

MSN

Identity

Other names **moesin (membrane-organising extension spike protein)**
 Hugo **MSN**
 Location Xq11

DNA/RNA

Transcription 3879 bp mRNA with a 1733 bp of coding sequence

Protein

Description 576 amino acids, 75 kDa; contains in N-term a globular membrane binding domain (band 4.1 like domain (amino acids 57 to 224), known also as the four-point-one/ezrin/radixin/moesin domain, an alpha helix domain, and in C-term a domain which interact with actin filaments
 Expression wide; expressed differentially in microvilli and cell adhesion sites
 Function cytoskeleton protein; binds to the plasma membrane and interacts with actin/myosin; role in cell-cell recognition and signaling
 Homology Ezrin, radixin, moesin are called the ERM proteins; they are members of the band 4.1 superfamily

Implicated in

Entity [t\(X;2\)\(q11;p23\)](#) --> MSN- [ALK](#)
 Disease found in a case of ALK+ [anaplastic large cell lymphoma](#)
 Abnormal Protein 1005 amino acids, 125 kDa; membrane restricted; ;448 N-term amino acid from MSN, containing the band 4.1 like domain and most of the alpha helix domain, fused to the 557 (instead of the usual 562) C-term amino acids from ALK (i.e. the cytoplasmic portion of ALK with the tyrosine kinase domain).
 Oncogenesis tyrosine kinase activity.

External links

Nomenclature
[Hugo](#) [MSN](#)
[GDB](#) [MSN](#)
[Entrez Gene](#) [MSN 4478](#) moesin

Cards
[Atlas](#) [MSNID363](#)
[GeneCards](#) [MSN](#)
[Ensembl](#) [MSN](#)
[CancerGene](#) [MSN](#)
[Genatlas](#) [MSN](#)
[GeneLynx](#) [MSN](#)
[eGenome](#) [MSN](#)
[euGene](#) [4478](#)

Genomic and cartography
[GoldenPath](#) [MSN - Xq11](#) [chrX:64670532-64744813 + Xq12](#) (hg17-May_2004)

[Ensembl](#) [MSN - Xq12 \[CytoView\]](#)
[NCBI](#) [Genes Cyto](#) [Gene Seq](#) [Map View - NCBI]
[OMIM](#) [Disease map \[OMIM\]](#)
[HomoloGene](#) [MSN](#)

Gene and transcription

[Genbank](#) [BC001112](#) [SRS] [BC001112](#) [ENTREZ]
[Genbank](#) [BC011827](#) [SRS] [BC011827](#) [ENTREZ]
[Genbank](#) [BC017293](#) [SRS] [BC017293](#) [ENTREZ]
[Genbank](#) [M69066](#) [SRS] [M69066](#) [ENTREZ]
[RefSeq](#) [NM_002444](#) [SRS] [NM_002444](#) [ENTREZ]
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[AceView](#) [MSN](#) AceView - NCBI
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[Unigene](#) [Hs.87752](#) [SRS] [Hs.87752](#) [NCBI] [HS87752](#) [spliceNest]

Protein : pattern, domain, 3D structure

[SwissProt](#) [P26038](#) [SRS] [P26038](#) [EXPASY] [P26038](#) [INTERPRO]
[Prosite](#) [PS00660 FERM_1](#) [SRS] [PS00660 FERM_1](#) [Expasy]
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[Interpro](#) [IPR000798 Ez/rad/moesin](#) [SRS] [IPR000798 Ez/rad/moesin](#) [EBI]
[Interpro](#) [IPR009065 FERM](#) [SRS] [IPR009065 FERM](#) [EBI]
[Interpro](#) [IPR008954 Moesin](#) [SRS] [IPR008954 Moesin](#) [EBI]
[Interpro](#) [IPR011036 PH_related](#) [SRS] [IPR011036 PH_related](#) [EBI]
[CluSTr](#) [P26038](#)
[Pfam](#) [PF00373 Band_41](#) [SRS] [PF00373 Band_41](#) [Sanger] [pfam00373](#) [NCBI-CDD]
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[PDB](#) [1E5W](#) [SRS] [1E5W](#) [PdbSum], [1E5W](#) [IMB]
[PDB](#) [1EF1](#) [SRS] [1EF1](#) [PdbSum], [1EF1](#) [IMB]

Polymorphism : SNP, mutations, diseases

[OMIM](#) [309845](#) [map]
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General knowledge

[Family Browser](#) [MSN](#) [UCSC Family Browser]
[SOURCE](#) [NM_002444](#)
[SMD](#) [Hs.87752](#)
[SAGE](#) [Hs.87752](#)
[Amigo](#) [process|cell motility](#)
[Amigo](#) [component|cytoplasm](#)
[Amigo](#) [function|cytoskeletal protein binding](#)
[Amigo](#) [component|cytoskeleton](#)
[Amigo](#) [component|plasma membrane](#)
[Amigo](#) [function|structural constituent of cytoskeleton](#)
[PubGene](#) [MSN](#)

Other databases

Probes

[Probe](#)

[MSN Related clones \(RZPD - Berlin\)](#)

PubMed

[PubMed](#)

[16 Pubmed reference\(s\) in LocusLink](#)

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