

Gene Report

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List Id: P35427	ribosomal protein L13A(Rpl13a)	Related Genes	Rattus norvegicus
CHROMOSOME	1,		
CYTOGENETIC_LOCATION	1q22,		
ENSEMBL_GENE_ID	ENSRNOG00000020618,		
ENTREZ_GENE_ID	317646,		
GENERIF_SUMMARY	Data show that EF1alpha, RPL13a and YWHAZ are suitable genes for the RT-qPCR analysis and comparison of several sources of human MSC during in vitro characterization and differentiation as well as in an ex vivo animal model of global cerebral ischemia., We evaluated copy number variation (CNV) for four genes in rat strains differing in nervous system excitability. rpl13a copy number is significantly reduced in hippocampus and bone marrow in rats with a high excitability threshold and stress,		
UNIPROT_ID	A0A1W2Q602_RAT, Q5RK10_RAT, RL13A_RAT,		
UP_COMMENT_FUNCTION	Associated with ribosomes but is not required for canonical ribosome function and has extra-ribosomal functions. Component of the GAIT (gamma interferon-activated inhibitor of translation) complex which mediates interferon-gamma-induced transcript-selective translation inhibition in inflammation processes. Upon interferon-gamma activation and subsequent phosphorylation dissociates from the ribosome and assembles into the GAIT complex which binds to stem loop-containing GAIT elements in the 3'-UTR of diverse inflammatory mRNAs (such as ceruplasmin) and suppresses their translation. In the GAIT complex interacts with m7G cap-bound eIF4G at or near the eIF3-binding site and blocks the recruitment of the 43S ribosomal complex. Involved in methylation of rRNA. {ECO:0000250 UniProtKB:P40429},,		
UP_COMMENT_PTM	Citruillinated by PADI4. {ECO:0000250 UniProtKB:P19253},, Phosphorylation at Ser-77 upon interferon-gamma treatment in macrophages involves a DAPK1-DAPK3 kinase cascade and is causing release from the ribosome, association with the GAIT complex and subsequent involvement in transcript-selective translation inhibition. {ECO:0000250 UniProtKB:P19253},,		
UP_COMMENT_SIMILARITY	Belongs to the universal ribosomal protein uL13 family. {ECO:0000256 ARBA:ARBA00006227, ECO:0000256 RuleBase:RU003877},, Belongs to the universal ribosomal protein uL13 family. {ECO:0000256 ARBA:ARBA00006227},, Belongs to the universal ribosomal protein uL13 family. {ECO:0000305},,		
UP_COMMENT_SUBCELLULAR_LOCATION	Cytoplasm {ECO:0000250 UniProtKB:P40429},,		
UP_COMMENT_SUBUNIT	Component of the 60S ribosome. Component of the GAIT complex. Interacts with EIF4G1. {ECO:0000250 UniProtKB:P40429},, Component of the 60S ribosome. Component of the GAIT complex. Interacts with EIF4G1. {ECO:0000256 ARBA:ARBA00026018},,		
List Id: F1LSW7	ribosomal protein L14(Rpl14)	Related Genes	Rattus norvegicus
CHROMOSOME	8,		
CYTOGENETIC_LOCATION	8q32,		
ENSEMBL_GENE_ID	ENSRNOG00000019007,		
ENTREZ_GENE_ID	65043,		
UNIPROT_ID	A0A0G2K570_RAT, A0A8I5ZPM1_RAT, B5DEM5_RAT, F1LSW7_RAT, RL14_RAT,		
UP_COMMENT_FUNCTION	Component of the large ribosomal subunit. The ribosome is a large ribonucleoprotein complex responsible for the synthesis of proteins in the cell. {ECO:0000250 UniProtKB:P50914},,		
UP_COMMENT_SIMILARITY	Belongs to the eukaryotic ribosomal protein eL14 family. {ECO:0000256 ARBA:ARBA00006592},, Belongs to the eukaryotic ribosomal protein eL14 family. {ECO:0000305},,		
UP_COMMENT_SUBCELLULAR_LOCATION	Cytoplasm {ECO:0000250 UniProtKB:P50914},,		
UP_COMMENT_SUBUNIT	Component of the large ribosomal subunit. {ECO:0000250 UniProtKB:P50914},,		

List Id: Q0QEW8	ribosomal protein L18(Rpl18)	Related Genes	Rattus norvegicus
CHROMOSOME	1,		
CYTOGENETIC_LOCATION	1q22,		
ENSEMBL_GENE_ID	ENSRNOG00000021035,		
ENTREZ_GENE_ID	81766,		
UNIPROT_ID	A0A0H2UHS7_RAT, A0A8I5YC25_RAT, A0A8I6A4M9_RAT, A0A8I6B2T7_RAT, A0A8I6GD73_RAT, Q0QEW8_RAT, RL18_RAT,		
UP_COMMENT_FUNCTION	Component of the large ribosomal subunit. The ribosome is a large ribonucleoprotein complex responsible for the synthesis of proteins in the cell. {ECO:0000250 UniProtKB:Q07020}., Component of the large ribosomal subunit. {ECO:0000256 ARBA:ARBA00002814}.,		
UP_COMMENT_SIMILARITY	Belongs to the eukaryotic ribosomal protein eL18 family. {ECO:0000256 ARBA:ARBA00006815}., Belongs to the eukaryotic ribosomal protein eL18 family. {ECO:0000305}.,		
UP_COMMENT_SUBCELLULAR_LOCATION	Cytoplasm, cytosol {ECO:0000250 UniProtKB:Q07020}. Cytoplasm {ECO:0000250 UniProtKB:Q07020}. Rough endoplasmic reticulum {ECO:0000250 UniProtKB:Q95342}. Note=Detected on cytosolic polysomes (By similarity). Detected in ribosomes that are associated with the rough endoplasmic reticulum (By similarity). {ECO:0000250 UniProtKB:Q07020, ECO:0000250 UniProtKB:Q95342}., Endoplasmic reticulum {ECO:0000256 ARBA:ARBA00004240}. Rough endoplasmic reticulum {ECO:0000256 ARBA:ARBA00004427}.,		
UP_COMMENT_SUBUNIT	Component of the large ribosomal subunit. {ECO:0000250 UniProtKB:Q07020}., Component of the large ribosomal subunit. {ECO:0000256 ARBA:ARBA00011133}.,		
List Id: Q6PDV8	ribosomal protein L22, pseudogene 2(Rpl22-ps2)	Related Genes	Rattus norvegicus
CHROMOSOME	4,		
CYTOGENETIC_LOCATION	4q34,		
ENSEMBL_GENE_ID	ENSRNOG00000011104, ENSRNOG00000028747,		
ENTREZ_GENE_ID	100360057,		
UNIPROT_ID	A0A8J8XZ98_RAT, Q6PDV8_RAT,		
UP_COMMENT_SIMILARITY	Belongs to the eukaryotic ribosomal protein eL22 family. {ECO:0000256 ARBA:ARBA00007817}.,		
List Id: F1M013	ribosomal protein L7A(Rpl7a)	Related Genes	Rattus norvegicus
CHROMOSOME	3,		
CYTOGENETIC_LOCATION	3p13,		
ENSEMBL_GENE_ID	ENSRNOG00000047737, ENSRNOG00000070974,		
ENTREZ_GENE_ID	296596,		
UNIPROT_ID	A0A8J8Y1F6_RAT, B0K021_RAT, F1M013_RAT, RL7A_RAT,		
UP_COMMENT_FUNCTION	Component of the large ribosomal subunit. The ribosome is a large ribonucleoprotein complex responsible for the synthesis of proteins in the cell. {ECO:0000250 UniProtKB:P62424}., Component of the ribosome. {ECO:0000256 RuleBase:RU367042}.,		
UP_COMMENT_SIMILARITY	Belongs to the eukaryotic ribosomal protein eL8 family. {ECO:0000256 ARBA:ARBA00007337, ECO:0000256 RuleBase:RU367042}., Belongs to the eukaryotic ribosomal protein eL8 family. {ECO:0000305}.,		
UP_COMMENT_SUBCELLULAR_LOCATION	Cytoplasm {ECO:0000250 UniProtKB:P62424}.,		
UP_COMMENT_SUBUNIT	Component of the large ribosomal subunit (By similarity). Interacts with CRY1 (By similarity). Interacts with DICER1, AGO2, TARBP2, MOV10 and EIF6; they form a large RNA-induced silencing complex (RISC) (By similarity). {ECO:0000250 UniProtKB:P12970, ECO:0000250 UniProtKB:P62424}.,		
List Id: P62250	ribosomal protein S16(Rps16)	Related Genes	Rattus norvegicus
CHROMOSOME	1,		
CYTOGENETIC_LOCATION	1q21,		
ENSEMBL_GENE_ID	ENSRNOG00000019578,		
ENTREZ_GENE_ID	140655,		
UNIPROT_ID	A0A1W2Q531_RAT, A0A8L2QED1_RAT, B0K038_RAT, Q5XFV9_RAT, Q6P3E1_RAT, RS16_RAT,		
UP_COMMENT_SIMILARITY	Belongs to the universal ribosomal protein uS9 family. {ECO:0000256 ARBA:ARBA00005251, ECO:0000256 RuleBase:RU003815}., Belongs to the universal ribosomal protein uS9 family. {ECO:0000305}.,		
List Id: M0RA26	ribosomal protein S27-like(LOC100362987)	Related Genes	Rattus norvegicus
CHROMOSOME	9,		
CYTOGENETIC_LOCATION	9q12,		
ENSEMBL_GENE_ID	ENSRNOG000000021159,		
ENTREZ_GENE_ID	100362987,		
UNIPROT_ID	M0RA26_RAT,		
UP_COMMENT_COFACTOR	Name=Zn(2+); Xref=ChEBI:CHEBI:29105; Evidence={ECO:0000256 ARBA:ARBA00001947}.,		
UP_COMMENT_SIMILARITY	Belongs to the eukaryotic ribosomal protein eS27 family. {ECO:0000256 ARBA:ARBA00010919}.,		
List Id: P62275	ribosomal protein S29(Rps29)	Related Genes	Rattus norvegicus
CHROMOSOME	6,		
CYTOGENETIC_LOCATION	6q24,		
ENSEMBL_GENE_ID	ENSRNOG00000004196,		
ENTREZ_GENE_ID	25348,		
UNIPROT_ID	A0A8I6GMA6_RAT, RS29_RAT,		
UP_COMMENT_COFACTOR	Name=Zn(2+); Xref=ChEBI:CHEBI:29105; Evidence={ECO:0000250 UniProtKB:P62273}; Note=Binds 1 zinc ion per subunit. {ECO:0000250 UniProtKB:P62273}., Name=Zn(2+); Xref=ChEBI:CHEBI:29105; Evidence={ECO:0000256 ARBA:ARBA00001947}.,		
UP_COMMENT_SIMILARITY	Belongs to the universal ribosomal protein uS14 family. {ECO:0000256 ARBA:ARBA00009083}., Belongs to the universal ribosomal protein uS14 family. {ECO:0000305}.,		
UP_COMMENT_SUBCELLULAR_LOCATION	Cytoplasm, cytosol {ECO:0000250 UniProtKB:P62273}. Cytoplasm {ECO:0000250 UniProtKB:P62273}. Rough endoplasmic reticulum {ECO:0000250 UniProtKB:Q6QAP6}. Note=Detected on cytosolic polysomes (By similarity). Detected in ribosomes that are associated with the rough endoplasmic reticulum (By similarity). {ECO:0000250 UniProtKB:P62273, ECO:0000250 UniProtKB:Q6QAP6}.,		
UP_COMMENT_SUBUNIT	Component of the 40S small ribosomal subunit. {ECO:0000250 UniProtKB:Q6QAP6}., Component of the 40S small ribosomal subunit. {ECO:0000256 ARBA:ARBA00011542}.,		

List Id: P62909	ribosomal protein S3(Rps3)	Related Genes	Rattus norvegicus
CHROMOSOME	1,		
CYTOGENETIC_LOCATION	1q32,		
ENSEMBL_GENE_ID	ENSRNOG00000017418 ,		
ENTREZ_GENE_ID	140654 ,		
GENERIF_SUMMARY	Findings define an extraribosomal role of RPS3 as a molecular switch that accommodates apoptotic induction to DNA repair through Akt-mediated phosphorylation.		
UNIPROT_ID	A0A815ZK30 RAT, A0A816A8D6 RAT, A0A8L2QCQ7 RAT, RS3 RAT,		
UP_COMMENT_CATALYTIC_ACTIVITY	Reaction=2'-deoxyribonucleotide-(2'-deoxyribose 5'-phosphate)-2'- deoxyribonucleotide-DNA = a 3'-end 2'-deoxyribonucleotide-(2,3- dehydro-2,3-deoxyribose 5'-phosphate)-DNA + a 5'-end 5'-monophospho- 2'-deoxyribonucleoside-DNA + H(+); Xref=Rhea:RHEA:66592, Rhea:RHEA- COMP:13180, Rhea:RHEA-COMP:16897, Rhea:RHEA-COMP:17067, ChEBI:ChEBI:15378, ChEBI:ChEBI:136412, ChEBI:ChEBI:157695, ChEBI:ChEBI:167181; EC=4.2.99.18; Evidence={ECO:0000250 UniProtKB:P23396};, Reaction=2'-deoxyribonucleotide-(2'-deoxyribose 5'-phosphate)-2'- deoxyribonucleotide-DNA = a 3'-end 2'-deoxyribonucleotide-(2,3- dehydro-2,3-deoxyribose 5'-phosphate)-DNA + a 5'-end 5'-monophospho- 2'-deoxyribonucleoside-DNA + H(+); Xref=Rhea:RHEA:66592, Rhea:RHEA- COMP:13180, Rhea:RHEA-COMP:16897, Rhea:RHEA-COMP:17067, ChEBI:ChEBI:15378, ChEBI:ChEBI:136412, ChEBI:ChEBI:157695, ChEBI:ChEBI:167181; EC=4.2.99.18; Evidence={ECO:0000256 ARBA:ARBA00024490};,		
UP_COMMENT_FUNCTION	Involved in translation as a component of the 40S small ribosomal subunit (By similarity). Has endonuclease activity and plays a role in repair of damaged DNA (PubMed:7775413). Cleaves phosphodiester bonds of DNAs containing altered bases with broad specificity and cleaves supercoiled DNA more efficiently than relaxed DNA (By similarity). Displays high binding affinity for 7,8-dihydro-8- oxoguanine (8-oxoG), a common DNA lesion caused by reactive oxygen species (ROS) (By similarity). Has also been shown to bind with similar affinity to intact and damaged DNA (By similarity). Stimulates the N- glycosylase activity of the base excision protein OGG1 (By similarity). Enhances the uracil excision activity of UNG1 (By similarity). Also stimulates the cleavage of the phosphodiester backbone by APEX1 (By similarity). When located in the mitochondrion, reduces cellular ROS levels and mitochondrial DNA damage. Has also been shown to negatively regulate DNA repair in cells exposed to hydrogen peroxide (By similarity). Plays a role in regulating transcription as part of the NF-kappa-B p65-p50 complex where it binds to the RELA/p65 subunit, enhances binding of the complex to DNA and promotes transcription of target genes (By similarity). Represses its own translation by binding to its cognate mRNA (By similarity). Binds to and protects TP53/p53 from MDM2-mediated ubiquitination (By similarity). Involved in spindle formation and chromosome movement during mitosis by regulating microtubule polymerization (By similarity). Involved in induction of apoptosis through its role in activation of CASP8 (By similarity). Induces neuronal apoptosis by interacting with the E2F1 transcription factor and acting synergistically with it to up-regulate pro-apoptotic proteins BCL2L1/BIM and HRK/Dp5 (By similarity). Interacts with TRADD following exposure to UV radiation and induces apoptosis by caspase-dependent JNK activation (By similarity). {ECO:0000250 UniProtKB:P23396, ECO:0000269 PubMed:7775413};,		
UP_COMMENT_PTM	Methylation by PRMT1 is required for import into the nucleolus and for ribosome assembly. {ECO:0000250 UniProtKB:P23396};, Phosphorylation at Thr-221 by CDK1 occurs mainly in G2/M phase. Phosphorylation by PRKCD occurs on a non-ribosomal-associated form which results in translocation of RPS3 to the nucleus and enhances its endonuclease activity. Phosphorylation on Ser-209 by IKKB in response to activation of the NF-kappa-B p65-p50 complex which enhances the association of RPS3 with importin-alpha and mediates the nuclear translocation of RPS3. Phosphorylation by MAPK is required for translocation to the nucleus following exposure of cells to DNA damaging agents such as hydrogen peroxide. Phosphorylation by PKB/AKT mediates RPS3 nuclear translocation, enhances RPS3 endonuclease activity and suppresses RPS3-induced neuronal apoptosis. {ECO:0000250 UniProtKB:P23396};, Sumoylation by SUMO1 enhances protein stability through increased resistance to proteolysis. Sumoylation occurs at one or more of the three consensus sites, Lys-18, Lys-214 and Lys-230. {ECO:0000250 UniProtKB:P23396};, Ubiquitinated. This is prevented by interaction with HSP90 which stabilizes the protein. Monoubiquitinated at Lys-214 by ZNF598 when a ribosome has stalled during translation of poly(A) sequences, leading to preclude synthesis of a long poly-lysine tail and initiate the ribosome quality control (RQC) pathway to degrade the potentially detrimental aberrant nascent polypeptide. {ECO:0000250 UniProtKB:P23396};, Ufmylated by UFL1. {ECO:0000250 UniProtKB:P62908};,		
UP_COMMENT_SIMILARITY	Belongs to the universal ribosomal protein uS3 family. {ECO:0000256 ARBA:ARBA00010761};, Belongs to the universal ribosomal protein uS3 family. {ECO:0000305};,		
UP_COMMENT_SUBCELLULAR_LOCATION	Cytoplasm {ECO:0000250 UniProtKB:P23396}. Nucleus {ECO:0000250 UniProtKB:P23396}. Nucleus, nucleolus {ECO:0000250 UniProtKB:P23396}. Mitochondrion inner membrane {ECO:0000250 UniProtKB:P23396}; Peripheral membrane protein {ECO:0000250 UniProtKB:P23396}. Cytoplasm, cytoskeleton, spindle {ECO:0000250 UniProtKB:P23396}. Note=In normal cells, located mainly in the cytoplasm with small amounts in the nucleus but translocates to the nucleus in cells undergoing apoptosis. Nuclear translocation is induced by DNA damaging agents such as hydrogen peroxide. Accumulates in the mitochondrion in response to increased ROS levels. Localizes to the spindle during mitosis. Localized in cytoplasmic mRNP granules containing untranslated mRNAs. {ECO:0000250 UniProtKB:P23396, ECO:0000250 UniProtKB:P62908};, Cytoplasm, cytoskeleton, spindle {ECO:0000256 ARBA:ARBA00004186}. Membrane {ECO:0000256 ARBA:ARBA00004170}; Peripheral membrane protein {ECO:0000256 ARBA:ARBA00004170}. Mitochondrion inner membrane {ECO:0000256 ARBA:ARBA00004637}; Peripheral membrane protein {ECO:0000256 ARBA:ARBA00004637}. Nucleus, nucleolus {ECO:0000256 ARBA:ARBA00004604};, Membrane {ECO:0000256 ARBA:ARBA00004170}; Peripheral membrane protein {ECO:0000256 ARBA:ARBA00004170}. Mitochondrion inner membrane {ECO:0000256 ARBA:ARBA00004637}; Peripheral membrane protein {ECO:0000256 ARBA:ARBA00004637};,		
UP_COMMENT_SUBUNIT	Component of the 40S small ribosomal subunit. Identified in a IGF2BP1-dependent mRNP granule complex containing untranslated mRNAs. Interacts with HNRPD. Interacts with PRMT1; the interaction methylates RPS3. Interacts with SUMO1; the interaction sumoylates RPS3. Interacts with UBC9. Interacts with CDK1; the interaction phosphorylates RPS3. Interacts with PRKCD; the interaction phosphorylates RPS3. Interacts with PKB/AKT; the interaction phosphorylates RPS3. Interacts with E2F1; the interaction occurs in the absence of nerve growth factor and increases transcription of pro-apoptotic proteins BCL2L1/BIM and HRK/Dp5. Interacts with the base excision repair proteins APEX1 and OGG1; interaction with OGG1 increases OGG1 N-glycosylase activity. Interacts with UNG; the interaction increases the uracil excision activity of UNG1. Interacts with HSP90; the interaction prevents the ubiquitination and proteasome-dependent degradation of RPS3 and is suppressed by increased ROS levels. Interacts with TOM70; the interaction promotes translocation of RPS3 to the mitochondrion. Interacts (via N-terminus) with RELA (via N-terminus); the interaction enhances the DNA-binding activity of the NF-kappa-B p65-p50 complex. Interacts with NFKBIA; the interaction is direct and may bridge the interaction between RPS3 and RELA. Interacts with IKKB; the interaction phosphorylates RPS3 and enhances its translocation to the nucleus. Interacts (via KH domain) with MDM2 and TP53. Interacts with TRADD. Interacts with CRY1. {ECO:0000250 UniProtKB:P23396, ECO:0000250 UniProtKB:P62908};,		
List Id: P62083	ribosomal protein S7(Rps7)	Related Genes	Rattus norvegicus
CHROMOSOME	6,		
CYTOGENETIC_LOCATION	6q16,		
ENSEMBL_GENE_ID	ENSRNOG00000008373 ,		
ENTREZ_GENE_ID	29258 ,		
UNIPROT_ID	A0A816ABK7 RAT, A0A8L2Q5A3 RAT, A0A8L2RB77 RAT, B5DEL9 RAT, RS7 RAT,		
UP_COMMENT_FUNCTION	Required for rRNA maturation. {ECO:0000250 UniProtKB:P62081};, Required for rRNA maturation. {ECO:0000256 ARBA:ARBA00003567};,		
UP_COMMENT_PTM	Phosphorylated by NEK6. {ECO:0000250 UniProtKB:P62081};, Ubiquitinated. Deubiquitinated by DESI2, leading to its stabilization. {ECO:0000250 UniProtKB:P62081};,		
UP_COMMENT_SIMILARITY	Belongs to the eukaryotic ribosomal protein eS7 family. {ECO:0000256 ARBA:ARBA00007820, ECO:0000256 RuleBase:RU364105};, Belongs to the eukaryotic ribosomal protein eS7 family. {ECO:0000305};,		
UP_COMMENT_SUBCELLULAR_LOCATION	Cytoplasm, cytoskeleton, microtubule organizing center, centrosome {ECO:0000250 UniProtKB:P62081}. Cytoplasm {ECO:0000250 UniProtKB:P62081}. Nucleus {ECO:0000250 UniProtKB:P62081}. Note=Although RPS7 is functional within the cytoplasm, the assembly of ribosomal subunits occurs in the nucleus. RPS7 nuclear import is mediated by IPO5/RanBP5, IPO7/RanBP7, KPNB1/importin-beta or TPNO1/Trn (By similarity). Colocalizes with NEK6 in the centrosome (By similarity). {ECO:0000250 UniProtKB:P62081};,		
UP_COMMENT_SUBUNIT	Binds IPO9 with high affinity (By similarity). Interacts with NEK6 (By similarity). Interacts with DESI2 (By similarity). Interacts with IPO5, IPO7 and KPNB1; these interactions may be involved in RPS7 nuclear import for the assembly of ribosomal subunits (By similarity). {ECO:0000250 UniProtKB:P62081};,		
List Id: A0A0H2UHU0	ribosomal protein s25(Rps25)	Related Genes	Rattus norvegicus
CHROMOSOME	8,		
CYTOGENETIC_LOCATION	8q22,		
ENSEMBL_GENE_ID	ENSRNOG000000027503 ,		
ENTREZ_GENE_ID	122799 ,		
UNIPROT_ID	A0A0H2UHU0 RAT, A0A815ZLX3 RAT, A0A816GLY7 RAT, RS25 RAT,		
UP_COMMENT_SIMILARITY	Belongs to the eukaryotic ribosomal protein eS25 family. {ECO:0000256 ARBA:ARBA00009106, ECO:0000256 RuleBase:RU366057};, Belongs to the eukaryotic ribosomal protein eS25 family. {ECO:0000305};,		