

DHX36

Probable ATP-dependent RNA helicase DHX36 also known as **DEAH box protein 36** (DHX36) or **MLE-like protein 1** (MLEL1) or **G4 resolvase 1** (G4R1) or **RNA helicase associated with AU-rich elements** (RHAU) is an [enzyme](#) that in humans is encoded by the *DHX36* [gene](#).^{[4][5]}

Structure

Structurally, DHX36 is a 1008 amino acid-long modular [protein](#) that has been crystallized in a complex with a DNA G-quadruplex.^[6] It consists of a ~440-amino acid [helicase](#) core comprising all signature motifs of the DEAH/RHA family of [helicases](#) with N- and C-terminal flanking regions of ~180 and ~380 amino acids, respectively. Part of the N-terminal flanking region forms an [alpha-helix](#) called the DHX36-specific motif, which recognizes the 5'-most G-quadruplex quartet. The [OB-fold](#) domain binds to the 3'-most G-tract sugar-phosphate backbone.^[7] Like all the DEAH/RHA helicases, the helicase associated domain is located adjacent to the helicase core region and occupies 75% of the C-terminal region.^[8]

Function

DEAH/RHA proteins are RNA and DNA helicases typically characterized by low [processivity](#) translocation on substrates and the capability to bind/unwind non-canonical nucleic acid secondary structures.^[9] They are implicated in a number of cellular processes involving alteration of [RNA secondary structure](#) such as translation initiation, [nuclear](#) and [mitochondrial splicing](#), and [ribosome](#) and [spliceosome](#) assembly. Based on their distribution patterns, some members of this DEAH/RHA [protein family](#) are believed to be involved in [embryogenesis](#), [spermatogenesis](#), and cellular growth and division.^[4]

DHX36 exhibits a unique ATP-dependent [guanine-quadruplex](#) (G4) resolvase activity and specificity for its substrate *in vitro*.^{[10][11]} DHX36 displays repetitive unwinding activity as a function of the thermal stability of the G-quadruplex substrate, characteristic of a number of other G-quadruplex resolvases such as the BLM/WRN helicases.^{[12][13]} DHX36 binds G4-nucleic acid with sub-nanomolar affinity and unwinds G4 structures much more efficiently than double-stranded nucleic acid. Consistent with these biochemical observations, DHX36 was also identified as the major source of tetramolecular RNA-resolving activity in HeLa cell lysates.

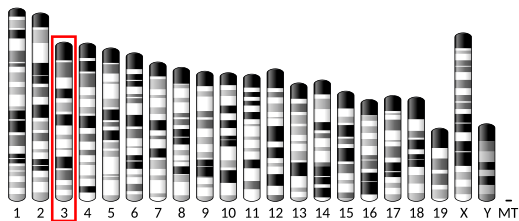
Previous work showed that DHX36 associates with mRNAs and re-localises to [stress granules](#) (SGs) upon translational arrest induced by various environmental stresses.^{[14][15]} A region of the first

105 amino acid was shown to be critical for RNA binding and re-localisation to SGs.

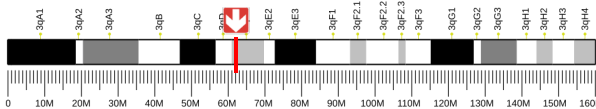
| DHX36 | |
|--|--|
| Available structures | |
| PDB | Ortholog search: PDBe (https://www.ebi.ac.uk/pdbe/searchResults.html?display=both&term=Q8VHK9%20or%20Q9H2U1) RCSB (https://www.rcsb.org/search?q=rcsb_polymer_entity_container_identifiers.reference_sequence_identifiers.database_name:UniProt%20AND%20rcsb_polymer_entity_container_identifiers.reference_sequence_identifiers.database_accession:Q8VHK9,Q9H2U1) |
| List of PDB id codes | |
| 2N16 (https://www.rcsb.org/structure/2N16), 2N21 (https://www.rcsb.org/structure/2N21) | |
| Identifiers | |
| Aliases | DHX36 (https://www.genenames.org/data/gene-symbol-report/#!/hgnc_id/14410), DDX36, G4R1, MLEL1, RHAU, DEAH-box helicase 36 |
| External IDs | OMIM: 612767 (https://omim.org/entry/612767); MGI: 1919412 (http://www.informatics.jax.org) |

[g/marker/MGI:1919412](#)); HomoloGene: 6356 (https://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=homologene&dopt=HomoloGene&list_uids=6356); GeneCards: DHX36 (<https://www.genecards.org/cgi-bin/carddisp.pl?gene=DHX36>); OMA:DHX36 - orthologs (<https://oma.abrowser.org/oma/vps/n/a>)

Gene location (Mouse)



Chr. Chromosome 3 (mouse)^[1]



| | | | |
|------|--------|-------|------------------------------|
| Band | 3 3 E1 | Start | 62,468,013 bp ^[1] |
| | | End | 62,507,004 bp ^[1] |

Gene ontology

Molecular function

- nucleotide binding (<http://amigo.geneontology.org/amigo/term/GO:0000166>)
- DNA binding (<http://amigo.geneontology.org/amigo/term/GO:0003677>)
- ATP-dependent activity, acting on DNA (<http://amigo.geneontology.org/amigo/term/GO:0008094>)
- helicase activity (<http://amigo.geneontology.org/amigo/term/GO:0004386>)
- G-quadruplex RNA binding (<http://amigo.geneontology.org/amigo/term/GO:0002151>)
- histone deacetylase binding (<http://amigo.geneontology.org/amigo/term/GO:0042826>)
- G-quadruplex DNA binding (<http://amigo.geneontology.org/amigo/term/GO:0051880>)
- protein binding (<http://amigo.geneontology.org/amigo/term/GO:0005515>)
- nucleic acid binding (<http://amigo.geneontology.org/amigo/term/GO:0003676>)
- double-stranded RNA binding (<http://amigo.geneontology.org/amigo/term/GO:0003676>)

eontology.org/amigo/term/GO:0003725)

- hydrolase activity (<http://amigo.geneontology.org/amigo/term/GO:0016787>)
- ATP binding (<http://amigo.geneontology.org/amigo/term/GO:0005524>)
- telomerase RNA binding (<http://amigo.geneontology.org/amigo/term/GO:0070034>)
- RNA binding (<http://amigo.geneontology.org/amigo/term/GO:0003723>)
- single-stranded DNA binding (<http://amigo.geneontology.org/amigo/term/GO:0003697>)
- magnesium ion binding (<http://amigo.geneontology.org/amigo/term/GO:0000287>)
- RNA polymerase II cis-regulatory region sequence-specific DNA binding (<http://amigo.geneontology.org/amigo/term/GO:0000978>)
- mRNA 3'-UTR binding (<http://amigo.geneontology.org/amigo/term/GO:0003730>)
- DNA helicase activity (<http://amigo.geneontology.org/amigo/term/GO:0003730>)

| | |
|---------------------------|---|
| | <p>rg/amigo/term/GO:0003678)</p> <ul style="list-style-type: none">• 3'-5' RNA helicase activity (http://amigo.geneontology.org/amigo/term/GO:0034458)• mRNA 3'-UTR AU-rich region binding (http://amigo.geneontology.org/amigo/term/GO:0035925)• metal ion binding (http://amigo.geneontology.org/amigo/term/GO:0046872)• mRNA 5'-UTR binding (http://amigo.geneontology.org/amigo/term/GO:0048027)• pre-miRNA binding (http://amigo.geneontology.org/amigo/term/GO:0070883) |
| Cellular component | <ul style="list-style-type: none">• chromosome (http://amigo.geneontology.org/amigo/term/GO:0005694)• telomere (http://amigo.geneontology.org/amigo/term/GO:0000781)• extracellular exosome (http://amigo.geneontology.org/amigo/term/GO:0070062)• cytosol (http://amigo.geneontology.org/amigo/term/GO:0005829) |

- nucleus (<http://amigo.geneontology.org/amigo/term/GO:0005634>)
- cytoplasm (<http://amigo.geneontology.org/amigo/term/GO:0005737>)
- mitochondrion (<http://amigo.geneontology.org/amigo/term/GO:0005739>)
- cytoplasmic stress granule (<http://amigo.geneontology.org/amigo/term/GO:0010494>)
- nuclear speck (<http://amigo.geneontology.org/amigo/term/GO:0016607>)
- axon (<http://amigo.geneontology.org/amigo/term/GO:0030424>)
- dendrite (<http://amigo.geneontology.org/amigo/term/GO:0030425>)
- cell projection (<http://amigo.geneontology.org/amigo/term/GO:0042995>)
- perikaryon (<http://amigo.geneontology.org/amigo/term/GO:0043204>)

Biological process

- RNA processing (<http://amigo.geneontology.org/amigo/term/GO:0006396>)
- regulation of transcription, DNA-templated (<http://amigo.geneontology.org/amigo/term/GO:0006355>)

- ossification (<http://amigo.geneontology.org/amigo/term/GO:0001503>)
- response to exogenous dsRNA (<http://amigo.geneontology.org/amigo/term/GO:0043330>)
- response to virus (<http://amigo.geneontology.org/amigo/term/GO:0009615>)
- transcription, DNA-templated (<http://amigo.geneontology.org/amigo/term/GO:0006351>)
- positive regulation of telomere maintenance (<http://amigo.geneontology.org/amigo/term/GO:0032206>)
- RNA secondary structure unwinding (<http://amigo.geneontology.org/amigo/term/GO:0010501>)
- positive regulation of type I interferon production (<http://amigo.geneontology.org/amigo/term/GO:0032481>)
- positive regulation of transcription by RNA polymerase II (<http://amigo.geneontology.org/amigo/term/GO:0045944>)
- telomerase RNA stabilization (<http://amigo.geneontology.org/amigo/term/GO:0045944>)

o.geneontology.org/amigo/term/GO:0090669)

- immune system process (<http://amigo.geneontology.org/amigo/term/GO:0002376>)
- positive regulation of myeloid dendritic cell cytokine production (<http://amigo.geneontology.org/amigo/term/GO:0002735>)
- regulation of transcription by RNA polymerase III (<http://amigo.geneontology.org/amigo/term/GO:0006359>)
- regulation of translation (<http://amigo.geneontology.org/amigo/term/GO:0006417>)
- multicellular organism development (<http://amigo.geneontology.org/amigo/term/GO:0007275>)
- spermatogenesis (<http://amigo.geneontology.org/amigo/term/GO:0007283>)
- positive regulation of gene expression (<http://amigo.geneontology.org/amigo/term/GO:0010628>)
- negative regulation of translation (<http://amigo.geneontology.org/amigo/term/GO:0017148>)

- cell differentiation (<http://amigo.geneontology.org/amigo/term/GO:0030154>)
- positive regulation of mRNA 3'-end processing (<http://amigo.geneontology.org/amigo/term/GO:0031442>)
- DNA duplex unwinding (<http://amigo.geneontology.org/amigo/term/GO:0032508>)
- cellular response to heat (<http://amigo.geneontology.org/amigo/term/GO:0034605>)
- cellular response to UV (<http://amigo.geneontology.org/amigo/term/GO:0034644>)
- positive regulation of I-kappaB kinase/NF-kappaB signaling (<http://amigo.geneontology.org/amigo/term/GO:0043123>)
- regulation of mRNA stability (<http://amigo.geneontology.org/amigo/term/GO:0043488>)
- G-quadruplex DNA unwinding (<http://amigo.geneontology.org/amigo/term/GO:0044806>)
- innate immune response (<http://amigo.geneontology.org/amigo/term/GO:0044806>)

[gy.org/amigo/term/GO:0045087](http://amigo.geneontology.org/amigo/term/GO:0045087))

- regulation of embryonic development (<http://amigo.geneontology.org/amigo/term/GO:0045995>)
- defense response to virus (<http://amigo.geneontology.org/amigo/term/GO:0051607>)
- positive regulation of cardioblast differentiation (<http://amigo.geneontology.org/amigo/term/GO:0051891>)
- positive regulation of transcription initiation from RNA polymerase II promoter (<http://amigo.geneontology.org/amigo/term/GO:0060261>)
- positive regulation of dendritic spine morphogenesis (<http://amigo.geneontology.org/amigo/term/GO:0061003>)
- 3'-UTR-mediated mRNA destabilization (<http://amigo.geneontology.org/amigo/term/GO:0061158>)
- positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (<http://amigo.geneontology.org/amigo/term/GO:1900153>)

- positive regulation of hematopoietic progenitor cell differentiation (<http://amigo.geneontology.org/amigo/term/GO:1901534>)
- cellular response to arsenite ion (<http://amigo.geneontology.org/amigo/term/GO:1903843>)
- positive regulation of telomere maintenance via telomere lengthening (<http://amigo.geneontology.org/amigo/term/GO:1904358>)
- positive regulation of intracellular mRNA localization (<http://amigo.geneontology.org/amigo/term/GO:1904582>)
- positive regulation of cytoplasmic translation (<http://amigo.geneontology.org/amigo/term/GO:2000767>)

Sources: Amigo (<http://amigo.geneontology.org/>) / QuickGO (<https://www.ebi.ac.uk/QuickGO/>)

| Orthologs | | |
|-----------|--|---|
| Species | Human | Mouse |
| Entrez | 170506 (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=retrieve&dopt=default&list_uids=170506&rn=1) | 72162 (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=retrieve&dopt=default&list_uids=72162&rn=1) |
| Ensembl | n/a | ENSMUSE00000000000 (http://www.ensembl.org/Mus_musculus/Mus_musculus/View?g=ENSMUSE00000000000) |
| UniProt | Q9H2U1 (http://www.uniprot.org/uniprot/Q9H2U1) | Q8VH01 (http://www.uniprot.org/uniprot/Q8VH01) |

| | | |
|-----------------------------|---|--|
| RefSeq (mRNA) | NM_020865 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NLM_020865) NM_001114397 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NLM_001114397) | NM_020865 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NLM_020865) NM_001114397 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NLM_001114397) |
| RefSeq (protein) | NP_001107869 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_001107869) NP_065916 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_065916) | NP_001107869 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_001107869) NP_065916 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_065916) |
| Location (UCSC) | n/a | Chr 3: 62,000,000-62,000,000 (https://genome.ucsc.edu/cgi-bin/gTrack?position=chr3:62000000-62000000) |
| PubMed search | [2] | [3] |

| | |
|---------------------------------|---------------------------------|
| Wikidata | |
| View/Edit Human | View/Edit Mouse |

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2. "Human PubMed Reference:" (https://www.ncbi.nlm.nih.gov/sites/entrez?db=gene&cmd=Link&LinkName=gene_pubmed&from_uid=170506) . *National Center for Biotechnology Information, U.S. National Library of Medicine.*
3. "Mouse PubMed Reference:" (https://www.ncbi.nlm.nih.gov/sites/entrez?db=gene&cmd=Link&LinkName=gene_pubmed&from_uid=72162) . *National Center for Biotechnology Information, U.S. National Library of Medicine.*
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Further reading

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External links

- Group Yoshikuni Nagamine homepage (<https://web.archive.org/web/20100621120450/http://www.fmi.ch/research/groupleader/?group=27>)
- Group Steven Akman homepage (https://crchd.cancer.gov/research/pi_akman.html)

Portal:  **Biology**



This article on a *gene* on human *chromosome 3* is a *stub*. You can help Wikipedia by *expanding* it (<https://en.wikipedia.org/w/index.php?title=DHX36&action=edit>).