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PANTHER GENE INFORMATION ?

Gene ID: [MGI:1349462](#)Protein ID: [Q9DBK7](#)

Gene Name: MCG18845, isoform CRA_d

Gene Symbol(s): Uba7

Organism: Mus musculus

Alternate Ids: NP_076227(refSeq) AL731808(SwissProt ID)
Q9DBK7(Alias Gene Symbol) BAB23650(SwissProt accession)
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PANTHER CLASSIFICATION

PANTHER Family: [UBIQUITIN-ACTIVATING ENZYME E1 \(PTHR10953\)](#)PANTHER Subfamily: [UBIQUITIN-LIKE MODIFIER-ACTIVATING ENZYME 7 \(PTHR10953:SF170\)](#)[Tree](#) [MSA](#) [Evolutionary History](#)PANTHER GO-slim Molecular Function: [catalytic activity](#)↳ [ligase activity](#)↳ [ubiquitin-protein ligase activity](#)PANTHER GO-slim Biological Process: [metabolic process](#)↳ [catabolic process](#)[cellular process](#)↳ [primary metabolic process](#)↳ [protein metabolic process](#)↳ [cellular protein modification process](#)↳ [proteolysis](#)

PANTHER GO-slim Cellular Component:

[cell part](#)
 ↳ [intracellular](#)
 ↳ [cytoplasm](#)
 ↳ [cytosol](#)

[organelle](#)
 ↳ [nucleus](#)

PANTHER protein class:

[ligase](#)
[transfer/carrier protein](#)

Pathway Categories:

[Ubiquitin proteasome pathway](#)
 ↳ [Ubiquitin activating enzyme E1](#)

[Ubiquitin proteasome pathway](#)
 ↳ [Ubiquitin protein ligase E3](#)

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GO MF Complete: [ubiquitin-protein transferase activity](#), [ISG15 activating enzyme activity](#), [ubiquitin activating enzyme activity](#)GO BP Complete: [ISG15-protein conjugation](#), [cellular protein modification process](#), [modification-dependent protein catabolic process](#)GO CC Complete: [nucleus](#), [cytosol](#)

ORTHOLOGS

ID	Organism	Type 
HUMAN HGNC=12471 UniProtKB=P41226	Homo sapiens	LDO
PANTR Ensembl=ENSPTRG00000014936 UniProtKB=H2QMM5	Pan troglodytes	LDO
MACMU Ensembl=ENSMMUG00000020980 UniProtKB=F7HMU2	Macaca mulatta	LDO
RAT RGD=1308323 UniProtKB=A0A0G2K735	Rattus norvegicus	LDO
BOVIN Ensembl=ENSBTAG00000012335 UniProtKB=Q5GF34	Bos taurus	LDO
PIG Ensembl=ENSSSCG00000011393 UniProtKB=F1SPR0	Sus scrofa	LDO
HORSE Ensembl=ENSECAG00000019670 UniProtKB=F7CFS8	Equus caballus	LDO
FELCA Ensembl=ENSFCAG00000010680 UniProtKB=M3WDO3	Felis catus	LDO
CANFA Ensembl=ENSCAFG00000011164 UniProtKB=E2OYA0	Canis familiaris	LDO
MONDO Ensembl=ENSMODG00000012394 UniProtKB=F6PN80	Monodelphis domestica	O
MONDO Ensembl=ENSMODG00000010677 UniProtKB=F7C1J2	Monodelphis domestica	O
ORNANI Ensembl=ENSOANG00000012650 UniProtKB=F7BTM7	Ornithorhynchus anatinus	O
CHICK Ensembl=ENSGALG00000002521 UniProtKB=F1P543	Gallus gallus	O
ANOCA Ensembl=ENSACAG00000007320 UniProtKB=G1KGJ3	Anolis carolinensis	O

ANOCA Ensembl=ENSACAG00000005270 UniProtKB=G1KE14	Anolis carolinensis	O
XENTRI Gene=Xenbase=XB-GENE-5874064 UniProtKB=F6UG64	Xenopus tropicalis	O
TAKRUJ Ensembl=ENSTRUG00000009466 UniProtKB=H2TGI0	Takifugu rubripes	O
DANRE ZFIN=ZDB-GENE-121120-4 UniProtKB=E7EYF3	Danio rerio	O
TAKRUJ Ensembl=ENSTRUG00000010472 UniProtKB=H2TNX7	Takifugu rubripes	O
DANRE ZFIN=ZDB-GENE-040426-2009 UniProtKB=F1RCA1	Danio rerio	O
BRAFL Gene=BRAFLDRAFT_255626 UniProtKB=C3ZZI8	Branchiostoma floridae	O
CIOINI Ensembl=ENSCING00000007869 UniProtKB=F6U4V1	Ciona intestinalis	O
STRPU EnsemblGenome=SPU_021701 UniProtKB=W4ZOR6	Strongylocentrotus purpuratus	O
CAEEL WormBase=WBGene00006699 UniProtKB=Q27481	Caenorhabditis elegans	O
CAEBRI Gene=CBG03440 UniProtKB=A8WV26	Caenorhabditis briggsae	O
PRIPA Gene=PPA11652 UniProtKB=H3EPF1	Pristionchus pacificus	O
DROME FlyBase=FBgn0023143 UniProtKB=Q8T0L3	Drosophila melanogaster	O
DAPPU EnsemblGenome=DAPPUDRAFT_186898 UniProtKB=E9FRU9	Daphnia pulex	O
IXOSC EnsemblGenome=ISCW019123 UniProtKB=B7PR84	Ixodes scapularis	O
SCHMA EnsemblGenome=Smp_162630 UniProtKB=G4VH12	Schistosoma mansoni	O
NEMVE EnsemblGenome=NEMVEDRAFT_v1q129964 UniProtKB=A7SSG6	Nematostella vectensis	O
NEMVE EnsemblGenome=NEMVEDRAFT_v1q69055 UniProtKB=A7T5P1	Nematostella vectensis	O
TRIAD EnsemblGenome=TriadG25768 UniProtKB=B3RWM5	Trichoplax adhaerens	O
MONBE Gene=33365 UniProtKB=A9V503	Monosiga brevicollis	O
YEAST SGD=S000001693 UniProtKB=P22515	Saccharomyces cerevisiae	O
ASHGO EnsemblGenome=AGOS_AFR433C UniProtKB=Q752Y8	Ashbya gossypii	O
CANAL Gene=CGD=CAL0005518 UniProtKB=Q5A2X3	Candida albicans	O
YARLI EnsemblGenome=YALIO_E06017q UniProtKB=Q6C6V1	Yarrowia lipolytica	O
EMENI EnsemblGenome=CADANIAG00008853 UniProtKB=C8VMA9	Emericella nidulans	O
NEUCRI EnsemblGenome=EFNCRG00000005233 UniProtKB=Q7RWR0	Neurospora crassa	O
SCLS1 EnsemblGenome=SS1G_08259 UniProtKB=A7ESF4	Sclerotinia sclerotiorum	O
PHANO EnsemblGenome=SNOG_08557 UniProtKB=Q0UI57	Phaeosphaeria nodorum	O
SCHPO PomBase=SPBC1604.21c UniProtKB=O94609	Schizosaccharomyces pombe	O
CRYNJ EnsemblGenome=CNA01230 UniProtKB=Q5KPX3	Cryptococcus neoformans	O
USTMA Gene=UMAG_06188 UniProtKB=A0A0D1CFJ5	Ustilago maydis	O
PUCGT EnsemblGenome=PGTG_07941 UniProtKB=E3KBL0	Puccinia graminis	O
BATDJ Gene=BATDEDRAFT_19117 UniProtKB=F4NY58	Batrachochytrium dendrobatidis	O
ENTHI EnsemblGenome=EH1_038690 UniProtKB=B1N360	Entamoeba histolytica	O
ENTHI EnsemblGenome=EH1_020270 UniProtKB=C4M7T9	Entamoeba histolytica	O
DICDI dictyBase=DDB_G0270272 UniProtKB=Q55C16	Dictyostelium discoideum	O
DICPU Gene=DICPUDRAFT_96719 UniProtKB=F0ZAP3	Dictyostelium purpureum	O
PLAF7 EnsemblGenome=PF13_0264 UniProtKB=C0H5H9	Plasmodium falciparum	O
PLAF7 EnsemblGenome=PF13_0182 UniProtKB=Q8IDZ6	Plasmodium falciparum	O

PLAF7 EnsemblGenome=PF11_0457 UniProtKB=Q8IHS2	Plasmodium falciparum	O
PLAF7 EnsemblGenome=PFL1245w UniProtKB=Q8I5F9	Plasmodium falciparum	O
TETTS EnsemblGenome=TTHERM_00519760 UniProtKB=I7M167	Tetrahymena thermophila	O
TETTS EnsemblGenome=TTHERM_00450930 UniProtKB=Q238S6	Tetrahymena thermophila	O
TETTS EnsemblGenome=TTHERM_00481290 UniProtKB=I7M1M7	Tetrahymena thermophila	O
TETTS EnsemblGenome=TTHERM_00997780 UniProtKB=Q23QY3	Tetrahymena thermophila	O
TETTS EnsemblGenome=TTHERM_00149190 UniProtKB=I7ML74	Tetrahymena thermophila	O
TETTS EnsemblGenome=TTHERM_00311940 UniProtKB=Q22KT5	Tetrahymena thermophila	O
TETTS EnsemblGenome=TTHERM_00125358 UniProtKB=A4VDU7	Tetrahymena thermophila	O
TETTS EnsemblGenome=TTHERM_00028560 UniProtKB=Q22N18	Tetrahymena thermophila	O
TETTS EnsemblGenome=TTHERM_00241900 UniProtKB=I7M407	Tetrahymena thermophila	O
THAPS Gene=Thaps262047 UniProtKB=B8C120	Thalassiosira pseudonana	O
THAPS Gene=Thaps268541 UniProtKB=B8BYU7	Thalassiosira pseudonana	O
PHYIT EnsemblGenome=PITG_07036 UniProtKB=D0N735	Phytophthora infestans	O
PHYIT EnsemblGenome=PITG_05690 UniProtKB=D0N3G3	Phytophthora infestans	O
LEIMA EnsemblGenome=LmjF.35.3060 UniProtKB=E9AFD0	Leishmania major	O
TRYB2 Gene=Tb09.211.3610 UniProtKB=Q38DE8	Trypanosoma brucei	O
LEIMA EnsemblGenome=LmjF.23.0550 UniProtKB=Q9NF77	Leishmania major	O
TRYB2 Gene=Tb927.8.2640 UniProtKB=Q57XC5	Trypanosoma brucei	O
GIAIC EnsemblGenome=GL50803_10661 UniProtKB=A8BBP6	Giardia intestinalis	O
TRIVA Gene=TVAG_300590 UniProtKB=A2EP39	Trichomonas vaginalis	O
TRIVA Gene=TVAG_369470 UniProtKB=A2G7V0	Trichomonas vaginalis	O
TRIVA Gene=TVAG_006110 UniProtKB=A2E718	Trichomonas vaginalis	O
TRIVA Gene=TVAG_446890 UniProtKB=A2E8P8	Trichomonas vaginalis	O
TRIVA Gene=TVAG_455710 UniProtKB=A2G060	Trichomonas vaginalis	O
CHLRE EnsemblGenome=CHLREDRAFT_170220 UniProtKB=A8IPB5	Chlamydomonas reinhardtii	O
CHLRE EnsemblGenome=CHLREDRAFT_191903 UniProtKB=A8J1C1	Chlamydomonas reinhardtii	O
SORBI EnsemblGenome=Sb01q038300 UniProtKB=C5WNH5	Sorghum bicolor	O
ORYSJ Gene=LOC_Os03q18380 UniProtKB=Q10MU6	Oryza sativa	O
BRADI EnsemblGenome=BRADI1G65330 UniProtKB=I1H6H7	Brachypodium distachyon	O
SORBI EnsemblGenome=Sb02q043880 UniProtKB=C5X6F4	Sorghum bicolor	O
ORYSJ Gene=Os07q0692900 UniProtKB=Q84NQ2	Oryza sativa	O
BRADI EnsemblGenome=BRADI1G16680 UniProtKB=I1GOV9	Brachypodium distachyon	O
SOYBN EnsemblGenome=GLYMA14G37610 UniProtKB=I1MBE2	Glycine max	O
SOYBN EnsemblGenome=GLYMA02G39495 UniProtKB=K7KA83	Glycine max	O
SORBI EnsemblGenome=Sb05q000520 UniProtKB=C5Y2Z7	Sorghum bicolor	O
SORBI EnsemblGenome=Sb08q000540 UniProtKB=C5YQ24	Sorghum bicolor	O
ORYSJ EnsemblGenome=OS11G0106400 UniProtKB=Q2RBM4	Oryza sativa	O
BRADI EnsemblGenome=BRADI4G44880 UniProtKB=I1IV69	Brachypodium distachyon	O

BRADI EnsemblGenome=BRADI4G26790 UniProtKB=I1INX4	Brachypodium distachyon	O
SOLLC EnsemblGenome=Solyc06g007320.2 UniProtKB=K4C3B5	Solanum lycopersicum	O
SOLLC EnsemblGenome=Solyc09g018450.2 UniProtKB=K4CSA9	Solanum lycopersicum	O
VITVI EnsemblGenome=VIT_08s0058g00320 UniProtKB=F6GXU4	Vitis vinifera	O
VITVI EnsemblGenome=VIT_06s0004g07060 UniProtKB=F6GUM1	Vitis vinifera	O
ARATH TAIR=AT2G30110 UniProtKB=P93028	Arabidopsis thaliana	O
ARATH TAIR=AT5G06460 UniProtKB=P92974	Arabidopsis thaliana	O
SOYBN EnsemblGenome=GLYMA11G29302 UniProtKB=K7LR00	Glycine max	O
SOYBN EnsemblGenome=GLYMA18G06620 UniProtKB=I1MZW3	Glycine max	O
POPTR EnsemblGenome=POPTR_0009s07950 UniProtKB=B9HNB1	Populus trichocarpa	O
POPTR EnsemblGenome=POPTR_0001s28750 UniProtKB=B9GGR5	Populus trichocarpa	O
POPTR EnsemblGenome=POPTR_0009s07960 UniProtKB=B9HNB0	Populus trichocarpa	O
PHYPA Gene=PHYPADRAFT_139758 UniProtKB=A9T3V0	Physcomitrella patens	O
PHYPA Gene=PHYPADRAFT_150825 UniProtKB=A9TU56	Physcomitrella patens	O
PHYPA Gene=PHYPADRAFT_129081 UniProtKB=A9SFQ4	Physcomitrella patens	O
PHYPA Gene=PHYPADRAFT_174245 UniProtKB=A9REZ6	Physcomitrella patens	O
KORCO EnsemblGenome=Kcr_0737 UniProtKB=B1L4V7	Korarchaeum cryptofilum	O
SULSO EnsemblGenome=SSO0298 UniProtKB=Q980J4	Sulfolobus solfataricus	O
PYRAE EnsemblGenome=PAE1056 UniProtKB=Q8ZXW7	Pyrobaculum aerophilum	O
METAC EnsemblGenome=MA_0255 UniProtKB=Q8TU19	Methanosarcina acetivorans	O
HALSA EnsemblGenome=VNG_0084G UniProtKB=Q9HST5	Halobacterium salinarum	O
PYRKO EnsemblGenome=TK2117 UniProtKB=Q5JEX2	Pyrococcus kodakaraensis	O
CLOBH EnsemblGenome=CLC_1879 UniProtKB=A5I358	Clostridium botulinum	O
STAA8 EnsemblGenome=SAOUHSC_02545 UniProtKB=Q2FVX7	Staphylococcus aureus	O
LISMO Gene=CAC99127 UniProtKB=Q8Y868	Listeria monocytogenes	O
BACSU EnsemblGenome=BSU14270 UniProtKB=O31702	Bacillus subtilis	O
BACSU EnsemblGenome=BSU11700 UniProtKB=O31619	Bacillus subtilis	O
BACCR EnsemblGenome=BC_4723 UniProtKB=Q816U3	Bacillus cereus	O
BACCR EnsemblGenome=BC_2124 UniProtKB=Q81E67	Bacillus cereus	O
BACCR EnsemblGenome=BC_0750 UniProtKB=Q81HQ4	Bacillus cereus	O
STRCO Gene=CAC01308 UniProtKB=Q9FCL0	Streptomyces coelicolor	O
MYCTU EnsemblGenome=P425_03247 UniProtKB=L7N674	Mycobacterium tuberculosis	O
MYCTU EnsemblGenome=Rv3116 UniProtKB=L7N674	Mycobacterium tuberculosis	O
MYCTU EnsemblGenome=RVBD_3116 UniProtKB=L7N674	Mycobacterium tuberculosis	O
MYCTU EnsemblGenome=Rv3206c UniProtKB=P9WMN7	Mycobacterium tuberculosis	O
DEIRA EnsemblGenome=DR_2269 UniProtKB=Q9RS58	Deinococcus radiodurans	O
CHLAA EnsemblGenome=Caur_3492 UniProtKB=A9W9Z4	Chloroflexus aurantiacus	O
GLOVI Gene=BAC91353 UniProtKB=Q7NFW2	Gloeobacter violaceus	O
SYNY3 Gene=BAD02110 UniProtKB=Q6YRV1	Synechocystis	O

SYNY3 Gene=BAA18438 UniProtKB=P74344	Synechocystis	O
BACTNI EnsemblGenome=BT_0648 UniProtKB=Q8AA17	Bacteroides thetaiotaomicron	O
AQUAE EnsemblGenome=aq_1329 UniProtKB=O67348	Aquifex aeolicus	O
RHOBAL EnsemblGenome=RB12145 UniProtKB=Q7UJ43	Rhodopirellula baltica	O
THEYD EnsemblGenome=THEYE_A1987 UniProtKB=B5YIE5	Thermodesulfovibrio yellowstonii	O
GEOSLI EnsemblGenome=GSU0654 UniProtKB=Q74FF5	Geobacter sulfurreducens	O
GEOSLI EnsemblGenome=GSU0907 UniProtKB=Q74EQ5	Geobacter sulfurreducens	O
GEOSLI EnsemblGenome=GSU1350 UniProtKB=Q74DG6	Geobacter sulfurreducens	O
BRAJAL Gene=BAC46030 UniProtKB=Q89WC6	Bradyrhizobium japonicum	O
SHEONI EnsemblGenome=SO_2443 UniProtKB=Q8EED9	Shewanella oneidensis	O
VIBCHI EnsemblGenome=VC_0063 UniProtKB=Q9KVS6	Vibrio cholerae	O
SALTY EnsemblGenome=STM4162 UniProtKB=Q9L9I9	Salmonella typhimurium	O
YERPE EnsemblGenome=y0489 UniProtKB=Q7CKT8	Yersinia pestis	O
YERPE EnsemblGenome=YP_3104 UniProtKB=Q7CKT8	Yersinia pestis	O
YERPE EnsemblGenome=DJ56_3464 UniProtKB=Q7CKT8	Yersinia pestis	O
ECOLI EcoGene=EG11587 UniProtKB=P30138	Escherichia coli	O
COXBU EnsemblGenome=CBU_0876 UniProtKB=Q83D65	Coxiella burnetii	O
HAEIN EnsemblGenome=HI_1449 UniProtKB=P45211	Haemophilus influenzae	O
SHEONI EnsemblGenome=SO_0137 UniProtKB=Q8EKF6	Shewanella oneidensis	O
VIBCHI EnsemblGenome=VC_A0618 UniProtKB=Q9KLX3	Vibrio cholerae	O
XANCP EnsemblGenome=XCC1989 UniProtKB=Q8P977	Xanthomonas campestris	O
PSEAE EnsemblGenome=PA4663 UniProtKB=Q9HVC9	Pseudomonas aeruginosa	O
PSEAE EnsemblGenome=PA2103 UniProtKB=Q9I212	Pseudomonas aeruginosa	O
SALTY EnsemblGenome=STM0845 UniProtKB=Q56067	Salmonella typhimurium	O
YERPE Gene=YPO1494 UniProtKB=Q0WGS8	Yersinia pestis	O
ECOLI EcoGene=EG10154 UniProtKB=P12282	Escherichia coli	O

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