



Stem Cell Research Literatures

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Abstract: Stem cells are derived from embryonic and non-embryonic tissues. Most stem cell studies are for animal stem cells and plants have also stem cell. Stem cells were discovered in 1981 from early mouse embryos. Stem cells have the potential to develop into all different cell types in the living body. Stem cell is a body repair system. When a stem cell divides it can be still a stem cell or become adult cell, such as a brain cell. Stem cells are unspecialized cells and can renew themselves by cell division, and stem cells can also differentiate to adult cells with special functions. Stem cells replace the old cells and repair the damaged tissues. Embryonic stem cells can become all cell types of the body because they are pluripotent. Adult stem cells are thought to be limited to differentiating into different cell types of their tissue of origin. This article introduces recent research reports as references in the related studies.

[Herbert M. **Stem Cell Research Literatures**. *Stem Cell* 2020;11(4):30-110]. ISSN: 1945-4570 (print); ISSN: 1945-4732 (online). <http://www.sciencepub.net/stem>. 4. doi: [10.7537/marsscj110420.04](https://doi.org/10.7537/marsscj110420.04).

Key words: stem cell; life; research; literature; gene

Introduction

The stem cell is the origin of an organism's life that has the potential to develop into many different types of cells in life bodies. In many tissues stem cells serve as a sort of internal repair system, dividing essentially without limit to replenish other cells as long as the person or animal is still alive. When a stem cell divides, each new cell has the potential either to remain a stem cell or become another type of cell with a more specialized function, such as a red blood cell or a brain cell. This article introduces recent research reports as references in the related studies.

The following introduces stem cell gens as references in the related studies.

Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

NCBI Reference Sequence: NC_045512.2

LOCUS NC_045512 29903 bp ss-RNA linear VRL 18-JUL-2020

DEFINITION Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome.

ACCESSION NC_045512

VERSION NC_045512.2

DBLINK BioProject: [PRJNA485481](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA485481)

KEYWORDS RefSeq.

SOURCE Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)

ORGANISM [Severe acute respiratory syndrome coronavirus 2](#)

Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;
Nidovirales; Coronaviridae; Orthocoronavirinae;
Betacoronavirus; Sarbecovirus.

REFERENCE 1 (bases 1 to 29903)

AUTHORS Wu,F., Zhao,S., Yu,B., Chen,Y.M., Wang,W., Song,Z.G., Hu,Y.,
Tao,Z.W., Tian,J.H., Pei,Y.Y., Yuan,M.L., Zhang,Y.L., Dai,F.H.,
Liu,Y., Wang,Q.M., Zheng,J.J., Xu,L., Holmes,E.C. and Zhang,Y.Z.

TITLE A new coronavirus associated with human respiratory disease in
China

JOURNAL Nature 579 (7798), 265-269 (2020)

PUBMED [32015508](https://pubmed.ncbi.nlm.nih.gov/32015508/)

REMARK Erratum:[Nature. 2020 Apr;580(7803):E7. PMID: 32296181]

REFERENCE 2 (bases 13476 to 13503)
 AUTHORS Baranov,P.V., Henderson,C.M., Anderson,C.B., Gesteland,R.F.,
 Atkins,J.F. and Howard,M.T.
 TITLE Programmed ribosomal frameshifting in decoding the SARS-CoV genome
 JOURNAL Virology 332 (2), 498-510 (2005)
 PUBMED [15680415](#)

REFERENCE 3 (bases 29728 to 29768)
 AUTHORS Robertson,M.P., Igel,H., Baertsch,R., Haussler,D., Ares,M. Jr. and
 Scott,W.G.
 TITLE The structure of a rigorously conserved RNA element within the SARS
 virus genome
 JOURNAL PLoS Biol 3 (1), e5 (2005)
 PUBMED [15630477](#)

REFERENCE 4 (bases 29609 to 29657)
 AUTHORS Williams,G.D., Chang,R.Y. and Brian,D.A.
 TITLE A phylogenetically conserved hairpin-type 3' untranslated region
 pseudoknot functions in coronavirus RNA replication
 JOURNAL J Virol 73 (10), 8349-8355 (1999)
 PUBMED [10482585](#)

REFERENCE 5 (bases 1 to 29903)
 CONSRTM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (17-JAN-2020) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

REFERENCE 6 (bases 1 to 29903)
 AUTHORS Wu,F., Zhao,S., Yu,B., Chen,Y.-M., Wang,W., Hu,Y., Song,Z.-G.,
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 Dai,F.-H., Liu,Y., Wang,Q.-M., Zheng,J.-J., Xu,L., Holmes,E.C. and
 Zhang,Y.-Z.
 TITLE Direct Submission
 JOURNAL Submitted (05-JAN-2020) Shanghai Public Health Clinical Center &
 School of Public Health, Fudan University, Shanghai, China

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The
 reference sequence is identical to [MN908947](#).
 On Jan 17, 2020 this sequence version replaced [NC_045512.1](#).
 Annotation was added using homology to SARSr-CoV NC_004718.3. ###
 Formerly called 'Wuhan seafood market pneumonia virus.' If you have
 questions or suggestions, please email us at info@ncbi.nlm.nih.gov
 and include the accession number NC_045512.### Protein structures
 can be found at
<https://www.ncbi.nlm.nih.gov/structure/?term=sars-cov-2.###> Find
 all other Severe acute respiratory syndrome coronavirus 2
 (SARS-CoV-2) sequences at
<https://www.ncbi.nlm.nih.gov/genbank/sars-cov-2-seqs/>

##Assembly-Data-START##
 Assembly Method :: Megahit v. V1.1.3
 Sequencing Technology :: Illumina
 ##Assembly-Data-END##
 COMPLETENESS: full length.

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[mat peptide](#) 266..805

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/product="leader protein"

/note="nsp1; produced by both pp1a and pp1ab"

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3'UTR 29675..29903

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 (NC_004718.3)"
 /function="Coronavirus 3' stem-loop II-like motif (s2m)"

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Rattus norvegicus troponin T2, cardiac type (Tnnt2), mRNA

NCBI Reference Sequence: NM_012676.1

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LOCUS NM_012676 1096 bp mRNA linear ROD 06-DEC-2020

DEFINITION Rattus norvegicus troponin T2, cardiac type (Tnnt2), mRNA.

ACCESSION NM_012676

VERSION NM_012676.1

KEYWORDS RefSeq.

SOURCE *Rattus norvegicus* (Norway rat)

ORGANISM [Rattus norvegicus](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Muridae; Murinae; *Rattus*.

REFERENCE 1 (bases 1 to 1096)

AUTHORS Muslimovic A, Friden V, Tenstad O, Starnberg K, Nystrom S, Wesen E,
Esbjorner EK, Granholm K, Lindahl B and Hammarsten O.

TITLE The Liver and Kidneys mediate clearance of cardiac troponin in the
rat

JOURNAL Sci Rep 10 (1), 6791 (2020)

PUBMED [32322013](#)

REMARK GeneRIF: The Liver and Kidneys mediate clearance of cardiac
troponin in the rat.

Publication Status: Online-Only

REFERENCE 2 (bases 1 to 1096)

AUTHORS Liu Y, Liao W, Wan L, Xiang T and Zhang W.

TITLE Correlation Between Relative Nasopharyngeal Virus RNA Load and
Lymphocyte Count Disease Severity in Patients with COVID-19

JOURNAL Viral Immunol (2020) In press

PUBMED [32297828](#)

REMARK Publication Status: Available-Online prior to print

REFERENCE 3 (bases 1 to 1096)

AUTHORS Wijnker PJ, Li Y, Zhang P, Foster DB, dos Remedios C, Van Eyk JE,
Stienen GJ, Murphy AM and van der Velden J.

TITLE A novel phosphorylation site, Serine 199, in the C-terminus of
cardiac troponin I regulates calcium sensitivity and susceptibility
to calpain-induced proteolysis

JOURNAL J Mol Cell Cardiol 82, 93-103 (2015)

PUBMED [25771144](#)

REFERENCE 4 (bases 1 to 1096)

AUTHORS Hao J, Galindo CL, Tran TL and Sawyer DB.

TITLE Neuregulin-1beta induces embryonic stem cell cardiomyogenesis via
ErbB3/ErbB2 receptors

JOURNAL Biochem J 458 (2), 335-341 (2014)

PUBMED [24364879](#)

REFERENCE 5 (bases 1 to 1096)

AUTHORS Gollapudi SK, Gallon CE and Chandra M.

TITLE The tropomyosin binding region of cardiac troponin T modulates
crossbridge recruitment dynamics in rat cardiac muscle fibers

JOURNAL J Mol Biol 425 (9), 1565-1581 (2013)

PUBMED [23357173](#)

REMARK GeneRIF: Replacement of the functionally corresponding N-terminal
end portion of rat fast skeletal cardiac muscle (RfsTnT) into
cardiac muscle troponin T (RcTnT), the observed functional
differences associate with a sequence variation.

REFERENCE 6 (bases 1 to 1096)

AUTHORS Watkins H, McKenna WJ, Thierfelder L, Suk HJ, Anan R, O'Donoghue A,
Spirito P, Matsumori A, Moravec CS, Seidman JG et al.

TITLE Mutations in the genes for cardiac troponin T and alpha-tropomyosin
in hypertrophic cardiomyopathy

JOURNAL N Engl J Med 332 (16), 1058-1064 (1995)

PUBMED [7898523](#)

REFERENCE 7 (bases 1 to 1096)

AUTHORS Thierfelder L, Watkins H, MacRae C, Lamas R, McKenna W, Vosberg HP, Seidman JG and Seidman CE.
 TITLE Alpha-tropomyosin and cardiac troponin T mutations cause familial hypertrophic cardiomyopathy: a disease of the sarcomere
 JOURNAL Cell 77 (5), 701-712 (1994)
 PUBMED [8205619](#)
 REFERENCE 8 (bases 1 to 1096)
 AUTHORS Jin JP, Huang QQ, Yeh HI and Lin JJ.
 TITLE Complete nucleotide sequence and structural organization of rat cardiac troponin T gene. A single gene generates embryonic and adult isoforms via developmentally regulated alternative splicing
 JOURNAL J Mol Biol 227 (4), 1269-1276 (1992)
 PUBMED [1433301](#)
 REFERENCE 9 (bases 1 to 1096)
 AUTHORS Solaro RJ, el-Saleh SC and Kentish JC.
 TITLE Ca²⁺, pH and the regulation of cardiac myofilament force and ATPase activity
 JOURNAL Mol Cell Biochem 89 (2), 163-167 (1989)
 PUBMED [2530435](#)
 REFERENCE 10 (bases 1 to 1096)
 AUTHORS Jin JP and Lin JJ.
 TITLE Isolation and characterization of cDNA clones encoding embryonic and adult isoforms of rat cardiac troponin T
 JOURNAL J Biol Chem 264 (24), 14471-14477 (1989)
 PUBMED [2760070](#)
 COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final NCBI review. The reference sequence was derived from [M26051.1](#).

Summary: tropomyosin-binding subunit of troponin; confers calcium-sensitivity to actinomyosin ATPase activity in striated muscle [RGD, Feb 2006].

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: M26051.1 [ECO:0000332]
 RNAseq introns :: single sample supports all introns
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 [ECO:0000348]

##Evidence-Data-END##

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 /db_xref="RGD:[3882](#)"
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ORIGIN

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 1081 cacattgctg acatgg

The above contents are the collected information from Internet and public resources to offer to the people for the convenient reading and information disseminating and sharing.

References

1. Baidu. <http://www.baidu.com>. 2020.
2. Cancer Biology. <http://www.cancerbio.net>. 2020.
3. Google. <http://www.google.com>. 2020.
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8. Ma H, Cherng S. Nature of Life. Life Science Journal 2005;2(1):7-15. doi:[10.7537/marslsj020105.03](https://doi.org/10.7537/marslsj020105.03). <http://www.lifesciencesite.com/lj/life0201/life-0201-03.pdf>.
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10. Ma H. The Nature of Time and Space. Nature and science 2003;1(1):1-11. doi:[10.7537/marsnsj010103.01](https://doi.org/10.7537/marsnsj010103.01). <http://www.sciencepub.net/nature/0101/01-ma.pdf>.
11. Marsland Press. <http://www.sciencepub.net>. 2020.
12. Marsland Press. <http://www.sciencepub.org>. 2020.
13. National Center for Biotechnology Information, U.S. National Library of Medicine. <http://www.ncbi.nlm.nih.gov/pubmed>. 2020.
14. Nature and Science. <http://www.sciencepub.net/nature>. 2020.
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16. Wikipedia. The free encyclopedia. <http://en.wikipedia.org>. 2020.

Homo sapiens microRNA 1207 (MIR1207), microRNA

NCBI Reference Sequence: NR_031612.1

[FASTA Graphics](#)

[Go to:](#)

LOCUS NR_031612 87 bp RNA linear PRI 09-DEC-2020

DEFINITION Homo sapiens microRNA 1207 (MIR1207), microRNA.

ACCESSION NR_031612

VERSION NR_031612.1

KEYWORDS RefSeq.

- SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
- REFERENCE 1 (bases 1 to 87)
AUTHORS Bertolazzi G, Cipollina C, Benos PV, Tumminello M and Coronello C.
TITLE miR-1207-5p Can Contribute to Dysregulation of Inflammatory
Response in COVID-19 via Targeting SARS-CoV-2 RNA
JOURNAL Front Cell Infect Microbiol 10, 586592 (2020)
PUBMED [33194826](#)
REMARK GeneRIF: miR-1207-5p Can Contribute to Dysregulation of
Inflammatory Response in COVID-19 via Targeting SARS-CoV-2 RNA.
Publication Status: Online-Only
- REFERENCE 2 (bases 1 to 87)
AUTHORS Yan Y, Su M and Qin B.
TITLE CircHIPK3 promotes colorectal cancer cells proliferation and
metastasis via modulating of miR-1207-5p/FMNL2 signal
JOURNAL Biochem Biophys Res Commun 524 (4), 839-846 (2020)
PUBMED [32046858](#)
REMARK GeneRIF: CircHIPK3 promotes colorectal cancer cells proliferation
and metastasis via modulating of miR-1207-5p/FMNL2 signal.
- REFERENCE 3 (bases 1 to 87)
AUTHORS Cui M, Chang Y, Fang QG, Du W, Wu JF, Wang JH, Liu ST and Luo SX.
TITLE Non-Coding RNA Pvt1 Promotes Cancer Stem Cell-Like Traits in
Nasopharyngeal Cancer via Inhibiting miR-1207
JOURNAL Pathol Oncol Res 25 (4), 1411-1422 (2019)
PUBMED [30141114](#)
REMARK GeneRIF: Low expression of MIR1207 is associated with
Nasopharyngeal Cancer.
- REFERENCE 4 (bases 1 to 87)
AUTHORS Chao PC, Cui MY, Li XA, Jiang Y, Lin BC and Li ZB.
TITLE Correlation between miR-1207-5p expression with steroid-induced
necrosis of femoral head and VEGF expression
JOURNAL Eur Rev Med Pharmacol Sci 23 (7), 2710-2718 (2019)
PUBMED [31002120](#)
REMARK GeneRIF: Correlation between miR-1207-5p expression with
steroid-induced necrosis of femoral head and VEGF expression.
- REFERENCE 5 (bases 1 to 87)
AUTHORS Song P and Yin SC.
TITLE Long non-coding RNA 319 facilitates nasopharyngeal carcinoma
carcinogenesis through regulation of miR-1207-5p/KLF12 axis
JOURNAL Gene 680, 51-58 (2019)
PUBMED [30243935](#)
REMARK GeneRIF: Data found that miR-1207 expression was decreased in
nasopharyngeal carcinoma (NPC) tissues, and LINC00319 facilitated
cell proliferation in vitro via sponging miR-1207-5p in NPC cells.
- REFERENCE 6 (bases 1 to 87)
AUTHORS Chen L, Lu MH, Zhang D, Hao NB, Fan YH, Wu YY, Wang SM, Xie R, Fang
DC, Zhang H, Hu CJ and Yang SM.
TITLE miR-1207-5p and miR-1266 suppress gastric cancer growth and
invasion by targeting telomerase reverse transcriptase
JOURNAL Cell Death Dis 5, e1034 (2014)
PUBMED [24481448](#)
REMARK GeneRIF: MiR-1207-5p and miR-1266 suppress gastric cancer growth
and invasion by targeting TERT.

Publication Status: Online-Only

REFERENCE 7 (bases 1 to 87)

AUTHORS Alvarez ML, Khosroheidari M, Eddy E and Kiefer J.

TITLE Role of microRNA 1207-5P and its host gene, the long non-coding RNA Pvt1, as mediators of extracellular matrix accumulation in the kidney: implications for diabetic nephropathy

JOURNAL PLoS One 8 (10), e77468 (2013)

PUBMED [24204837](https://pubmed.ncbi.nlm.nih.gov/24204837/)

REMARK GeneRIF: miR-1207-5p, a PVT1-derived microRNA, is abundantly expressed in kidney cells, and is upregulated by glucose and TGF-beta1.

Erratum:[PLoS One. 2016 Dec 9;11(12):e0168353. PMID: 27936176]

Publication Status: Online-Only

REFERENCE 8 (bases 1 to 87)

AUTHORS Papagregoriou G, Erguler K, Dweep H, Voskarides K, Koupepidou P, Athanasiou Y, Pierides A, Gretz N, Felekis KN and Deltas C.

TITLE A miR-1207-5p binding site polymorphism abolishes regulation of HBEGF and is associated with disease severity in CFHR5 nephropathy

JOURNAL PLoS One 7 (2), e31021 (2012)

PUBMED [22319602](https://pubmed.ncbi.nlm.nih.gov/22319602/)

REMARK GeneRIF: variant 1936T prevents hsa-miR-1207-5p from down-regulating HBEGF in podocytes

REFERENCE 9 (bases 1 to 87)

AUTHORS Huppi K, Volfovsky N, Runfola T, Jones TL, Mackiewicz M, Martin SE, Mushinski JF, Stephens R and Caplen NJ.

TITLE The identification of microRNAs in a genomically unstable region of human chromosome 8q24

JOURNAL Mol Cancer Res 6 (2), 212-221 (2008)

PUBMED [18314482](https://pubmed.ncbi.nlm.nih.gov/18314482/)

REFERENCE 10 (bases 1 to 87)

AUTHORS Griffiths-Jones S, Grocock RJ, van Dongen S, Bateman A and Enright AJ.

TITLE miRBase: microRNA sequences, targets and gene nomenclature

JOURNAL Nucleic Acids Res 34 (Database issue), D140-D144 (2006)

PUBMED [16381832](https://pubmed.ncbi.nlm.nih.gov/16381832/)

COMMENT PROVISIONAL [REFSEQ](https://www.ncbi.nlm.nih.gov/RefSeq/): This record is based on preliminary annotation provided by NCBI staff in collaboration with miRBase. The reference sequence was derived from [AC103705.5](https://www.ncbi.nlm.nih.gov/RefSeq/AC103705.5/).

Summary: microRNAs (miRNAs) are short (20-24 nt) non-coding RNAs that are involved in post-transcriptional regulation of gene expression in multicellular organisms by affecting both the stability and translation of mRNAs. miRNAs are transcribed by RNA polymerase II as part of capped and polyadenylated primary transcripts (pri-miRNAs) that can be either protein-coding or non-coding. The primary transcript is cleaved by the Drosha ribonuclease III enzyme to produce an approximately 70-nt stem-loop precursor miRNA (pre-miRNA), which is further cleaved by the cytoplasmic Dicer ribonuclease to generate the mature miRNA and antisense miRNA star (miRNA*) products. The mature miRNA is incorporated into a RNA-induced silencing complex (RISC), which recognizes target mRNAs through imperfect base pairing with the miRNA and most commonly results in translational inhibition or destabilization of the target mRNA. The RefSeq represents the predicted microRNA stem-loop. [provided by RefSeq, Sep 2009].

Sequence Note: This record represents a predicted microRNA stem-loop as defined by miRBase. Some sequence at the 5' and 3' ends may not be included in the intermediate precursor miRNA produced by Drosha cleavage.

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

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Rattus norvegicus ferritin heavy chain 1 (Fth1), mRNA

NCBI Reference Sequence: NM_012848.2

[FASTA Graphics](#)[Go to:](#)

LOCUS NM_012848 828 bp mRNA linear ROD 11-OCT-2020

DEFINITION Rattus norvegicus ferritin heavy chain 1 (Fth1), mRNA.

ACCESSION NM_012848

VERSION NM_012848.2

KEYWORDS RefSeq.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM [Rattus norvegicus](#)Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 828)

AUTHORS Zhang Y, Li H, Zhang J, Cao Y, Zhao X, Yu N, Gao Y, Ma J, Zhang H,
Zhang J, Guo X and Liu X.TITLE The clinical characteristics and outcomes of patients with diabetes
and secondary hyperglycaemia with coronavirus disease 2019: A
single-centre, retrospective, observational study in Wuhan

JOURNAL Diabetes Obes Metab 22 (8), 1443-1454 (2020)

PUBMED [32406594](#)

REFERENCE 2 (bases 1 to 828)

AUTHORS Hou H, Zhang B, Huang H, Luo Y, Wu S, Tang G, Liu W, Mao L, Mao L,
Wang F and Sun Z.TITLE Using IL-2R/lymphocytes for predicting the clinical progression of
patients with COVID-19

JOURNAL Clin Exp Immunol 201 (1), 76-84 (2020)

PUBMED [32365221](#)

REFERENCE 3 (bases 1 to 828)

AUTHORS Mu T, Qin Y, Liu B, He X, Liao Y, Sun J, Qiu J, Li X, Zhong Y and
Cai J.TITLE In Vitro Neural Differentiation of Bone Marrow Mesenchymal Stem
Cells Carrying the FTH1 Reporter Gene and Detection with MRI

JOURNAL Biomed Res Int 2018, 1978602 (2018)

PUBMED [30046590](#)REMARK GeneRIF: FTH1 gene expression did not affect mesenchymal stem cell
differentiation into neurons and was not affected by neural
differentiation

Publication Status: Online-Only

REFERENCE 4 (bases 1 to 828)

AUTHORS Festa L, Gutoskey CJ, Graziano A, Waterhouse BD and Meucci O.

TITLE Induction of Interleukin-1beta by Human Immunodeficiency Virus-1
Viral Proteins Leads to Increased Levels of Neuronal Ferritin Heavy
Chain, Synaptic Injury, and Deficits in Flexible Attention

JOURNAL J Neurosci 35 (29), 10550-10561 (2015)

PUBMED [26203149](#)REMARK GeneRIF: This work demonstrates the key role of the cytokine
IL-1beta in the regulation of a novel intracellular mediator [i.e.,
the protein ferritin heavy chain (FHC)] of HIV-induced dendritic
damage and the resulting neurocognitive impairment.

REFERENCE 5 (bases 1 to 828)

AUTHORS Lane DJ, Merlot AM, Huang ML, Bae DH, Jansson PJ, Sahni S,
Kalinowski DS and Richardson DR.

TITLE Cellular iron uptake, trafficking and metabolism: Key molecules and

mechanisms and their roles in disease
 JOURNAL Biochim Biophys Acta 1853 (5), 1130-1144 (2015)
 PUBMED [25661197](#)
 REMARK Review article
 REFERENCE 6 (bases 1 to 828)
 AUTHORS Wu CG, Groenink M, Bosma A, Reitsma PH, van Deventer SJ and Chamuleau RA.
 TITLE Rat ferritin-H: cDNA cloning, differential expression and localization during hepatocarcinogenesis
 JOURNAL Carcinogenesis 18 (1), 47-52 (1997)
 PUBMED [9054589](#)
 REFERENCE 7 (bases 1 to 828)
 AUTHORS Ursini MV and de Francis V.
 TITLE TSH regulation of ferritin H chain messenger RNA levels in the rat thyroids
 JOURNAL Biochem Biophys Res Commun 150 (1), 287-295 (1988)
 PUBMED [2827671](#)
 REFERENCE 8 (bases 1 to 828)
 AUTHORS Murray MT, White K and Munro HN.
 TITLE Conservation of ferritin heavy subunit gene structure: implications for the regulation of ferritin gene expression
 JOURNAL Proc Natl Acad Sci U S A 84 (21), 7438-7442 (1987)
 PUBMED [3478702](#)
 REFERENCE 9 (bases 1 to 828)
 AUTHORS Krawetz, S.A., Connor, W., Cannon, P.D. and Dixon, G.H.
 TITLE A vector-primer-cloner-sequencer plasmid for the construction of cDNA libraries: evidence for a rat glyceraldehyde-3-phosphate dehydrogenase-like mRNA and a ferritin mRNA within testis
 JOURNAL DNA 5 (5), 427-435 (1986)
 PUBMED [3780374](#)
 REMARK Erratum:[DNA 1986 Oct;6(3):281]
 REFERENCE 10 (bases 1 to 828)
 AUTHORS Leibold, E.A., Aziz, N., Brown, A.J. and Munro, H.N.
 TITLE Conservation in rat liver of light and heavy subunit sequences of mammalian ferritin. Presence of unique octopeptide in the light subunit
 JOURNAL J Biol Chem 259 (7), 4327-4334 (1984)
 PUBMED [6546756](#)
 COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final NCBI review. The reference sequence was derived from [U58829.1](#). On Aug 30, 2012 this sequence version replaced [NM_012848.1](#).

Summary: overexpressed during hepatic tumor development; used as an early marker for hepatocellular carcinoma [RGD, Feb 2006].

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: U58829.1, FQ229789.1 [ECO:0000332]
 RNAseq introns :: single sample supports all introns
 SAMD00052296, SAMD00052297
 [ECO:0000348]

##Evidence-Data-END##

PRIMARY REFSEQ_SPAN PRIMARY_IDENTIFIER PRIMARY_SPAN COMP

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Anguilla japonica esrs34e10-5 mRNA for spermatogonial stem-cell renewal factor, complete cds

GenBank: AB097149.1

[FASTA Graphics](#)[Go to:](#)

LOCUS AB097149 1711 bp mRNA linear VRT 03-DEC-2003

DEFINITION *Anguilla japonica* esrs34e10-5 mRNA for spermatogonial stem-cell renewal factor, complete cds.

ACCESSION AB097149

VERSION AB097149.1

KEYWORDS .

SOURCE *Anguilla japonica* (Japanese eel)ORGANISM [Anguilla japonica](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Anguillidae; *Anguilla*.

REFERENCE 1

AUTHORS Miura,T., Ohta,T., Miura,C.I. and Yamauchi,K.

TITLE Complementary deoxyribonucleic acid cloning of spermatogonial stem cell renewal factor

JOURNAL Endocrinology 144 (12), 5504-5510 (2003)

PUBMED [12960007](#)

REFERENCE 2 (bases 1 to 1711)

AUTHORS Miura,T.

TITLE Direct Submission

JOURNAL Submitted (28-NOV-2002) Takeshi Miura, Ehime University, Laboratory of Fish Reproductive Physiology, Faculty of Agriculture; 3-5-7Tarumi, Matuyama, Ehime 790-8566, Japan (E-mail:miutake@agr.ehime-u.ac.jp, Tel:81-89-946-9818, Fax:81-89-977-4364)

FEATURES Location/Qualifiers

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WO 2017078176-A/1: A method for producing immortal stem cell and a sell produced

GenBank: LX157047.1

[FASTA Graphics](#)[Go to:](#)

LOCUS LX157047 3928 bp DNA linear PAT 28-SEP-2017

DEFINITION WO 2017078176-A/1: A method for producing immortal stem cell and a sell produced.

ACCESSION LX157047

VERSION LX157047.1

KEYWORDS WO 2017078176-A/1.

SOURCE synthetic construct

ORGANISM [synthetic construct](#)

other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 3928)

AUTHORS Yamashita,Y.

TITLE A method for producing immortal stem cell and a sell produced

JOURNAL Patent: WO 2017078176-A 1 11-MAY-2017;

Quarrymen and Co Inc

COMMENT OS Artificial Sequence

PN WO 2017078176-A/1

PD 11-MAY-2017

PF 07-NOV-2016 WO 2016JP082975

PR 05-NOV-2015 JP 2015-217428

PA Quarrymen and Co Inc

PI yasuhiko yamashita

PT 'A method for producing immortal stem cell and a sell

PT produced'

PS N1

CC SYN4122-1-7

FH Key Location/Qualifiers

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FEATURES Location/Qualifiers

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/organism="synthetic construct"

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WO 2017078176-A/2: A method for producing immortal stem cell and a sell produced

GenBank: LX157048.1

[FASTA Graphics](#)[Go to:](#)

LOCUS LX157048 2556 bp DNA linear PAT 28-SEP-2017

DEFINITION WO 2017078176-A/2: A method for producing immortal stem cell and a sell produced.

ACCESSION LX157048
 VERSION LX157048.1
 KEYWORDS WO 2017078176-A/2.
 SOURCE synthetic construct
 ORGANISM [synthetic construct](#)
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 2556)
 AUTHORS Yamashita,Y.
 TITLE A method for producing immortal stem cell and a sell produced
 JOURNAL Patent: WO 2017078176-A 2 11-MAY-2017;
 Quarrymen and Co Inc
 COMMENT OS Artificial Sequence
 PN WO 2017078176-A/2
 PD 11-MAY-2017
 PF 07-NOV-2016 WO 2016JP082975
 PR 05-NOV-2015 JP 2015-217428
 PA Quarrymen and Co Inc
 PI yasuhiko yamashita
 PT 'A method for producing immortal stem cell and a sell
 PT produced'
 PS N2
 CC SYN4122-2-2
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Hydra vulgaris FoxO transcription factor mRNA, complete cds

GenBank: JX118843.1

[FASTA Graphics](#)

[Go to:](#)

LOCUS JX118843 2206 bp mRNA linear INV 29-NOV-2012

DEFINITION Hydra vulgaris FoxO transcription factor mRNA, complete cds.

ACCESSION JX118843

VERSION JX118843.1

KEYWORDS .

SOURCE Hydra vulgaris (swiftwater hydra)

ORGANISM [Hydra vulgaris](#)

Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidolina;

Anthoathecata; Aplanulata; Hydridae; Hydra.

REFERENCE 1 (bases 1 to 2206)

AUTHORS Boehm,A.M., Khalturin,K., Anton-Erxleben,F., Hemmrich,G.,
Klostermeier,U.C., Lopez-Quintero,J.A., Oberg,H.H., Puchert,M.,
Rosenstiel,P., Wittlieb,J. and Bosch,T.C.

TITLE FoxO is a critical regulator of stem cell maintenance in immortal
Hydra

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 109 (48), 19697-19702 (2012)

PUBMED [23150562](#)

REFERENCE 2 (bases 1 to 2206)

AUTHORS Boehm,A.-M., Hemmrich,G., Khalturin,K., Puchert,M.,
Anton-Erxleben,F., Wittlieb,J., Klostermeier,U.C., Rosenstiel,P.,
Oberg,H.-H. and Bosch,T.C.G.

TITLE Direct Submission

JOURNAL Submitted (30-MAY-2012) Zoological Institute, Christian-Albrechts
University, Olshausenstrasse 40, Kiel 24098, Germany

FEATURES Location/Qualifiers

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Hydra vulgaris PIWI mRNA, complete cds

GenBank: JX118847.1

[FASTA Graphics](#)[Go to:](#)

LOCUS JX118847 3231 bp mRNA linear INV 29-NOV-2012

DEFINITION Hydra vulgaris PIWI mRNA, complete cds.

ACCESSION JX118847

VERSION JX118847.1

KEYWORDS .

SOURCE Hydra vulgaris (swiftwater hydra)

ORGANISM [Hydra vulgaris](#)Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidolina;
Anthoathecata; Aplanulata; Hydridae; Hydra.

REFERENCE 1 (bases 1 to 3231)

AUTHORS Boehm,A.M., Khalturin,K., Anton-Erxleben,F., Hemmrich,G.,
Klostermeier,U.C., Lopez-Quintero,J.A., Oberg,H.H., Puchert,M.,
Rosenstiel,P., Wittlieb,J. and Bosch,T.C.TITLE FoxO is a critical regulator of stem cell maintenance in immortal
Hydra

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 109 (48), 19697-19702 (2012)

PUBMED [23150562](#)

REFERENCE 2 (bases 1 to 3231)

AUTHORS Boehm,A.-M., Hemmrich,G., Khalturin,K., Puchert,M.,
Anton-Erxleben,F., Wittlieb,J., Klostermeier,U.C., Rosenstiel,P.,
Oberg,H.-H. and Bosch,T.C.G.

TITLE Direct Submission

JOURNAL Submitted (30-MAY-2012) Zoological Institute, Christian-Albrechts
University, Olshausenstrasse 40, Kiel 24098, Germany

FEATURES Location/Qualifiers

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Echinococcus multilocularis argonaute-like protein 2 (ago2-A) mRNA, partial cds

GenBank: KF768022.1

[FASTA Graphics](#)

[Go to:](#)

LOCUS KF768022 2410 bp mRNA linear INV 12-APR-2014

DEFINITION Echinococcus multilocularis argonaute-like protein 2 (ago2-A) mRNA,
partial cds.

ACCESSION KF768022

VERSION KF768022.1

KEYWORDS .

SOURCE Echinococcus multilocularis

ORGANISM [Echinococcus multilocularis](#)Eukaryota; Metazoa; Spiralia; Lophotrochozoa; Platyhelminthes;
Cestoda; Eucestoda; Cyclophyllidea; Taeniidae; Echinococcus.

REFERENCE 1 (bases 1 to 2410)

AUTHORS Koziol,U., Rauschendorfer,T., Zanon Rodriguez,L., Krohne,G. and
Brehm,K.TITLE The unique stem cell system of the immortal larva of the human
parasite Echinococcus multilocularis

JOURNAL Evodevo 5 (1), 10 (2014)

PUBMED [24602211](#)

REMARK Publication Status: Online-Only

REFERENCE 2 (bases 1 to 2410)

AUTHORS Koziol,U., Rauschendorfer,T., Zanon Rodriguez,L. and Brehm,K.

TITLE Direct Submission

JOURNAL Submitted (25-OCT-2013) Institute for Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider-Strasse 2 / Bau E1,
Wuerzburg, Bayern 97080, Germany

FEATURES Location/Qualifiers

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 2401 gaccaaatgt

Echinococcus multilocularis hdac1 (hdac1) mRNA, complete cds

GenBank: KF768025.1

[FASTA Graphics](#)

[Go to:](#)

LOCUS KF768025 1739 bp mRNA linear INV 12-APR-2014

DEFINITION Echinococcus multilocularis hdac1 (hdac1) mRNA, complete cds.

ACCESSION KF768025

VERSION KF768025.1

KEYWORDS .

SOURCE Echinococcus multilocularis

ORGANISM [Echinococcus multilocularis](#)

Eukaryota; Metazoa; Spiralia; Lophotrochozoa; Platyhelminthes;

Cestoda; Eucestoda; Cyclophyllidea; Taeniidae; Echinococcus.

REFERENCE 1 (bases 1 to 1739)

AUTHORS Koziol,U., Rauschendorfer,T., Zanon Rodriguez,L., Krohne,G. and Brehm,K.

TITLE The unique stem cell system of the immortal larva of the human parasite Echinococcus multilocularis

JOURNAL Evodevo 5 (1), 10 (2014)

PUBMED [24602211](#)

REMARK Publication Status: Online-Only

REFERENCE 2 (bases 1 to 1739)

AUTHORS Koziol,U., Rauschendorfer,T., Zanon Rodriguez,L. and Brehm,K.

TITLE Direct Submission

JOURNAL Submitted (25-OCT-2013) Institute for Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider-Strasse 2 / Bau E1,
Wuerzburg, Bayern 97080, Germany

FEATURES Location/Qualifiers

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Homo sapiens prostate stem cell antigen (PSCA), RefSeqGene on chromosome 8

NCBI Reference Sequence: NG_011722.3

[FASTA Graphics](#)

[Go to:](#)

LOCUS NG_011722 19418 bp DNA linear PRI 16-DEC-2020

DEFINITION Homo sapiens prostate stem cell antigen (PSCA), RefSeqGene on chromosome 8.

ACCESSION NG_011722

VERSION NG_011722.3

KEYWORDS RefSeq; RefSeqGene.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 19418)

AUTHORS Wu C, Wang G, Yang M, Huang L, Yu D, Tan W and Lin D.

TITLE Two genetic variants in prostate stem cell antigen and gastric cancer susceptibility in a Chinese population

JOURNAL Mol Carcinog 48 (12), 1131-1138 (2009)

PUBMED [19554573](#)

REFERENCE 2 (bases 1 to 19418)

AUTHORS Matsuo K, Tajima K, Suzuki T, Kawase T, Watanabe M, Shitara K, Misawa K, Ito S, Sawaki A, Muro K, Nakamura T, Yamao K, Yamamura Y, Hamajima N, Hiraki A and Tanaka H.

TITLE Association of prostate stem cell antigen gene polymorphisms with the risk of stomach cancer in Japanese

JOURNAL Int J Cancer 125 (8), 1961-1964 (2009)

PUBMED [19582881](#)

REFERENCE 3 (bases 1 to 19418)

AUTHORS Wu,X., Ye,Y., Kiemeny,L.A., Sulem,P., Rafnar,T., Matullo,G., Seminara,D., Yoshida,T., Saeki,N., Andrew,A.S., Dinney,C.P., Czerniak,B., Zhang,Z.F., Kiltie,A.E., Bishop,D.T., Vineis,P., Porru,S., Buntinx,F., Kellen,E., Zeegers,M.P., Kumar,R., Rudnai,P., Gurzau,E., Koppova,K., Mayordomo,J.I., Sanchez,M., Saez,B., Lindblom,A., de Verdier,P., Steineck,G., Mills,G.B., Schned,A., Guarrera,S., Polidoro,S., Chang,S.C., Lin,J., Chang,D.W., Hale,K.S., Majewski,T., Grossman,H.B., Thorlacius,S., Thorsteinsdottir,U., Aben,K.K., Witjes,J.A., Stefansson,K., Amos,C.I., Karagas,M.R. and Gu,J.

TITLE Genetic variation in the prostate stem cell antigen gene PSCA confers susceptibility to urinary bladder cancer

JOURNAL Nat Genet 41 (9), 991-995 (2009)

PUBMED [19648920](#)

REMARK Erratum:[Nat Genet. 2009 Oct;41(10):1156. Guarrera, Simonetta [added]; Polidoro, Silvia [added]]

REFERENCE 4 (bases 1 to 19418)

AUTHORS Sakamoto H, Yoshimura K, Saeki N, Katai H, Shimoda T, Matsuno Y, Saito D, Sugimura H, Tanioka F, Kato S, Matsukura N, Matsuda N, Nakamura T, Hyodo I, Nishina T, Yasui W, Hirose H, Hayashi M, Toshiro E, Ohnami S, Sekine A, Sato Y, Totsuka H, Ando M, Takemura R, Takahashi Y, Ohdaira M, Aoki K, Honmyo I, Chiku S, Aoyagi K, Sasaki H, Ohnami S, Yanagihara K, Yoon KA, Kook MC, Lee YS, Park

SR, Kim CG, Choi IJ, Yoshida T, Nakamura Y and Hirohashi S.
 CONSRTM Study Group of Millennium Genome Project for Cancer
 TITLE Genetic variation in PSCA is associated with susceptibility to
 diffuse-type gastric cancer
 JOURNAL Nat Genet 40 (6), 730-740 (2008)
 PUBMED [18488030](#)
 REFERENCE 5 (bases 1 to 19418)
 AUTHORS Schlosser E, Otero C, Wuensch C, Kessler B, Edelmann M, Brunisholz
 R, Drexler I, Legler DF and Groettrup M.
 TITLE A novel cytosolic class I antigen-processing pathway for
 endoplasmic-reticulum-targeted proteins
 JOURNAL EMBO Rep 8 (10), 945-951 (2007)
 PUBMED [17853904](#)
 COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The
 reference sequence was derived from [AC108002.3](#) and [KC877375.1](#).
 This sequence is a reference standard in the [RefSeqGene](#) project.
 On Jan 20, 2016 this sequence version replaced [NG_011722.2](#).

Summary: This gene encodes a glycosylphosphatidylinositol-anchored cell membrane glycoprotein. In addition to being highly expressed in the prostate it is also expressed in the bladder, placenta, colon, kidney, and stomach. This gene is up-regulated in a large proportion of prostate cancers and is also detected in cancers of the bladder and pancreas. This gene includes a polymorphism that results in an upstream start codon in some individuals; this polymorphism is thought to be associated with a risk for certain gastric and bladder cancers. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Feb 2010].

PRIMARY	REFSEQ_SPAN	PRIMARY_IDENTIFIER	PRIMARY_SPAN	COMP
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6975-7519	KC877375.1	1-545		
7520-19418	AC108002.3	47394-59292	c	

FEATURES Location/Qualifiers

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ORIGIN

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Homo sapiens HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1 (HUWE1), mRNA

NCBI Reference Sequence: NM_031407.7

[FASTA Graphics](#)

Go to:

LOCUS NM_031407 14731 bp mRNA linear PRI 12-DEC-2020
DEFINITION Homo sapiens HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1 (HUWE1), mRNA.
ACCESSION NM_031407 NM_005703 NM_017627 XM_497119
VERSION NM_031407.7
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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 14731)
AUTHORS Crawford LJ, Campbell DC, Morgan JJ, Lawson MA, Down JM, Chauhan D, McAvera RM, Morris TC, Hamilton C, Krishnan A, Rajalingam K, Chantry AD and Irvine AE.
TITLE The E3 ligase HUWE1 inhibition as a therapeutic strategy to target MYC in multiple myeloma
JOURNAL Oncogene 39 (27), 5001-5014 (2020)
PUBMED [32523091](#)
REMARK GeneRIF: The E3 ligase HUWE1 inhibition as a therapeutic strategy to target MYC in multiple myeloma.
REFERENCE 2 (bases 1 to 14731)
AUTHORS Zhang Y, Zhang Y and Xu H.
TITLE LIMCH1 suppress the growth of lung cancer by interacting with HUWE1 to sustain p53 stability
JOURNAL Gene 712, 143963 (2019)
PUBMED [31279706](#)
REMARK GeneRIF: LIMCH1 is a negative regulator involved in a new molecular mechanism for the pathogenesis of lung cancer with HUWE1 and p53
REFERENCE 3 (bases 1 to 14731)
AUTHORS Lee HJ, Li CF, Ruan D, He J, Montal ED, Lorenz S, Girmun GD and Chan CH.
TITLE Non-proteolytic ubiquitination of Hexokinase 2 by HectH9 controls tumor metabolism and cancer stem cell expansion
JOURNAL Nat Commun 10 (1), 2625 (2019)
PUBMED [31201299](#)
REMARK GeneRIF: Study in cancer cell lines identify that K63-linked ubiquitination by HECTH9 regulates the mitochondrial localization and function of hexokinase 2 (HK2). Histological analyses show that HECTH9 expression is upregulated and correlated with disease progression in prostate cancer. Results suggest that HECTH9 is a novel regulator of HK2 and cancer metabolism.
Publication Status: Online-Only
REFERENCE 4 (bases 1 to 14731)
AUTHORS Bernassola F, Karin M, Ciechanover A and Melino G.
TITLE The HECT family of E3 ubiquitin ligases: multiple players in cancer development
JOURNAL Cancer Cell 14 (1), 10-21 (2008)
PUBMED [18598940](#)
REMARK Review article
REFERENCE 5 (bases 1 to 14731)
AUTHORS Zhong Q, Gao W, Du F and Wang X.
TITLE Mule/ARF-BP1, a BH3-only E3 ubiquitin ligase, catalyzes the polyubiquitination of Mcl-1 and regulates apoptosis
JOURNAL Cell 121 (7), 1085-1095 (2005)

PUBMED [15989957](#)

REMARK GeneRIF: Mule is both required and sufficient for the polyubiquitination of Mcl-1; Mule is a unique BH3-containing E3 ubiquitin ligase apical to Bcl-2 family proteins during DNA damage-induced apoptosis
GeneRIF: Mule (HUWE1) poly-ubiquitinates anti-apoptotic gene Mcl-1.

REFERENCE 6 (bases 1 to 14731)

AUTHORS Chen D, Kon N, Li M, Zhang W, Qin J and Gu W.
TITLE ARF-BP1/Mule is a critical mediator of the ARF tumor suppressor
JOURNAL Cell 121 (7), 1071-1083 (2005)
PUBMED [15989956](#)

REMARK GeneRIF: study modifies the current view of ARF-mediated p53 activation and reveals that ARF-BP1 is a critical mediator of both the p53-independent and p53-dependent tumor suppressor functions of ARF
GeneRIF: Ubiquitin ligase activity of ARF-BP1 (HUWE1) is inhibited by Arf.

REFERENCE 7 (bases 1 to 14731)

AUTHORS Liu Z, Oughtred R and Wing SS.
TITLE Characterization of E3Histone, a novel testis ubiquitin protein ligase which ubiquitinates histones
JOURNAL Mol Cell Biol 25 (7), 2819-2831 (2005)
PUBMED [15767685](#)

REFERENCE 8 (bases 1 to 14731)

AUTHORS Gu J, Dubner R, Fornace AJ Jr and Iadarola MJ.
TITLE UREB1, a tyrosine phosphorylated nuclear protein, inhibits p53 transactivation
JOURNAL Oncogene 11 (10), 2175-2178 (1995)
PUBMED [7478539](#)

REFERENCE 9 (bases 1 to 14731)

AUTHORS Turner G, Gedeon A and Mulley J.
TITLE X-linked mental retardation with heterozygous expression and macrocephaly: pericentromeric gene localization
JOURNAL Am J Med Genet 51 (4), 575-580 (1994)
PUBMED [7943042](#)

REFERENCE 10 (bases 1 to 14731)

AUTHORS Gu J, Ren K, Dubner R and Iadarola MJ.
TITLE Cloning of a DNA binding protein that is a tyrosine kinase substrate and recognizes an upstream initiator-like sequence in the promoter of the preprodynorphin gene
JOURNAL Brain Res Mol Brain Res 24 (1-4), 77-88 (1994)
PUBMED [7968380](#)

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [DQ097177.1](#), [BX323845.7](#), [AY772009.1](#), [AC231658.3](#), [AB002310.3](#) and [R60532.1](#). This sequence is a reference standard in the [RefSeqGene](#) project. On Nov 22, 2018 this sequence version replaced [NM_031407.6](#).

Summary: This gene encodes a protein containing a C-terminal HECT (E6AP type E3 ubiquitin protein ligase) domain that functions as an E3 ubiquitin ligase. The encoded protein is required for the ubiquitination and subsequent degradation of the anti-apoptotic protein Mcl1 (myeloid cell leukemia sequence 1 (BCL2-related)). This protein also ubiquitinates the p53 tumor suppressor, core histones, and DNA polymerase beta. Mutations in this gene are associated with Turner type X-linked syndromic cognitive

disability. [provided by RefSeq, Aug 2013].

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: DQ097177.1 [ECO:0000332]
 RNAseq introns :: mixed/partial sample support
 SAMEA1965299, SAMEA1966682
 [ECO:0000350]

##Evidence-Data-END##

##RefSeq-Attributes-START##

MANE Ensembl match :: ENST00000262854.11/ ENSP00000262854.6
 RefSeq Select criteria :: based on conservation

##RefSeq-Attributes-END##

COMPLETENESS: full length.

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13296-13296	AC231658.3	136442-136442		
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 /evidence=ECO:0000244|PubMed:18220336, ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:21406692; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 4495..4497
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 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:18669648, ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:23186163, ECO:0000244|PubMed:24275569; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 4501..4503
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 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:19690332; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 4537..4539
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 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:23186163; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 4576..4578
 /gene="HUWE1"
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 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:16964243, ECO:0000244|PubMed:19690332, ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:23186163, ECO:0000244|PubMed:24275569;

propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3);
phosphorylation site"

misc feature 5557..5559

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/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
MRXST; MULE; URE-B1; UREB1"
/note="Phosphothreonine.
/evidence=ECO:0000244|PubMed:20068231,
ECO:0000244|PubMed:23186163; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc feature 6112..6114

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MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine.
/evidence=ECO:0000244|PubMed:16964243,
ECO:0000244|PubMed:18669648, ECO:0000244|PubMed:19690332,
ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:21406692,
ECO:0000244|PubMed:23186163; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc feature 6496..6498

/gene="HUWE1"
/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
MRXST; MULE; URE-B1; UREB1"
/note="Phosphothreonine.
/evidence=ECO:0000244|PubMed:24275569; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc feature 7189..7191

/gene="HUWE1"
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MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine.
/evidence=ECO:0000244|PubMed:23186163; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc feature 7192..7194

/gene="HUWE1"
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MRXST; MULE; URE-B1; UREB1"
/note="N6-acetyllysine.
/evidence=ECO:0000250|UniProtKB:Q7TMY8; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); acetylation site"

misc feature 7477..7479

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MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine.
/evidence=ECO:0000244|PubMed:16964243,
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ECO:0000244|PubMed:18691976, ECO:0000244|PubMed:19690332,
ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:21406692,
ECO:0000244|PubMed:23186163; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc feature 7486..7488

/gene="HUWE1"
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MRXST; MULE; URE-B1; UREB1"

/note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:18669648,
 ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:21406692,
 ECO:0000244|PubMed:23186163; propagated from
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misc feature 7564..7566

/gene="HUWE1"
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 /evidence=ECO:0000244|PubMed:19690332; propagated from
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misc feature 7972..7974

/gene="HUWE1"
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 /evidence=ECO:0000244|PubMed:23186163; propagated from
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misc feature 7987..7989

/gene="HUWE1"
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 /evidence=ECO:0000244|PubMed:23186163; propagated from
 UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc feature 7996..7998

/gene="HUWE1"
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 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:23186163; propagated from
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misc feature 8053..8055

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 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphothreonine.
 /evidence=ECO:0000244|PubMed:23186163; propagated from
 UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc feature 8143..8145

/gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:24275569; propagated from
 UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc feature 8176..8178

/gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:19690332,
 ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:23186163;
 propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3);
 phosphorylation site"

- misc_feature 8248..8250
/gene="HUWE1"
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/note="Phosphoserine."
/evidence=ECO:0000244|PubMed:19690332; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
- misc_feature 8644..8646
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/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
/note="Phosphothreonine."
/evidence=ECO:0000244|PubMed:19690332; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
- misc_feature 8869..8871
/gene="HUWE1"
/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine."
/evidence=ECO:0000244|PubMed:24275569; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
- misc_feature 8890..8892
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/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine."
/evidence=ECO:0000244|PubMed:24275569; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
- misc_feature 8896..8898
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/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine."
/evidence=ECO:0000244|PubMed:24275569; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
- misc_feature 8974..8976
/gene="HUWE1"
/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine."
/evidence=ECO:0000244|PubMed:24275569; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
- misc_feature 9052..9054
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/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine."
/evidence=ECO:0000244|PubMed:16964243, ECO:0000244|PubMed:18669648, ECO:0000244|PubMed:19690332, ECO:0000244|PubMed:23186163; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
- misc_feature 9055..9057
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/note="Phosphoserine."

/evidence=ECO:0000244|PubMed:23186163; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
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 /note="Phosphothreonine.
 /evidence=ECO:0000244|PubMed:23186163; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
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 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:16964243; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 9739..9741
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:19690332, ECO:0000244|PubMed:23186163; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 9742..9744
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 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:23186163; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 9757..9759
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 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:23186163; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 9772..9774
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 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:23186163; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 9796..9798
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1; MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:23186163; propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 9838..9840
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;

MRXST; MULE; URE-B1; UREB1"
 /note="Omega-N-methylarginine.
 /evidence=ECO:0000250|UniProtKB:Q7TMY8; propagated from
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misc_feature 11056..11058

/gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:23186163; propagated from
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misc_feature 11377..11379

/gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:18669648,
 ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:23186163;
 propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3);
 phosphorylation site"

misc_feature 11647..11649

/gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:19690332,
 ECO:0000244|PubMed:23186163; propagated from
 UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc_feature 11662..11664

/gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:19690332,
 ECO:0000244|PubMed:20068231, ECO:0000244|PubMed:23186163,
 ECO:0000244|PubMed:24275569; propagated from
 UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc_feature 11668..11670

/gene="HUWE1"
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 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:24275569; propagated from
 UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc_feature 11671..11673

/gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphoserine.
 /evidence=ECO:0000244|PubMed:20068231,
 ECO:0000244|PubMed:23186163; propagated from
 UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc_feature 11815..11817

/gene="HUWE1"
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 MRXST; MULE; URE-B1; UREB1"

/note="Phosphoserine.
/evidence=ECO:0000244|PubMed:19690332,
ECO:0000244|PubMed:23186163; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 11839..11841
/gene="HUWE1"
/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine.
/evidence=ECO:0000244|PubMed:19690332,
ECO:0000244|PubMed:23186163, ECO:0000244|PubMed:24275569;
propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3);
phosphorylation site"
[misc_feature](#) 11872..11874
/gene="HUWE1"
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MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine.
/evidence=ECO:0000244|PubMed:23186163,
ECO:0000244|PubMed:24275569; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 11881..11883
/gene="HUWE1"
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MRXST; MULE; URE-B1; UREB1"
/note="Phosphothreonine.
/evidence=ECO:0000244|PubMed:23186163; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 12109..12111
/gene="HUWE1"
/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine.
/evidence=ECO:0000244|PubMed:24275569; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
[misc_feature](#) 12148..12150
/gene="HUWE1"
/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
MRXST; MULE; URE-B1; UREB1"
/note="Phosphoserine.
/evidence=ECO:0000244|PubMed:18669648,
ECO:0000244|PubMed:19690332, ECO:0000244|PubMed:20068231,
ECO:0000244|PubMed:24275569; propagated from
UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"
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/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
MRXST; MULE; URE-B1; UREB1"
/note="Phosphothreonine.
/evidence=ECO:0000244|PubMed:18669648,
ECO:0000244|PubMed:19690332, ECO:0000244|PubMed:24275569;
propagated from UniProtKB/Swiss-Prot (Q7Z6Z7.3);
phosphorylation site"
[misc_feature](#) 12172..12174
/gene="HUWE1"
/gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;

MRXST; MULE; URE-B1; UREB1"
 /note="Phosphothreonine."
 /evidence=ECO:0000244|PubMed:18669648,
 ECO:0000244|PubMed:24275569; propagated from
 UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

misc feature 13204..13206
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /note="Phosphotyrosine."
 /evidence=ECO:0000250|UniProtKB:P51593; propagated from
 UniProtKB/Swiss-Prot (Q7Z6Z7.3); phosphorylation site"

exon 439..537
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /inference="alignment:Splign:2.1.0"

exon 538..744
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
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 /inference="alignment:Splign:2.1.0"

exon 745..897
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /inference="alignment:Splign:2.1.0"

exon 898..960
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /inference="alignment:Splign:2.1.0"

exon 961..1038
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /inference="alignment:Splign:2.1.0"

exon 1039..1086
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /inference="alignment:Splign:2.1.0"

exon 1087..1155
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /inference="alignment:Splign:2.1.0"

exon 1156..1255
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
 /inference="alignment:Splign:2.1.0"

exon 1256..1356
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"

exon /inference="alignment:Splign:2.1.0"
 1357..1507
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 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
exon /inference="alignment:Splign:2.1.0"
 1508..1635
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
exon /inference="alignment:Splign:2.1.0"
 1636..1776
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
exon /inference="alignment:Splign:2.1.0"
 1777..1882
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
exon /inference="alignment:Splign:2.1.0"
 1883..1984
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
exon /inference="alignment:Splign:2.1.0"
 1985..2065
 /gene="HUWE1"
 /gene_synonym="ARF-BP1; HECTH9; HSPC272; Ib772; LASU1;
 MRXST; MULE; URE-B1; UREB1"
exon /inference="alignment:Splign:2.1.0"
 2066..2172
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ORIGIN

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