Cell_Line	GEO_Accession	Sample_ID	Filename	QC	Cell Line Authentication	Phenotype Assignment
DOK	GSE57083	GSM1374468	GSM1374468.CEL	Passed	Authenticated	NonNociceptive
DOK	GSE10063	GSM254364	GSM254364.CEL	Passed	Unknown	---
DOK	GSE10063	GSM254369	GSM254369.CEL	Passed	Unknown	---
DOK	GSE10063	GSM254374	GSM254374.CEL	Passed	Unknown	---
DOK	GSE10063	GSM254379	GSM254379.CEL	Passed	Unknown	---
DOK	GSE10063	GSM254384	GSM254384.CEL	Passed	Unknown	---
DOK	GSE10063	GSM254389	GSM254389.CEL	Passed	Unknown	---
HaCaT	GSE41445	GSM1017467	GSM1017467.CEL	Passed	Authenticated	NonNociceptive
HaCaT	GSE39293	GSM960294	GSM960294.CEL	Passed	Unknown	---
HaCaT	GSE20297	GSM508815	GSM508815.CEL	Passed	Unknown	---
HaCaT	GSE20297	GSM508816	GSM508816.CEL	Passed	Unknown	---
HaCaT	GSE20297	GSM508817	GSM508817.CEL	Passed	Unknown	---
HaCaT	GSE70512	GSM1808252	GSM1808252.CEL	Passed	Unknown	---
HaCaT	GSE70512	GSM1808253	GSM1808253.CEL	Passed	Unknown	---
HaCaT	GSE41445	GSM1017466	GSM1017466.CEL	Failed QC	Authenticated	---
HaCaT	GSE41445	GSM1017468	GSM1017468.CEL	Failed QC	Authenticated	---
HSC-3	GSE32056	GSM794751	GSM794751.CEL	Passed	Authenticated	Nociceptive
HSC-3	GSE32056	GSM794752	GSM794752.CEL	Passed	Authenticated	Nociceptive
HSC-3	GSE32056	GSM794753	GSM794753.CEL	Passed	Authenticated	Nociceptive
HSC-3	GSE68722	GSM1679826	GSM1679826.CEL	Passed	Unknown	---
HSC-3	GSE75127	GSM1943674	GSM1943674.CEL	Passed	Unknown	---
HSC-3	GSE43862	GSM1072426	GSM1072426.CEL	Passed	Unknown	---
HSC-3	GSE38058	GSM933267	GSM933267.CEL	Passed	Unknown	---
HSC-3	GSE38058	GSM933268	GSM933268.CEL	Passed	Unknown	---
HSC-3	GSE24783	GSM610399	GSM610399.CEL	Passed	Unknown	---
NOK	GSE59843	GSM1422231	GSM1422231.CEL	Passed	Authenticated	NonNociceptive
NOK	GSE59843	GSM1422232	GSM1422232.CEL	Passed	Authenticated	NonNociceptive
NOK	GSE57636	GSM1385756	GSM1385756.CEL	Passed	Unknown	---
NOK	GSE57636	GSM1385757	GSM1385757.CEL	Passed	Unknown	---
PANC-1	GSE23952	GSM590166	GSM590166.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE23952	GSM590167	GSM590167.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE23952	GSM590168	GSM590168.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE64337	GSM1568739	GSM1568739.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE64337	GSM1568740	GSM1568740.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE64337	GSM1568741	GSM1568741.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE35351	GSM866688	GSM866688.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE35351	GSM866689	GSM866689.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE35351	GSM866690	GSM866690.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE35351	GSM866691	GSM866691.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE46385	GSM1129598	GSM1129598.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE44946	GSM1094286	GSM1094286.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE44946	GSM1094288	GSM1094288.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE21654	GSM540395	GSM540395.CEL	Passed	Authenticated	Nociceptive
PANC-1	GSE44946	GSM1094287	GSM1094287.CEL	Passed	Authenticated	Nociceptive
SCC-4	GSE36133	GSM887560	GSM887560.CEL	Failed QC	Authenticated	---
SCC-4	GSE57083	GSM1374865	GSM1374865.CEL	Passed	Authenticated	Nociceptive
SCC-4	GSE893029	GSM593029	GSM593029.CEL	Passed	Unknown	---
SCC-9	GSE57083	GSM1374866	GSM1374866.CEL	Passed	Authenticated	Nociceptive
SKMel-28	GSE41445	GSM1017502	GSM1017502.CEL	Passed	Authenticated	NonNociceptive
SKMel-28	GSE41445	GSM1017503	GSM1017503.CEL	Passed	Authenticated	NonNociceptive
SKMel-28	GSE41445	GSM1017504	GSM1017504.CEL	Passed	Authenticated	NonNociceptive
SKMel-28	GSE34211	GSM844690	GSM844690.CEL	Passed	Authenticated	NonNociceptive
SKMel-28	GSE8332	GSM206543	GSM206543.CEL	Passed	Authenticated	NonNociceptive
SKMel-28	GSE7127	GSM171012	GSM171012.CEL	Passed	Authenticated	NonNociceptive
SKMel-28	GSE10843	GSM274690	GSM274690.CEL	Passed	Unknown	---

Aggregated Papers from Proteomic Literature Search		
Gene Name	**Protein Name**	**Paper (PMID)**
LGALS3BP	Galectin-3-binding protein	22905270
PFN1	Pro ilin-1	22905270
ANXA3	Annexin A3	22905270
ANXA5	Annexin A5	22905270
RAC1	so orm A o Ras-related C3 botulinum toxin substrate 1	22905270
ENO3	so orm 1 o Beta-enolase	22905270
ENO1	so orm alpha-enolase o Alpha-enolase	22905270
ANXA8L2	so orm 2 o Annexin A8-like protein 2	22905270
SLC3A2	so orm 2 o 4F2 cell-sur ace antigen heavy chain	22905270
PKP3	Plakophilin-3	22905270
CALR	Calreticulin	22905270
CLTC	so orm 1 o Clathrin heavy chain 1	22905270
PLEC	so orm 1 o Plectin-1	22905270
MDH1	Putative uncharacterized protein MDH1	22905270
TLN1	alin-1	22905270
CTSD	Cathepsin D	22905270
CTSH	Cathepsin H	22905270
MMP1	nterstitial collagenase	22905270
KLK0	Kallikrein-10	22905270
THBS1	hrombospondin-1	22905270
GSN	so orm 1 o Gelsolin	22905270
SDC1	Syndecan-1	22905270
RANGAP1	Ran G Pase-activating protein 1	22905270
ANXA1	Annexin A1	22905270
FN1	so orm 1 o Fibronectin	22905270
LAMA3	so orm 1 o Laminin subunit alpha-3	22905270
LAMB3	Laminin subunit beta-3	22905270
LAMA5	Laminin subunit alpha-5	22905270
EZH2	enhancer zeste homolog 2	26604082
CDC7	Cdc7	23684929
ANX1	Annexin A1	26234610
CDABP0047	Glyceraldehyde-3-phosphate dehydrogenase	26234610
GAR1	H/ACA ribonucleoprotein complex subunit 1	26234610
---	cDNA FLJ54303 highly similar to Heat shock 70 kDa protein 1	26234610
CKAP4	63 kDa membrane protein	26234610
ANX2LG	Calpactin light chain	26234610
ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 amily member A	26234610
ALPP	Alkaline phosphatase Regan isozyme	26234610
CYK18	Cell proli eration-inducing gene 46 protein	26234610
EPIPL	450 kDa epidermal antigen	26234610
G22P2	86 kDa subunit o Ku antigen	26234610
SET	HLA-DR-associated protein	26234610
SPTAN1	Putative uncharacterized protein SP AN1	26234610
G19P1	80K-H protein	26234610
HSPA1	Heat shock 70 kDa protein 1/2	26234610
PFN1	Pro ilin	26234610
CCT5	CC -epsilon	26234610
ALDC	Brain-type aldolase	26234610
NAP1L1	NAP-1-related protein	26234610
ANX2	Annexin A2	26234610
FNRB	Fibronectin receptor subunit beta	26234610
JUP	cDNA FLJ60424 highly similar to Junction plakoglobin	26234610
OIP3	Cytosolic thyroid hormone-binding protein	26234610
CDC21	CDC21 homolog	26234610
Ov Br septin	cDNA FLJ55422 highly similar to Septin-9	26234610
MDU1	4F2 cell-sur ace antigen heavy chain	26234610
EDMD	Emerin	26234610
RPL17	60S ribosomal protein L17	26234610
ERAB	17-beta-hydroxysteroid dehydrogenase 10	26234610
ALDA	Fructose-bisphosphate aldolase A	26234610
EZR	Cytovillin	26234610
HSP90A	Heat shock 86 kDa	26234610
CDHF5	Cadherin amily member 5	26234610
FUBP1	DNA helicase V	26234610
NDUFB10	Complex -PDSW	26234610
HNRNPA1	Helix-destabilizing protein	26234610
EEF1D	elongation actor 1 delta (guanine nucleotide exchange protein) (EEF1D)	26234610
RCN	Reticulocalbin-1	26234610
TPM4	M30p1	26234610
ZNF207	Zinc inger protein 207 variant	26234610
HDGF	Hepatoma-derived growth actor (High-mobility group protein 1-like)	26234610
UQCRC2	Complex subunit 2	26234610
hCG 22755	umor protein D52-like 2	26234610
ILF2	nterleukin enhancer-binding actor 2	26234610
FTH1	Ferritin	26234610
ECHS1	Enoyl-CoA hydratase 1	26234610

BCLAF1	Bcl-2-associated transcription actor 1	26234610
CCDC86	Coiled-coil domain-containing protein 86	26234610
AHNAK	Desmoyokin	26234610
BAT1	56 kDa U2AF65-associated protein	26234610
C21orf33	ES1 protein homolog mitochondrial	26234610
PC4	Activated RNA polymerase transcriptional coactivator p15	26234610
CPD	Carboxypeptidase D	26234610
TUFM	Elongation actor u mitochondrial	26234610
NUDC	Nuclear distribution protein C homolog	26234610
YWHAE	14-3-3 protein epsilon	26234610
NPM	Nucleolar phosphoprotein B23	26234610
SNRPD3	Small nuclear ribonucleoprotein Sm D3	26234610
RPS13	40S ribosomal protein S13	26234610
RPL8	60S ribosomal protein L8	26234610
KIAA0568	190 kDa paraneoplastic pemphigus antigen	26234610
MIG10	Cell migration-inducing gene 10 protein	26234610
SAFB	SAFB protein	26234610
EWSR1	PRO E N EWS	26234610
NAP1L4	Nucleosome assembly protein 1-like 4	26234610
IKBIP	nhibitor o nuclear actor kappa-B kinase-interacting protein	26234610
BM28	cDNA FLJ53276 moderately similar to DNA replication licensing actor MCM2	26234610
RBM4	La k homolog	26234610
STIP1	phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (S P1) mRNA	26234610
EEF2	Elongation actor 2	26234610
DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 iso orm CRA a	26234610
G3BP	A P-dependent DNA helicase V	26234610
DRBF	Double-stranded RNA-binding protein 76	26234610
CLTB	Clathrin light chain B	26234610
HSP105	Antigen NY-CO-25	26234610
hCG 25936	riosephosphate isomerase	26234610
C21orf50	Bax antagonist selected in saccharomyces 1	26234610
SPTB2	Beta- spectrin	26234610
DKFZp686E2459	Putative uncharacterized protein DKFZp686E2459	26234610
GLT25D1	Glycosyltrans erase 25 amily member 1	26234610
BAZ1B	Bromodomain adjacent to zinc inger domain protein 1B	26234610
AKAP12	A-kinase anchor protein 12	26234610
RAB11FIP1	Rab11 amily-interacting protein 1	26234610
DUT	Deoxyuridine 5-triphosphate nucleotidohydrolase mitochondrial	26234610
hCG 2031827	PABPC4 protein	26234610
ACLY variant prot	ACLY variant protein	26234610
RPL7	60S ribosomal protein L7	26234610
MYH9	Cellular myosin heavy chain type A	26234610
PLEC1	Hemidesmosomal protein 1	26234610
SFRS7	Splicing actor 9G8	26234610
OK SW-cl.56	ubulin beta chain	26234610
CG1	CG-1 antigen	26234610
FUS	75 kDa DNA-pairing protein	26234610
COX5A	Cytochrome c oxidase polypeptide Va	26234610
H1F4	Histone H1 4	26234610
HNRNPA3	Heterogeneous nuclear ribonucleoprotein A3	26234610
C1orf77	Uncharacterized protein C1or 77	26234610
CTA-216E10.8-00	NHP2 non-histone chromosome protein 2-like 1 (S cerevisiae)	26234610
ERP57	58 kDa glucose-regulated protein	26234610
ATP2A2	Calcium pump 2	26234610
HNRNPUL2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	26234610
IGF2BP3	GF- mRNA-binding protein 3	26234610
TMED10	21 kDa transmembrane-tra icking protein	26234610
KIAA0719	Mitochondrial import receptor subunit OM70	26234610
PDHA1	cDNA FLJ59461 highly similar to Pyruvate dehydrogenase E1 component alp	26234610
ATP5B	A P synthase subunit beta mitochondrial	26234610
DLD	Dihydrolipoamide dehydrogenase	26234610
DLST	2-oxoglutarate dehydrogenase complex component E2	26234610
TRP32	32 kDa thioredoxin-related protein	26234610
ERBA2L	Cellular thyroid hormone-binding protein	26234610
GRP94	94 kDa glucose-regulated protein	26234610
CAS	Cellular apoptosis susceptibility protein	26234610
ABBP1	APOBEC1-binding protein 1	26234610
ATP5A	A P synthase subunit alpha mitochondrial	26234610
KIAA0268	C219-reactive peptide	26234610
NDUFV2	NADH dehydrogenase [ubiquinone lavoprotein 2 mitochondrial	26234610
TIM9	Mitochondrial import inner membrane translocase subunit im9	26234610
MDH2	Malate dehydrogenase mitochondrial	26234610
LRRC59	Leucine-rich repeat-containing protein 59	26234610
CBP1	47 kDa heat shock protein	26234610
H2AFC	Histone H2A type 1	26234610
SDH2	cDNA FLJ37560 is clone BRCOC2000333 highly similar to Succinate dehyd	26234610
H4 A	Histone H4	26234610
ANT2	Adenine nucleotide translocator 2	26234610

HIBADH	3-hydroxyisobutyrate dehydrogenase mitochondrial	26234610
TARDBP	AR DNA-binding protein 43	26234610
hCG 17250	NADH-ubiquinone oxidoreductase 75 kDa subunit	26234610
H2BFD	Histone H2B	26234610
OPA1	Putative uncharacterized protein OPA1	26234610
H2AFZ	Histone H2A Z	26234610
DNAJB11	APOBEC1-binding protein 2	26234610
OXCT	3-oxoacid-CoA trans erase 1	26234610
CGI-33	H RA-interacting protein 5	26234610
ORCA	EB 3-associated protein o 60 kDa	26234610
DC2	Hydrophobic protein HSF-28	26234610
PCK2	Phosphoenolpyruvate carboxykinase [G P mitochondrial	26234610
hBD-1	Human Beta-de ensin-1	24658581
CD68	CD68	26769084
CD163	CD163	26769084
CDH1	E-cadherin	26769084
VIM	vimentin	26769084
EPLIN	Epithelial protein lost in neoplasm	16083295
PRDX2	Peroxiredoxin 2	16083295
MCM7	DNA replication licensing actor MCM7	16083295
CCT8	-complex protein 1 θ subunit	16083295
PTMA	Prothymosin α	16083295
DCK	Deoxycytidine kinase	16083295
NAP1L1	Nucleosome assembly protein 1-like 1	16083295
ACSL4	Long-chain- atty-acid- -CoA ligase 4	16083295
ANXA2	Annexin A2	16083295
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase liver	16083295
SLC3A2	4F2 cell-sur ace antigen heavy chain	16083295
N A	Collagen-binding protein 2 precursor	16083295
N A	Glyceraldehyde-3-phosphate dehydrogenase muscle	16083295
RRBP1	Ribosome-binding protein 1	16083295
CLTC	Clathrin heavy chain 1	16083295
TFRC	rans errin receptor protein 1	16083295
RBM3	Putative RNA-binding protein 3	16083295
PLOD1	5-dioxygenase 1 precursor	16083295
CALD1	Caldesmon	16083295
P4HA2	Prolyl 4-hydroxylase α-2 subunit precursor	16083295
COL1A1	Collagen α 1( ) chain precursor	16083295
CA9	Carbonic anhydrase X precursor	16083295
NPM1	Nucleophosmin	16083295
TAGLN	ransgelin	16083295
CTNND1	p120 catenin	16083295
NEDD8	Neddylin	16083295
TPI1	riosephosphate isomerase	16083295
CALR	Calreticulin precursor	16083295
TCOF1	reacle protein	16083295
SLC7A5	Large neutral amino acids transporter small subunit 1	16083295
TUBB4A	ubulin β-4 chain	16083295
CAV1	Caveolin-1	16083295
EHD2	EH-domain containing protein 2	16083295
CTNNA1	α-1 catenin	16083295
ENAH	Enabled protein homolog	16083295
TBL2	ransducin β-like 2 protein	16083295
GLG1	Golgi apparatus protein 1 precursor	16083295
KTN1	Kinectin	16083295
PRDX4	Peroxiredoxin 4	16083295
P4HA1	Prolyl 4-hydroxylase α-1 subunit precursor	16083295
COL5A1	Collagen α 1(V) chain precursor	16083295
PLOD2	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 2 precursor	16083295
COL3A1	Collagen α 1( ) chain precursor	16083295
ANXA6	Annexin A6	16083295
CTTN	Src substrate cortactin	16083295
SEC61A1	Protein transport protein Sec61 α subunit iso orm 1	16083295
TPM1	ropomyosin 1 α chain	16083295
TPM2	ropomyosin β chain	16083295
PRKCA	Protein kinase C α type	16083295
PRKCB	Protein kinase C β type	16083295
KRT18	Keratin type cytoskeletal 18	16083295
APG16L	APG16 Autophagy 16-like iso orm 3	15942644
CAPG	Capping Protein gelsolin-like	15942644
C15orf29	chromosome 15 open reading rame 29	15942644
LMNA	Lamin A/C	15942644
PSAT1	Phosphoserine aminotrans erase so orm 1	15942644
SEPTIN 1	Septin 1	15942644
SERPINB1	Serine protease inhibitor clade B member 1	15942644
STMN1	Stathmin 1	15942644
ZNF322A	Zinc inger protein 322A	15942644
ANXA1	ANNEX N A1	15942644

CTSB	CA HEPS N B	15942644
CTSB	CHA N B CA HEPS N B	15942644
ECH1	Enoyl co enzyme a hydratae 1 peroxisomal	15942644
FKBP9	FK506 binding protein 9	15942644
HSPB1	Heat shock 27kDA protein	15942644
IFNA2	nter ero alpha 2	15942644
1L1RA	nterleukin 1 receptor antagonist	15942644
KRT13	Keratin 13	15942644
SOD2	Superoxide dismutase 2 mitochondrial	15942644
OAT	Ornithine aminotras erase	15942644
SERPINB5	Serine protease inhibitor clade B member 5	15942644
ZSCAN5	Zinc inger protein 495	15942644
QPCT	Glutaminyl-peptide cyclotras erase	25484078
CXCL8	Chemokine Ligand 8	25484078
LIF	Leukemia nhibitory Factor	25484078
SDCBP	Syndecan Binding Protein	25484078
IL1B	nterleukin 1 beta	25484078
APOD	Apolipoprotein D	25484078
FAM3C	Family with sequence similarity 3 member C	25484078
ECM1	Extracellular Matrix Protein 1	25484078
DKK3	Dickkop WN signaling pathway inhibitor 3	25484078
ANXA1	Annexin A1	25484078
GM2A	GM2 ganglioside activator	25484078
AGRN	Agrin	25484078
TIMP2	MP metalopeptidase inhibitor 2	25484078
AKR1B1	Aldo-keto reductase amily 1 member B1	25484078
TIMP1	MP metallopeptidase inhibitor 1	25484078
UBA1	Ubiquitin-like modi ier activating enzyme 1	25484078
ACTG1P2	Actin-gamma 1 pseudogene 2	25484078
LAMB1	Laminin beta 1	25484078
CST3	cystatin C	25484078
GLCCI1	Glucocorticoid induced trascript 1	25484078
PRIC	peptidylprolyd isomerase C	25484078
PTGR1	Protaglandin reductase 1	25484078
ANGPTL3	Angiopoitin like 3	25484078
VIM	vimentin	25484078
GOT1	Glutamic oxaloacetic trasaminase 1	25484078
MIA	Melanoma inhibitory activity	25484078
LCN2	Lipocalin 2	25484078
CYTL1	Cytokine-like 1	25484078
CXCL8	L8	25484078
ILF	nterleukin 1 B	25484078
DKK3	Di ckkop WN signalling	25484078
IL-1Ba	nterleukin 1 beta	25204733
IL-6	nterleukin 6	25204733
IL-8	nterleukin 8	25204733
EGFR	epidermal growth actor receptor	22902387
OAT	ornithine aminotrans erase	22902387
TPT	ranslationally-controlled tumor protein	22902387
ITGA6	ntegrin alpha-6	22902387
G3BP1	Ras G Pase-activating protein-binding protein 1	22902387
CB39L	Calcium-binding protein 39-like	22902387
MIR-19a	microRNA 192	22902387
MIR-203	microRNA 203	22902387
MIR-377	microRNA 377	22902387
CD82	nducible membrane protein R2	22902387
ADRB2	β2-Adrenergic receptor	23090842
HCAR1	Nicotinic acid receptor 1	23090842
PTGER2	Prostaglandin E2 receptor EP2 subtype	23090842
F2RL1	Proteinase-activated receptor 2 precursor	23090842
CTNNB1	Catenin β1	23090842
CTNND1	Catenin δ1	23090842
CD44	CD44 antigen precursor	23090842
ITGA3	ntegrin α3 precursor	23090842
ITGA6	ntegrin α6 precursor	23090842
ITGB4	ntegrin β4 precursor	23090842
PKP3	Plakophilin 3	23090842
PLEC	Plectin 1	23090842
SLC12A6	Solute carrier amily 12 member 6	23090842
SLC38A1	Sodium-coupled neutral amino acid transporter 1	23090842
SLC9A1	Sodium/hydrogen exchanger 1	23090842
ABCC1	Multidrug resistance-associated protein 1	23090842
EGFR	Epidermal growth actor receptor precursor	23090842
PRKD2	Serine/threonine-protein kinase D2	23090842
WNK1	Serine/threonine-protein kinase Wnk1	23090842
ADAM17	ADAM17 precursor	23090842
HSPB1	Heat shock protein β1	23090842
NCOA3	Nuclear receptor coactivator 3	23090842

SHC1	SHC-trans orming protein 1	23090842
F3	issue actor precursor	23090842
AER61	Uncharacterized glycosyltrans erase AER61 precursor	23090842
AGL	Amylo-1 6-glucosidase	23090842
AHSA1	Activator o 90 kDa heat shock protein A Pase homolog 1	23090842
ASPH	Aspartyl/asparaginyl beta-hydroxylase	23090842
ATP1A1	Sodium/potassium-transporting A Pase subunit alpha-1 precursor	23090842
ATP1B3	Sodium/potassium-transporting A Pase subunit beta-3	23090842
ATP2B4	Plasma membrane calcium-transporting A Pase 4	23090842
BTN3A3	Butyrophilin sub amily 3 member A3 precursorantigen	23090842
C3orf1	Uncharacterized protein C3or 1 Protein M5-14	23090842
CAD	CAD protein	23090842
CALR	Calreticulin precursor	23090842
CAPN2	Calpain-2 catalytic subunit precursor	23090842
CBR4	Carbonyl reductase 4	23090842
CCT4	CP-1-delta	23090842
HLADRB1	HLA class histocompatibility antigen gamma chain	23090842
CDC2	Cell division control protein 2 homolog	23090842
CTBS	Di-N-acetylchitobiase precursor	23090842
CTNND1	Catenin delta-1 p120 catenin	23090842
DARS	Aspartyl-tRNA synthetase cytoplasmic	23090842
DDR1	Discoidin domain receptor amily member 1	23090842
DHRS7B	Dehydrogenase/reductase SDR amily member 7B	23090842
DNAJA4	DnaJ (Hsp40) homolog sub amily A member 4 iso orm CRA b	23090842
HSPA4	Heat shock 40 kDa protein 4	23090842
DNAJA2	DnaJ homolog sub amily A member 2	23090842
EXT2	Exostosin-2	23090842
FAS	Fatty acid synthase	23090842
FAT	Cadherin-related tumor suppressor homolog precursor Protein at homolog	23090842
FBLN1	Fibulin-1 precursor	23090842
FGFBP1	Fibroblast growth actor-binding protein 1 precursor	23090842
GANAB	Neutral alpha-glucosidase AB precursor	23090842
GYS1	Glycogen [starch synthase muscle	23090842
GDH	Glucose 1-dehydrogenase	23090842
HAX1	HCLS1 associated protein X-1	23090842
HMGCR	3-hydroxy-3-methylglutaryl-coenzyme A reductase	23090842
HNRPF	Heterogeneous nuclear ribonucleoprotein F	23090842
HSP90AB1	Heat shock protein HSP 90-beta	23090842
HSPA1A	Heat shock 70 kDa protein 1	23090842
HSPA5	78 kDa glucose-regulated protein precursor	23090842
IGSF3	Uncharacterized protein GSF3	23090842
IMPAD1	nositol monophosphatase 3	23090842
ITPR2	nositol 1 4 5-trisphosphate receptor type 2	23090842
ITPR3	nositol 1 4 5-trisphosphate receptor type 3	23090842
KIAA0152	Uncharacterized protein K AA0152 precursor	23090842
KPNB1	mportin subunit beta-1	23090842
KTEL1	K EL moti -containing protein 1 precursor	23090842
LAMA3	Laminin subunit alpha-3 precursor	23090842
LAMA2	Laminin subunit beta-2 precursor	23090842
MAN2A1	Alpha-mannosidase 2	23090842
MCM7	DNA replication licensing actor MCM7	23090842
NUP62	Nuclear pore glycoprotein p62	23090842
NUP88	Nuclear pore complex protein Nup88	23090842
NUP93	Nuclear pore complex protein Nup93	23090842
OAS2	2'-5'-oligoadenylate synthetase 2	23090842
PCDH7	Protocadherin-7 precursor	23090842
PCDHGC3	Protocadherin gamma C3 precursor	23090842
PCNA	Proli erating cell nuclear antigen	23090842
PDB1	Pyruvate dehydrogenase E1 component subunit beta mitochondrial precurso	23090842
PSMA3	Proteasome subunit alpha type-3	23090842
PSMC6	26S protease regulatory subunit S10B	23090842
PSMD8	26S proteasome non-A Pase regulatory subunit 8	23090842
PYGB	Glycogen phosphorylase brain orm	23090842
NXF1	mRNA export actor	23090842
RARS	Arginyl-tRNA synthetase cytoplasmic	23090842
MSMO1	C-4 methylsterol oxidase	23090842
SEPT 9	Septin-9	23090842
SERPINE1	Plasminogen activator inhibitor 1 precursor	23090842
SLC25A5	ADP/A P translocase 2	23090842
SLC44A1	Choline transporter-like protein 1	23090842
STAT1	Signal transducer and activator o transcription 1-alpha/beta	23090842
STOM	Erythrocyte band 7 integral membrane protein	23090842
TAPBP	AP binding protein	23090842
TIMM50	mport inner membrane translocase subunit M50 mitochondrial precursor	23090842
TLR2	oll-like receptor 2 precursor	23090842
TMED2	ransmembrane emp24 domain-containing protein 2 precursor Membrane pro	23090842
TMTC3	ransmembrane and PR repeat-containing protein 3	23090842
TNPO1	ransportin-1	23090842

TRIP13	hyroid receptor-interacting protein 13	23090842
TUBB	ubulin beta chain	23090842
UB	Ubiquitin	23090842
UNC93B1	Protein unc-93 homolog B1	23090842
USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	23090842
VDAC1	Voltage-dependent anion-selective channel protein 1	23090842
VDAC2	Voltage-dependent anion-selective channel protein 2	23090842
VDAC3	Voltage-dependent anion-selective channel protein 3	23090842
PKD1	Polycystic kidney disease 1-related protein	23090842
XRN1	5'-3' exoribonuclease 1 Strand-exchange protein 1 homolog	23090842
MMP9	MMP9	18485796
MMP2	MMP2	18485796
SDC1	Syndecan-1	23352437
TGFB1	integrin beta 1	26850833
MMP3	matrix metalloproteinase-3	26850833
MIA	Melanoma inhibitory activity	18616526
HMGB1	high mobility group box-1	18616526
NFkBp65	nuclear actor kB	18616526
VEGF	vascular endothelial growth actor	18616526
IL4RA	nterleukin-4 receptor α	23563734
HMGB1	High-mobility group protein B1	25828589
STMN1	Stathmin	24495306
MYOM1	Myomesin-1	24495306
MATR3	Matrin-3	24495306
NAP1L4	Nucleosome assembly protein 1-like 4	24495306
NAP1L4b	Nucleosome assembly protein 1-like 4	24495306
LAMA3	Laminin subunit alpha-3	24495306
PRPS2	Ribose-phosphate pyrophosphokinase 2 Ribose-phosphate pyrophosphokina	24495306
PRPS1L1	Ribose-phosphate pyrophosphokinase 2 Ribose-phosphate pyrophosphokina	24495306
PRPS1	Ribose-phosphate pyrophosphokinase 2 Ribose-phosphate pyrophosphokina	24495306
NAP1L1	Nucleosome assembly protein 1-like 1	24495306
SOD2	Superoxide dismutase [Mn mitochondrial Superoxide dismutase	24495306
HARS	Histidine--tRNA ligase cytoplasmic	24495306
CNN3	Calponin-3	24495306
IDH2	socitrate dehydrogenase [NADP mitochondrial socitrate dehydrogenase [N	24495306
COMMD9	COMM domain-containing protein 9	24495306
DPYSL2	Dihydropyrimidinase-related protein 2	24495306
MST4	Serine/threonine-protein kinase 24 Serine/threonine-protein kinase 24 36 kDa	24495306
STK24	Serine/threonine-protein kinase 24 Serine/threonine-protein kinase 24 36 kDa	24495306
STK25	Serine/threonine-protein kinase 24 Serine/threonine-protein kinase 24 36 kDa	24495306
FGB	Fibrinogen beta chain Fibrinopeptide B Fibrinogen beta chain	24495306
HADHB	ri unctional enzyme subunit beta mitochondrial 3-ketoacyl-CoA thiolase	24495306
RPS9	40S ribosomal protein S9	24495306
RAN	G P-binding nuclear protein Ran	24495306
ENO2	Gamma-enolase Enolase	24495306
LUC7L2	Putative RNA-binding protein Luc7-like 2	24495306
HSPA9	Stress-70 protein mitochondrial	24495306
FHL1	Four and a hal L M domains protein 1	24495306
DECR1	2 4-dienoyl-CoA reductase mitochondrial	24495306
PARVA	Alpha-parvin	24495306
PCMT1	Protein-L-isoaspartate O-methyltrans erase Protein-L-isoaspartate(D-aspartate	24495306
PPP2R5E	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon is	24495306
MYBPC1	Myosin-binding protein C slow-type	24495306
IMMT	Mitochondrial inner membrane protein	24495306
PDCD10	Programmed cell death protein 10	24495306
FGG	Fibrinogen gamma chain	24495306
CYCS	Cytochrome c	24495306
RPS3A	40S ribosomal protein S3a	24495306
COL12A1	Collagen alpha-1(X) chain	24495306
TKT	ransketolase	24495306
NDUFV2	NADH dehydrogenase [ubiquinone lavoprotein 2 mitochondrial	24495306
RPL15	60S ribosomal protein L15 Ribosomal protein L15	24495306
THBS4	hrombospondin-4	24495306
U2SURP	U2 snRNP-associated SURP moti -containing protein	24495306
SRP68	Signal recognition particle 68 kDa protein	24495306
TCOF1	reacle protein	24495306
UGP2	U P--glucose-1-phosphate uridylyltrans erase	24495306
G6PD	Glucose-6-phosphate 1-dehydrogenase	24495306
NUCB2	Nucleobindin-2	24495306
HYOU1	Hypoxia up-regulated protein 1	24495306
USO1	General vesicular transport actor p115	24495306
MDH1	Malate dehydrogenase Malate dehydrogenase cytoplasmic	24495306
PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	24495306
ACADVL	Very long-chain speci ic acyl-CoA dehydrogenase mitochondrial	24495306
CACNB1	Voltage-dependent L-type calcium channel subunit beta-1	24495306
PGM1	Phosphoglucomutase-1	24495306
RRBP1	Ribosome-binding protein 1	24495306
DSC2	Desmocollin-2	24495306

DKFZp686I11137	Desmocollin-2	24495306
NEB	Nebulin	24495306
CAPRIN1	Caprin-1	24495306
DLAT	Dihydrolipoyllysine-residue acetyltrans erase component o pyruvate dehydrog	24495306
SLC25A11	Mitochondrial 2-oxoglutarate/malate carrier protein	24495306
DDX39A	A P-dependent RNA helicase DDX39A	24495306
DDX39	A P-dependent RNA helicase DDX39A	24495306
CLIC1	Chloride intracellular channel protein 1	24495306
IGF2BP3	nsulin-like growth actor 2 mRNA-binding protein 3	24495306
ATP2A1	Sarcoplasmic/endoplasmic reticulum calcium A Pase 1	24495306
IDH3B	socitrate dehydrogenase [NAD subunit beta mitochondrial	24495306
KBTBD10	Kelch repeat and B B domain-containing protein 10	24495306
LDB3	L M domain-binding protein 3	24495306
NDUFS2	NADH dehydrogenase [ubiquinone iron-sul ur protein 2 mitochondrial	24495306
PDCD6	Programmed cell death protein 6	24495306
FLNB	Filamin-B	24495306
SLC25A12	Calcium-binding mitochondrial carrier protein Aralar1	24495306
GLS	Glutaminase kidney iso orm mitochondrial	24495306
GOT2	Aspartate aminotrans erase mitochondrial Aspartate aminotrans erase	24495306
PGK1	Phosphoglycerate kinase 1 Phosphoglycerate kinase	24495306
AK1	Adenylate kinase isoenzyme 1	24495306
OAT	Ornithine aminotrans erase mitochondrial Ornithine aminotrans erase hepatic	24495306
RPN2	Dolichyl-diphosphooligosaccharide–protein glycosyltrans erase subunit 2	24495306
ALDH2	Aldehyde dehydrogenase mitochondrial	24495306
SLC25A5	ADP/A P translocase 2	24495306
P4HB	Protein disul ide-isomerase	24495306
CTSD	Cathepsin D Cathepsin D light chain Cathepsin D heavy chain	24495306
TPM2	ropomyosin beta chain	24495306
PFKM	6-phospho ructokinase muscle type	24495306
TPM1	ropomyosin alpha-1 chain	24495306
HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1 Heterogeneous nuclear ribonuc	24495306
HNRNPA1L2	Heterogeneous nuclear ribonucleoprotein A1 Heterogeneous nuclear ribonuc	24495306
LAMC1	Laminin subunit gamma-1	24495306
HSPA8	Heat shock cognate 71 kDa protein	24495306
PDHB	Pyruvate dehydrogenase E1 component subunit beta mitochondrial	24495306
PYGM	Glycogen phosphorylase muscle orm Phosphorylase	24495306
PCNA	Proli erating cell nuclear antigen	24495306
COL6A2	Collagen alpha-2(V) chain	24495306
ACTN1	Alpha-actinin-1	24495306
MYH1	Myosin-1	24495306
RNH1	Ribonuclease inhibitor	24495306
EEF2	Elongation actor 2	24495306
PKM2	Pyruvate kinase isozymes M1/M2 Pyruvate kinase	24495306
COX6B1	Cytochrome c oxidase subunit 6B1	24495306
FABP4	Fatty acid-binding protein adipocyte	24495306
UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	24495306
DSP	Desmoplakin	24495306
H2AFX	Histone H2A x Histone H2A type 1-A Histone H2A type 2-B	24495306
HIST2H2AB	Histone H2A x Histone H2A type 1-A Histone H2A type 2-B	24495306
HIST1H2AA	Histone H2A x Histone H2A type 1-A Histone H2A type 2-B	24495306
ACADS	Short-chain speci ic acyl-CoA dehydrogenase mitochondrial	24495306
ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium A Pase 2	24495306
GOT1	Aspartate aminotrans erase cytoplasmic Aspartate aminotrans erase	24495306
CKMT2	Creatine kinase S-type mitochondrial	24495306
UQCRC2	Cytochrome b-c1 complex subunit 2 mitochondrial	24495306
ACAT1	Acetyl-CoA acetyltrans erase mitochondrial	24495306
MYL9	Myosin regulatory light polypeptide 9	24495306
MCM3	DNA replication licensing actor MCM3	24495306
MSN	Moesin	24495306
CALML3	Calmodulin-like protein 3	24495306
APEX1	DNA-(apurinic or apyrimidinic site) lyase DNA-(apurinic or apyrimidinic site) lyas	24495306
PSMB5	Proteasome subunit beta type-5	24495306
NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit mitochondrial	24495306
SERPINB3	Serpin B3	24495306
ERP29	Endoplasmic reticulum resident protein 29	24495306
BLVRB	Flavin reductase (NADPH)	24495306
PRDX5	Peroxiredoxin-5 mitochondrial	24495306
SFN	14-3-3 protein sigma	24495306
STIP1	Stress-induced-phosphoprotein 1	24495306
DSG3	Desmoglein-3	24495306
SHMT2	Serine hydroxymethyltrans erase mitochondrial Serine hydroxymethyltrans era	24495306
SPRR1A	Corni in-A	24495306
SPRR2A	Small proline-rich protein 2A Small proline-rich protein 2E Small proline-rich pro	24495306
SPRR2E	Small proline-rich protein 2A Small proline-rich protein 2E Small proline-rich pro	24495306
SPRR2D	Small proline-rich protein 2A Small proline-rich protein 2E Small proline-rich pro	24495306
SPRR2B	Small proline-rich protein 2A Small proline-rich protein 2E Small proline-rich pro	24495306
AGL	Glycogen debranching enzyme 4-alpha-glucanotrans erase Amylo-alpha-1 6-g	24495306
ACTN2	Alpha-actinin-2	24495306

DLST	Dihydrolipoyllysine-residue succinyltrans erase component o 2-oxoglutarate d	24495306
ETFB	Electron trans er lavoprotein subunit beta	24495306
EIF4A3	Eukaryotic initiation actor 4A-	24495306
NNMT	Nicotinamide N-methyltrans erase	24495306
MDH2	Malate dehydrogenase mitochondrial Malate dehydrogenase	24495306
SKIV2L2	Superkiller viralicidic activity 2-like 2	24495306
LRPPRC	Leucine-rich PPR moti -containing protein mitochondrial	24495306
ACAA2	3-ketoacyl-CoA thiolase mitochondrial	24495306
CCT5	-complex protein 1 subunit epsilon	24495306
TUFM	Elongation actor u mitochondrial	24495306
ALDH7A1	Alpha-aminoadipic semialdehyde dehydrogenase	24495306
AARS	Alanine--tRNA ligase cytoplasmic	24495306
PSMB2	Proteasome subunit beta type-2	24495306
GMPS	GMP synthase [glutamine-hydrolyzing	24495306
IDH3A	socitrate dehydrogenase [NAD subunit alpha mitochondrial	24495306
PRELP	Prolargin	24495306
KPNA2	mportin subunit alpha-2	24495306
HNRNPF	Heterogeneous nuclear ribonucleoprotein F Heterogeneous nuclear ribonucle	24495306
MYOM2	Myomesin-2	24495306
OXCT1	Succinyl-CoA 3-ketoacid-coenzyme A trans erase 1 mitochondrial	24495306
EIF3E	Eukaryotic translation initiation actor 3 subunit E	24495306
HNRNPK	Heterogeneous nuclear ribonucleoprotein K	24495306
PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit Serine/threo	24495306
SNRPD2	Small nuclear ribonucleoprotein Sm D2	24495306
PSMC6	26S protease regulatory subunit 10B	24495306
RPS4X	40S ribosomal protein S4 X iso orm	24495306
GNB2	Guanine nucleotide-binding protein G( )/G(S)/G( ) subunit beta-2 Guanine nu	24495306
GNB4	Guanine nucleotide-binding protein G( )/G(S)/G( ) subunit beta-2 Guanine nu	24495306
ACTG1	Actin cytoplasmic 2 Actin cytoplasmic 2 N-terminally processed	24495306
TPM4	ropomyosin alpha-4 chain	24495306
RBM3	Putative RNA-binding protein 3	24495306
FABP5	Fatty acid-binding protein epidermal	24495306
TAGLN	ransgelin	24495306
DSG1	Desmoglein-1	24495306
SRSF11	Serine/arginine-rich splicing actor 11	24495306
SFRS11	Serine/arginine-rich splicing actor 11	24495306
DHX9	A P-dependent RNA helicase A	24495306
AHNAK	Neuroblast di erentiation-associated protein AHNAK	24495306
FLII	Protein lightless-1 homolog	24495306
SELENBP1	Selenium-binding protein 1	24495306
CAMK2B	Calcium/calmodulin-dependent protein kinase type subunit beta	24495306
LAMB3	Laminin subunit beta-3	24495306
PKP1	Plakophilin-1	24495306
TUBB2A	ubulin beta-2A chain ubulin beta-2B chain	24495306
TUBB2B	ubulin beta-2A chain ubulin beta-2B chain	24495306
DPYSL3	Dihydropyrimidinase-related protein 3	24495306
DSC3	Desmocollin-3	24495306
SEC23B	Protein transport protein Sec23B	24495306
LAMA4	Laminin subunit alpha-4	24495306
FSCN1	Fascin	24495306
ADCK3	Chaperone activity o bc1 complex-like mitochondrial	24495306
CABC1	Chaperone activity o bc1 complex-like mitochondrial	24495306
NAPRT1	Nicotinate phosphoribosyltrans erase	24495306
HUWE1	E3 ubiquitin-protein ligase HUWE1	24495306
ADSSL1	Adenylosuccinate synthetase isozyme 1	24495306
GPD1L	Glycerol-3-phosphate dehydrogenase 1-like protein	24495306
SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	24495306
IPO4	mportin-4	24495306
TTN	itin	24495306
TNPO1	ransportin-1	24495306
SUCLG2	Succinyl-CoA ligase [GDP- orming subunit beta mitochondrial	24495306
FAM129B	Niban-like protein 1	24495306
ACO2	Aconitate hydratase mitochondrial	24495306
ASPN	Asporin	24495306
NT5C3	Cytosolic 5-nucleotidase 3	24495306
HDHD2	Haloacid dehalogenase-like hydrolase domain-containing protein 2	24495306
SYNPO2L	Synaptopodin 2-like protein	24495306
NIT2	Omega-amidase N 2	24495306
PDLIM7	PDZ and L M domain protein 7	24495306
SAR1A	G P-binding protein SAR1a	24495306
SAR1B	G P-binding protein SAR1a	24495306
ABRACL	Costars amily protein ABRACL	24495306
MYOT	Myotilin	24495306
UBQLN2	Ubiquilin-2	24495306
DBNL	Drebrin-like protein	24495306
HN1	Hematological and neurological expressed 1 protein	24495306
BAIAP2	Brain-speci ic angiogenesis inhibitor 1-associated protein 2	24495306
C14orf166	UPF0568 protein C14or 166	24495306

RUVBL2	RuvB-like 2	24495306
CFL2	Co ilin-2	24495306
YARS2	yrosine--tRNA ligase mitochondrial	24495306
PKP3	Plakophilin-3	24495306
AURKA	Aurora kinase A	23481312
SERPINB1	serine protease inhibitor clade B member 1	19213596
CDC23	Cell division cycle protein 23 homolog	24211406
CHD8	Chromodomain-helicase-DNA-binding protein 8	24211406
HIRIP3	H RA-interacting protein 3	24211406
TMPO	Lamina-associated polypeptide 2<comma> iso orm alpha	24211406
AHNAK	Neuroblast di erentiation-associated protein AHNAK	24211406
PCDH1	Protocadherin-1	24211406
SRRM2	Serine/arginine repetitive matrix protein 2	24211406
SVIL	Supervillin	24211406
SMARCC2	SW /SNF complex subunit SMARCC2	24211406
TSPYL2	estis-speci ic Y-encoded-like protein 2	24211406
TJP2	ight junction protein ZO-2	24211406
ABCF1	A P-binding cassette sub- amily F member 1	24211406
ACIN1	Apoptotic chromatin condensation inducer in the nucleus	24211406
AIM1L	Absent in Melanoma 1-like protein	24211406
BAG3	BAG amily molecular chaperone regulator 3	24211406
CBX3	Chromobox protein homolog 3	24211406
CTNNA1	Catenin alpha-1	24211406
CTNNA2	Catenin alpha-2	24211406
DENND1A	DENN domain-containing protein 1A	24211406
EHBP1	EH domain-binding protein 1	24211406
FAM83H	Protein FAM83H	24211406
FOXK1	Forkhead box protein K1	24211406
IRF2BPL	nter eron regulatory actor 2-binding protein-like	24211406
ITGB4	ntegrin beta-4	24211406
IWS1	Protein WS1 homolog	24211406
MAP7D1	MAP7 domain-containing protein 1	24211406
MLLT4	A adin	24211406
MYH14	Myosin-14	24211406
NSUN2	tRNA (cytosine(34)-C(5))-methyltrans erase	24211406
PHACTR4	Phosphatase and actin regulator 4	24211406
PHIP	PH-interacting protein	24211406
PRRC2B	Protein PRRC2B	24211406
SART3	Squamous cell carcinoma antigen recognized by -cells 3	24211406
SCRIB	Protein scribble homolog	24211406
SENP3	Sentrin-speci ic protease 3	24211406
SLTM	SAFB-like transcription modulator	24211406
SNIP1	Smad nuclear-interacting protein 1	24211406
SRRM2	Serine/arginine repetitive matrix protein 2	24211406
TACC2	rans orming acidic coiled-coil-containing protein 2	24211406
TMPO	Lamina-associated polypeptide 2<comma> iso orm alpha	24211406
TNKS1BP1	182 kDa tankyrase-1-binding protein	24211406
ZC3H13	Zinc inger CCCH domain-containing protein 13	24211406
UBE2O	Ubiquitin-conjugating enzyme E2 O	24211406
LGALS3BP	Mac-2-binding protein	18458027
HSP90AA1	Heat shock protein 90-alpha	18458027
HSPA5	BiP protein	18458027
MSN	Moesin	18458027
PDIA3	Disul ide-isomerase ER60	18458027
HSPA8	HSP70 amily HSPA8 protein	18458027
HSPA2	HSP70-2	18458027
TGFBI	GF beta-induced protein B GH3	18458027
PKM	Pyruvate kinase isozymes M1/M2	18458027
EZR	Ezrin	18458027
FSCN1	Fascin	18458027
ENO-1	Alpha enolase	18458027
PGK1	Phosphoglycerate kinase 1	18458027
ALDOA	Fructose-bisphosphate aldolase A	18458027
GAPDH	Glyceraldehyde 3-phophate dehydrogenase	18458027
TPM4	ropomyosin alpha-4 chain iso orm 2	18458027
SFN	14-3-3 protein sigma	18458027
HSPB1	Heat shock 27 kDa protein 1	18458027
YWHAZ	14-3-3 protein zeta chain A	18458027
TPI	riosephosphate isomerase	18458027
GSTP1	Glutathione s-trans erase P	18458027
PRDX1	Peroxiredoxin-1	18458027
NGAL	Neutrophil gelatinase-associated lipocalin	18458027
NME1	Nucleoside diphosphate kinase chain R	18458027
PPIA	Peptidylprolyly isomerase A (cyclophilin A)	18458027
PFN1	Pro ilin chain A	18458027
UBC	etraubiquitin	18458027

Proteomics /DEG Match	DGIDb Gene Name	Interaction Claim Source	Interaction Types	Drug Claim Primary Name	PMID(s)
ADAM17	*ADAM17*	Guide oPharmacology nteractions	inhibitor	K-862	---
	ADAM17	D	inhibitor	DPC-333	---
	ADAM17	Guide oPharmacology nteractions	inhibitor	LOMAS A	---
	ADAM17	Guide oPharmacology nteractions	inhibitor	APRA AS A	---
	ADAM17	dgClinical rial	---	NCB7839	---
	ADAM17	Guide oPharmacology nteractions	inhibitor	BMS-561392	---
	ADAM17	D	inhibitor	GW-3333	---
	EGFR	NC	---	E HANOL	10092515
	EGFR	CKB	---	EGFRBi-armed autologous activated cells	16397041
	EGFR	CKB	---	AV-412	17888033
	EGFR	C ViC	---	PF 00299804	18089823
	EGFR	CKB	---	AEE788	19147750
	EGFR	CKB	---	CUDC-101	20388807
	EGFR	DoCM	---	GEF N B	21274259
	EGFR	CKB	---	Gedatolisib	21325073
	EGFR	CKB	---	AC480	21576284
	EGFR	C ViC	---	CR ZO N B	21791641
	EGFR	OncoKB	---	Cetuximab	22001862
	EGFR	C ViC	---	CARBOPLA N	22139083
	EGFR	C ViC	---	PACL AXEL	22139083
	EGFR	CKB	---	Ponatinib	22238366
	EGFR	DoCM	---	PAN UMUMAB	22270724
	EGFR	CKB	---	matinib	22323597
	EGFR	CKB	---	XL647	22722787
	EGFR	CKB	---	Golvatinib	22789825
	EGFR	DoCM	---	LAPA N B	22885469
	EGFR	CKB	---	GA201	23209031
	EGFR	CKB	---	BMS-690514	23490650
	EGFR	CKB	---	Everolimus	23629727
	EGFR	CKB	---	Regora enib	23629727
	EGFR	CKB	---	Pimasertib	23629727
	EGFR	C ViC	---	C SPLA N	23764753
	EGFR	CKB	---	AK-285	23983820
	EGFR	CKB	---	emsirolimus	24470557
	EGFR	C ViC	---	PEME REXED	24636847
	EGFR	CKB	---	Sirolimus	24813888
	EGFR	CKB	---	Decitabine	24874286
	EGFR	CKB	---	Paclitaxel	24886365
	EGFR	C ViC	---	RAPAMYC N (S ROL MUS)	24934779
	EGFR	CKB	---	Ganetespib	25077897
	EGFR	CKB	---	Nimotuzumab	25185971
	EGFR	C ViC	---	R NDOPEP MU	25586468
	EGFR	CKB	---	AUY922	25870087
	EGFR	CKB	---	AB -806	25895099
	EGFR	CKB	---	Vandetanib	25910950
	EGFR	CKB	---	AE226	26090892
	EGFR	CKB	---	MK2206	26106072
	EGFR	CKB	---	Sonidegib	26124204
	EGFR	CKB	---	PF3644022	26140595
	EGFR	CKB	---	PF-477736	26140595
	EGFR	CKB	---	BGB-283	26208524
	EGFR	CKB	---	AMG 337	26432108
	EGFR	CKB	---	Linsitinib	26561558
	EGFR	CKB	---	BMS-754807	26561558
	EGFR	CKB	---	GC1118	26586721
	EGFR	CKB	---	EGF816	26825170
	EGFR	OncoKB	---	EGF816	26825170
	EGFR	OncoKB	---	AP32788	26825170
	EGFR	CKB	---	AB -414	26846818
	EGFR	C ViC	---	SYM004	26888827
	EGFR	CKB	---	AZD4547	26936917
	EGFR	CKB	---	Cisplatin	27040853
	EGFR	CKB	---	ER2	27040853
	EGFR	CKB	---	Sunitinib	27149458
	EGFR	CKB	---	K-756	27196752
	EGFR	CKB	---	EGFR antibody	27196767
	EGFR	CKB	---	ERBB3 antibody	27196767
	EGFR	CKB	---	GF-1R antibody	27196767
	EGFR	CKB	---	unspeci ied EGFR antibody	27196767
	EGFR	CKB	---	unspeci ied ERBB3 antibody	27196767
	EGFR	CKB	---	unspeci ied GF-1R antibody	27196767
	EGFR	CKB	---	Etoposide	27216155
	EGFR	CKB	---	JNJ-61186372	27216193
	EGFR	CKB	---	Pembrolizumab	27225694
	EGFR	CKB	---	Durvalumab	27225694
	EGFR	CKB	---	Atezolizumab	27225694
	EGFR	CKB	---	EA 045	27251290

EGFR	CKB	---	Amlexanox	27287717
EGFR	CKB	---	Vemura enib	27312529
EGFR	CKB	---	Dabra enib	27312529
EGFR	CKB	---	Encora enib	27312529
EGFR	CKB	---	SCH772984	27312529
EGFR	CKB	---	SHP099	27362227
EGFR	CKB	---	AC0010MA	27573423
EGFR	CKB	---	Savolitinib	27694386
EGFR	CKB	---	NG -1	27694802
EGFR	CKB	---	S63845	27760111
EGFR	CKB	---	PF-431396	27793840
EGFR	CKB	---	PF-573228	27793840
EGFR	CKB	---	cabozantinib	27825638
EGFR	CKB	---	AZD3759	27928026
EGFR	C ViC	---	BR GA N B PAN UMUMAB CE UX MAB	28287083
EGFR	CKB	---	JNJ-42756493	28341788
EGFR	CKB	---	Bevacizumab	28408243
EGFR	CKB	---	Dasatinib	28416483
EGFR	CKB	---	GSK2334470	28416483
EGFR	CKB	---	BKM120	28416483
EGFR	CKB	---	Saracatinib	28416483
EGFR	CKB	---	Bosutinib	28416483
EGFR	CKB	---	PF-573328	28416483
EGFR	CKB	---	AK-632	28416483
EGFR	CKB	---	NC280	28783719
EGFR	CKB	---	Pelitinib	1 671E+15
EGFR	C ViC	---	AEE788	1 82275E+15
EGFR	C ViC	---	LAPA N B	1 84088E+15
EGFR	CG	---	Ge itinib	2 12743E+15
EGFR	CKB	---	rinotecan	2 3209E+15
EGFR	CKB	---	BEZ235	2 36297E+15
EGFR	CKB	---	NPS-1034	2 41652E+15
EGFR	C ViC	---	PAN UMUMAB	2 46536E+15
EGFR	CKB	---	S-222611	2 48373E+15
EGFR	CKB	---	Sapitinib	2 48864E+15
EGFR	CKB	---	Osimertinib	2 58701E+15
EGFR	CKB	---	emozolomide	2 5911E+15
EGFR	CKB	---	MM-151	2 59117E+15
EGFR	C ViC	---	DACOM N B	2 67682E+15
EGFR	OncoKB	---	Osimertinib	2 71984E+15
EGFR	CKB	---	Nivolumab	2 72257E+15
EGFR	CKB	---	Cabozantinib	2 76944E+15
EGFR	CKB	---	AP26113	2 78367E+15
EGFR	CKB	---	N/A	2 83519E+15
EGFR	CKB	---	PF-05212384	1 67317E+23
EGFR	CKB	---	EK -285	1 70857E+23
EGFR	CKB	---	Sora enib	2 36297E+23
EGFR	C ViC	---	ROC LE N B	2 40657E+23
EGFR	CKB	---	PHA-665752	2 41652E+23
EGFR	DoCM	---	S ROL MUS	2 49348E+23
EGFR	CKB	---	Radiotherapy	2 55895E+23
EGFR	CKB	---	Crizotinib	2 75955E+23
EGFR	C ViC	---	EGFR NH B OR	2 2056E+31
EGFR	CKB	---	WZ4002	2 59643E+31
EGFR	CG	---	Cetuximab	2 60594E+31
EGFR	CKB	---	Panitumumab	2 68432E+31
EGFR	CKB	---	SYM004	2 68888E+31
EGFR	CKB	---	Lapatinib	2 75955E+31
EGFR	CKB	---	rametinib	2 87837E+31
EGFR	CKB	---	Selumetinib	2 49391E+39
EGFR	CKB	---	cotinib	2 4533E+46
EGFR	OncoKB	---	Ge itnib	1 4571E+47
EGFR	CKB	---	Neratinib	2 04794E+47
EGFR	C ViC	---	CE UX MAB	2 46536E+55
EGFR	C ViC	---	OS MER N B	2 48939E+55
EGFR	CKB	---	CO1686	2 40657E+63
EGFR	C ViC	---	AFA N B	2 39826E+71
EGFR	CKB	---	Dacomitinib	2 48571E+71
EGFR	CKB	---	Cetuximab	2 7149E+103
EGFR	CKB	---	AZD9291	2 7694E+127
EGFR	C ViC	---	ERLO N B	1 7878E+167
EGFR	C ViC	---	GEF N B	2 35E+175
EGFR	OncoKB	---	A atinib	23371856 20808254 14570950 22370314 15710947 25589191 26051236 25179728 24893891 15638953 23969006 20573926 19692680 23328547 21764376 16187797 24353160 22452895 24285021 23816963 23566546 23816960 22285168 15897572 18676761 24065731 17285735 23912954 15118073 20022809 18408761 26286086 22422421 23749122 25521405 25130612 1867676 19536777 22190593 21949883 19625781 16011858 15737014 21670455 26206867 21531810 18000506 24478319 17686547 21252719

EGFR	OncoKB	---	Erlotinib	23371856 20808254 14570950 22370314 15710947 25589191 26051236 25179728 24893891 15638953 23969006 20573926 19692680 23328547 21764376 16187797 24353160 22452895 24285021 23816963 23566546 23816960 22285168 15897572 18676761 24065731 17285735 23912954 15118073 20022809 18408761 26286086 21422421 23749122 25521405 25130612 1867676 19536777 22190593 21949883 19625781 16011858 22001862 15737014 21670455 26206867 21531810 18000506 24478319 17686547 21252719
EGFR	OncoKB	---	Ge itinib	23371856 20808254 14570950 22370314 15710947 25589191 26051236 25179728 24893891 15638953 23969006 20573926 19692680 23328547 21764376 16187797 24353160 22452895 24285021 23816963 23566546 26980463 23816960 22285168 15897572 18676761 24065731 23912954 15118073 20022809 18408761 26286086 21422421 23749122 25130612 1867676 19536777 22190593 21949883 19625781 28537764 16011858 15737014 21670455 26206867 25070024 21531810 18000506 24478319 17686547 21252719
EGFR	CKB	---	Ge itinib	24533047 27468240 28089594 22789825 26936917 24410791 17463250 19692680 24165158 25964297 27196752 23980091 17085664 27793840 24353160 25573954 25870145 24736073 22263058 18981003 17349580 26561558 26124204 23344264 20942962 24874286 21422421 25948633 22997455 19147750 22323597 27312529 15737014 26206867 25931286 23542356 27612490
EGFR	CKB	---	Erlotinib	26324372 25870087 27468240 28089594 27694386 27102076 27216155 23917401 24410791 26341921 19015641 27760111 26106072 27207775 27793840 24353160 25573954 18981003 17349580 23344264 20942962 25077897 27825638 26286086 27913578 22190593 26720423 19147750 24868098 28408243 26206867 25931286 28343545 17177598 24470557 19010870
EGFR	DoCM	---	AFA N B	26619011 19455431 22452896 23102728 20068085 16707764 17653080 15710947 20479403 25668228 16912157 24893891 15728811 20573926 16258541 19692680 15118125 18227510 24658966 18199554 19922469 20033049 26515464 25923549 21783417 19692684 22753918 16187797 22452895 23945392 15329413 24636847 23816963 24729716 23816960 22285168 19096302 16204070 24894453 16043828 22215752 21194487 24065731 15118073 20022809 23948351 16115929 18458038 17332364 24623981 19147750 25157968 16011858 21430269 2302402 15737014 26720284 21670455 21233402 23242437 25923550 22588155 21531810 18303429 19671738
EGFR	DoCM	---	ERLO N B	26619011 19455431 22452896 23102728 20068085 16707764 17653080 15710947 20479403 25668228 16912157 24893891 15728811 20573926 16258541 19692680 15118125 18227510 24658966 18199554 19922469 20033049 26515464 25923549 21783417 19692684 22753918 16187797 22452895 23945392 15329413 24636847 23816963 24729716 23816960 22285168 19096302 16204070 24894453 16043828 22215752 21194487 24065731 15118073 20022809 23948351 16115929 18458038 17332364 24623981 19147750 25157968 16011858 21430269 2302402 15737014 26720284 21670455 21233402 23242437 17177598 25923550 22588155 21531810 18303429 19671738
EGFR	DoCM	---	CE UX MAB	26619011 19455431 22452896 24934779 23102728 20068085 16707764 17653080 15710947 20479403 25668228 16912157 24893891 15728811 20573926 16258541 19692680 15118125 18227510 24658966 18199554 19922469 20033049 26515464 25923549 21783417 19692684 22753918 16187797 22452895 23945392 15329413 24636847 23816963 24729716 23816960 22285168 19096302 16204070 22270724 24894453 16043828 22215752 21194487 24065731 15118073 20022809 23948351 16115929 18458038 17332364 24623981 19147750 25157968 16011858 21430269 23578570 2302402 15737014 26720284 21670455 21233402 23242437 25923550 22588155 21531810 18303429 19671738 18089823
EGFR	CKB	---	A atinib	28169392 27044931 27694386 27102076 26051236 26354527 26341921 25589492 27083334 25964297 28363995 27207775 28145866 24353160 25559287 25870145 24813888 23816960 17349580 23344264 25077897 26286086 27913578 25948633 22190593 24790411 26206867 23991291 26862733 21617858
EGFR	ALC	inhibitor	AZD8931	---
EGFR	Chembl nteractions	inhibitor	ERLO N B HYDROCHLOR DE	---
EGFR	MyCancerGenomeClinical rial	inhibitor	ERLO N B HYDROCHLOR DE	---
EGFR	Guide oPharmacology nteractions	inhibitor	PP121	---
EGFR	Guide oPharmacology nteractions	inhibitor	AFA N B	---
EGFR	MyCancerGenome	inhibitor	AFA N B	---
EGFR	MyCancerGenomeClinical rial	inhibitor	AFA N B	---
EGFR	ALC	inhibitor	AFA N B	---
EGFR	CG	---	A atinib	---
EGFR	FDA	---	A atinib	---
EGFR	dgClinical rial	---	AFA N B	---
EGFR	MyCancerGenomeClinical rial	inhibitor	B BW 2992	---
EGFR	D	inhibitor	B BW 2992	---
EGFR	CancerCommons	inhibitor	B BW2992	---
EGFR	Guide oPharmacology nteractions	---	BE ACELLUL N	---
EGFR	Chembl nteractions	inhibitor	LAPA N B D OSYLA E	---
EGFR	MyCancerGenomeClinical rial	inhibitor	LAPA N B D OSYLA E	---
EGFR	D	inhibitor	YKERB	---
EGFR	CancerCommons	antibody	CE UX MAB	---
EGFR	Guide oPharmacology nteractions	antibody	CE UX MAB	---
EGFR	MyCancerGenome	antibody	CE UX MAB	---
EGFR	ALC	antibody	CE UX MAB	---
EGFR	D	antibody	CE UX MAB	---
EGFR	Chembl nteractions	inhibitor	CE UX MAB	---
EGFR	ClearityFoundationBiomarkers	---	CE UX MAB	---
EGFR	FDA	---	Cetuximab	---
EGFR	dgClinical rial	---	CE UX MAB	---
EGFR	END	---	CE UX MAB	---
EGFR	END	---	RAS UZUMAB	---
EGFR	ClearityFoundationBiomarkers	---	PAN UMUMAB	---
EGFR	dgClinical rial	---	PAN UMUMAB	---

	EGFR	Guide oPharmacology nteractions	agonist	PAN UMUMAB	---
	EGFR	MyCancerGenome	antibody	PAN UMUMAB	---
	EGFR	ALC	antibody	PAN UMUMAB	---
	EGFR	Chembl nteractions	inhibitor	PAN UMUMAB	---
	EGFR	CG	---	Panitumumab	---
	EGFR	FDA	---	Panitumumab	---
	EGFR	END	---	PAN UMUMAB	---
	EGFR	D	---	PAN UMUMAB	---
	EGFR	Guide oPharmacology nteractions	inhibitor	WZ4002	---
	EGFR	D	inhibitor	PAZOPAN B + YVERB/ YKERB	---
	EGFR	Guide oPharmacology nteractions	---	EGF	---
	EGFR	D	inhibitor	AK165	---
	EGFR	Chembl nteractions	inhibitor	AK-285	---
	EGFR	Chembl nteractions	inhibitor	AC-480	---
	EGFR	dgClinical rial	---	AC480	---
	EGFR	Guide oPharmacology nteractions	inhibitor	BMS-599626	---
	EGFR	MyCancerGenome	inhibitor	BMS-599626	---
EGFR	*EGFR*	ALC	inhibitor	BMS-599626	---
	EGFR	D	inhibitor	BMS-599626	---
	EGFR	Guide oPharmacology nteractions	antibody	NEC UMUMAB	---
	EGFR	MyCancerGenome	antibody	NEC UMUMAB	---
	EGFR	Chembl nteractions	inhibitor	NEC UMUMAB	---
	EGFR	ALC	inhibitor	NEC UMUMAB	---
	EGFR	dgClinical rial	---	NEC UMUMAB	---
	EGFR	Guide oPharmacology nteractions	inhibitor	BP Q-	---
	EGFR	D	inhibitor	HK -272	---
	EGFR	Chembl nteractions	inhibitor	NERA N B	---
	EGFR	Guide oPharmacology nteractions	inhibitor	NERA N B	---
	EGFR	ALC	inhibitor	NERA N B	---
	EGFR	dgClinical rial	---	NERA N B	---
	EGFR	Guide oPharmacology nteractions	inhibitor	BRU N B	---
	EGFR	Guide oPharmacology nteractions	inhibitor	COMPOUND 56 [PM D 8568816	---
	EGFR	Guide oPharmacology nteractions	inhibitor	PF-670462	---
	EGFR	Chembl nteractions	inhibitor	PK -166	---
	EGFR	Guide oPharmacology nteractions	inhibitor	PK 166	---
	EGFR	Chembl nteractions	inhibitor	CEP-32496	---
	EGFR	Guide oPharmacology nteractions	inhibitor	CO N B	---
	EGFR	MyCancerGenome	inhibitor	CO N B	---
	EGFR	MyCancerGenomeClinical rial	inhibitor	CO N B	---
	EGFR	ALC	inhibitor	CO N B	---
	EGFR	Chembl nteractions	inhibitor	VARL N B	---
	EGFR	Chembl nteractions	inhibitor	AFA N B D MALEA E	---
	EGFR	Chembl nteractions	inhibitor	DACOM N B HYDRA E	---
	EGFR	dgClinical rial	---	HUMAX-EGFR	---
	EGFR	Chembl nteractions	antagonist	ZALU UMUMAB	---
	EGFR	ALC	antibody	ZALU UMUMAB	---
	EGFR	dgClinical rial	---	R NDOPEP MU	---
	EGFR	Chembl nteractions	inhibitor	MA UZUMAB	---
	EGFR	D	activator	HEGF	---
	EGFR	MyCancerGenome	antibody	N MO UZUMAB	---
	EGFR	ALC	antibody	N MO UZUMAB	---
	EGFR	CG	---	Nimotuzumab	---
	EGFR	dgClinical rial	---	N MO UZUMAB	---
	EGFR	MyCancerGenome	antibody	SYM004	---
	EGFR	dgClinical rial	---	SYM004	---
	EGFR	MyCancerGenome	antibody	RO5083945	---
	EGFR	ALC	antibody	RO5083945	---
	EGFR	Chembl nteractions	inhibitor	mAb-425	---
	EGFR	Chembl nteractions	---	MDX-447	---
	EGFR	Chembl nteractions	antagonist	RG-7160	---
	EGFR	Chembl nteractions	inhibitor	DACOM N B	---
	EGFR	Guide oPharmacology nteractions	inhibitor	DACOM N B	---
	EGFR	MyCancerGenome	inhibitor	DACOM N B	---
	EGFR	MyCancerGenomeClinical rial	inhibitor	DACOM N B	---
	EGFR	ALC	inhibitor	DACOM N B	---
	EGFR	dgClinical rial	---	DACOM N B	---
	EGFR	CancerCommons	inhibitor	PF-00299804	---
	EGFR	ALC	inhibitor	AEE 788	---
	EGFR	Guide oPharmacology nteractions	---	EP REGUL N	---
	EGFR	Chembl nteractions	inhibitor	SAP N B	---
	EGFR	Guide oPharmacology nteractions	inhibitor	SAP N B	---

EGFR	Chembl nteractions	inhibitor	VANDE AN B	---
EGFR	Guide oPharmacology nteractions	inhibitor	VANDE AN B	---
EGFR	MyCancerGenome	inhibitor	VANDE AN B	---
EGFR	MyCancerGenomeClinical rial	inhibitor	VANDE AN B	---
EGFR	ALC	inhibitor	VANDE AN B	---
EGFR	D	inhibitor	VANDE AN B	---
EGFR	ClearityFoundationBiomarkers	---	VANDE AN B	---
EGFR	ClearityFoundationClinical rial	---	VANDE AN B	---
EGFR	dgClinical rial	---	VANDE AN B	---
EGFR	CKB	---	MGCD265	---
EGFR	Chembl nteractions	inhibitor	FALN DAMOL	---
EGFR	Guide oPharmacology nteractions	inhibitor	FALN DAMOL	---
EGFR	Guide oPharmacology nteractions	inhibitor	ORAN N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	PP1	---
EGFR	ALC	antibody	MEHD7945 A	---
EGFR	MyCancerGenome	antibody	MEHD7945A	---
EGFR	Guide oPharmacology nteractions	inhibitor	CANER N B	---
EGFR	MyCancerGenome	inhibitor	CANER N B	---
EGFR	Chembl nteractions	inhibitor	OS MER N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	OS MER N B	---
EGFR	MyCancerGenome	inhibitor	OS MER N B	---
EGFR	CG	---	Osimertinib	---
EGFR	FDA	---	Osimertinib	---
EGFR	Chembl nteractions	inhibitor	Pyrotinib	---
EGFR	Chembl nteractions	inhibitor	ESEVA N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	ESEVA N B	---
EGFR	MyCancerGenome	inhibitor	XL647	---
EGFR	ALC	inhibitor	XL647	---
EGFR	dgClinical rial	---	XL647	---
EGFR	Chembl nteractions	inhibitor	MP-412	---
EGFR	Chembl nteractions	inhibitor	OS MER N B MESYLA E	---
EGFR	Chembl nteractions	inhibitor	Puquitinib	---
EGFR	Chembl nteractions	inhibitor	Epitinib	---
EGFR	CKB	---	Epitinib	---
EGFR	Chembl nteractions	inhibitor	JNJ-26483327	---
EGFR	Chembl nteractions	inhibitor	Poziotinib	---
EGFR	Guide oPharmacology nteractions	inhibitor	POZ O N B	---
EGFR	MyCancerGenomeClinical rial	inhibitor	POZ O N B	---
EGFR	CKB	---	poziotinib	---
EGFR	Chembl nteractions	inhibitor	heliatinib	---
EGFR	Chembl nteractions	inhibitor	PD-0166285	---
EGFR	Chembl nteractions	inhibitor	S-222611	---
EGFR	D	inhibitor	S-222611	---
EGFR	Chembl nteractions	inhibitor	EGF816	---
EGFR	Chembl nteractions	inhibitor	Simotinib	---
EGFR	Chembl nteractions	inhibitor	Allitinib	---
EGFR	Guide oPharmacology nteractions	inhibitor	BGB-283	---
EGFR	ALC	inhibitor	CO 1686	---
EGFR	MyCancerGenome	inhibitor	CO-1686	---
EGFR	Chembl nteractions	inhibitor	ROC LE N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	ROC LE N B	---
EGFR	CG	---	Rociletinib	---
EGFR	MyCancerGenomeClinical rial	inhibitor	AP26113	---
EGFR	ALC	inhibitor	AP26113	---
EGFR	Chembl nteractions	inhibitor	BR GA N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	BR GA N B	---
EGFR	Chembl nteractions	inhibitor	BMS-690514	---
EGFR	Guide oPharmacology nteractions	inhibitor	BMS-690514	---
EGFR	MyCancerGenome	inhibitor	BMS-690514	---
EGFR	ALC	inhibitor	BMS-690514	---
EGFR	Chembl nteractions	inhibitor	HM-61713	---
EGFR	CKB	---	ASP8273	---
EGFR	Guide oPharmacology nteractions	inhibitor	NAQUO N B	---
EGFR	MyCancerGenome	antibody	AB -806	---
EGFR	Guide oPharmacology nteractions	inhibitor	ACALABRU N B	---
EGFR	CG	---	HM61713	---
EGFR	CKB	---	HM61713	---
EGFR	Guide oPharmacology nteractions	inhibitor	OLMU N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	EGFR NH B OR	---
EGFR	CG	---	Sirolimus	---
EGFR	Chembl nteractions	inhibitor	AZD-4769	---

EGFR	D	inhibitor	AZD4769	---
EGFR	Guide oPharmacology nteractions	inhibitor	DOV N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	PD 158780	---
EGFR	Chembl nteractions	inhibitor	CANER N B D HYDROCHLOR DE	---
EGFR	CancerCommons	inhibitor	ERLO N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	ERLO N B	---
EGFR	MyCancerGenome	inhibitor	ERLO N B	---
EGFR	ALC	inhibitor	ERLO N B	---
EGFR	D	inhibitor	ERLO N B	---
EGFR	CG	---	Erlotinib	---
EGFR	ClearityFoundationBiomarkers	---	ERLO N B	---
EGFR	ClearityFoundationClinical rial	---	ERLO N B	---
EGFR	FDA	---	Erlotinib	---
EGFR	dgClinical rial	---	ERLO N B	---
EGFR	END	---	ERLO N B	---
EGFR	ClearityFoundationClinical rial	---	LAPA N B	---
EGFR	CancerCommons	inhibitor	LAPA N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	LAPA N B	---
EGFR	ALC	inhibitor	LAPA N B	---
EGFR	D	inhibitor	LAPA N B	---
EGFR	CG	---	Lapatinib	---
EGFR	dgClinical rial	---	LAPA N B	---
EGFR	END	---	LAPA N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	AG 490	---
EGFR	Chembl nteractions	inhibitor	AEE-788	---
EGFR	Guide oPharmacology nteractions	inhibitor	AEE788	---
EGFR	MyCancerGenome	inhibitor	AEE788	---
EGFR	Chembl nteractions	inhibitor	CUDC-101	---
EGFR	Guide oPharmacology nteractions	inhibitor	CUDC-101	---
EGFR	ALC	inhibitor	CUDC-101	---
EGFR	dgClinical rial	---	CUDC-101	---
EGFR	Chembl nteractions	inhibitor	PEL N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	PEL N B	---
EGFR	MyCancerGenome	inhibitor	PEL N B	---
EGFR	ALC	inhibitor	PEL N B	---
EGFR	D	activator	DWP-401	---
EGFR	dgClinical rial	---	L DOCA NE	---
EGFR	Guide oPharmacology nteractions	inhibitor	AG1478	---
EGFR	Chembl nteractions	inhibitor	GEF N B	---
EGFR	Guide oPharmacology nteractions	inhibitor	GEF N B	---
EGFR	MyCancerGenome	inhibitor	GEF N B	---
EGFR	MyCancerGenomeClinical rial	inhibitor	GEF N B	---
EGFR	D	inhibitor	GEF N B	---
EGFR	ClearityFoundationBiomarkers	---	GEF N B	---
EGFR	FDA	---	Ge itinib	---
EGFR	dgClinical rial	---	GEF N B	---
EGFR	END	---	GEF N B	---
EGFR	ALC	inhibitor	GEF N B RESSA	---
EGFR	CancerCommons	inhibitor	GELF N B	---
EGFR	CKB	---	ABBV-221	---
EGFR	CKB	---	AFM24	---
EGFR	Guide oPharmacology nteractions	inhibitor	AG 112	---
EGFR	Guide oPharmacology nteractions	inhibitor	AG 9	---
EGFR	ClearityFoundationClinical rial	---	AKOS004227608	---
EGFR	dgClinical rial	---	AL -110	---
EGFR	Guide oPharmacology nteractions	---	AMPH REGUL N	---
EGFR	D	antibody	AN -HER3/EGFR DAF	---
EGFR	CKB	---	AP32788	---
EGFR	dgClinical rial	---	ARRY-334543	---
EGFR	dgClinical rial	---	AV-412	---
EGFR	CKB	---	AV D100	---
EGFR	MyCancerGenome	inhibitor	AZD8931	---
EGFR	D	inhibitor	BEVAC ZUMAB+ERLO N B	---
EGFR	D	inhibitor	C -1033	---
EGFR	Guide oPharmacology nteractions	inhibitor	COMPOUND 38 [PM D 24915291	---
EGFR	CKB	---	DS-1205b	---
EGFR	Guide oPharmacology nteractions	inhibitor	EGFR/ERBB-2 NH B OR	---
EGFR	Guide oPharmacology nteractions	inhibitor	EGFR/ERBB-2/ERBB-4 NH B OR	---
EGFR	Guide oPharmacology nteractions	---	EP GEN	---
EGFR	D	inhibitor	ERLO N B+BEVAC ZUMAB	---

	EGFR	Guide oPharmacology nteractions	---	HB-EGF	---
	EGFR	Guide oPharmacology nteractions	inhibitor	JAK3 NH B OR	---
	EGFR	dgClinical rial	---	MDX-214	---
	EGFR	Guide oPharmacology nteractions	antibody	MM-151	---
	EGFR	MyCancerGenome	antibody	MM-151	---
	EGFR	ALC	antibody	MM151	---
	EGFR	Guide oPharmacology nteractions	inhibitor	NAZAR N B	---
	EGFR	Guide oPharmacology nteractions	inhibitor	PD 174265	---
	EGFR	Guide oPharmacology nteractions	inhibitor	PD166285	---
	EGFR	D	inhibitor	PF-299804	---
	EGFR	Guide oPharmacology nteractions	inhibitor	ARLOXO N B	---
	EGFR	Guide oPharmacology nteractions	---	GFŒ±	---
	EGFR	CKB	---	H-4000	---
	EGFR	D	inhibitor	YVERB/ YKERB	---
	EGFR	D	inhibitor	XL647	---
	EGFR	Guide oPharmacology nteractions	inhibitor	ZM-306416	---
	F2RL1	NC	---	MACROL DES	18212111
	F2RL1	Guide oPharmacology nteractions	agonist	RANS-C NNAMOYL-L GRLO [N-[3H PROP ONYL -NH2	---
	F2RL1	Guide oPharmacology nteractions	agonist	AC-55541	---
	F2RL1	Guide oPharmacology nteractions	agonist	AC-98170	---
	F2RL1	Guide oPharmacology nteractions	agonist	2-FUROYL-L GRLO-AM DE	---
	F2RL1	Guide oPharmacology nteractions	agonist	GB110	---
	F2RL1	Guide oPharmacology nteractions	agonist	AC264613	---
	F2RL1	Guide oPharmacology nteractions	agonist	[3H 2-FUROYL-L GRL-NH2	---
	F2RL1	Guide oPharmacology nteractions	agonist	2-FUROYL-L GRL[N-(ALEXA FLUOR 594)-O -NH2	---
F2RL1	*F2RL1*	Guide oPharmacology nteractions	agonist	2-FUROYL-L GRL[N[3H PROP ONYL -O-NH2	---
	F2RL1	Guide oPharmacology nteractions	agonist	AY77	---
	F2RL1	Guide oPharmacology nteractions	allosteric mo	AZ3451	---
	F2RL1	Guide oPharmacology nteractions	antagonist	AZ7188	---
	F2RL1	Guide oPharmacology nteractions	antagonist	AZ8838	---
	F2RL1	Guide oPharmacology nteractions	antagonist	C391	---
	F2RL1	Guide oPharmacology nteractions	antagonist	GB88	---
	F2RL1	Guide oPharmacology nteractions	antagonist	P2PAL18S	---
	F2RL1	Guide oPharmacology nteractions	agonist	SL GKV-NH2	---
	F2RL1	Guide oPharmacology nteractions	agonist	SL GRL-NH2	---
ITGA3	*ITGA3*	Guide oPharmacology nteractions	---	PEP DE L GAND 2 [PM D 19055415	---
	ITGB1	Guide oPharmacology nteractions	antibody	NA AL ZUMAB	---
	ITGB1	Chembl nteractions	inhibitor	NA AL ZUMAB	---
	ITGB1	ALC	antibody	V AX N	---
	ITGB1	Chembl nteractions	antagonist	N E UMUMAB	---
	ITGB1	dgClinical rial	---	R1295	---
	ITGB1	Chembl nteractions	antagonist	F RA EGRAS	---
	ITGB1	dgClinical rial	---	F RA EGRAS	---
	ITGB1	dgClinical rial	---	AN HYMOCY E GLOBUL N	---
	ITGB1	D	antagonist	R411	---
	ITGB1	Chembl nteractions	antagonist	VOLOC X MAB	---
	ITGB1	ALC	antibody	VOLOC X MAB	---
	ITGB1	dgClinical rial	---	VOLOC X MAB	---
	ITGB1	Chembl nteractions	inhibitor	D 17E6	---
ITGB1	*ITGB1*	ALC	antibody	PF-04605412	---
	ITGB1	Guide oPharmacology nteractions	inhibitor	B O1211	---
	ITGB1	dgClinical rial	---	A L1102	---
	ITGB1	dgClinical rial	---	F200	---
	ITGB1	dgClinical rial	---	GLPG0187	---
	ITGB1	D	antagonist	JSM 6427	---
	ITGB1	dgClinical rial	---	JSM 6427	---
	ITGB1	Guide oPharmacology nteractions	inhibitor	OB US A N	---
	ITGB1	dgClinical rial	---	SAN-300	---

	ITGB1	Guide oPharmacology nteractions	inhibitor	C 15	---
	ITGB1	Guide oPharmacology nteractions	inhibitor	CS2314	---
KRT19	*KRT19*	NC	---	PD-98059	15793288
	KRT19	NC	---	DEXAME HASONE	15793288
LAMB1	*LAMB1*	NC	---	HEPARAN SULFA E	8873769
	LAMB1	Chembl nteractions	---	OCR PLASM N	---
LIF	*LIF*	NC	---	L-1	1908322
	LIF	NC	---	RE NO C AC D	2119291
	LIF	NC	---	HROMB N	7007650
	LIF	NC	---	DEXAME HASONE	8392465
	LIF	NC	---	CAPSA C N	9138695
	LIF	NC	---	OES RAD OL	10508216
	LIF	NC	---	DA DZE N	10508216
	LIF	NC	---	M FEPR S ONE	10717784
	LIF	NC	---	BUP VACA NE	10838161
	LIF	NC	---	AN SENSE OL GONUCLEO DES	10843995
	LIF	NC	---	HORMONES	11589623
	LIF	NC	---	PACL AXEL	11800022
	LIF	NC	---	CLOM PHENE C RA E	12012626
	LIF	NC	---	AZACY D NE	12543079
	LIF	NC	---	L-13	12620497
	LIF	NC	---	5-AZA-2&APOS -DEOXYCY D NE	14647063
	LIF	NC	---	S MVAS A N	16797728
	LIF	NC	---	HUMAN CHOR ON C GONADO ROP N	9 76435E+14
	LIF	NC	---	C SPLA N	1 18E+15
PLAU	*PLAU*	NC	---	RE NOL	1576255
	PLAU	NC	---	ONOMYC N	1701176
	PLAU	NC	---	COR SOL	2115769
	PLAU	NC	---	NORD HYDROGUA ARE C AC D	2122915
	PLAU	NC	---	DEX RAN SULFA E	2465792
	PLAU	NC	---	17 BE A-ES RAD OL	2492346
	PLAU	NC	---	PHOSPHOD ES ERASE NH B OR	3021458
	PLAU	NC	---	CALC R OL	3139763
	PLAU	NC	---	PRO E N K NASE C NH B OR	7684044
	PLAU	NC	---	L F	7782459
	PLAU	NC	---	D FFEREN A ON NDUCER	8595156
	PLAU	NC	---	BCNU	9219734
	PLAU	NC	---	C SPLA N	9219734
	PLAU	NC	---	RAZOXANE	9378540
	PLAU	NC	---	DACARBAZ NE	9378540
	PLAU	NC	---	AN OX DAN	9573532
	PLAU	NC	---	VERAPAM L	9579573
	PLAU	NC	---	PRO E N K NASE NH B OR	9579573
	PLAU	NC	---	OES RAD OL	9662256
	PLAU	NC	---	AZACY D NE	10209960
	PLAU	NC	---	RAN ES	10559777
	PLAU	NC	---	RAPAMYC N	11245436
	PLAU	NC	---	HERB MYC N A	11245436
	PLAU	NC	---	YROS NE K NASE NH B OR	11245436
	PLAU	NC	---	RU 486	11742418
	PLAU	NC	---	B SPHOSPHONA ES	11984068
	PLAU	NC	---	ALENDRONA E	11984068
	PLAU	NC	---	ZOLEDRONA E	11984068
	PLAU	NC	---	CLODRONA E	11984068
	PLAU	NC	---	R CHOS A N A	12198113
	PLAU	NC	---	AN NFLAMMA ORY DRUGS	12234061
	PLAU	NC	---	GELDANAMYC N	12724357
	PLAU	NC	---	AN B O C	12724357
	PLAU	NC	---	PAPAVER NE	16099300
	PLAU	NC	---	CELECOX B	16172791
	PLAU	NC	---	BLM	16224526
	PLAU	NC	---	RESSA	16263158
	PLAU	NC	---	G-CSF	16331631
	PLAU	NC	---	PMSG	2 50665E+13
	PLAU	Guide oPharmacology nteractions	inhibitor	WX-UK1	---
	PLAU	dgClinical rial	---	WX-UK1	---
	PLAU	Guide oPharmacology nteractions	inhibitor	UK-356202	---
	PLAU	dgClinical rial	---	UROK NASE	---
	PLAU	D	activator	AMED PLASE	---
	PLAU	Guide oPharmacology nteractions	inhibitor	COMPOUND 4 [PM D 18163548	---
	PLAU	dgClinical rial	---	MRX-801	---
	PLAU	Guide oPharmacology nteractions	inhibitor	UPAMOS A	---
	PLAU	dgClinical rial	---	WX-671	---
PSMA3	*PSMA3*	Chembl nteractions	inhibitor	OPROZOM B	---
	PSMA3	Chembl nteractions	inhibitor	BOR EZOM B	---
	PSMA3	MyCancerGenome	inhibitor	BOR EZOM B	---
	PSMA3	Chembl nteractions	inhibitor	XAZOM B C RA E	---

	PSMA3	Chembl nteractions	inhibitor	MAR ZOM B	---
	PSMA3	Chembl nteractions	inhibitor	CARF LZOM B	---
	PSMA3	MyCancerGenome	inhibitor	CARF LZOM B	---
PSMC6	*PSMC6*	Chembl nteractions	inhibitor	OPROZOM B	---
	PSMC6	Chembl nteractions	inhibitor	BOR EZOM B	---
	PSMC6	MyCancerGenome	inhibitor	BOR EZOM B	---
	PSMC6	Chembl nteractions	inhibitor	XAZOM B C RA E	---
	PSMC6	Chembl nteractions	inhibitor	CARF LZOM B	---
	PSMC6	MyCancerGenome	inhibitor	CARF LZOM B	---
PYGB	*PYGB*	D	inhibitor	PSN357	---
	PYGB	dgClinical rial	---	PSN357	---
TUBB	*TUBB*	Chembl nteractions	inhibitor	COLCH C NE	---
	TUBB	Guide oPharmacology nteractions	inhibitor	COLCH C NE	---
	TUBB	Chembl nteractions	inhibitor	PL NABUL N	---
	TUBB	Chembl nteractions	inhibitor	CABAZ AXEL	---
	TUBB	Guide oPharmacology nteractions	inhibitor	CABAZ AXEL	---
	TUBB	Chembl nteractions	inhibitor	XABEP LONE	---
	TUBB	Guide oPharmacology nteractions	inhibitor	XABEP LONE	---
	TUBB	Guide oPharmacology nteractions	inhibitor	V NBLAS NE	---
	TUBB	Chembl nteractions	inhibitor	ER BUL N MESYLA E	---
	TUBB	Guide oPharmacology nteractions	inhibitor	ER BUL N	---
	TUBB	Chembl nteractions	inhibitor	BREN UX MAB VEDO N	---
	TUBB	Chembl nteractions	inhibitor	RAS UZUMAB EM ANS NE	---
	TUBB	Chembl nteractions	---	DAVUNE DE	---
	TUBB	Chembl nteractions	inhibitor	CROL BUL N	---
	TUBB	Chembl nteractions	---	FOSBRE ABUL N ROME HAM NE	---
	TUBB	Chembl nteractions	---	PACL AXEL POL GLUMEX	---
	TUBB	Chembl nteractions	inhibitor	V NFLUN NE	---
	TUBB	Chembl nteractions	---	SAGOP LONE	---
	TUBB	Chembl nteractions	inhibitor	FOSBRE ABUL N D SOD UM	---
	TUBB	Chembl nteractions	inhibitor	DOCE AXEL HYDRA E	---
	TUBB	Chembl nteractions	inhibitor	V NBLAS NE SULFA E	---
	TUBB	Chembl nteractions	inhibitor	PACL AXEL	---
	TUBB	Guide oPharmacology nteractions	inhibitor	PACL AXEL	---
	TUBB	Chembl nteractions	---	VERUBUL N	---
	TUBB	Chembl nteractions	inhibitor	ND BUL N	---
	TUBB	Chembl nteractions	inhibitor	V NCR S NE SULFA E	---
	TUBB	Chembl nteractions	inhibitor	V NORELB N D AR RA E	---
	TUBB	Chembl nteractions	inhibitor	LEX BUL N	---
	TUBB	Guide oPharmacology nteractions	inhibitor	V NCR S NE	---
	TUBB	Guide oPharmacology nteractions	inhibitor	DOCE AXEL	---

Gene Ontology ID	Term	Ont	N	DE	P.DE
GO 0008150	biological process	BP	9721	1610	4 92E-07
GO 0009987	cellular process	BP	9039	1512	7 49E-07
GO 0008152	metabolic process	BP	7168	1187	0 00961494
GO 0065007	biological regulation	BP	6726	1173	4 65E-08
GO 0071704	organic substance metabolic process	BP	6867	1147	0 00310563
GO 0044237	cellular metabolic process	BP	6810	1131	0 00924209
GO 0044238	primary metabolic process	BP	6647	1116	0 00170217
GO 0050789	regulation of biological process	BP	6363	1114	9 88E-08
GO 0006807	nitrogen compound metabolic process	BP	6403	1083	0 00064792
GO 0050794	regulation of cellular process	BP	5986	1057	5 39E-08
GO 0043170	macromolecule metabolic process	BP	5920	1015	0 00012943
GO 0044260	cellular macromolecule metabolic process	BP	5276	921	2 12E-05
GO 0050896	response to stimulus	BP	4838	825	0 00298664
GO 0071840	cellular component organization or biogenesis	BP	4312	773	3 73E-06
GO 0016043	cellular component organization	BP	4153	751	1 39E-06
GO 0034641	cellular nitrogen compound metabolic process	BP	4345	749	0 00170027
GO 0019222	regulation of metabolic process	BP	4152	736	4 83E-05
GO 1901564	organonitrogen compound metabolic process	BP	4384	735	0 03176763
GO 1901360	organic cyclic compound metabolic process	BP	4102	711	0 00134939
GO 0006725	cellular aromatic compound metabolic process	BP	3989	697	0 00061297
GO 0051716	cellular response to stimulus	BP	4027	692	0 00421834
GO 0031323	regulation of cellular metabolic process	BP	3824	691	6 54E-06
GO 0046483	heterocycle metabolic process	BP	3973	691	0 00114264
GO 0060255	regulation of macromolecule metabolic process	BP	3821	690	7 41E-06
GO 0006139	nucleobase-containing compound metabolic process	BP	3888	681	0 00056452
GO 0080090	regulation of primary metabolic process	BP	3729	680	2 03E-06
GO 0009058	biosynthetic process	BP	4005	679	0 01669311
GO 1901576	organic substance biosynthetic process	BP	3970	674	0 01527959
GO 0044249	cellular biosynthetic process	BP	3912	667	0 01097478
GO 0051171	regulation of nitrogen compound metabolic process	BP	3624	666	8 43E-07
GO 0048518	positive regulation of biological process	BP	3597	660	1 28E-06
GO 0051179	localization	BP	3839	645	0 04098004
GO 0019538	protein metabolic process	BP	3717	643	0 00340821
GO 0032501	multicellular organismal process	BP	3639	623	0 01056772
GO 0010467	gene expression	BP	3579	611	0 01457396
GO 0090304	nucleic acid metabolic process	BP	3445	610	0 00042955
GO 0048522	positive regulation of cellular process	BP	3251	605	6 59E-07
GO 0044267	cellular protein metabolic process	BP	3432	603	0 00109426
GO 0032502	developmental process	BP	3356	593	0 00068714
GO 0048519	negative regulation of biological process	BP	3227	570	0 00097324
GO 0023052	signaling	BP	3317	559	0 04919217
GO 0009059	macromolecule biosynthetic process	BP	3237	556	0 01332922
GO 0044271	cellular nitrogen compound biosynthetic process	BP	3199	547	0 01982119
GO 0048856	anatomical structure development	BP	3115	546	0 00271127
GO 0034645	cellular macromolecule biosynthetic process	BP	3159	545	0 01032857
GO 0016070	RNA metabolic process	BP	3052	533	0 00428634
GO 0048523	negative regulation of cellular process	BP	2860	528	1 51E-05
GO 0043412	macromolecule modification	BP	2845	524	2 20E-05
GO 0006996	organelle organization	BP	2763	523	6 88E-07
GO 0006464	cellular protein modification process	BP	2693	499	1 96E-05
GO 0036211	protein modification process	BP	2693	499	1 96E-05
GO 0010468	regulation of gene expression	BP	2810	490	0 00737702
GO 0009889	regulation of biosynthetic process	BP	2649	489	3 80E-05
GO 0007275	multicellular organism development	BP	2835	489	0 01622677
GO 1901362	organic cyclic compound biosynthetic process	BP	2792	487	0 0074291
GO 0031326	regulation of cellular biosynthetic process	BP	2598	481	3 30E-05
GO 0018130	heterocycle biosynthetic process	BP	2711	477	0 00423476
GO 0019438	aromatic compound biosynthetic process	BP	2706	475	0 00519021
GO 0019219	regulation of nucleobase-containing compound metabolic process	BP	2560	471	8 06E-05
GO 0010556	regulation of macromolecule biosynthetic process	BP	2521	466	5 53E-05
GO 0034654	nucleobase-containing compound biosynthetic process	BP	2665	466	0 00757368
GO 2000112	regulation of cellular macromolecule biosynthetic process	BP	2448	450	0 00013681
GO 0048731	system development	BP	2547	441	0 01826338
GO 0009893	positive regulation of metabolic process	BP	2282	432	1 04E-05
GO 0051252	regulation of RNA metabolic process	BP	2357	427	0 00078296
GO 0048869	cellular developmental process	BP	2278	421	0 0001512
GO 0006950	response to stress	BP	2344	420	0 00210278
GO 0044085	cellular component biogenesis	BP	2236	416	9 06E-05
GO 0010604	positive regulation of macromolecule metabolic process	BP	2125	411	1 90E-06
GO 0032774	RNA biosynthetic process	BP	2295	410	0 00300744
GO 0097659	nucleic acid-templated transcription	BP	2286	408	0 00330987
GO 0006351	transcription DNA-templated	BP	2255	402	0 0038823
GO 0031325	positive regulation of cellular metabolic process	BP	2107	401	1 45E-05
GO 0051173	positive regulation of nitrogen compound metabolic process	BP	2026	398	5 26E-07
GO 0030154	cell differentiation	BP	2139	391	0 00069902
GO 2001141	regulation of RNA biosynthetic process	BP	2165	389	0 00264751
GO 1903506	regulation of nucleic acid-templated transcription	BP	2162	388	0 00292067
GO 0022607	cellular component assembly	BP	2026	383	4 58E-05
GO 0051641	cellular localization	BP	2062	383	0 00021937
GO 0006355	regulation of transcription DNA-templated	BP	2121	377	0 00641805
GO 0033036	macromolecule localization	BP	2102	375	0 00518334
GO 0008104	protein localization	BP	1902	345	0 00264066
GO 0065009	regulation of molecular function	BP	1881	341	0 00291275
GO 0009892	negative regulation of metabolic process	BP	1920	341	0 01018677

GO 0051246	regulation of protein metabolic process	BP	1763	324	0 00157384
GO 0010605	negative regulation of macromolecule metabolic process	BP	1775	316	0 01185103
GO 0031324	negative regulation of cellular metabolic process	BP	1647	312	0 00024058
GO 0032268	regulation of cellular protein metabolic process	BP	1649	305	0 0014711
GO 0051128	regulation of cellular component organization	BP	1639	299	0 00380902
GO 0035556	intracellular signal transduction	BP	1687	296	0 02959923
GO 0007049	cell cycle	BP	1344	293	1 08E-09
GO 0051172	negative regulation of nitrogen compound metabolic process	BP	1543	290	0 00070774
GO 0051649	establishment of localization in cell	BP	1590	287	0 00819669
GO 0043933	protein-containing complex subunit organization	BP	1569	282	0 01091449
GO 0045184	establishment of protein localization	BP	1481	267	0 01141108
GO 0070727	cellular macromolecule localization	BP	1402	265	0 0008778
GO 0034613	cellular protein localization	BP	1392	264	0 0007295
GO 0051704	multi-organism process	BP	1381	263	0 00057697
GO 0050790	regulation of catalytic activity	BP	1447	263	0 0080913
GO 0033554	cellular response to stress	BP	1454	263	0 01026301
GO 0009653	anatomical structure morphogenesis	BP	1452	262	0 01169637
GO 0032879	regulation of localization	BP	1471	257	0 04896785
GO 0065003	protein-containing complex assembly	BP	1343	255	0 00084707
GO 0046907	intracellular transport	BP	1394	249	0 02169567
GO 0007399	nervous system development	BP	1285	245	0 000849
GO 0008219	cell death	BP	1384	244	0 03877728
GO 0009891	positive regulation of biosynthetic process	BP	1292	237	0 00775061
GO 0031328	positive regulation of cellular biosynthetic process	BP	1278	236	0 00572793
GO 0010628	positive regulation of gene expression	BP	1279	235	0 00741477
GO 0012501	programmed cell death	BP	1306	232	0 03263183
GO 0010557	positive regulation of macromolecule biosynthetic process	BP	1232	231	0 00294542
GO 0044093	positive regulation of molecular function	BP	1123	230	1 31E-05
GO 0045935	positive regulation of nucleobase-containing compound metabolic	BP	1257	226	0 02177913
GO 0006915	apoptotic process	BP	1231	225	0 01105068
GO 0048468	cell development	BP	1144	224	0 00031847
GO 0006928	movement of cell or subcellular component	BP	1094	219	9 74E-05
GO 0051247	positive regulation of protein metabolic process	BP	1055	218	1 23E-05
GO 0031399	regulation of protein modification process	BP	1142	218	0 00156764
GO 0008283	cell proliferation	BP	1189	217	0 01331583
GO 0006468	protein phosphorylation	BP	1146	212	0 00808234
GO 0022402	cell cycle process	BP	976	209	1 54E-06
GO 0009890	negative regulation of biosynthetic process	BP	1039	203	0 00069631
GO 0031327	negative regulation of cellular biosynthetic process	BP	1023	202	0 00040444
GO 0032270	positive regulation of cellular protein metabolic process	BP	992	201	9 45E-05
GO 0051254	positive regulation of RNA metabolic process	BP	1124	200	0 04298421
GO 0045934	negative regulation of nucleobase-containing compound metaboli	BP	985	197	0 00023637
GO 0009057	macromolecule catabolic process	BP	1054	195	0 0108828
GO 0010558	negative regulation of macromolecule biosynthetic process	BP	988	194	0 0007106
GO 1902680	positive regulation of RNA biosynthetic process	BP	1058	194	0 01574449
GO 0030030	cell projection organization	BP	915	193	1 11E-05
GO 1903508	positive regulation of nucleic acid-templated transcription	BP	1057	193	0 01877098
GO 0051276	chromosome organization	BP	915	192	1 64E-05
GO 0010941	regulation of cell death	BP	1044	192	0 01450714
GO 0007010	cytoskeleton organization	BP	874	191	1 12E-06
GO 0022008	neurogenesis	BP	877	190	2 19E-06
GO 0051174	regulation of phosphorus metabolic process	BP	1047	190	0 02455805
GO 0120036	plasma membrane bounded cell projection organization	BP	894	189	1 19E-05
GO 0019220	regulation of phosphate metabolic process	BP	1045	189	0 02803232
GO 0040011	locomotion	BP	965	188	0 00127136
GO 0051726	regulation of cell cycle	BP	870	185	1 03E-05
GO 2000113	negative regulation of cellular macromolecule biosynthetic process	BP	944	184	0 00139846
GO 0043085	positive regulation of catalytic activity	BP	905	183	0 0002215
GO 0045893	positive regulation of transcription DNA-templated	BP	987	182	0 01549504
GO 0048699	generation of neurons	BP	819	181	1 02E-06
GO 0042981	regulation of apoptotic process	BP	961	180	0 00881524
GO 0043067	regulation of programmed cell death	BP	975	180	0 01534298
GO 0033043	regulation of organelle organization	BP	907	179	0 00089731
GO 0051240	positive regulation of multicellular organismal process	BP	916	173	0 00735515
GO 0051253	negative regulation of RNA metabolic process	BP	886	172	0 00238964
GO 0044265	cellular macromolecule catabolic process	BP	916	171	0 01196775
GO 0000278	mitotic cell cycle	BP	760	169	1 61E-06
GO 0042325	regulation of phosphorylation	BP	918	168	0 02533063
GO 1901565	organonitrogen compound catabolic process	BP	896	164	0 02679439
GO 0030182	neuron differentiation	BP	737	162	5 48E-06
GO 0048870	cell motility	BP	843	160	0 00814397
GO 0051674	localization of cell	BP	843	160	0 00814397
GO 0001932	regulation of protein phosphorylation	BP	839	158	0 01132783
GO 0034622	cellular protein-containing complex assembly	BP	838	157	0 01386503
GO 1902679	negative regulation of RNA biosynthetic process	BP	821	156	0 00856589
GO 1903507	negative regulation of nucleic acid-templated transcription	BP	821	156	0 00856589
GO 0070647	protein modification by small protein conjugation or removal	BP	836	155	0 02046061
GO 0051130	positive regulation of cellular component organization	BP	800	152	0 00941836
GO 0016477	cell migration	BP	777	151	0 00416663
GO 0018193	peptidyl-amino acid modification	BP	818	150	0 0314287
GO 0045892	negative regulation of transcription DNA-templated	BP	789	149	0 01246043
GO 1903047	mitotic cell cycle process	BP	661	146	1 25E-05
GO 0031401	positive regulation of protein modification process	BP	724	146	0 00108816
GO 0051336	regulation of hydrolase activity	BP	783	146	0 02011601
GO 0006259	DNA metabolic process	BP	754	143	0 01232138

GO 0030163	protein catabolic process	BP	705	142	0 00133386
GO 0051094	positive regulation of developmental process	BP	741	139	0 01911756
GO 0006974	cellular response to DNA damage stimulus	BP	683	137	0 00190302
GO 0033365	protein localization to organelle	BP	716	136	0 01375122
GO 0045944	positive regulation of transcription by RNA polymerase	BP	741	136	0 03820239
GO 0006952	defense response	BP	745	136	0 04421753
GO 0032989	cellular component morphogenesis	BP	650	131	0 00198282
GO 0048666	neuron development	BP	610	128	0 00044461
GO 0007017	microtubule-based process	BP	503	127	2 76E-08
GO 0044087	regulation of cellular component biogenesis	BP	630	126	0 0031725
GO 0006325	chromatin organization	BP	584	125	0 00022279
GO 0000902	cell morphogenesis	BP	601	124	0 00106997
GO 0044257	cellular protein catabolic process	BP	605	123	0 00195585
GO 0044419	interspecies interaction between organisms	BP	619	123	0 0044268
GO 0044403	symbiont process	BP	607	122	0 00308042
GO 0032446	protein modification by small protein conjugation	BP	645	120	0 03491968
GO 0010564	regulation of cell cycle process	BP	547	119	0 00015757
GO 0031175	neuron projection development	BP	555	118	0 00043714
GO 0060341	regulation of cellular localization	BP	594	118	0 0052981
GO 0051603	proteolysis involved in cellular protein catabolic process	BP	560	117	0 00091582
GO 0007167	enzyme linked receptor protein signaling pathway	BP	611	117	0 01691962
GO 0032880	regulation of protein localization	BP	613	117	0 01856959
GO 0016032	viral process	BP	577	115	0 00527603
GO 0051640	organelle localization	BP	501	113	4 87E-05
GO 0051301	cell division	BP	477	112	8 14E-06
GO 0016567	protein ubiquitination	BP	601	112	0 03888567
GO 0042327	positive regulation of phosphorylation	BP	589	109	0 04855059
GO 0001934	positive regulation of protein phosphorylation	BP	559	107	0 02191019
GO 0043632	modification-dependent macromolecule catabolic process	BP	499	106	0 00087057
GO 0007417	central nervous system development	BP	535	106	0 00861489
GO 0007346	regulation of mitotic cell cycle	BP	472	103	0 00038315
GO 0019941	modification-dependent protein catabolic process	BP	488	103	0 00128266
GO 0006511	ubiquitin-dependent protein catabolic process	BP	482	102	0 00123482
GO 0000226	microtubule cytoskeleton organization	BP	374	99	8 82E-08
GO 0060284	regulation of cell development	BP	521	98	0 04122893
GO 0051960	regulation of nervous system development	BP	502	96	0 02941617
GO 0051345	positive regulation of hydrolase activity	BP	488	95	0 01957525
GO 0051129	negative regulation of cellular component organization	BP	471	94	0 01059062
GO 0009607	response to biotic stimulus	BP	501	94	0 04736816
GO 0000904	cell morphogenesis involved in differentiation	BP	425	92	0 00101022
GO 0045786	negative regulation of cell cycle	BP	453	92	0 00707857
GO 0030029	actin filament-based process	BP	456	91	0 01179573
GO 0050767	regulation of neurogenesis	BP	459	91	0 0139734
GO 0006281	DNA repair	BP	440	90	0 00630105
GO 0060322	head development	BP	446	90	0 00912074
GO 0032990	cell part morphogenesis	BP	384	87	0 00030208
GO 0007420	brain development	BP	414	87	0 00335546
GO 0044770	cell cycle phase transition	BP	445	87	0 02233622
GO 0010638	positive regulation of organelle organization	BP	453	87	0 03346565
GO 0120039	plasma membrane bounded cell projection morphogenesis	BP	365	85	0 00013436
GO 0048858	cell projection morphogenesis	BP	366	85	0 00014829
GO 0044772	mitotic cell cycle phase transition	BP	415	85	0 00751595
GO 0048812	neuron projection morphogenesis	BP	355	84	8 23E-05
GO 0016569	covalent chromatin modification	BP	372	84	0 00042664
GO 0007169	transmembrane receptor protein tyrosine kinase signaling pathway	BP	433	84	0 02906921
GO 0070201	regulation of establishment of protein localization	BP	439	84	0 03909552
GO 0010498	proteasomal protein catabolic process	BP	384	83	0 00182427
GO 0097435	supramolecular fiber organization	BP	413	83	0 01320397
GO 0030036	actin cytoskeleton organization	BP	420	83	0 01971164
GO 0016570	histone modification	BP	367	82	0 0006992
GO 0030031	cell projection assembly	BP	385	82	0 00296915
GO 0051347	positive regulation of transferase activity	BP	416	82	0 02159297
GO 0120031	plasma membrane bounded cell projection assembly	BP	378	81	0 00264077
GO 0051493	regulation of cytoskeleton organization	BP	353	79	0 00082601
GO 0048609	multicellular organismal reproductive process	BP	402	79	0 02541901
GO 0032504	multicellular organism reproduction	BP	404	79	0 02829451
GO 0051656	establishment of organelle localization	BP	341	76	0 00116154
GO 1903827	regulation of cellular protein localization	BP	381	76	0 02025877
GO 0048667	cell morphogenesis involved in neuron differentiation	BP	322	75	0 00032457
GO 0007264	small GTPase mediated signal transduction	BP	370	74	0 02054977
GO 0045596	negative regulation of cell differentiation	BP	374	74	0 02584129
GO 0010563	negative regulation of phosphorus metabolic process	BP	382	74	0 03967082
GO 0043161	proteasome-mediated ubiquitin-dependent protein catabolic proce	BP	333	73	0 00227932
GO 0048285	organelle fission	BP	335	72	0 00409547
GO 0043254	regulation of protein complex assembly	BP	327	70	0 00508448
GO 1902532	negative regulation of intracellular signal transduction	BP	352	70	0 02668871
GO 0000280	nuclear division	BP	304	69	0 0011616
GO 0044089	positive regulation of cellular component biogenesis	BP	353	69	0 03862266
GO 0061564	axon development	BP	277	68	0 00012134
GO 0040017	positive regulation of locomotion	BP	327	66	0 0229475
GO 0007276	gamete generation	BP	336	66	0 03868878
GO 0007409	axonogenesis	BP	252	64	6 60E-05
GO 0051272	positive regulation of cellular component movement	BP	316	64	0 02319421
GO 0045860	positive regulation of protein kinase activity	BP	326	64	0 04164677
GO 0042176	regulation of protein catabolic process	BP	297	63	0 00928676

GO 0051169	nuclear transport	BP	293	62	0 01033351
GO 0051052	regulation of DNA metabolic process	BP	306	62	0 0249368
GO 0007265	Ras protein signal transduction	BP	297	61	0 01999964
GO 0016049	cell growth	BP	299	61	0 02277779
GO 0006913	nucleocytoplasmic transport	BP	290	60	0 01813019
GO 1901990	regulation of mitotic cell cycle phase transition	BP	298	60	0 03035142
GO 0030335	positive regulation of cell migration	BP	303	60	0 04080667
GO 0032386	regulation of intracellular transport	BP	300	59	0 04741958
GO 0010639	negative regulation of organelle organization	BP	274	58	0 01271279
GO 0006935	chemotaxis	BP	290	58	0 03686633
GO 0042330	taxis	BP	291	58	0 03912143
GO 0033044	regulation of chromosome organization	BP	272	57	0 01634372
GO 0051962	positive regulation of nervous system development	BP	277	57	0 02306719
GO 0009617	response to bacterium	BP	279	57	0 0263114
GO 1904951	positive regulation of establishment of protein localization	BP	280	56	0 03969674
GO 0140014	mitotic nuclear division	BP	236	55	0 00189751
GO 0007059	chromosome segregation	BP	251	55	0 0074806
GO 0006260	DNA replication	BP	233	54	0 00236007
GO 0030900	forebrain development	BP	203	53	0 00012774
GO 0044782	cilium organization	BP	245	52	0 01673993
GO 0060249	anatomical structure homeostasis	BP	259	52	0 04334415
GO 0060271	cilium assembly	BP	241	51	0 01865376
GO 1903829	positive regulation of cellular protein localization	BP	251	51	0 03725715
GO 0051056	regulation of small GTPase mediated signal transduction	BP	210	46	0 0136489
GO 0007018	microtubule-based movement	BP	171	45	0 00033086
GO 0070997	neuron death	BP	210	45	0 02112135
GO 0000209	protein polyubiquitination	BP	213	45	0 02656262
GO 0019058	viral life cycle	BP	218	45	0 03801909
GO 0006302	double-strand break repair	BP	183	44	0 00275943
GO 1901214	regulation of neuron death	BP	183	43	0 00478454
GO 0007568	aging	BP	195	43	0 01491642
GO 0009895	negative regulation of catabolic process	BP	208	43	0 0408897
GO 0031589	cell-substrate adhesion	BP	209	43	0 04380964
GO 0022406	membrane docking	BP	149	42	0 00010198
GO 0007249	-kappaB kinase/NF-kappaB signaling	BP	189	42	0 01406845
GO 0071375	cellular response to peptide hormone stimulus	BP	197	42	0 02726921
GO 0006310	DNA recombination	BP	198	42	0 02944397
GO 0010721	negative regulation of cell development	BP	184	41	0 01446561
GO 0044839	cell cycle G2/M phase transition	BP	185	41	0 01580305
GO 0051258	protein polymerization	BP	191	41	0 02607052
GO 0140056	organelle localization by membrane tethering	BP	141	40	0 00012691
GO 0032886	regulation of microtubule-based process	BP	155	40	0 00104257
GO 0045732	positive regulation of protein catabolic process	BP	166	40	0 00401706
GO 1903320	regulation of protein modification by small protein conjugation or re	BP	189	40	0 0340353
GO 0021537	telencephalon development	BP	138	39	0 00016737
GO 0070507	regulation of microtubule cytoskeleton organization	BP	139	39	0 00019748
GO 0050768	negative regulation of neurogenesis	BP	163	39	0 00507097
GO 0043122	regulation of -kappaB kinase/NF-kappaB signaling	BP	168	39	0 00858873
GO 0000086	G2/M transition of mitotic cell cycle	BP	169	39	0 00949314
GO 0051961	negative regulation of nervous system development	BP	176	39	0 01827068
GO 0031330	negative regulation of cellular catabolic process	BP	185	39	0 03800838
GO 0051235	maintenance of location	BP	188	39	0 04732459
GO 0007159	leukocyte cell-cell adhesion	BP	175	38	0 02650091
GO 0042063	gliogenesis	BP	155	37	0 0064754
GO 0032496	response to lipopolysaccharide	BP	166	37	0 01933601
GO 0002237	response to molecule of bacterial origin	BP	172	37	0 0322353
GO 0032868	response to insulin	BP	177	37	0 04735721
GO 0051783	regulation of nuclear division	BP	152	36	0 00815689
GO 0097191	extrinsic apoptotic signaling pathway	BP	156	36	0 0123418
GO 1903050	regulation of proteolysis involved in cellular protein catabolic proce	BP	172	36	0 04910628
GO 2001252	positive regulation of chromosome organization	BP	140	35	0 00366063
GO 0007088	regulation of mitotic nuclear division	BP	143	35	0 00526022
GO 0051701	interaction with host	BP	154	35	0 0169305
GO 0043393	regulation of protein binding	BP	162	35	0 03443631
GO 0000819	sister chromatid segregation	BP	164	35	0 04045452
GO 0031396	regulation of protein ubiquitination	BP	165	35	0 04374548
GO 0007051	spindle organization	BP	139	34	0 00595112
GO 0051091	positive regulation of DNA-binding transcription factor activity	BP	161	34	0 04894973
GO 0046578	regulation of Ras protein signal transduction	BP	144	33	0 01775604
GO 0007163	establishment or maintenance of cell polarity	BP	144	33	0 01775604
GO 1902749	regulation of cell cycle G2/M phase transition	BP	144	33	0 01775604
GO 0007160	cell-matrix adhesion	BP	136	32	0 01333135
GO 0043123	positive regulation of -kappaB kinase/NF-kappaB signaling	BP	136	32	0 01333135
GO 0070372	regulation of ERK1 and ERK2 cascade	BP	148	32	0 04129587
GO 0071559	response to transforming growth factor beta	BP	149	32	0 04483234
GO 1901215	negative regulation of neuron death	BP	119	31	0 00310617
GO 0010389	regulation of G2/M transition of mitotic cell cycle	BP	130	31	0 01214863
GO 0045665	negative regulation of neuron differentiation	BP	135	31	0 02052325
GO 1902275	regulation of chromatin organization	BP	136	31	0 02264658
GO 0051402	neuron apoptotic process	BP	142	31	0 03921265
GO 0051321	meiotic cell cycle	BP	143	31	0 04268628
GO 0071560	cellular response to transforming growth factor beta stimulus	BP	144	31	0 046384
GO 0032869	cellular response to insulin stimulus	BP	144	31	0 046384
GO 0021543	pallium development	BP	101	30	0 00036197
GO 0031023	microtubule organizing center organization	BP	105	30	0 00074351

GO 2000058	regulation of ubiquitin-dependent protein catabolic process	BP	120	30	0 0067938
GO 0048588	developmental cell growth	BP	128	30	0 01706838
GO 0030705	cytoskeleton-dependent intracellular transport	BP	130	30	0 02098765
GO 0007411	axon guidance	BP	134	30	0 03092362
GO 0097485	neuron projection guidance	BP	134	30	0 03092362
GO 0043542	endothelial cell migration	BP	136	30	0 03707872
GO 0010970	transport along microtubule	BP	114	29	0 00595381
GO 0099111	microtubule-based transport	BP	114	29	0 00595381
GO 0043523	regulation of neuron apoptotic process	BP	121	29	0 01394073
GO 0050890	cognition	BP	133	29	0 04558014
GO 0006479	protein methylation	BP	134	29	0 04962813
GO 0008213	protein alkylation	BP	134	29	0 04962813
GO 0006275	regulation of DNA replication	BP	91	28	0 00029592
GO 0007098	centrosome cycle	BP	97	28	0 00092271
GO 0010001	glial cell differentiation	BP	115	28	0 01255617
GO 1902850	microtubule cytoskeleton organization involved in mitosis	BP	111	27	0 01423805
GO 0051100	negative regulation of binding	BP	119	27	0 03354008
GO 0006333	chromatin assembly or disassembly	BP	123	27	0 04861863
GO 0000724	double-strand break repair via homologous recombination	BP	94	26	0 00268428
GO 0000725	recombinational repair	BP	95	26	0 00314687
GO 0019827	stem cell population maintenance	BP	102	26	0 00865098
GO 0098727	maintenance of cell number	BP	104	26	0 01120683
GO 0051017	actin filament bundle assembly	BP	106	26	0 01434148
GO 0061572	actin filament bundle organization	BP	108	26	0 01814032
GO 1903364	positive regulation of cellular protein catabolic process	BP	112	26	0 02808489
GO 0007179	transforming growth factor beta receptor signaling pathway	BP	115	26	0 03794695
GO 0051494	negative regulation of cytoskeleton organization	BP	91	25	0 00354002
GO 0008286	insulin receptor signaling pathway	BP	93	25	0 00482458
GO 0032434	regulation of proteasomal ubiquitin-dependent protein catabolic p	BP	100	25	0 01271394
GO 0045216	cell-cell junction organization	BP	104	25	0 02058816
GO 0051302	regulation of cell division	BP	107	25	0 02866751
GO 1903046	meiotic cell cycle process	BP	109	25	0 03526753
GO 0051053	negative regulation of DNA metabolic process	BP	111	25	0 04294566
GO 0060759	regulation of response to cytokine stimulus	BP	111	25	0 04294566
GO 0097711	ciliary basal body-plasma membrane docking	BP	84	24	0 00241222
GO 0061351	neural precursor cell proliferation	BP	85	24	0 00286335
GO 0031333	negative regulation of protein complex assembly	BP	90	24	0 00632702
GO 0030260	entry into host cell	BP	93	24	0 00971011
GO 0044409	entry into host	BP	93	24	0 00971011
GO 0051806	entry into cell of other organism involved in symbiotic interaction	BP	93	24	0 00971011
GO 0051828	entry into other organism involved in symbiotic interaction	BP	93	24	0 00971011
GO 1990138	neuron projection extension	BP	98	24	0 01848318
GO 0001959	regulation of cytokine-mediated signaling pathway	BP	103	24	0 03252746
GO 0021987	cerebral cortex development	BP	69	23	0 00027756
GO 0051261	protein depolymerization	BP	70	23	0 00035187
GO 0046718	viral entry into host cell	BP	83	23	0 00447667
GO 1903052	positive regulation of proteolysis involved in cellular protein catabo	BP	95	23	0 0236557
GO 0030010	establishment of cell polarity	BP	96	23	0 02656216
GO 1902904	negative regulation of supramolecular fiber organization	BP	81	22	0 00693077
GO 0006892	post-Golgi vesicle-mediated transport	BP	86	22	0 01431838
GO 0006633	fatty acid biosynthetic process	BP	88	22	0 01862264
GO 0007052	mitotic spindle organization	BP	94	22	0 03770735
GO 0140013	meiotic nuclear division	BP	94	22	0 03770735
GO 0018022	peptidyl-lysine methylation	BP	96	22	0 0465145
GO 0051651	maintenance of location in cell	BP	70	21	0 00229625
GO 0031109	microtubule polymerization or depolymerization	BP	79	21	0 01061773
GO 0048771	tissue remodeling	BP	79	21	0 01061773
GO 0021953	central nervous system neuron differentiation	BP	82	21	0 01626117
GO 0007043	cell-cell junction assembly	BP	84	21	0 02117511
GO 1901800	positive regulation of proteasomal protein catabolic process	BP	84	21	0 02117511
GO 0051225	spindle assembly	BP	86	21	0 02716328
GO 0072384	organelle transport along microtubule	BP	62	20	0 00108508
GO 0048675	axon extension	BP	73	20	0 0088238
GO 1903305	regulation of regulated secretory pathway	BP	76	20	0 0139364
GO 0045185	maintenance of protein location	BP	77	20	0 01608238
GO 0043524	negative regulation of neuron apoptotic process	BP	81	20	0 02734991
GO 0051817	modification of morphology or physiology of other organism involve	BP	81	20	0 02734991
GO 0036503	ERAD pathway	BP	82	20	0 03092692
GO 0035023	regulation of Rho protein signal transduction	BP	85	20	0 04375609
GO 0034968	histone lysine methylation	BP	85	20	0 04375609
GO 0043297	apical junction assembly	BP	54	19	0 00042719
GO 0051303	establishment of chromosome localization	BP	63	19	0 00340607
GO 0050000	chromosome localization	BP	64	19	0 00413449
GO 0017156	calcium ion regulated exocytosis	BP	73	19	0 01826845
GO 0002705	positive regulation of leukocyte mediated immunity	BP	74	19	0 02101272
GO 0032091	negative regulation of protein binding	BP	75	19	0 02406281
GO 0043244	regulation of protein complex disassembly	BP	75	19	0 02406281
GO 2000060	positive regulation of ubiquitin-dependent protein catabolic proces	BP	75	19	0 02406281
GO 0008643	carbohydrate transport	BP	76	19	0 02743828
GO 1905269	positive regulation of chromatin organization	BP	78	19	0 03524157
GO 1901879	regulation of protein depolymerization	BP	54	18	0 00124102
GO 0005976	polysaccharide metabolic process	BP	63	18	0 00799185
GO 0002576	platelet degranulation	BP	69	18	0 02076462
GO 0034502	protein localization to chromosome	BP	72	18	0 03127329
GO 0000726	non-recombinational repair	BP	74	18	0 0401955

GO 0140029	exocytic process	BP	52	17	0 00213018
GO 0032507	maintenance of protein location in cell	BP	57	17	0 00616686
GO 0044264	cellular polysaccharide metabolic process	BP	58	17	0 00745636
GO 0048010	vascular endothelial growth factor receptor signaling pathway	BP	60	17	0 01068288
GO 0032436	positive regulation of proteasomal ubiquitin-dependent protein cat	BP	65	17	0 02361802
GO 0006303	double-strand break repair via nonhomologous end joining	BP	69	17	0 04055493
GO 0015749	monosaccharide transmembrane transport	BP	55	16	0 01002027
GO 0034219	carbohydrate transmembrane transport	BP	56	16	0 01200272
GO 0098693	regulation of synaptic vesicle cycle	BP	58	16	0 01687966
GO 0021782	glial cell development	BP	59	16	0 01982866
GO 0002702	positive regulation of production of molecular mediator of immune	BP	61	16	0 02688374
GO 0070317	negative regulation of G0 to G1 transition	BP	35	15	0 00014035
GO 0070316	regulation of G0 to G1 transition	BP	38	15	0 00041611
GO 0045023	G0 to G1 transition	BP	39	15	0 00057752
GO 0070830	bicellular tight junction assembly	BP	45	15	0 00308641
GO 0120192	tight junction assembly	BP	46	15	0 00391655
GO 0120193	tight junction organization	BP	47	15	0 00492028
GO 0048278	vesicle docking	BP	51	15	0 01119579
GO 1904659	glucose transmembrane transport	BP	52	15	0 01347265
GO 0008645	hexose transmembrane transport	BP	54	15	0 01908808
GO 0044786	cell cycle DNA replication	BP	56	15	0 02632477
GO 0046785	microtubule polymerization	BP	58	15	0 03542181
GO 0010827	regulation of glucose transmembrane transport	BP	41	14	0 00326732
GO 0016445	somatic diversification of immunoglobulins	BP	41	14	0 00326732
GO 1901880	negative regulation of protein depolymerization	BP	42	14	0 00419417
GO 0007080	mitotic metaphase plate congression	BP	44	14	0 0066843
GO 0043242	negative regulation of protein complex disassembly	BP	46	14	0 01023092
GO 0006112	energy reserve metabolic process	BP	46	14	0 01023092
GO 0051781	positive regulation of cell division	BP	46	14	0 01023092
GO 0002200	somatic diversification of immune receptors	BP	46	14	0 01023092
GO 2000177	regulation of neural precursor cell proliferation	BP	50	14	0 02158255
GO 0006220	pyrimidine nucleotide metabolic process	BP	51	14	0 02551267
GO 0031110	regulation of microtubule polymerization or depolymerization	BP	53	14	0 0349222
GO 0051310	metaphase plate congression	BP	53	14	0 0349222
GO 0051702	interaction with symbiont	BP	54	14	0 04046414
GO 1901216	positive regulation of neuron death	BP	55	14	0 04660216
GO 0062014	negative regulation of small molecule metabolic process	BP	55	14	0 04660216
GO 0021885	forebrain cell migration	BP	35	13	0 00192984
GO 0008156	negative regulation of DNA replication	BP	36	13	0 00258586
GO 0006221	pyrimidine nucleotide biosynthetic process	BP	38	13	0 00444378
GO 0005977	glycogen metabolic process	BP	42	13	0 01129528
GO 0006073	cellular glucan metabolic process	BP	42	13	0 01129528
GO 0044042	glucan metabolic process	BP	42	13	0 01129528
GO 0002011	morphogenesis of an epithelial sheet	BP	42	13	0 01129528
GO 0034724	DNA replication-independent nucleosome organization	BP	43	13	0 01388318
GO 0034508	centromere complex assembly	BP	44	13	0 01690206
GO 0007062	sister chromatid cohesion	BP	47	13	0 02895082
GO 0072528	pyrimidine-containing compound biosynthetic process	BP	47	13	0 02895082
GO 0021766	hippocampus development	BP	48	13	0 0340942
GO 0002753	cytoplasmic pattern recognition receptor signaling pathway	BP	48	13	0 0340942
GO 0014812	muscle cell migration	BP	49	13	0 03986109
GO 0046928	regulation of neurotransmitter secretion	BP	49	13	0 03986109
GO 1904377	positive regulation of protein localization to cell periphery	BP	49	13	0 03986109
GO 0017158	regulation of calcium ion-dependent exocytosis	BP	50	13	0 04628328
GO 0051851	modification by host of symbiont morphology or physiology	BP	50	13	0 04628328
GO 0000245	spliceosomal complex assembly	BP	50	13	0 04628328
GO 0016447	somatic recombination of immunoglobulin gene segments	BP	34	12	0 00464143
GO 0006904	vesicle docking involved in exocytosis	BP	35	12	0 00605617
GO 0033627	cell adhesion mediated by integrin	BP	39	12	0 01538413
GO 0002562	somatic diversification of immune receptors via germline recombina	BP	39	12	0 01538413
GO 0016444	somatic cell DNA recombination	BP	39	12	0 01538413
GO 0021954	central nervous system neuron development	BP	40	12	0 01887071
GO 0031122	cytoplasmic microtubule organization	BP	41	12	0 02291488
GO 0006336	DNA replication-independent nucleosome assembly	BP	42	12	0 02756272
GO 0019083	viral transcription	BP	42	12	0 02756272
GO 0043627	response to estrogen	BP	43	12	0 03285803
GO 1901224	positive regulation of N K/NF-kappaB signaling	BP	44	12	0 03884151
GO 0038095	Fc-epsilon receptor signaling pathway	BP	45	12	0 04555009
GO 0034067	protein localization to Golgi apparatus	BP	24	11	0 00054633
GO 0046323	glucose import	BP	33	11	0 01065823
GO 0022029	telencephalon cell migration	BP	33	11	0 01065823
GO 0002381	immunoglobulin production involved in immunoglobulin mediated i	BP	33	11	0 01065823
GO 0030042	actin filament depolymerization	BP	34	11	0 01353582
GO 0046626	regulation of insulin receptor signaling pathway	BP	34	11	0 01353582
GO 0051058	negative regulation of small GTPase mediated signal transduction	BP	35	11	0 016964
GO 0045840	positive regulation of mitotic nuclear division	BP	35	11	0 016964
GO 0018023	peptidyl-lysine trimethylation	BP	36	11	0 02099998
GO 1900076	regulation of cellular response to insulin stimulus	BP	36	11	0 02099998
GO 0031055	chromatin remodeling at centromere	BP	36	11	0 02099998
GO 0002042	cell migration involved in sprouting angiogenesis	BP	38	11	0 03111435
GO 0071385	cellular response to glucocorticoid stimulus	BP	38	11	0 03111435
GO 2000300	regulation of synaptic vesicle exocytosis	BP	39	11	0 03729408
GO 0046782	regulation of viral transcription	BP	39	11	0 03729408
GO 0043266	regulation of potassium ion transport	BP	40	11	0 04428225
GO 0051568	histone H3-K4 methylation	BP	40	11	0 04428225

GO 0043486	histone exchange	BP	40	11	0 04428225
GO 0051383	kinetochore organization	BP	21	10	0 00067363
GO 0021795	cerebral cortex cell migration	BP	27	10	0 00645798
GO 0007019	microtubule depolymerization	BP	28	10	0 00863555
GO 0046324	regulation of glucose import	BP	29	10	0 01133415
GO 0002204	somatic recombination of immunoglobulin genes involved in immur	BP	31	10	0 01857752
GO 0002208	somatic diversification of immunoglobulins involved in immune resp	BP	31	10	0 01857752
GO 0045190	isotype switching	BP	31	10	0 01857752
GO 0030834	regulation of actin filament depolymerization	BP	32	10	0 02326124
GO 0034080	CENP-A containing nucleosome assembly	BP	32	10	0 02326124
GO 0061641	CENP-A containing chromatin organization	BP	32	10	0 02326124
GO 0007405	neuroblast proliferation	BP	33	10	0 02874082
GO 0072595	maintenance of protein localization in organelle	BP	34	10	0 03507623
GO 0043954	cellular component maintenance	BP	34	10	0 03507623
GO 0043525	positive regulation of neuron apoptotic process	BP	35	10	0 04232112
GO 0045880	positive regulation of smoothened signaling pathway	BP	19	9	0 00131836
GO 0007435	salivary gland morphogenesis	BP	22	9	0 00451351
GO 0030835	negative regulation of actin filament depolymerization	BP	24	9	0 00878819
GO 0007431	salivary gland development	BP	24	9	0 00878819
GO 0051642	centrosome localization	BP	24	9	0 00878819
GO 0061842	microtubule organizing center localization	BP	25	9	0 01182494
GO 0070423	nucleotide-binding oligomerization domain containing signaling pa	BP	26	9	0 01558017
GO 0046579	positive regulation of Ras protein signal transduction	BP	26	9	0 01558017
GO 0006298	mismatch repair	BP	27	9	0 02014127
GO 0035872	nucleotide-binding domain leucine rich repeat containing recepto	BP	27	9	0 02014127
GO 0033173	calcineurin-NFAT signaling cascade	BP	27	9	0 02014127
GO 0097720	calcineurin-mediated signaling	BP	27	9	0 02014127
GO 0045910	negative regulation of DNA recombination	BP	27	9	0 02014127
GO 0051984	positive regulation of chromosome segregation	BP	27	9	0 02014127
GO 2000179	positive regulation of neural precursor cell proliferation	BP	27	9	0 02014127
GO 0043276	anoikis	BP	28	9	0 02559135
GO 0051057	positive regulation of small GTPase mediated signal transduction	BP	29	9	0 03200708
GO 0007099	centriole replication	BP	29	9	0 03200708
GO 0097300	programmed necrotic cell death	BP	30	9	0 0394567
GO 0035272	exocrine system development	BP	30	9	0 0394567
GO 0045103	intermediate filament-based process	BP	30	9	0 0394567
GO 0045104	intermediate filament cytoskeleton organization	BP	30	9	0 0394567
GO 0098534	centriole assembly	BP	30	9	0 0394567
GO 0051898	negative regulation of protein kinase B signaling	BP	31	9	0 04799818
GO 1901985	positive regulation of protein acetylation	BP	31	9	0 04799818
GO 0062033	positive regulation of mitotic sister chromatid segregation	BP	17	8	0 00259137
GO 0000729	DNA double-strand break processing	BP	20	8	0 0085967
GO 0021955	central nervous system neuron axonogenesis	BP	20	8	0 0085967
GO 0051693	actin filament capping	BP	22	8	0 0162449
GO 2000781	positive regulation of double-strand break repair	BP	22	8	0 0162449
GO 0032467	positive regulation of cytokinesis	BP	23	8	0 02150582
GO 0050919	negative chemotaxis	BP	23	8	0 02150582
GO 0014009	glial cell proliferation	BP	23	8	0 02150582
GO 0033014	tetrapyrrole biosynthetic process	BP	24	8	0 02786463
GO 0090504	epiboly	BP	24	8	0 02786463
GO 0045191	regulation of isotype switching	BP	24	8	0 02786463
GO 0090169	regulation of spindle assembly	BP	24	8	0 02786463
GO 0046039	GTP metabolic process	BP	25	8	0 03541272
GO 2000758	positive regulation of peptidyl-lysine acetylation	BP	25	8	0 03541272
GO 0001953	negative regulation of cell-matrix adhesion	BP	26	8	0 04422719
GO 0031111	negative regulation of microtubule polymerization or depolymeriza	BP	26	8	0 04422719
GO 0044818	mitotic G2/M transition checkpoint	BP	26	8	0 04422719
GO 0017145	stem cell division	BP	26	8	0 04422719
GO 0002931	response to ischemia	BP	26	8	0 04422719
GO 0051016	barbed-end actin filament capping	BP	15	7	0 00512114
GO 0070050	neuron cellular homeostasis	BP	15	7	0 00512114
GO 1904385	cellular response to angiotensin	BP	16	7	0 00786519
GO 1901685	glutathione derivative metabolic process	BP	16	7	0 00786519
GO 1901687	glutathione derivative biosynthetic process	BP	16	7	0 00786519
GO 0034643	establishment of mitochondrion localization microtubule-mediated	BP	16	7	0 00786519
GO 0047497	mitochondrion transport along microtubule	BP	16	7	0 00786519
GO 0090322	regulation of superoxide metabolic process	BP	17	7	0 01155686
GO 0071514	genetic imprinting	BP	17	7	0 01155686
GO 1901673	regulation of mitotic spindle assembly	BP	17	7	0 01155686
GO 2000209	regulation of anoikis	BP	18	7	0 01635402
GO 1990776	response to angiotensin	BP	18	7	0 01635402
GO 0051654	establishment of mitochondrion localization	BP	18	7	0 01635402
GO 0060706	cell differentiation involved in embryonic placenta development	BP	19	7	0 02240425
GO 0034453	microtubule anchoring	BP	19	7	0 02240425
GO 0046627	negative regulation of insulin receptor signaling pathway	BP	19	7	0 02240425
GO 1900077	negative regulation of cellular response to insulin stimulus	BP	19	7	0 02240425
GO 0045830	positive regulation of isotype switching	BP	20	7	0 02983908
GO 0032885	regulation of polysaccharide biosynthetic process	BP	21	7	0 03876916
GO 0033028	myeloid cell apoptotic process	BP	21	7	0 03876916
GO 0007064	mitotic sister chromatid cohesion	BP	21	7	0 03876916
GO 2000404	regulation of T cell migration	BP	22	7	0 04928048
GO 0071549	cellular response to dexamethasone stimulus	BP	22	7	0 04928048
GO 0051567	histone H3-K9 methylation	BP	22	7	0 04928048
GO 0043921	modulation by host of viral transcription	BP	22	7	0 04928048
GO 0052472	modulation by host of symbiont transcription	BP	22	7	0 04928048

GO 0051095	regulation of helicase activity	BP	12	6	0 00633276
GO 0051315	attachment of mitotic spindle microtubules to kinetochore	BP	13	6	0 01019016
GO 0035313	wound healing spreading of epidermal cells	BP	13	6	0 01019016
GO 0008356	asymmetric cell division	BP	13	6	0 01019016
GO 0001990	regulation of systemic arterial blood pressure by hormone	BP	14	6	0 01546045
GO 0035024	negative regulation of Rho protein signal transduction	BP	14	6	0 01546045
GO 0060972	left/right pattern formation	BP	14	6	0 01546045
GO 0001945	lymph vessel development	BP	15	6	0 02235333
GO 0031468	nuclear envelope reassembly	BP	15	6	0 02235333
GO 1900181	negative regulation of protein localization to nucleus	BP	15	6	0 02235333
GO 0051385	response to mineralocorticoid	BP	16	6	0 03104621
GO 0005979	regulation of glycogen biosynthetic process	BP	16	6	0 03104621
GO 0010962	regulation of glucan biosynthetic process	BP	16	6	0 03104621
GO 0070828	heterochromatin organization	BP	16	6	0 03104621
GO 0051382	kinetochore assembly	BP	16	6	0 03104621
GO 0031338	regulation of vesicle fusion	BP	17	6	0 04167676
GO 1901522	positive regulation of transcription from RNA polymerase promot	BP	17	6	0 04167676
GO 0046794	transport of virus	BP	17	6	0 04167676
GO 0070493	thrombin-activated receptor signaling pathway	BP	7	5	0 00162755
GO 0051096	positive regulation of helicase activity	BP	7	5	0 00162755
GO 0034085	establishment of sister chromatid cohesion	BP	8	5	0 00376941
GO 0050901	leukocyte tethering or rolling	BP	9	5	0 00737104
GO 0071801	regulation of podosome assembly	BP	9	5	0 00737104
GO 0034770	histone H4-K20 methylation	BP	9	5	0 00737104
GO 0090343	positive regulation of cell aging	BP	9	5	0 00737104
GO 0051482	positive regulation of cytosolic calcium ion concentration involved	BP	9	5	0 00737104
GO 0035520	monoubiquitinated protein deubiquitination	BP	9	5	0 00737104
GO 0003081	regulation of systemic arterial blood pressure by renin-angiotensin	BP	10	5	0 0128216
GO 0010560	positive regulation of glycoprotein biosynthetic process	BP	10	5	0 0128216
GO 0006241	CTP biosynthetic process	BP	10	5	0 0128216
GO 0046036	CTP metabolic process	BP	10	5	0 0128216
GO 0046628	positive regulation of insulin receptor signaling pathway	BP	10	5	0 0128216
GO 0010842	retina layer formation	BP	10	5	0 0128216
GO 0006349	regulation of gene expression by genetic imprinting	BP	11	5	0 02045912
GO 0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	BP	11	5	0 02045912
GO 0016024	CDP-diacylglycerol biosynthetic process	BP	11	5	0 02045912
GO 0007100	mitotic centrosome separation	BP	11	5	0 02045912
GO 1903020	positive regulation of glycoprotein metabolic process	BP	11	5	0 02045912
GO 0006983	ER overload response	BP	11	5	0 02045912
GO 0090161	Golgi ribbon formation	BP	11	5	0 02045912
GO 0035437	maintenance of protein localization in endoplasmic reticulum	BP	11	5	0 02045912
GO 0061756	leukocyte adhesion to vascular endothelial cell	BP	12	5	0 03054939
GO 0003071	renal system process involved in regulation of systemic arterial blo	BP	12	5	0 03054939
GO 0071800	podosome assembly	BP	12	5	0 03054939
GO 0034086	maintenance of sister chromatid cohesion	BP	12	5	0 03054939
GO 0034088	maintenance of mitotic sister chromatid cohesion	BP	12	5	0 03054939
GO 0009208	pyrimidine ribonucleoside triphosphate metabolic process	BP	12	5	0 03054939
GO 0046341	CDP-diacylglycerol metabolic process	BP	12	5	0 03054939
GO 0051299	centrosome separation	BP	12	5	0 03054939
GO 1900078	positive regulation of cellular response to insulin stimulus	BP	12	5	0 03054939
GO 0002566	somatic diversification of immune receptors via somatic mutation	BP	12	5	0 03054939
GO 0016446	somatic hypermutation of immunoglobulin genes	BP	12	5	0 03054939
GO 0045777	positive regulation of blood pressure	BP	13	5	0 0432739
GO 2000811	negative regulation of anoikis	BP	13	5	0 0432739
GO 0032486	Rap protein signal transduction	BP	13	5	0 0432739
GO 0080182	histone H3-K4 trimethylation	BP	13	5	0 0432739
GO 0032232	negative regulation of actin filament bundle assembly	BP	13	5	0 0432739
GO 0051497	negative regulation of stress fiber assembly	BP	13	5	0 0432739
GO 2000042	negative regulation of double-strand break repair via homologous	BP	13	5	0 0432739
GO 0003084	positive regulation of systemic arterial blood pressure	BP	5	4	0 00282041
GO 1903251	multi-ciliated epithelial cell differentiation	BP	5	4	0 00282041
GO 0045719	negative regulation of glycogen biosynthetic process	BP	5	4	0 00282041
GO 0070874	negative regulation of glycogen metabolic process	BP	5	4	0 00282041
GO 0043570	maintenance of DNA repeat elements	BP	5	4	0 00282041
GO 0048172	regulation of short-term neuronal synaptic plasticity	BP	5	4	0 00282041
GO 0071921	cohesin loading	BP	6	4	0 00738968
GO 1905634	regulation of protein localization to chromatin	BP	6	4	0 00738968
GO 0044359	modulation of molecular function in other organism	BP	7	4	0 01507252
GO 0052205	modulation of molecular function in other organism involved in sym	BP	7	4	0 01507252
GO 0097709	connective tissue replacement	BP	7	4	0 01507252
GO 0036462	TRA L-activated apoptotic signaling pathway	BP	8	4	0 02637563
GO 0060707	trophoblast giant cell differentiation	BP	8	4	0 02637563
GO 0060253	negative regulation of glial cell proliferation	BP	8	4	0 02637563
GO 2000774	positive regulation of cellular senescence	BP	8	4	0 02637563
GO 0006621	protein retention in ER lumen	BP	8	4	0 02637563
GO 0019896	axonal transport of mitochondrion	BP	8	4	0 02637563
GO 0099640	axo-dendritic protein transport	BP	8	4	0 02637563
GO 0006013	mannose metabolic process	BP	8	4	0 02637563
GO 0051657	maintenance of organelle location	BP	8	4	0 02637563
GO 0051451	myoblast migration	BP	9	4	0 0415793
GO 0043619	regulation of transcription from RNA polymerase promoter in resp	BP	9	4	0 0415793
GO 0051412	response to corticosterone	BP	9	4	0 0415793
GO 0032530	regulation of microvillus organization	BP	9	4	0 0415793
GO 0042532	negative regulation of tyrosine phosphorylation of STAT protein	BP	9	4	0 0415793
GO 0060307	regulation of ventricular cardiac muscle cell membrane repolarizati	BP	9	4	0 0415793

GO 0071888	macrophage apoptotic process	BP	9	4	0 0415793
GO 0043922	negative regulation by host of viral transcription	BP	9	4	0 0415793
GO 0018026	peptidyl-lysine monomethylation	BP	9	4	0 0415793
GO 0035385	Roundabout signaling pathway	BP	3	3	0 00405706
GO 0000710	meiotic mismatch repair	BP	3	3	0 00405706
GO 2000465	regulation of glycogen (starch) synthase activity	BP	3	3	0 00405706
GO 2000466	negative regulation of glycogen (starch) synthase activity	BP	3	3	0 00405706
GO 0097742	de novo centriole assembly	BP	3	3	0 00405706
GO 0098535	de novo centriole assembly involved in multi-ciliated epithelial cell	BP	3	3	0 00405706
GO 0010269	response to selenium ion	BP	4	3	0 0142889
GO 0090324	negative regulation of oxidative phosphorylation	BP	4	3	0 0142889
GO 0099509	regulation of presynaptic cytosolic calcium ion concentration	BP	4	3	0 0142889
GO 2000675	negative regulation of type B pancreatic cell apoptotic process	BP	4	3	0 0142889
GO 0007079	mitotic chromosome movement towards spindle pole	BP	4	3	0 0142889
GO 0031033	myosin filament organization	BP	4	3	0 0142889
GO 0048625	myoblast fate commitment	BP	4	3	0 0142889
GO 0061072	iris morphogenesis	BP	4	3	0 0142889
GO 1903912	negative regulation of endoplasmic reticulum stress-induced e F2	BP	4	3	0 0142889
GO 1903373	positive regulation of endoplasmic reticulum tubular network organ	BP	4	3	0 0142889
GO 0006102	isocitrate metabolic process	BP	5	3	0 03149163
GO 0052428	modulation by host of symbiont molecular function	BP	5	3	0 03149163
GO 0018197	peptidyl-aspartic acid modification	BP	5	3	0 03149163
GO 0098915	membrane repolarization during ventricular cardiac muscle cell act	BP	5	3	0 03149163
GO 0015014	heparan sulfate proteoglycan biosynthetic process polysaccharid	BP	5	3	0 03149163
GO 0061419	positive regulation of transcription from RNA polymerase promot	BP	5	3	0 03149163
GO 0048853	forebrain morphogenesis	BP	5	3	0 03149163
GO 0014010	Schwann cell proliferation	BP	5	3	0 03149163
GO 0000920	septum digestion after cytokinesis	BP	5	3	0 03149163
GO 0071922	regulation of cohesin loading	BP	5	3	0 03149163
GO 0021800	cerebral cortex tangential migration	BP	5	3	0 03149163
GO 0042796	snRNA transcription by RNA polymerase	BP	5	3	0 03149163
GO 0045053	protein retention in Golgi apparatus	BP	5	3	0 03149163
GO 1903722	regulation of centriole elongation	BP	5	3	0 03149163
GO 0034093	positive regulation of maintenance of sister chromatid cohesion	BP	5	3	0 03149163
GO 0034184	positive regulation of maintenance of mitotic sister chromatid cohe	BP	5	3	0 03149163
GO 1903371	regulation of endoplasmic reticulum tubular network organization	BP	5	3	0 03149163
GO 0043366	beta selection	BP	2	2	0 02544967
GO 0071386	cellular response to corticosterone stimulus	BP	2	2	0 02544967
GO 0021502	neural fold elevation formation	BP	2	2	0 02544967
GO 2000620	positive regulation of histone H4-K16 acetylation	BP	2	2	0 02544967
GO 0052203	modulation of catalytic activity in other organism involved in symbio	BP	2	2	0 02544967
GO 1905123	regulation of glucosylceramidase activity	BP	2	2	0 02544967
GO 0008228	opsonization	BP	2	2	0 02544967
GO 1904124	microglial cell migration	BP	2	2	0 02544967
GO 1904139	regulation of microglial cell migration	BP	2	2	0 02544967
GO 1904141	positive regulation of microglial cell migration	BP	2	2	0 02544967
GO 0021523	somatic motor neuron differentiation	BP	2	2	0 02544967
GO 1900133	regulation of renin secretion into blood stream	BP	2	2	0 02544967
GO 2000077	negative regulation of type B pancreatic cell development	BP	2	2	0 02544967
GO 0001766	membrane raft polarization	BP	2	2	0 02544967
GO 0031580	membrane raft distribution	BP	2	2	0 02544967
GO 0006097	glyoxylate cycle	BP	2	2	0 02544967
GO 0038165	oncostatin-M-mediated signaling pathway	BP	2	2	0 02544967
GO 0048861	leukemia inhibitory factor signaling pathway	BP	2	2	0 02544967
GO 1905150	regulation of voltage-gated sodium channel activity	BP	2	2	0 02544967
GO 0075732	viral penetration into host nucleus	BP	2	2	0 02544967
GO 1902594	multi-organism nuclear import	BP	2	2	0 02544967
GO 0043000	Golgi to plasma membrane CFTR protein transport	BP	2	2	0 02544967
GO 0070494	regulation of thrombin-activated receptor signaling pathway	BP	2	2	0 02544967
GO 0070495	negative regulation of thrombin-activated receptor signaling pathw	BP	2	2	0 02544967
GO 0045105	intermediate filament polymerization or depolymerization	BP	2	2	0 02544967
GO 0043385	mycotoxin metabolic process	BP	2	2	0 02544967
GO 0043387	mycotoxin catabolic process	BP	2	2	0 02544967
GO 0046222	aflatoxin metabolic process	BP	2	2	0 02544967
GO 0046223	aflatoxin catabolic process	BP	2	2	0 02544967
GO 1901376	organic heteropentacyclic compound metabolic process	BP	2	2	0 02544967
GO 1901377	organic heteropentacyclic compound catabolic process	BP	2	2	0 02544967
GO 0019541	propionate metabolic process	BP	2	2	0 02544967
GO 0014040	positive regulation of Schwann cell differentiation	BP	2	2	0 02544967
GO 0090618	DNA clamp unloading	BP	2	2	0 02544967
GO 0000350	generation of catalytic spliceosome for second transesterification s	BP	2	2	0 02544967
GO 1990116	ribosome-associated ubiquitin-dependent protein catabolic proces	BP	2	2	0 02544967
GO 0061709	reticulophagy	BP	2	2	0 02544967
GO 0006548	histidine catabolic process	BP	2	2	0 02544967
GO 0052805	imidazole-containing compound catabolic process	BP	2	2	0 02544967
GO 0034087	establishment of mitotic sister chromatid cohesion	BP	2	2	0 02544967
GO 0060382	regulation of DNA strand elongation	BP	2	2	0 02544967
GO 0032472	Golgi calcium ion transport	BP	2	2	0 02544967
GO 0042144	vacuole fusion non-autophagic	BP	2	2	0 02544967
GO 0097576	vacuole fusion	BP	2	2	0 02544967
GO 0048250	iron import into the mitochondrion	BP	2	2	0 02544967
GO 1990166	protein localization to site of double-strand break	BP	2	2	0 02544967
GO 0005575	cellular component	CC	10123	1662	1 96E-06
GO 0005623	cell	CC	9668	1601	9 93E-07
GO 0044464	cell part	CC	9659	1599	1 36E-06

GO 0005622	intracellular	CC	9233	1552	5 38E-09
GO 0044424	intracellular part	CC	9136	1540	2 58E-09
GO 0043226	organelle	CC	8520	1461	5 47E-11
GO 0043229	intracellular organelle	CC	8194	1411	1 66E-10
GO 0043227	membrane-bounded organelle	CC	8057	1366	9 54E-07
GO 0005737	cytoplasm	CC	7500	1269	2 63E-05
GO 0043231	intracellular membrane-bounded organelle	CC	7343	1254	2 54E-06
GO 0044422	organelle part	CC	6571	1139	7 82E-07
GO 0044446	intracellular organelle part	CC	6482	1129	2 71E-07
GO 0044444	cytoplasmic part	CC	6503	1099	0 00061742
GO 0005634	nucleus	CC	5046	908	4 76E-08
GO 0031974	membrane-enclosed lumen	CC	3991	712	2 93E-05
GO 0043233	organelle lumen	CC	3991	712	2 93E-05
GO 0070013	intracellular organelle lumen	CC	3991	712	2 93E-05
GO 0005829	cytosol	CC	3779	684	5 95E-06
GO 0044428	nuclear part	CC	3501	650	2 50E-07
GO 0032991	protein-containing complex	CC	3721	649	0 00136376
GO 0031981	nuclear lumen	CC	3241	605	4 11E-07
GO 0043228	non-membrane-bounded organelle	CC	2966	551	3 81E-06
GO 0043232	intracellular non-membrane-bounded organelle	CC	2962	550	4 17E-06
GO 0005654	nucleoplasm	CC	2825	539	1 31E-07
GO 0005856	cytoskeleton	CC	1380	279	4 03E-06
GO 0044430	cytoskeletal part	CC	1061	216	3 71E-05
GO 0120025	plasma membrane bounded cell projection	CC	1105	196	0 04968218
GO 0015630	microtubule cytoskeleton	CC	862	187	2 42E-06
GO 0005694	chromosome	CC	819	176	8 95E-06
GO 0044451	nucleoplasm part	CC	911	169	0 01561629
GO 0097458	neuron part	CC	887	161	0 0364153
GO 0044427	chromosomal part	CC	714	153	4 16E-05
GO 1990234	transferase complex	CC	656	125	0 01610277
GO 0005815	microtubule organizing center	CC	554	122	7 53E-05
GO 0016604	nuclear body	CC	610	116	0 02107382
GO 0098590	plasma membrane region	CC	588	113	0 01690457
GO 0045202	synapse	CC	599	111	0 04540064
GO 0099512	supramolecular fiber	CC	506	102	0 00594146
GO 0099081	supramolecular polymer	CC	510	102	0 00750568
GO 0099080	supramolecular complex	CC	511	102	0 00794777
GO 0005813	centrosome	CC	407	92	0 00022283
GO 0099513	polymeric cytoskeletal fiber	CC	405	88	0 00114255
GO 0000785	chromatin	CC	406	81	0 01690854
GO 0098687	chromosomal region	CC	291	74	1 75E-05
GO 0005635	nuclear envelope	CC	355	70	0 03161558
GO 0030424	axon	CC	314	65	0 01421588
GO 0005874	microtubule	CC	288	62	0 00708529
GO 0005819	spindle	CC	283	61	0 00731256
GO 0005667	transcription factor complex	CC	236	59	0 00019844
GO 0005911	cell-cell junction	CC	289	59	0 02447938
GO 0031252	cell leading edge	CC	264	53	0 04176216
GO 0000793	condensed chromosome	CC	173	52	2 10E-06
GO 0000775	chromosome centromeric region	CC	173	50	1 11E-05
GO 0033267	axon part	CC	205	48	0 00322499
GO 0150034	distal axon	CC	153	39	0 0015324
GO 0044450	microtubule organizing center part	CC	132	38	0 00013257
GO 0098978	glutamatergic synapse	CC	178	38	0 03374955
GO 0000776	kinetochore	CC	125	37	8 57E-05
GO 0044798	nuclear transcription factor complex	CC	146	37	0 00222507
GO 0000779	condensed chromosome centromeric region	CC	108	33	0 00010343
GO 0000777	condensed chromosome kinetochore	CC	97	31	6 52E-05
GO 0030427	site of polarized growth	CC	112	31	0 00109411
GO 0030426	growth cone	CC	111	30	0 00196207
GO 0090575	RNA polymerase transcription factor complex	CC	122	29	0 01558058
GO 0005814	centriole	CC	97	28	0 00092271
GO 0043296	apical junction complex	CC	103	25	0 01833303
GO 0070160	tight junction	CC	91	24	0 00732535
GO 0005923	bicellular tight junction	CC	87	22	0 01635945
GO 0097223	sperm part	CC	79	20	0 02114351
GO 0072686	mitotic spindle	CC	85	20	0 04375609
GO 0032155	cell division site part	CC	54	17	0 00333847
GO 0032153	cell division site	CC	57	17	0 00616686
GO 0032154	cleavage furrow	CC	46	16	0 0013708
GO 0001669	acrosomal vesicle	CC	46	15	0 00391655
GO 0090734	site of DNA damage	CC	55	15	0 0224885
GO 0005657	replication fork	CC	57	15	0 03062643
GO 0005871	kinesin complex	CC	39	13	0 00571023
GO 0031091	platelet alpha granule	CC	44	13	0 01690206
GO 0045171	intercellular bridge	CC	45	13	0 02039293
GO 1990391	DNA repair complex	CC	38	12	0 01240755
GO 0035861	site of double-strand break	CC	44	12	0 03884151
GO 0031093	platelet alpha granule lumen	CC	31	10	0 01857752
GO 0071782	endoplasmic reticulum tubular network	CC	20	7	0 02983908
GO 0044295	axonal growth cone	CC	20	7	0 02983908
GO 0035327	transcriptionally active chromatin	CC	20	7	0 02983908
GO 0008305	integrin complex	CC	16	6	0 03104621
GO 0098636	protein complex involved in cell adhesion	CC	16	6	0 03104621
GO 0000242	pericentriolar material	CC	17	6	0 04167676

GO 0031010	SW -type complex	CC	8	5	0 00376941
GO 0036513	Derlin-1 retrotranslocation complex	CC	9	5	0 00737104
GO 0032300	mismatch repair complex	CC	9	5	0 00737104
GO 0008278	cohesin complex	CC	9	5	0 00737104
GO 0016471	vacuolar proton-transporting V-type ATPase complex	CC	13	5	0 0432739
GO 0031616	spindle pole centrosome	CC	13	5	0 0432739
GO 0031262	Ndc80 complex	CC	4	4	0 00064645
GO 0033391	chromatoid body	CC	6	4	0 00738968
GO 0035748	myelin sheath abaxonal region	CC	6	4	0 00738968
GO 0030123	AP-3 adaptor complex	CC	8	4	0 02637563
GO 0030877	beta-catenin destruction complex	CC	9	4	0 0415793
GO 1990023	mitotic spindle midzone	CC	9	4	0 0415793
GO 0048188	Set1C/COMPASS complex	CC	9	4	0 0415793
GO 0031414	N-terminal protein acetyltransferase complex	CC	9	4	0 0415793
GO 0098536	deuterosome	CC	3	3	0 00405706
GO 0098981	cholinergic synapse	CC	4	3	0 0142889
GO 0031415	NatA complex	CC	4	3	0 0142889
GO 0035061	interchromatin granule	CC	4	3	0 0142889
GO 0016589	NURF complex	CC	5	3	0 03149163
GO 1990590	ATF1-ATF4 transcription factor complex	CC	2	2	0 02544967
GO 1990589	ATF4-CREB1 transcription factor complex	CC	2	2	0 02544967
GO 1990617	CHOP-ATF4 complex	CC	2	2	0 02544967
GO 0032301	MutSalpha complex	CC	2	2	0 02544967
GO 0005674	transcription factor TF F complex	CC	2	2	0 02544967
GO 0005900	oncostatin-M receptor complex	CC	2	2	0 02544967
GO 0034667	integrin alpha3-beta1 complex	CC	2	2	0 02544967
GO 0032302	MutSbeta complex	CC	2	2	0 02544967
GO 0000308	cytoplasmic cyclin-dependent protein kinase holoenzyme complex	CC	2	2	0 02544967
GO 0031372	UBC13-MMS2 complex	CC	2	2	0 02544967
GO 0032807	DNA ligase V complex	CC	2	2	0 02544967
GO 0044308	axonal spine	CC	2	2	0 02544967
GO 0031213	RSF complex	CC	2	2	0 02544967
GO 0071020	post-spliceosomal complex	CC	2	2	0 02544967
GO 1990112	RQC complex	CC	2	2	0 02544967
GO 0032116	SMC loading complex	CC	2	2	0 02544967
GO 0090694	Scc2-Scc4 cohesin loading complex	CC	2	2	0 02544967
GO 0036502	Derlin-1-V MP complex	CC	2	2	0 02544967
GO 0042720	mitochondrial inner membrane peptidase complex	CC	2	2	0 02544967
GO 0003674	molecular function	MF	9800	1601	0 00089365
GO 0005488	binding	MF	8891	1476	6 85E-05
GO 0005515	protein binding	MF	7495	1290	6 15E-08
GO 0097159	organic cyclic compound binding	MF	3968	681	0 00528269
GO 1901363	heterocyclic compound binding	MF	3934	676	0 00487938
GO 0003824	catalytic activity	MF	3860	650	0 03387451
GO 0043168	anion binding	MF	1765	315	0 0104944
GO 0036094	small molecule binding	MF	1646	294	0 01289431
GO 0019899	enzyme binding	MF	1640	289	0 02595502
GO 0000166	nucleotide binding	MF	1467	275	0 00116533
GO 1901265	nucleoside phosphate binding	MF	1467	275	0 00116533
GO 0140096	catalytic activity acting on a protein	MF	1509	269	0 01889628
GO 0097367	carbohydrate derivative binding	MF	1426	268	0 00116209
GO 0017076	purine nucleotide binding	MF	1301	250	0 0004633
GO 0032553	ribonucleotide binding	MF	1294	249	0 00043689
GO 0032555	purine ribonucleotide binding	MF	1286	248	0 00039221
GO 0035639	purine ribonucleoside triphosphate binding	MF	1250	244	0 00020437
GO 0008144	drug binding	MF	1135	217	0 0014823
GO 0140110	transcription regulator activity	MF	1224	217	0 0409362
GO 0042802	identical protein binding	MF	1100	213	0 00083799
GO 0030554	adenyl nucleotide binding	MF	1066	206	0 00113752
GO 0032559	adenyl ribonucleotide binding	MF	1053	204	0 00105635
GO 0005524	ATP binding	MF	1019	200	0 00059992
GO 0046983	protein dimerization activity	MF	778	146	0 01637497
GO 0044877	protein-containing complex binding	MF	743	144	0 00562456
GO 0008092	cytoskeletal protein binding	MF	594	133	1 53E-05
GO 0016462	pyrophosphatase activity	MF	631	123	0 00838328
GO 0016817	hydrolase activity acting on acid anhydrides	MF	633	123	0 00927524
GO 0016818	hydrolase activity acting on acid anhydrides in phosphorus-conta	MF	633	123	0 00927524
GO 0017111	nucleoside-triphosphatase activity	MF	597	119	0 00457015
GO 0016301	kinase activity	MF	576	107	0 04605819
GO 0019904	protein domain specific binding	MF	496	102	0 00320067
GO 0004672	protein kinase activity	MF	437	84	0 03549126
GO 0003682	chromatin binding	MF	392	77	0 0273333
GO 0016887	ATPase activity	MF	311	67	0 00518074
GO 0004674	protein serine/threonine kinase activity	MF	336	66	0 03868878
GO 0015631	tubulin binding	MF	218	59	1 74E-05
GO 0003779	actin binding	MF	253	53	0 0201512
GO 0001228	DNA-binding transcription activator activity RNA polymerase -spe	MF	249	51	0 03270073
GO 0044389	ubiquitin-like protein ligase binding	MF	252	51	0 03971148
GO 0031625	ubiquitin protein ligase binding	MF	238	50	0 02235539
GO 0008017	microtubule binding	MF	163	44	0 0002087
GO 0003714	transcription corepressor activity	MF	174	42	0 00314787
GO 0061630	ubiquitin protein ligase activity	MF	153	35	0 01537163
GO 0061659	ubiquitin-like protein ligase activity	MF	157	35	0 02237973
GO 0042393	histone binding	MF	157	34	0 03558382
GO 0008234	cysteine-type peptidase activity	MF	135	30	0 03389516

GO 0030674	protein binding bridging	MF	115	29	0 00677818
GO 0060090	molecular adaptor activity	MF	133	29	0 04558014
GO 0051015	actin filament binding	MF	116	27	0 02478394
GO 0003697	single-stranded DNA binding	MF	88	26	0 00094866
GO 0005516	calmodulin binding	MF	103	26	0 00986173
GO 0001085	RNA polymerase transcription factor binding	MF	101	25	0 0144078
GO 0002020	protease binding	MF	85	21	0 02402673
GO 0036459	thiol-dependent ubiquitinyl hydrolase activity	MF	84	20	0 03911389
GO 0101005	ubiquitinyl hydrolase activity	MF	84	20	0 03911389
GO 0005178	integrin binding	MF	66	19	0 00597887
GO 0008094	DNA-dependent ATPase activity	MF	73	19	0 01826845
GO 0003684	damaged DNA binding	MF	60	18	0 00458169
GO 0004197	cysteine-type endopeptidase activity	MF	72	18	0 03127329
GO 0019208	phosphatase regulator activity	MF	68	17	0 03567906
GO 0003777	microtubule motor activity	MF	50	15	0 0092318
GO 0003705	transcription factor activity RNA polymerase distal enhancer sec	MF	60	15	0 04659875
GO 0030165	PDZ domain binding	MF	53	14	0 0349222
GO 0019905	syntaxin binding	MF	42	12	0 02756272
GO 0001618	virus receptor activity	MF	45	12	0 04555009
GO 0104005	hijacked molecular function	MF	45	12	0 04555009
GO 0016877	ligase activity forming carbon-sulfur bonds	MF	26	10	0 00473171
GO 0016830	carbon-carbon lyase activity	MF	35	10	0 04232112
GO 0000217	DNA secondary structure binding	MF	18	9	0 00080749
GO 0016831	carboxy-lyase activity	MF	24	9	0 00878819
GO 0046915	transition metal ion transmembrane transporter activity	MF	29	9	0 03200708
GO 0048487	beta-tubulin binding	MF	30	9	0 0394567
GO 0043531	ADP binding	MF	31	9	0 04799818
GO 0030275	LRR domain binding	MF	15	8	0 00092532
GO 0001205	distal enhancer DNA-binding transcription activator activity RNA p	MF	23	8	0 02150582
GO 0070717	poly-purine tract binding	MF	25	8	0 03541272
GO 0008143	poly(A) binding	MF	19	7	0 02240425
GO 0008171	O-methyltransferase activity	MF	21	7	0 03876916
GO 0004364	glutathione transferase activity	MF	15	6	0 02235333
GO 0008574	ATP-dependent microtubule motor activity plus-end-directed	MF	16	6	0 03104621
GO 0016878	acid-thiol ligase activity	MF	16	6	0 03104621
GO 0043522	leucine zipper domain binding	MF	9	5	0 00737104
GO 0097153	cysteine-type endopeptidase activity involved in apoptotic process	MF	11	5	0 02045912
GO 0030983	mismatched DNA binding	MF	11	5	0 02045912
GO 0016405	CoA-ligase activity	MF	12	5	0 03054939
GO 0016783	sulfurtransferase activity	MF	12	5	0 03054939
GO 0038191	neuropilin binding	MF	13	5	0 0432739
GO 1990381	ubiquitin-specific protease binding	MF	13	5	0 0432739
GO 0032135	DNA insertion or deletion binding	MF	5	4	0 00282041
GO 0043515	kinetochore binding	MF	6	4	0 00738968
GO 0031957	very long-chain fatty acid-CoA ligase activity	MF	7	4	0 01507252
GO 0140035	ubiquitination-like modification-dependent protein binding	MF	7	4	0 01507252
GO 0140036	ubiquitin-dependent protein binding	MF	7	4	0 01507252
GO 0030306	ADP-ribosylation factor binding	MF	7	4	0 01507252
GO 0032404	mismatch repair complex binding	MF	9	4	0 0415793
GO 0032357	oxidized purine DNA binding	MF	9	4	0 0415793
GO 0015645	fatty acid ligase activity	MF	9	4	0 0415793
GO 0032138	single base insertion or deletion binding	MF	3	3	0 00405706
GO 0032142	single guanine insertion binding	MF	3	3	0 00405706
GO 0032143	single thymine insertion binding	MF	3	3	0 00405706
GO 0032137	guanine/thymine mispair binding	MF	4	3	0 0142889
GO 0005138	interleukin-6 receptor binding	MF	4	3	0 0142889
GO 0034594	phosphatidylinositol trisphosphate phosphatase activity	MF	4	3	0 0142889
GO 0032405	MutLalpha complex binding	MF	5	3	0 03149163
GO 0004448	isocitrate dehydrogenase activity	MF	5	3	0 03149163
GO 0004445	inositol-polyphosphate 5-phosphatase activity	MF	5	3	0 03149163
GO 0004679	AMP-activated protein kinase activity	MF	5	3	0 03149163
GO 0004597	peptide-aspartate beta-dioxygenase activity	MF	2	2	0 02544967
GO 0099626	voltage-gated calcium channel activity involved in regulation of pre	MF	2	2	0 02544967
GO 0008240	tripeptidyl-peptidase activity	MF	2	2	0 02544967
GO 0004132	dCMP deaminase activity	MF	2	2	0 02544967
GO 0008597	calcium-dependent protein serine/threonine phosphatase regulato	MF	2	2	0 02544967
GO 0050508	glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylg	MF	2	2	0 02544967
GO 0050509	N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase	MF	2	2	0 02544967
GO 0015057	thrombin-activated receptor activity	MF	2	2	0 02544967
GO 0004450	isocitrate dehydrogenase (NADP+) activity	MF	2	2	0 02544967
GO 0004924	oncostatin-M receptor activity	MF	2	2	0 02544967
GO 0004572	mannosyl-oligosaccharide 1 3-1 6-alpha-mannosidase activity	MF	2	2	0 02544967
GO 0032181	dinucleotide repeat insertion binding	MF	2	2	0 02544967
GO 0000406	double-strand/single-strand DNA junction binding	MF	2	2	0 02544967
GO 0061860	DNA clamp unloader activity	MF	2	2	0 02544967
GO 0004649	poly(ADP-ribose) glycohydrolase activity	MF	2	2	0 02544967