

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0060589	nucleoside-triph	50/1295	353/17632	5.56E-06	0.003911297	0.003671164	ACAP3/AGAP3/ARHGAP33 /AGAP6/ARFGAP1/PLXNB 1/GPS2/RTKN/DNAJB4/AR HGAP39/SEC23A/RGS18/A LS2CL/RANGAP1/RALGDS /TOR1AIP1/ACAP2/FNIP2/ ARHGAP42/ARHGAP20/A GAP9/STXBP5/NPRL3/SOS 1/PLN/ARHGEF6/ARHGAP 15/PREX2/TNK2/GIT1/CPE B2/GNAQ/ARHGEF19/ELM OD2/ADGRB3/TSC2/PCP2/ TBC1D12/TBC1D16/RIN1/I QGAP1/LRRK2/ARHGAP31 /RABEP2/FAM13B/EVI5/HS PBP1/TAGAP/GDI1/ARHG AP5	50
GO:0030695	GTPase regulatc	45/1295	309/17632	7.85E-06	0.003911297	0.003671164	ACAP3/AGAP3/ARHGAP33 /AGAP6/ARFGAP1/PLXNB 1/GPS2/RTKN/ARHGAP39/ SEC23A/RGS18/ALS2CL/R ANGAP1/RALGDS/ACAP2/ ARHGAP42/ARHGAP20/A GAP9/STXBP5/NPRL3/SOS 1/ARHGEF6/ARHGAP15/P REX2/TNK2/GIT1/CPEB2/G NAQ/ARHGEF19/ELMOD2/ ADGRB3/TSC2/PCP2/TBC1 D12/TBC1D16/RIN1/IQGAP 1/LRRK2/ARHGAP31/RAB EP2/FAM13B/EVI5/TAGAP/	45

GO:0005096	GTPase activatc	39/1295	279/17632	7.74E-05	0.02396202	0.022490879	ACAP3/AGAP3/ARHGAP33 /AGAP6/ARFGAP1/PLXNB 1/ARHGAP39/SEC23A/RGS 18/ALS2CL/RANGAP1/AC AP2/ARHGAP42/ARHGAP2 0/AGAP9/STXBP5/NPRL3/S OS1/ARHGEF6/ARHGAP15 /PREX2/GIT1/GNAQ/ARHG EF19/ELMOD2/ADGRB3/T SC2/TBC1D12/TBC1D16/RI N1/IQGAP1/LRRK2/ARHG AP31/RABEP2/FAM13B/EV I5/TAGAP/GDI1/ARHGAP5	39
GO:0004674	protein serine/th	56/1295	455/17632	9.61E-05	0.02396202	0.022490879	CDK10/CLK2/PHKG2/MAP K15/ADCK5/FASTK/CSNK 1E/EIF2AK3/PKMYT1/SNR K/PASK/STK17B/STK36/N EK7/NEK1/STK25/RPS6KL 1/CAB39/CDC42/CAMK2D/ STK11/CDK3/NEK8/MAP3 K10/MAP2K4/PIK3CG/DCL K1/CSNK1G3/HIPK3/AKT2/ NRBP2/IRAK1/CSNK1G2/T NK2/GRK2/MAP3K2/CDKL 1/BMPR2/CAMK4/BMP2K/ MYLK/ULK1/LIMK1/CDK1 1A/LRRK2/PRKCB/RIOK3/ PRKACB/CDK18/MAPK1/P LK1/CDK14/CDK17/STK17 A/ERCC2/PHKB	56

GO:0008026	ATP-dependent	15/1295	75/17632	3.11E-04	0.042604779	0.039989071	RECQL4/PIF1/DHX34/DDX56/DDX11/DDX39B/SKIV2L/IGHMBP2/DHX37/MCM7/RECQL5/DDX54/DHX30/RUVBL2/ERCC2	15
GO:0070035	purine NTP-dep	15/1295	75/17632	3.11E-04	0.042604779	0.039989071	RECQL4/PIF1/DHX34/DDX56/DDX11/DDX39B/SKIV2L/IGHMBP2/DHX37/MCM7/RECQL5/DDX54/DHX30/RUVBL2/ERCC2	15
GO:0017124	SH3 domain bin	21/1295	127/17632	3.65E-04	0.042604779	0.039989071	RAD9A/MAPK15/INPPL1/NXA1/DRD4/EPS15/PLSCR4/MICAL1/QKI/SOS1/AKAP5/HIP1R/CRK/SH3BGR1/PLSCR3/WIPF1/SYNJ1/ADAM10/USP8/ARHGAP31/ABI1	21
GO:0140098	catalytic activity	44/1295	352/17632	3.71E-04	0.042604779	0.039989071	TRMT1/PIF1/DHX34/PUS1/TRMT2A/PAN2/DDX56/DDX39B/SKIV2L/DUS1L/QTRT1/TSEN54/IGHMBP2/DHX37/CARS2/POLR2H/DUS3L/TUT1/POLRMT/AARSD1/NOP2/POLR3E/VARS/TRMT61A/TERT/EXOSC2/WDR4/BUD23/NSUN3/DGCR8/SMG5/METTL14/CNOT6L/EXOSC5/AARS2/METTL3/METPCE/SARS2/DDX54/METTL1/FBL/EXOSC4/POP7/DHX30	44

GO:0004559	alpha-mannosid	6/1295	15/17632	4.35E-04	0.042604779	0.039989071	MAN2C1/MAN2A2/MAN1A2/MAN1A1/EDEM3/MANEA	6
GO:0019208	phosphatase reg	17/1295	94/17632	4.46E-04	0.042604779	0.039989071	PPP2R3B/PPP1R35/SHOC2/ZEB2/PPP1R16A/PPP2R5E/SBF1/FRS2/PPP1R37/PPP1R26/BMP2K/STYX/PPP2R3A/B3GAT3/RCAN1/PPP2R2B/PPP1R12A	17
GO:0140097	catalytic activity	27/1295	185/17632	4.70E-04	0.042604779	0.039989071	EME2/RECQL4/PIF1/RAD9A/DNASE1L2/DDX11/XRCC3/POLM/POLE/POLD1/MUTYH/IGHMBP2/NEIL1/MCM7/TOP1MT/TERT/LIG1/EME1/POLD2/POLL/RECQL5/TREX2/NTHL1/DNASE1/DHX30/RUVBL2/ERCC2	27