC1;CDK7;WRN;PMAIP1;TAF1;SMYD2;HIPK1;TP53BP2;TFDP2 |
| R-HSA-1483257 | Phospholipid metabolism | 22 | 2.082179 | 8.84E-04 | JMJD7-PLA2G4B;MTMR7;ETNK1;SBF2;SACM1L;TAZ;TNFAIP8L3;GPCPD1;GNPAT;PIKFYVE;MTMR9;PLB1;LPIN1;PIK3C2A;MTMR6;RAB5A;INPP5K;AGPAT5;MTMR1;GDPD5;PISD;PIP5K1A |
| R-HSA-162587 | HIV Life Cycle | 17 | 2.258933 | 0.00137 | CHMP3;NUP58;RNMT;TAF13;TAF4B;TAF9;TAF11;VPS4B;CCNK;NEDD4L;CDK7;CHMP2B;GTF2E1;TAF1;NUP85;NMT2;NUP214 |
| R-HSA-1660517 | Synthesis of PIPs at the late endosome membrane | 4 | 7.296232 | 0.00152 | MTMR7;PIKFYVE;MTMR9;PIK3C2A |
| R-HSA-8953854 | Metabolism of RNA | 51 | 1.518244 | 0.001721 | DDX39B;EIF4A1;HNRNPH2;SRSF10;RPL36AL;CSNK1E;SNRPN;RPP14;PNRC2;RPL36A;BOP1;TRMT13;NSUN6;C1D;PABPN1;RPL22L1;TRMU;NUP58;IGF2BP3;PPWD1;RNMT;LSM11;RPS10;PSMB7;CWC27;ZCRB1;PAN3;CDC40;TRNT1;PCF11;EIF4A2;ZRSR2;XPOT;WTAP;CDK7;SMNDC1;EXOSC7;HBS1L;CWC25;HEATR1;THOC2;UTP25;NXT1;PSME4;NUP85;SMG1;SLU7;RIOK3;RPL9;RPL12;NUP214 |
| R-HSA-5685938 | HDR through Single Strand Annealing (SSA) | 7 | 3.796013 | 0.002049 | ATRIP;ATM;RAD17;RMI2;BRIP1;ATR;WRN |
| R-HSA-5693616 | Presynaptic phase of homologous DNA pairing and strand exchange | 7 | 3.601345 | 0.002808 | ATRIP;ATM;RAD17;RMI2;BRIP1;ATR;WRN |
| R-HSA-6783310 | Fanconi Anemia Pathway | 7 | 3.511312 | 0.003261 | ATRIP;FANCL;ATR;FANCC;FAN1;WDR48;FANCE |
| R-HSA-3108214 | SUMOylation of DNA damage response and repair proteins | 10 | 2.640084 | 0.004279 | BMI1;EID3;TDG;NUP58;CBX8;WRN;STAG2;RNF168;NUP85;NUP214 |
| R-HSA-5693579 | Homologous DNA Pairing and Strand Exchange | 7 | 3.344106 | 0.004331 | ATRIP;ATM;RAD17;RMI2;BRIP1;ATR;WRN |
| R-HSA-1660499 | Synthesis of PIPs at the plasma membrane | 8 | 3.028625 | 0.00441 | SBF2;MTMR9;PIK3C2A;MTMR6;RAB5A;INPP5K;MTMR1;PIP5K1A |
| R-HSA-5663205 | Infectious disease | 31 | 1.628282 | 0.005044 | RPL36AL;CHMP3;RPL36A;SH3GL2;CTNND1;PABPN1;RPL22L1;NUP58;RNMT;RPS10;PSMB7;TAF13;TAF4B;TAF9;TAF11;VPS4B;CCNK;NEDD4L;EPS15;CDK7;CHMP2B;GTF2E1;TAF1;PSME4;NUP85;MET;NMT2;RPL9;IPO5;RPL12;NUP214 |
| R-HSA-2173793 | Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer | 7 | 3.192102 | 0.005647 | E2F5;CCNK;NEDD4L;PPM1A;CDK8;TFDP2;UBE2D3 |
| R-HSA-5685942 | HDR through Homologous Recombination (HRR) | 9 | 2.69525 | 0.00574 | ATRIP;RTEL1;ATM;RAD17;RMI2;BRIP1;ATR;WRN;POLH |
| R-HSA-212436 | Generic Transcription Pathway | 77 | 1.321623 | 0.005937 | ZNF197;ZNF26;ATRIP;ZNF761;BMI1;ZNF670;PRKAA2;CTSK;KCTD6;ZKSCAN4;RRAGD;ZNF195;RORA;E2F5;ZNF615;RABGGTB;ATM;RAD17;ZNF519;ZNF224;JMY;ZNF627;RFFL;ZNF124;RMI2;ZNF354B;MED23;CBX8;PSMB7;TAF13;RICTOR;BRIP1;SESN1;ATR;SGK1;ZNF394;ZNF485;TAF4B;TAF9;PPM1D;ZNF506;RRM2B;ZNF200;MDM4;CCNG1;TAF11;CCNK;ZNF484;NEDD4L;ZNF483;KDM5B;FANCC;AGO4;ZNF212;TSC1;ZNF266;ZKSCAN8;SOCS4;CDK7;WRN;ELF2;ZNF12;PPM1A;NR1D2;CDK8;PMAIP1;TAF1;RBBP5;PSME4;ITCH;SMYD2;HIPK1;MET;TP53BP2;TFDP2;UBE2D3;ZNF398 |
| R-HSA-936440 | Negative regulators of DDX58/IFIH1 signaling | 6 | 3.540819 | 0.006079 | HERC5;ATG12;TBK1;NLRC5;ITCH;UBE2D3 |
| R-HSA-8854691 | Interleukin-20 family signaling | 5 | 4.012928 | 0.006991 | IL24;IL20;JAK2;STAT2;JAK1 |
| R-HSA-6804757 | Regulation of TP53 Degradation | 6 | 3.344106 | 0.008096 | ATM;RFFL;RICTOR;SGK1;MDM4;CCNG1 |

# KD123 VS Control (Upregulated genes)



## 1

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| **Gene Set** | **GO Biological process description** | **Overlap** | **Enrichment Ratio** | **P Value** | **Gene ID** |
| GO:2001233 | regulation of apoptotic signaling pathway | 44 | 2.60203 | 6.36E-09 | TMBIM1;PARP1;NMT1;RAF1;PPP1CA;ITGA6;STX4;YWHAE;YWHAH;TPD52L1;BDKRB2;GSN;PARK7;TFAP4;BCAP31;BID;NOC2L;ARRB2;AKT1;MAP2K5;BAK1;ERP29;TIMP3;SOD1;GPX1;CREB3;BAD;SLC9A3R1;TMEM102;PYCARD;HYAL2;EYA2;LGALS9;FADD;HIGD1A;ERP27;RET;MUC1;TP73;MAPK8IP2;ACKR3;LCK;DBH;CIDEB |
| GO:2001235 | positive regulation of apoptotic signaling pathway | 23 | 3.098571 | 1.40E-06 | NMT1;PPP1CA;YWHAE;YWHAH;TPD52L1;GSN;PARK7;TFAP4;BCAP31;BID;BAK1;TIMP3;SOD1;BAD;SLC9A3R1;PYCARD;HYAL2;LGALS9;FADD;RET;TP73;LCK;CIDEB |
| GO:0007006 | mitochondrial membrane organization | 19 | 3.433234 | 2.46E-06 | ATP5F1B;NMT1;LETM1;YWHAE;HSP90AA1;YWHAH;BID;CHCHD6;BAK1;ATP5MC3;TIMM13;BAD;MAIP1;TMEM102;EYA2;ATP5ME;ATP5PO;SNCA;TP73 |
| GO:0097190 | apoptotic signaling pathway | 50 | 1.955993 | 4.59E-06 | TMBIM1;PARP1;NMT1;EP300;RAF1;PPP1CA;ITGA6;PERP;STX4;YWHAE;PDCD6;YWHAH;TPD52L1;BDKRB2;GSN;PARK7;TFAP4;BCAP31;BID;NOC2L;ARRB2;AKT1;MAP2K5;BAK1;ERP29;TIMP3;SOD1;GPX1;GGCT;CREB3;PDK2;BAD;FGFR3;SLC9A3R1;TMEM102;PYCARD;HYAL2;EYA2;LGALS9;FADD;HIGD1A;ERP27;RET;MUC1;TP73;MAPK8IP2;ACKR3;LCK;DBH;CIDEB |
| GO:1905475 | regulation of protein localization to membrane | 22 | 2.829891 | 1.06E-05 | TMBIM1;NMT1;STX4;YWHAE;AP2M1;YWHAH;GSN;RAB11A;BID;AKT1;LDLRAP1;VAMP8;LRP4;DMTN;DAG1;BAD;CSK;CDK5;WNT3A;TP73;LRP1;AGR2 |
| GO:0006887 | exocytosis | 67 | 1.706309 | 1.24E-05 | TMBIM1;SPTAN1;PSMD11;SNX19;ACLY;FUCA2;PYGB;RNASET2;STX4;OSTF1;HSP90AA1;DDOST;SRP14;MLEC;GSN;GIPC1;SNAP29;IMPDH1;RAB11A;PSMC3;PGAM1;AGPAT2;PKM;DYNLL1;PTPN6;TUBB4B;PSMD3;CYBA;SYNGR2;CHID1;LGALS3BP;SDC1;TIMP3;BACE1;RAB25;PA2G4;SVIP;VAMP8;SOD1;ATP6AP1;DMTN;LAMTOR2;ADGRE5;RAB8A;ANK1;PYCARD;PCDH7;CDK5;P2RY1;PTX3;LGALS9;TRAPPC1;CRISPLD2;JAGN1;SYT8;RAB24;CORO1A;SNCA;CFD;CPLX1;PRRT2;A1BG;CLEC5A;PRG2;SLC2A3;IL13;SELP |
| GO:0048589 | developmental growth | 51 | 1.863813 | 1.41E-05 | ATRN;TMED2;PIN1;HSP90AA1;ADAM15;CARM1;SH3PXD2B;GSN;PRPF19;RAB11A;PKM;POC1A;NKX2-5;LIMK1;STK40;RXRA;AKT1;SEMA3F;WDTC1;NRP2;SOD1;GPX1;LRP4;WWTR1;NDUFS6;GINS4;DUSP6;DAG1;RTN4R;KLF2;COL6A1;FGFR3;COL6A2;CDK5;RBP4;PTX3;MAP2;ATF5;TAF10;PAX7;RAPH1;VWA1;TLL2;SEMA3C;WNT3A;ILK;TP73;AGR2;L1CAM;TAL2;PDGFRB |
| GO:0051098 | regulation of binding | 35 | 2.171312 | 1.45E-05 | PARP1;EP300;PPP1CA;SUMO3;PIN1;EIF4G1;ADAM15;CARM1;PARK7;TFAP4;PCBD1;TXN;ARRB2;AKT1;BAK1;CDT1;LDLRAP1;ACD;TIRAP;PER2;PEX19;LDOC1;ID3;CDK5;LFNG;P2RY1;MAP2;TAF10;PAX7;WNT3A;ACE;LRP1;IRF4;TTBK1;ZBTB7C |
| GO:0097202 | activation of cysteine-type endopeptidase activity | 6 | 9.757611 | 1.56E-05 | PERP;BAK1;BAD;PYCARD;FADD;CIDEB |
| GO:0032757 | positive regulation of interleukin-8 production | 10 | 5.059502 | 1.98E-05 | PARK7;MYD88;TIRAP;ZNF580;DDX58;PYCARD;HYAL2;LGALS9;FADD;IL17D |
| GO:0010647 | positive regulation of cell communication | 111 | 1.458293 | 2.62E-05 | TRIM44;PARP1;NMT1;EP300;RAF1;PTBP1;PPP1CA;KHDRBS1;PPP5C;RUVBL1;STX4;YWHAE;PIN1;HSP90AA1;YWHAH;TPD52L1;GSN;GIPC1;PARK7;TFAP4;AGPAT2;DYNLL1;GLUL;BCAP31;PTPN6;TXN;MAP4K2;LASP1;NDFIP2;BID;CYBA;ABCA7;ARRB2;AKT1;PRMT1;MAP2K5;BAK1;ERP29;TIMP3;LDLRAP1;VAMP8;SOD1;GPX1;HCAR2;FBXL15;EMC10;MYD88;ATP6AP1;CTDNEP1;SCUBE3;TIRAP;DMTN;FAM53B;LAMTOR2;DUSP6;STAP2;RHOC;RTN4R;ERH;GBA;KCNN4;PHB;JAG2;RRAGC;BAD;EPHB3;BMP8A;FGFR3;SLC9A3R1;GIPR;CARD9;PYCARD;HYAL2;CSK;CDK5;RBP4;LFNG;P2RY1;NEO1;PAGR1;LGALS9;FADD;SECTM1;NRGN;SNCA;RET;WNT3A;ILK;CXXC5;TP73;EPHB6;FGD2;MAPK8IP2;RASGEF1A;AGR2;FGF3;ACKR3;NSG1;ARL2BP;MMP12;LCK;LEFTY1;NTSR1;IL13;IFNL1;SELP;ADCY8;CITED1;CALCR;CIDEB;PDGFRB |
| GO:0001775 | cell activation | 90 | 1.534905 | 2.63E-05 | TMBIM1;EP300;RAF1;SPTAN1;PSMD11;ACLY;FUCA2;PYGB;VAV2;RNASET2;STX4;OSTF1;HSP90AA1;DDOST;SRP14;MLEC;GSN;FIBP;SNAP29;IMPDH1;PSMC3;PGAM1;GNA11;AGPAT2;PKM;DYNLL1;PTPN6;TUBB4B;PSMD3;CYBA;ARRB2;AKT1;BAK1;IRF1;TRPV1;VSIR;PA2G4;SVIP;VAMP8;SOD1;RUNX3;EFNB1;TIRAP;DMTN;CCND3;LAMTOR2;PRR7;JAG2;CD320;NKAP;BAD;CD151;ADGRE5;PYCARD;HYAL2;CSK;LFNG;P2RY1;PTX3;LGALS9;TRAPPC1;FADD;CRISPLD2;RAB24;CORO1A;CEBPA;SNCA;TNFSF13;WNT3A;ILK;EGR3;NHEJ1;CFD;LRP1;CYGB;A1BG;CLEC5A;LY6D;IRF4;LCK;TTBK1;SLURP1;PRG2;CLEC4A;SLC2A3;IL13;IFNL1;SELP;DGKK;PDGFRB |
| GO:0023056 | positive regulation of signaling | 111 | 1.453261 | 3.04E-05 | TRIM44;PARP1;NMT1;EP300;RAF1;PTBP1;PPP1CA;KHDRBS1;PPP5C;RUVBL1;STX4;YWHAE;PIN1;HSP90AA1;YWHAH;TPD52L1;GSN;GIPC1;PARK7;TFAP4;AGPAT2;DYNLL1;GLUL;BCAP31;PTPN6;TXN;MAP4K2;LASP1;NDFIP2;BID;CYBA;ABCA7;ARRB2;AKT1;PRMT1;MAP2K5;BAK1;ERP29;TIMP3;LDLRAP1;VAMP8;SOD1;GPX1;HCAR2;FBXL15;EMC10;MYD88;ATP6AP1;CTDNEP1;SCUBE3;TIRAP;DMTN;FAM53B;LAMTOR2;DUSP6;STAP2;RHOC;RTN4R;ERH;GBA;KCNN4;PHB;JAG2;RRAGC;BAD;EPHB3;BMP8A;FGFR3;SLC9A3R1;GIPR;CARD9;PYCARD;HYAL2;CSK;CDK5;RBP4;LFNG;P2RY1;NEO1;PAGR1;LGALS9;FADD;SECTM1;NRGN;SNCA;RET;WNT3A;ILK;CXXC5;TP73;EPHB6;FGD2;MAPK8IP2;RASGEF1A;AGR2;FGF3;ACKR3;NSG1;ARL2BP;MMP12;LCK;LEFTY1;NTSR1;IL13;IFNL1;SELP;ADCY8;CITED1;CALCR;CIDEB;PDGFRB |
| GO:0046903 | secretion | 104 | 1.475294 | 3.06E-05 | TMBIM1;TRIM27;RAF1;SPTAN1;PSMD11;SNX19;ACLY;FUCA2;PYGB;RNASET2;STX4;OSTF1;HSP90AA1;DDOST;OAS2;ENSA;SRP14;BDKRB2;MLEC;GSN;GIPC1;PNKD;PARK7;SNAP29;IMPDH1;RAB11A;PSMC3;MTX1;PGAM1;AGPAT2;PKM;DYNLL1;GLUL;PTPN6;TUBB4B;PSMD3;CYBA;COMT;SYNGR2;UCP2;CHID1;LGALS3BP;ERP29;SDC1;TRPV1;TIMP3;GAPDH;BACE1;RAB25;PA2G4;SVIP;VAMP8;SOD1;HCAR2;SLC29A1;ATP6AP1;DMTN;LAMTOR2;KCNN4;PER2;BAD;ADGRE5;DDX58;BMP8A;RAB8A;CPT1A;SLC9A3R1;GIPR;ANK1;PYCARD;HYAL2;PCDH7;CDK5;RBP4;P2RY1;PTX3;LGALS9;TRAPPC1;SNCG;CRISPLD2;JAGN1;SYT8;RAB24;CORO1A;P2RY2;SNCA;ACE;NOX5;CFD;FBLN5;AGR2;CPLX1;ITGB6;PRRT2;A1BG;ARL2BP;MMP12;CLEC5A;PRG2;SLC2A3;NTSR1;IL13;SELP;ADCY8 |
| GO:0009887 | animal organ morphogenesis | 70 | 1.636287 | 3.11E-05 | EP300;ITGA6;CELSR1;PERP;TMED2;AP2M1;ADAM15;CARM1;SH3PXD2B;SHROOM2;IRX4;KDM2B;POC1A;NKX2-5;TSKU;STK40;RXRA;RFLNB;FOXO1;BCOR;AP2S1;ARRB2;BAK1;SDC1;SATB2;NECTIN1;NRP2;SOD1;LRP4;WWTR1;DAG1;SP6;HOXA1;GBA;JAG2;GBX2;IRX1;COL6A1;FGFR3;HOXB7;SLC9A3R1;ID3;HYAL2;COL6A2;RBP4;HOXB6;LFNG;PAX7;FGFRL1;VWA1;SEMA3C;CHAD;SMAD6;ACTA2;MMP2;DLX3;ROGDI;AQP3;WNT3A;ILK;HOXA4;WNT10A;PROX2;MGP;SOX8;CABP4;LEFTY1;CITED1;ASXL3;PDGFRB |
| GO:0002444 | myeloid leukocyte mediated immunity | 45 | 1.869615 | 4.19E-05 | TMBIM1;SPTAN1;PSMD11;ACLY;FUCA2;PYGB;RNASET2;STX4;OSTF1;HSP90AA1;DDOST;SRP14;MLEC;GSN;SNAP29;IMPDH1;PSMC3;PGAM1;AGPAT2;PKM;DYNLL1;PTPN6;TUBB4B;PSMD3;CYBA;PA2G4;SVIP;VAMP8;LAMTOR2;ADGRE5;DDX58;PYCARD;PTX3;LGALS9;TRAPPC1;CRISPLD2;JAGN1;RAB24;ACE;CFD;A1BG;CLEC5A;PRG2;SLC2A3;IL13 |
| GO:0001503 | ossification | 34 | 2.086533 | 4.33E-05 | ATP5F1B;CDK6;OSTF1;RRBP1;SH3PXD2B;RFLNB;BCOR;AKT1;SATB2;ATRAID;FBXL15;LRP4;WWTR1;ATP6AP1;FASN;KLF10;MN1;PHB;BMP8A;COL6A1;FGFR3;PTHLH;ID3;MINPP1;SMAD6;KREMEN2;MMP2;CEBPA;WNT3A;ILK;MGP;CLEC5A;SOX8;CITED1 |
| GO:0008637 | apoptotic mitochondrial changes | 16 | 3.140381 | 4.68E-05 | NMT1;YWHAE;YWHAH;BID;ARRB2;AKT1;BAK1;GPX1;GGCT;BAD;TMEM102;PYCARD;EYA2;HIGD1A;TP73;CIDEB |
| GO:0071496 | cellular response to external stimulus | 31 | 2.13879 | 5.87E-05 | ITGA6;EIF4G1;DEPDC5;GLUL;CYBA;COMT;FOXO1;UCP2;AKT1;BAK1;IRF1;RIPOR1;TRPV1;SOD1;MYD88;SLC39A4;KLF10;DAG1;KIF26A;GBA;EHMT2;RRAGC;PDK2;BAD;P2RY1;FADD;HIGD1A;P2RY2;AQP3;PDXP;IL13 |
| GO:0010942 | positive regulation of cell death | 51 | 1.759327 | 6.43E-05 | PARP1;NMT1;PPP1CA;ITGA6;VAV2;YWHAE;PIN1;EIF4G1;PDCD6;YWHAH;TPD52L1;GSN;PARK7;TFAP4;BCAP31;BID;FOXO1;UCP2;ARRB2;AKT1;BAK1;TRPV1;TIMP3;MYBL2;GAPDH;BACE1;DFFA;SOD1;HCAR2;DUSP6;PHB;BAD;SLC9A3R1;ID3;PYCARD;HYAL2;CDK5;LGALS9;FADD;EEF1A2;SNCA;RET;WNT3A;TP73;FGD2;LRP1;LCK;NTSR1;CALCR;CIDEB;PDGFRB |
| GO:0045055 | regulated exocytosis | 58 | 1.686501 | 6.68E-05 | TMBIM1;SPTAN1;PSMD11;ACLY;FUCA2;PYGB;RNASET2;STX4;OSTF1;HSP90AA1;DDOST;SRP14;MLEC;GSN;GIPC1;SNAP29;IMPDH1;PSMC3;PGAM1;AGPAT2;PKM;DYNLL1;PTPN6;TUBB4B;PSMD3;CYBA;SYNGR2;CHID1;LGALS3BP;TIMP3;BACE1;PA2G4;SVIP;VAMP8;SOD1;DMTN;LAMTOR2;ADGRE5;PYCARD;PCDH7;CDK5;P2RY1;PTX3;LGALS9;TRAPPC1;CRISPLD2;SYT8;RAB24;CORO1A;CFD;CPLX1;PRRT2;A1BG;CLEC5A;PRG2;SLC2A3;IL13;SELP |
| GO:0043299 | leukocyte degranulation | 43 | 1.850687 | 7.81E-05 | TMBIM1;SPTAN1;PSMD11;ACLY;FUCA2;PYGB;RNASET2;STX4;OSTF1;HSP90AA1;DDOST;SRP14;MLEC;GSN;SNAP29;IMPDH1;PSMC3;PGAM1;AGPAT2;PKM;DYNLL1;PTPN6;TUBB4B;PSMD3;CYBA;PA2G4;SVIP;VAMP8;LAMTOR2;ADGRE5;PYCARD;PTX3;LGALS9;TRAPPC1;CRISPLD2;RAB24;CORO1A;CFD;A1BG;CLEC5A;PRG2;SLC2A3;IL13 |
| GO:0002446 | neutrophil mediated immunity | 41 | 1.882012 | 7.90E-05 | TMBIM1;SPTAN1;PSMD11;ACLY;FUCA2;PYGB;RNASET2;OSTF1;HSP90AA1;DDOST;SRP14;MLEC;GSN;SNAP29;IMPDH1;PSMC3;PGAM1;AGPAT2;PKM;DYNLL1;PTPN6;TUBB4B;PSMD3;CYBA;PA2G4;SVIP;VAMP8;LAMTOR2;ADGRE5;PYCARD;PTX3;TRAPPC1;CRISPLD2;JAGN1;RAB24;ACE;CFD;A1BG;CLEC5A;PRG2;SLC2A3 |
| GO:1901264 | carbohydrate derivative transport | 12 | 3.692069 | 8.45E-05 | CYBA;SLC35A4;VAMP8;SLC29A1;SLC35D2;SLC29A3;SLC33A1;SLC25A42;SLC35C1;P2RY2;SLC29A4;AGR2 |
| GO:0016192 | vesicle-mediated transport | 119 | 1.395141 | 9.05E-05 | TMBIM1;TRIM27;ANXA11;SPTAN1;CUX1;PSMD11;SNX19;ACLY;FUCA2;PYGB;VAV2;RNASET2;TMED2;STX4;AP2M1;AP1M2;OSTF1;HSP90AA1;ACTR1A;DDOST;MGRN1;PDCD6;VPS37C;SRP14;MLEC;GSN;GIPC1;CNIH4;BET1L;SNAP29;KLC1;IMPDH1;RAB11A;PSMC3;PGAM1;AGPAT2;VPS25;PKM;DYNLL1;BCAP31;PTPN6;RAC3;MAP4K2;TUBB4B;LIMK1;PSMD3;CYBA;ABCA7;VPS37B;SYNGR2;AP2S1;CHID1;ARRB2;ARAP3;LYAR;LGALS3BP;SNX12;SDC1;PHETA1;TIMP3;LDLRAP1;AP1B1;BACE1;RAB25;PA2G4;SVIP;VAMP8;SOD1;EHD1;LRP4;ATP6AP1;ARF5;APOL1;DMTN;LAMTOR2;COG8;PROM2;KIF26A;AP5S1;RIN1;RAMP1;CD151;ADGRE5;RAB8A;ANK1;PYCARD;CSK;PCDH7;CDK5;P2RY1;PTX3;RHOBTB2;LGALS9;MAP2;TRAPPC1;CRISPLD2;JAGN1;SYT8;SH3BP1;RAB24;CORO1A;CHMP4A;SNCA;WNT3A;CFD;LRP1;CPLX1;ACKR3;PRRT2;A1BG;NSG1;FCGR1A;CFI;CLEC5A;PRG2;SLC2A3;IL13;SELP;GSG1L |

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| **Gene Set** | **GO Molecular function description** | **Overlap** | **Enrichment Ratio** | **P Value** | **Gene ID** |
| GO:0015932 | nucleobase-containing compound transmembrane transporter activity | 8 | 4.956076 | 1.63E-04 | SLC35A4;SLC29A1;SLC35D2;SLC29A3;SLC33A1;SLC25A42;SLC35C1;SLC29A4 |
| GO:1901505 | carbohydrate derivative transmembrane transporter activity | 8 | 4.714316 | 2.35E-04 | SLC35A4;SLC29A1;SLC35D2;SLC29A3;SLC33A1;SLC25A42;SLC35C1;SLC29A4 |
| GO:0047144 | 2-acylglycerol-3-phosphate O-acyltransferase activity | 4 | 10.73816 | 3.10E-04 | LPCAT4;CRLS1;MBOAT7;LPCAT3 |
| GO:0042802 | identical protein binding | 98 | 1.396088 | 3.89E-04 | PARP1;GLE1;TRIM27;RAF1;KHDRBS1;PLXNA2;THAP4;TRIP13;FOXJ2;ESYT1;PPP5C;YWHAE;NAA60;HSP90AA1;EIF4G1;CARM1;PDCD6;DCXR;YWHAH;TPD52L1;GIPC1;PARK7;PRPF19;TFAP4;PSMF1;PSMC3;PUF60;FHOD1;TK1;VPS25;PKM;DYNLL1;GLUL;PCBD1;NKX2-5;ARRB2;AKT1;PRMT1;DLK2;BAK1;ERP29;SDC1;PHETA1;TRPV1;MRFAP1L1;GAPDH;NECTIN1;VSIR;SOD1;EHD1;RILPL2;LRP4;MYD88;WWTR1;TIRAP;GGCT;GNPNAT1;KCTD1;FASN;SRM;ORAI1;HOXA1;RAD51;DRAP1;SCAND1;PDK2;KCTD17;DDX58;APOBEC3G;PRKG2;KCTD21;FGFR3;OLFML2A;HSCB;CPT1A;CARD9;PYCARD;CSK;PTX3;SDSL;FADD;ABCG2;VWA1;SMAD6;CORO1A;CHMP4A;CEBPA;SNCA;TP73;PDXP;FBLN5;AGR2;IL17D;LCK;NTSR1;ADCY8;CITED1;CIDEB |
| GO:0048156 | tau protein binding | 8 | 4.295266 | 4.58E-04 | EP300;PPP5C;PIN1;HSP90AA1;CDK5;MAP2;SNCA;TTBK1 |
| GO:0070182 | DNA polymerase binding | 5 | 7.106138 | 4.89E-04 | HSP90AA1;NABP2;CDT1;ACD;RAD51 |
| GO:0044212 | transcription regulatory region DNA binding | 57 | 1.53702 | 8.12E-04 | PARP1;EP300;CUX1;FOXJ2;FOXK2;ETV4;CARM1;PARK7;TFAP4;KDM2B;TCFL5;NKX2-5;NR2F6;RXRA;PITX1;BCOR;IRF1;PBX2;TEF;SATB2;MYBL2;RUNX3;KLF10;CREB3;PER2;PHB;NFE2L3;GBX2;ZNF239;EBF3;CIITA;HOXB7;HOXB6;ZNF668;ATF5;ZNF497;SMAD6;SOX12;SMARCE1;HOXC5;CEBPA;SNCA;YY2;MUC1;HOXA4;EGR3;TP73;ESX1;ASCL2;ONECUT3;NR2F1;POU2F3;MMP12;SOX8;IRF4;TAL2;CITED1 |
| GO:0001067 | regulatory region nucleic acid binding | 57 | 1.533596 | 8.56E-04 | PARP1;EP300;CUX1;FOXJ2;FOXK2;ETV4;CARM1;PARK7;TFAP4;KDM2B;TCFL5;NKX2-5;NR2F6;RXRA;PITX1;BCOR;IRF1;PBX2;TEF;SATB2;MYBL2;RUNX3;KLF10;CREB3;PER2;PHB;NFE2L3;GBX2;ZNF239;EBF3;CIITA;HOXB7;HOXB6;ZNF668;ATF5;ZNF497;SMAD6;SOX12;SMARCE1;HOXC5;CEBPA;SNCA;YY2;MUC1;HOXA4;EGR3;TP73;ESX1;ASCL2;ONECUT3;NR2F1;POU2F3;MMP12;SOX8;IRF4;TAL2;CITED1 |
| GO:0023023 | MHC protein complex binding | 5 | 6.358124 | 8.58E-04 | ANXA11;YWHAE;HSP90AA1;PKM;KLRC1 |
| GO:0001228 | DNA-binding transcription activator activity, RNA polymerase II-specific | 33 | 1.79574 | 8.76E-04 | PARP1;EP300;FOXJ2;FOXK2;ETV4;TFAP4;NKX2-5;PITX1;IRF1;PBX2;TEF;SATB2;MYBL2;KLF10;HOXA1;CREB3;ZNF572;GBX2;EBF3;HOXB7;HOXB6;ATF5;SOX12;DLX3;HOXC5;CEBPA;YY2;HOXA4;TP73;ONECUT3;POU2F3;SOX8;IRF4 |
| GO:0003841 | 1-acylglycerol-3-phosphate O-acyltransferase activity | 5 | 6.040217 | 0.001105 | LPCAT4;AGPAT2;CRLS1;MBOAT7;LPCAT3 |
| GO:0042171 | lysophosphatidic acid acyltransferase activity | 5 | 6.040217 | 0.001105 | LPCAT4;AGPAT2;CRLS1;MBOAT7;LPCAT3 |
| GO:0071617 | lysophospholipid acyltransferase activity | 5 | 6.040217 | 0.001105 | LPCAT4;AGPAT2;CRLS1;MBOAT7;LPCAT3 |
| GO:0016746 | transferase activity, transferring acyl groups | 22 | 2.060229 | 0.001111 | NMT1;EP300;ACLY;ZDHHC9;NAA60;ELOVL6;LPCAT4;AGPAT2;GLUL;CRLS1;MBOAT7;HAT1;CERS2;LPCAT3;GNPNAT1;FASN;NAA10;CIITA;CPT1A;TAF10;SMARCE1;GLYATL3 |
| GO:0016747 | transferase activity, transferring acyl groups other than amino-acyl groups | 20 | 2.13813 | 0.001171 | NMT1;EP300;ZDHHC9;NAA60;ELOVL6;LPCAT4;AGPAT2;GLUL;CRLS1;MBOAT7;HAT1;CERS2;LPCAT3;GNPNAT1;FASN;NAA10;CPT1A;TAF10;SMARCE1;GLYATL3 |
| GO:0015078 | proton transmembrane transporter activity | 14 | 2.543249 | 0.001231 | ATP5F1B;COX4I1;LETM1;COX6C;SLC15A3;ATP5MC3;CLCN4;ATP6AP1;SLC33A1;ATP6V0E2;ATP5ME;ATP5PO;NOX5;SLC9A9 |
| GO:0030246 | carbohydrate binding | 22 | 2.013406 | 0.001493 | ATRN;MLEC;NOMO2;CHID1;NECTIN1;GNPNAT1;ADGRL1;GALNT2;PTX3;LGALS9;BCAN;CNTN1;ATRNL1;CLEC5A;KLRC1;PRG2;CLEC4A;SLC2A3;ACR;SELP;DBH;KLRC3 |
| GO:0003713 | transcription coactivator activity | 25 | 1.911461 | 0.001532 | EP300;SMARCD1;RUVBL1;CARM1;PARK7;TFAP4;PCBD1;RXRA;PSMC3IP;WWTR1;PER2;NFE2L3;SCAND1;CIITA;ABT1;HYAL2;VGLL1;TAF10;SOX12;SMARCE1;CEBPA;WNT3A;NR2F1;ARL2BP;CITED1 |
| GO:0000977 | RNA polymerase II regulatory region sequence-specific DNA binding | 47 | 1.557697 | 0.001757 | PARP1;EP300;CUX1;FOXJ2;FOXK2;ETV4;TFAP4;KDM2B;TCFL5;NKX2-5;NR2F6;RXRA;PITX1;BCOR;IRF1;PBX2;TEF;SATB2;MYBL2;RUNX3;KLF10;CREB3;NFE2L3;GBX2;ZNF239;EBF3;HOXB7;HOXB6;ZNF668;ATF5;SMAD6;SMARCE1;HOXC5;CEBPA;YY2;MUC1;HOXA4;EGR3;TP73;ESX1;ASCL2;ONECUT3;NR2F1;POU2F3;SOX8;IRF4;TAL2 |
| GO:0017022 | myosin binding | 9 | 3.197762 | 0.001876 | GSN;GIPC1;RAB11A;KIRREL1;RAB25;RAB8A;SLC9A3R1;PYCARD;CORO1A |
| GO:0001012 | RNA polymerase II regulatory region DNA binding | 47 | 1.544981 | 0.002068 | PARP1;EP300;CUX1;FOXJ2;FOXK2;ETV4;TFAP4;KDM2B;TCFL5;NKX2-5;NR2F6;RXRA;PITX1;BCOR;IRF1;PBX2;TEF;SATB2;MYBL2;RUNX3;KLF10;CREB3;NFE2L3;GBX2;ZNF239;EBF3;HOXB7;HOXB6;ZNF668;ATF5;SMAD6;SMARCE1;HOXC5;CEBPA;YY2;MUC1;HOXA4;EGR3;TP73;ESX1;ASCL2;ONECUT3;NR2F1;POU2F3;SOX8;IRF4;TAL2 |
| GO:0005337 | nucleoside transmembrane transporter activity | 3 | 10.35466 | 0.00218 | SLC29A1;SLC29A3;SLC29A4 |
| GO:0000976 | transcription regulatory region sequence-specific DNA binding | 49 | 1.515855 | 0.002463 | PARP1;EP300;CUX1;FOXJ2;FOXK2;ETV4;TFAP4;KDM2B;TCFL5;NKX2-5;NR2F6;RXRA;PITX1;BCOR;IRF1;PBX2;TEF;SATB2;MYBL2;RUNX3;KLF10;CREB3;PER2;NFE2L3;GBX2;ZNF239;EBF3;HOXB7;HOXB6;ZNF668;ATF5;SMAD6;SOX12;SMARCE1;HOXC5;CEBPA;YY2;MUC1;HOXA4;EGR3;TP73;ESX1;ASCL2;ONECUT3;NR2F1;POU2F3;SOX8;IRF4;TAL2 |
| GO:1990837 | sequence-specific double-stranded DNA binding | 51 | 1.497211 | 0.002612 | PARP1;EP300;CUX1;FOXJ2;FOXK2;ETV4;TFAP4;KDM2B;TCFL5;NKX2-5;NR2F6;RXRA;PITX1;BCOR;MCM5;IRF1;PBX2;TEF;SATB2;MYBL2;LMNB1;RUNX3;KLF10;CREB3;PER2;NFE2L3;GBX2;ZNF239;EBF3;HOXB7;HOXB6;ZNF668;ATF5;SMAD6;SOX12;SMARCE1;HOXC5;CEBPA;YY2;MUC1;HOXA4;EGR3;TP73;ESX1;ASCL2;ONECUT3;NR2F1;POU2F3;SOX8;IRF4;TAL2 |
| GO:0023026 | MHC class II protein complex binding | 4 | 6.442899 | 0.002756 | ANXA11;YWHAE;HSP90AA1;PKM |

## 3

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| **Gene Set** | **KEGG pathway description** | **Overlap** | **Enrichment Ratio** | **P Value** | **Gene ID** |
| hsa05010 | Alzheimer disease | 23 | 2.814012 | 5.87E-06 | ATP5F1B;COX4I1;COX6C;NDUFB9;SDHC;BID;NDUFS4;CASP7;NDUFS8;CALM3;ATP5MC3;GAPDH;BACE1;NDUFS6;NDUFB5;BAD;NDUFA8;UQCR10;CDK5;ATP5PO;FADD;SNCA;LRP1 |
| hsa04714 | Thermogenesis | 24 | 2.192653 | 2.28E-04 | ATP5F1B;SMARCD1;COX4I1;COA4;ADCY3;COX6C;NDUFB9;SDHC;NDUFS4;NDUFS8;ATP5MC3;ACSL5;NDUFS6;CREB3;NDUFB5;NDUFA8;BMP8A;UQCR10;PRKG2;CPT1A;ATP5ME;ATP5PO;SMARCE1;ADCY8 |
| hsa00190 | Oxidative phosphorylation | 16 | 2.51688 | 5.68E-04 | ATP5F1B;COX4I1;COX6C;NDUFB9;SDHC;NDUFS4;NDUFS8;ATP5MC3;ATP6AP1;NDUFS6;NDUFB5;NDUFA8;UQCR10;ATP6V0E2;ATP5ME;ATP5PO |
| hsa05016 | Huntington disease | 20 | 2.168038 | 8.69E-04 | ATP5F1B;EP300;COX4I1;AP2M1;COX6C;NDUFB9;SDHC;NDUFS4;AP2S1;NDUFS8;ATP5MC3;SOD1;GPX1;NDUFS6;CREB3;NDUFB5;POLR2L;NDUFA8;UQCR10;ATP5PO |
| hsa05012 | Parkinson disease | 15 | 2.210025 | 0.003113 | ATP5F1B;COX4I1;PARK7;COX6C;NDUFB9;SDHC;NDUFS4;NDUFS8;ATP5MC3;NDUFS6;NDUFB5;NDUFA8;UQCR10;ATP5PO;SNCA |
| hsa04962 | Vasopressin-regulated water reabsorption | 7 | 3.328431 | 0.004458 | STX4;ADCY3;RAB11A;DYNLL1;CREB3;ARHGDIB;AQP3 |
| hsa04932 | Non-alcoholic fatty liver disease (NAFLD) | 15 | 2.106198 | 0.004915 | COX4I1;COX6C;NDUFB9;SDHC;BID;NDUFS4;RXRA;CASP7;AKT1;NDUFS8;NDUFS6;NDUFB5;NDUFA8;UQCR10;CEBPA |
| hsa05165 | Human papillomavirus infection | 27 | 1.66632 | 0.006032 | EP300;RAF1;LAMC1;ITGA6;CDK6;PKM;BCAP31;FOXO1;AKT1;BAK1;IRF1;ATP6AP1;CCND3;CREB3;BAD;COL6A1;SLC9A3R1;COL6A2;ATP6V0E2;LFNG;FADD;CHAD;WNT3A;WNT10A;ITGB6;IFNAR2;PDGFRB |
| hsa00790 | Folate biosynthesis | 5 | 4.023379 | 0.00695 | FPGS;PCBD1;DHFR;AKR1B10;ALPG |
| hsa04540 | Gap junction | 10 | 2.377451 | 0.008922 | RAF1;ADCY3;GNA11;TUBB4B;MAP2K5;TUBB6;PRKG2;TUBB3;ADCY8;PDGFRB |
| hsa04360 | Axon guidance | 15 | 1.793277 | 0.020049 | RAF1;PLXNA2;PLXNB2;RAC3;LIMK1;SEMA3F;EFNB1;EPHB3;CDK5;ABLIM2;SEMA3C;ILK;EPHB6;L1CAM;EFNA2 |
| hsa05152 | Tuberculosis | 15 | 1.753204 | 0.02405 | EP300;RAF1;BID;AKT1;CALM3;MYD88;ATP6AP1;TIRAP;BAD;CIITA;CARD9;FADD;IL10RB;CORO1A;FCGR1A |
| hsa04922 | Glucagon signaling pathway | 10 | 2.03122 | 0.024911 | EP300;PYGB;PGAM1;PKM;FOXO1;AKT1;PRMT1;CALM3;CREB3;CPT1A |
| hsa04510 | Focal adhesion | 16 | 1.682136 | 0.028442 | RAF1;LAMC1;PPP1CA;ITGA6;VAV2;PARVB;RAC3;AKT1;CCND3;BAD;COL6A1;COL6A2;CHAD;ILK;ITGB6;PDGFRB |
| hsa00604 | Glycosphingolipid biosynthesis | 3 | 4.184314 | 0.032107 | ST3GAL2;SLC33A1;ST8SIA5 |
| hsa04927 | Cortisol synthesis and secretion | 7 | 2.288297 | 0.032142 | ADCY3;GNA11;NCEH1;ORAI1;CREB3;PDE8B;ADCY8 |
| hsa01100 | Metabolic pathways | 76 | 1.218421 | 0.032668 | PGK1;ATP5F1B;FPGS;RRM2;COX4I1;ACLY;PYGB;MOGS;ITPK1;DDOST;DCXR;ST3GAL2;RPN1;PGD;COX6C;ELOVL6;NDUFB9;IMPDH1;LPCAT4;LAP3;SDHC;PGAM1;TK1;AGPAT2;PKM;GLUL;PCBD1;A4GALT;CRLS1;DPAGT1;NDUFS4;COMT;ACP2;NDUFS8;CERS2;ATP5MC3;ACSL5;ALDH1B1;TM7SF2;GAPDH;ATP6AP1;ALG3;ABO;GGCT;NDUFS6;FASN;HSD17B12;SRM;PGP;DHFR;GBA;NDUFB5;SLC33A1;POLR2L;NDUFA8;UQCR10;GALNT2;PYCR3;HYAL2;MINPP1;ATP6V0E2;ATP5ME;SDSL;ATP5PO;DHRS4;HPD;PDXP;CMPK2;DHRS4L1;HPSE2;ACOT4;ST8SIA5;DBH;AKR1B10;ALPG;DGKK |
| hsa05418 | Fluid shear stress and atherosclerosis | 12 | 1.806179 | 0.033658 | SUMO3;HSP90AA1;RAC3;TXN;CYBA;AKT1;MAP2K5;CALM3;SDC1;GPC1;KLF2;MMP2 |
| hsa04924 | Renin secretion | 7 | 2.253092 | 0.034605 | CALM3;ORAI1;PRKG2;ACE;CLCA2;CLCA4;PDE1A |
| hsa05230 | Central carbon metabolism in cancer | 7 | 2.253092 | 0.034605 | RAF1;PGAM1;PKM;AKT1;FGFR3;RET;PDGFRB |
| hsa05221 | Acute myeloid leukemia | 7 | 2.218954 | 0.03719 | RAF1;AKT1;DUSP6;PER2;BAD;CEBPA;FCGR1A |
| hsa04512 | ECM-receptor interaction | 8 | 2.041129 | 0.04139 | LAMC1;ITGA6;SDC1;DAG1;COL6A1;COL6A2;CHAD;ITGB6 |
| hsa05161 | Hepatitis B | 12 | 1.743464 | 0.042424 | EP300;RAF1;CDK6;AKT1;MYD88;ATP6AP1;TIRAP;CREB3;BAD;DDX58;FADD;EGR3 |
| hsa05200 | Pathways in cancer | 34 | 1.352345 | 0.042537 | EP300;RAF1;LAMC1;ITGA6;CDK6;HSP90AA1;TPM3;BDKRB2;ADCY3;GNA11;RAC3;BID;RXRA;FOXO1;CASP7;AKT1;BAK1;CALM3;CCND3;RAD51;JAG2;BAD;FGFR3;FADD;MMP2;CEBPA;RET;WNT3A;WNT10A;FGF3;IFNAR2;IL13;ADCY8;PDGFRB |
| hsa00480 | Glutathione metabolism | 6 | 2.241597 | 0.049738 | RRM2;PGD;LAP3;GPX1;GGCT;SRM |

## 4

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| **Gene Set** | **Reactome pathway description** | **Overlap** | **Enrichment Ratio** | **P Value** | **User ID** |
| R-HSA-109606 | Intrinsic Pathway for Apoptosis | 10 | 4.62165 | 4.14E-05 | NMT1;YWHAE;YWHAH;DYNLL1;BID;CASP7;AKT1;BAK1;BAD;TP73 |
| R-HSA-109581 | Apoptosis | 21 | 2.526867 | 8.14E-05 | NMT1;SPTAN1;PSMD11;YWHAE;YWHAH;GSN;PSMF1;PSMC3;DYNLL1;BCAP31;BID;PSMB8;PSMD3;CASP7;AKT1;BAK1;DFFA;LMNB1;BAD;FADD;TP73 |
| R-HSA-5357801 | Programmed Cell Death | 21 | 2.482793 | 1.05E-04 | NMT1;SPTAN1;PSMD11;YWHAE;YWHAH;GSN;PSMF1;PSMC3;DYNLL1;BCAP31;BID;PSMB8;PSMD3;CASP7;AKT1;BAK1;DFFA;LMNB1;BAD;FADD;TP73 |
| R-HSA-202131 | Metabolism of nitric oxide | 6 | 7.177151 | 1.07E-04 | HSP90AA1;NOSIP;DDAH2;AKT1;CALM3;CYGB |
| R-HSA-203765 | eNOS activation and regulation | 6 | 7.177151 | 1.07E-04 | HSP90AA1;NOSIP;DDAH2;AKT1;CALM3;CYGB |
| R-HSA-1474151 | Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation | 5 | 8.473025 | 1.67E-04 | HSP90AA1;AKT1;CALM3;DHFR;PRKG2 |
| R-HSA-203615 | eNOS activation | 5 | 7.821254 | 2.61E-04 | HSP90AA1;DDAH2;AKT1;CALM3;CYGB |
| R-HSA-163200 | Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. | 16 | 2.645237 | 3.34E-04 | ATP5F1B;COX4I1;COX6C;NDUFB9;SDHC;NDUFS4;UCP2;NDUFS8;ATP5MC3;NDUFS6;NDUFB5;NDUFA8;UQCR10;ATP5ME;ATP5PO;ETFB |
| R-HSA-114452 | Activation of BH3-only proteins | 7 | 4.744894 | 5.06E-04 | YWHAE;YWHAH;DYNLL1;BID;AKT1;BAD;TP73 |
| R-HSA-111447 | Activation of BAD and translocation to mitochondria | 5 | 6.77842 | 5.61E-04 | YWHAE;YWHAH;BID;AKT1;BAD |
| R-HSA-6798695 | Neutrophil degranulation | 39 | 1.655689 | 0.001295 | TMBIM1;SPTAN1;PSMD11;ACLY;FUCA2;PYGB;RNASET2;OSTF1;HSP90AA1;DDOST;SRP14;MLEC;GSN;SNAP29;IMPDH1;PSMC3;PGAM1;AGPAT2;PKM;DYNLL1;PTPN6;TUBB4B;PSMD3;CYBA;PA2G4;SVIP;VAMP8;LAMTOR2;ADGRE5;PYCARD;PTX3;TRAPPC1;CRISPLD2;RAB24;CFD;A1BG;CLEC5A;PRG2;SLC2A3 |
| R-HSA-1445148 | Translocation of SLC2A4 (GLUT4) to the plasma membrane | 10 | 2.905037 | 0.002104 | STX4;YWHAE;YWHAH;RAB11A;TUBB4B;AKT1;CALM3;TUBB6;RAB8A;TUBB3 |
| R-HSA-1428517 | The citric acid (TCA) cycle and respiratory electron transport | 18 | 2.103648 | 0.002258 | ATP5F1B;COX4I1;COX6C;NDUFB9;SDHC;NDUFS4;RXRA;UCP2;NDUFS8;ATP5MC3;NDUFS6;NDUFB5;PDK2;NDUFA8;UQCR10;ATP5ME;ATP5PO;ETFB |
| R-HSA-164938 | Nef-mediates down modulation of cell surface receptors by recruiting them to clathrin adapters | 5 | 5.083815 | 0.002363 | AP2M1;AP1M2;AP2S1;AP1B1;LCK |
| R-HSA-8978934 | Metabolism of cofactors | 5 | 5.083815 | 0.002363 | HSP90AA1;AKT1;CALM3;DHFR;PRKG2 |
| R-HSA-3928665 | EPH-ephrin mediated repulsion of cells | 8 | 3.189845 | 0.003184 | VAV2;AP2M1;AP2S1;EFNB1;EPHB3;MMP2;EPHB6;EFNA2 |
| R-HSA-8949613 | Cristae formation | 6 | 3.935857 | 0.003534 | ATP5F1B;MTX1;CHCHD6;ATP5MC3;ATP5ME;ATP5PO |
| R-HSA-83936 | Transport of nucleosides and free purine and pyrimidine bases across the plasma membrane | 3 | 8.715111 | 0.003567 | SLC29A1;SLC29A3;SLC29A4 |
| R-HSA-8862803 | Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models | 5 | 4.420709 | 0.00454 | YWHAE;PRDX2;LMNB1;CAPNS1;CDK5 |
| R-HSA-8863678 | Neurodegenerative Diseases | 5 | 4.420709 | 0.00454 | YWHAE;PRDX2;LMNB1;CAPNS1;CDK5 |
| R-HSA-1643685 | Disease | 70 | 1.350539 | 0.005254 | NMT1;EP300;RAF1;CUX1;MPRIP;PSMD11;MOGS;YWHAE;AP2M1;AP1M2;HSP90AA1;ANTXR1;VPS37C;DCXR;LIG1;PSMF1;PSMC3;DPAGT1;PSMB8;PSMD3;VPS37B;FOXO1;AP2S1;ARRB2;AKT1;CALM3;PRDX2;SDC1;RANBP1;AP1B1;RPS26;MYD88;UNC93B1;LMNB1;ALG3;TIRAP;SLC39A4;SLC29A3;DAG1;GPC1;PHB;JAG2;CAPNS1;CD320;SLC33A1;POLR2L;BAD;APOBEC3G;FGFR3;TCN2;CSK;SLC35C1;CDK5;RBP4;LFNG;TAF10;RNF43;BCAN;KREMEN2;CHMP4A;ABCG8;WNT3A;MUC1;FGF3;RPL3L;MUC3A;LCK;SLC6A19;SLC9A9;PDGFRB |
| R-HSA-449836 | Other interleukin signaling | 5 | 3.910627 | 0.00786 | STX4;SDC1;IL10RB;IL34;IFNL1 |
| R-HSA-167590 | Nef Mediated CD4 Down-regulation | 3 | 6.77842 | 0.00795 | AP2M1;AP2S1;LCK |
| R-HSA-3299685 | Detoxification of Reactive Oxygen Species | 6 | 3.29761 | 0.008701 | TXN;CYBA;PRDX2;SOD1;GPX1;NOX5 |
| R-HSA-6807878 | COPI-mediated anterograde transport | 11 | 2.259473 | 0.00918 | SPTAN1;TMED2;ACTR1A;BET1L;DYNLL1;TUBB4B;ARF5;TUBB6;COG8;ANK1;TUBB3 |