

## PML (Promyelocytic leukemia)

### Identity

Other names	<b>MYL (myelocytic leukemia)</b>
Hugo	<b><u>PML</u></b>
Location	15q22

### DNA/RNA

Description	9 coding exons; total gene sequence: 35 kb ?
Transcription	3 main mRNAs 4.6, 3.0 and 2.1 kb; alternative splicing generates at least 16 isoforms of mRNAs, varying in the region coding for the C-terminal part of the protein

### Protein

Description	560 amino acids, 70 KDa (longest isoform); composed successively, from the N- to the C-terminus, by: 1- a proline-rich N-terminus 2- a so-called "tripartite motif", cysteine-histidine rich, composed of a RING finger structure and 2 B box domains, with putative DNA-binding function 3- a coiled-coil motif corresponding to a dimerization interface 4- a basic sequence with a nuclear localization domain, and 5- a serine-proline rich C-terminal region, of unknown function, variable in length (alternative splicing) and containing phosphorylation sites
Expression	in a wide variety of tissues. In hematopoietic tissue, expression apparently restricted to myeloid precursors
Localisation	nuclear, as part of a multiproteic complex located into multiple subnuclear PML oncogenic domains (PODs)
Function	unknown to date; putative transcription factor; in conjunction with other proteins included in the PODs, it would play a role as tumor suppressor and in apoptosis
Homology	with (numerous) other RING finger / B box proteins

### Implicated in

Entity	<a href="#">t(15;17)(q22;q21)</a> / acute promyelocytic leukemia (APL) --> <a href="#">PML-RARA</a>
Disease	typical APL (or M3 ANLL, FAB classification), approximately 98% of APL cases; abnormal promyelocytes with Auer rods and bundles (faggots); disruption of the PODs with a microspeckled pattern; maturation response to all-trans retinoic acid (ATRA) therapy
Prognosis	immediate prognosis impaired by intravascular disseminated

coagulopathy; long term prognosis is favorable with treatment combining ATRA plus chemotherapy

Cytogenetics	variant or complex t(15;17) translocation in 5% of cases, no known prognosis implication; secondary chromosomal abnormalities in 30 to 35% of APL at diagnosis; association with <a href="#">+8</a> in 17 to 28% of cases; other associations are rare but recurrent: <a href="#">del(7q)</a> , <a href="#">del(9q)</a> , <a href="#">ider(17)t(15;17)</a> , <a href="#">+21</a>
Hybrid/Mutated Gene	<p>the crucial fusion transcript is 5'PML-3'RARA, encoded by der(15) chromosome; the counterpart 5'RARA-3'PML encoded by der(17) is inconstant</p> <p>breakpoint in RARA gene is always located in intron between A and B domains</p> <p>three breakpoint clusters in PML gene: bcr1 (70% of patients), bcr2 (10%) and bcr3 (20%), giving rise respectively to the long (L), intermediate (V) and short (S) length hybrid PML-RAR transcripts; V form would be linked to ATRA decreased sensitivity and S form to association with an excess of secondary chromosome changes.</p>
Abnormal Protein	106 Kda fusion protein; role in the leukemogenic process by probable interference with the signalling pathway leading to differentiation and maturation of myeloid precursors (mainly dysregulation of retinoid-inducible genes involved in myeloid differentiation)

## External links

	Nomenclature
<a href="#">Hugo</a>	<a href="#">PML</a>
<a href="#">GDB</a>	<a href="#">PML</a>
<a href="#">Entrez_Gene</a>	<a href="#">PML_5371</a> promyelocytic leukemia
	Cards
<a href="#">Atlas</a>	<a href="#">PMLID41</a>
<a href="#">GeneCards</a>	<a href="#">PML</a>
<a href="#">Ensembl</a>	<a href="#">PML</a>
<a href="#">Genatlas</a>	<a href="#">PML</a>
<a href="#">GeneLynx</a>	<a href="#">PML</a>
<a href="#">eGenome</a>	<a href="#">PML</a>
<a href="#">euGene</a>	<a href="#">5371</a>
	Genomic and cartography
<a href="#">GoldenPath</a>	<a href="#">PML - 15q22</a> <a href="#">chr15:72074067-72122769 + 15q24.1</a> (hg18-Mar_2006)
<a href="#">Ensembl</a>	<a href="#">PML - 15q24.1 [CytoView]</a>
<a href="#">NCBI</a>	<a href="#">Genes Cyto</a> <a href="#">Gene Seq</a> <small>[Map View - NCBI]</small>
<a href="#">OMIM</a>	<a href="#">Disease map [OMIM]</a>

[HomoloGene](#) [PML](#)

### Gene and transcription

[Genbank](#) [AB208950](#) [ENTREZ]

[Genbank](#) [AB209051](#) [ENTREZ]

[Genbank](#) [AB209411](#) [ENTREZ]

[Genbank](#) [AF230401](#) [ENTREZ]

[Genbank](#) [AF230402](#) [ENTREZ]

[RefSeq](#) [NM\\_002675](#) [SRS] [NM\\_002675](#) [ENTREZ]

[RefSeq](#) [NM\\_033238](#) [SRS] [NM\\_033238](#) [ENTREZ]

[RefSeq](#) [NM\\_033239](#) [SRS] [NM\\_033239](#) [ENTREZ]

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[AceView](#) [PML](#) AceView - NCBI

[TRASER](#) [PML](#) Traser - Stanford

[Unigene](#) [Hs.526464](#) [SRS] [Hs.526464](#) [NCBI] [HS526464](#) [spliceNest]

### Protein : pattern, domain, 3D structure

[SwissProt](#) [P29590](#) [SRS] [P29590](#) [EXPASY] [P29590](#) [INTERPRO]

[Prosite](#) [PS50119 ZF BBOX](#) [SRS] [PS50119 ZF BBOX](#) [Expasy]

[Prosite](#) [PS00518 ZF RING 1](#) [SRS] [PS00518 ZF RING 1](#) [Expasy]

[Prosite](#) [PS50089 ZF RING 2](#) [SRS] [PS50089 ZF RING 2](#) [Expasy]

[Interpro](#) [IPR000315 Znf Bbox](#) [SRS] [IPR000315 Znf Bbox](#) [EBI]

[Interpro](#) [IPR001841 Znf RING](#) [SRS] [IPR001841 Znf RING](#) [EBI]

[CluSTr](#) [P29590](#)

[Pfam](#) [PF00643 zf-B\\_box](#) [SRS] [PF00643 zf-B\\_box](#) [Sanger] [pfam00643](#) [NCBI-CDD]

[Pfam](#) [PF00097 zf-C3HC4](#) [SRS] [PF00097 zf-C3HC4](#) [Sanger] [pfam00097](#) [NCBI-CDD]

[Smart](#) [SM00336 BBOX](#) [EMBL]

[Smart](#) [SM00184 RING](#) [EMBL]

[Blocks](#) [P29590](#)

[PDB](#) [1BOR](#) [SRS] [1BOR](#) [PdbSum], [1BOR](#) [IMB]

### Protein Interaction databases

[DIP](#) [P29590](#)

[IntAct](#) [P29590](#)

### Polymorphism : SNP, mutations, diseases

[OMIM](#) [102578](#) [[map](#)]

[GENECLINICS](#) [102578](#)

[SNP](#) [PML](#) [dbSNP-NCBI]

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[SNP](#) [PML](#) [GeneSNPs - Utah] [PML](#) [HGBASE - SRS] [PML](#) [SNP - HAPMAP]

### General knowledge

[Family Browser](#) [PML](#) [UCSC Family Browser]

[SOURCE](#) [NM\\_002675](#)

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[SOURCE](#) [NM\\_033249](#)

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[SMD](#) [Hs.526464](#)

[SAGE](#) [Hs.526464](#)

[Amigo](#) [G1/S transition of mitotic cell cycle](#)

[Amigo](#) [nucleic acid binding](#)

[Amigo](#) [transcription factor activity](#)

[Amigo](#) [transcription coactivator activity](#)

[Amigo](#) [catalytic activity](#)

<a href="#">Amigo</a>	<a href="#">calcium ion binding</a>
<a href="#">Amigo</a>	<a href="#">protein binding</a>
<a href="#">Amigo</a>	<a href="#">protein binding</a>
<a href="#">Amigo</a>	<a href="#">intracellular</a>
<a href="#">Amigo</a>	<a href="#">intracellular</a>
<a href="#">Amigo</a>	<a href="#">insoluble fraction</a>
<a href="#">Amigo</a>	<a href="#">nucleus</a>
<a href="#">Amigo</a>	<a href="#">nucleoplasm</a>
<a href="#">Amigo</a>	<a href="#">nucleoplasm</a>
<a href="#">Amigo</a>	<a href="#">DNA repair</a>
<a href="#">Amigo</a>	<a href="#">transcription</a>
<a href="#">Amigo</a>	<a href="#">regulation of transcription, DNA-dependent</a>
<a href="#">Amigo</a>	<a href="#">protein complex assembly</a>
<a href="#">Amigo</a>	<a href="#">apoptosis</a>
<a href="#">Amigo</a>	<a href="#">induction of apoptosis</a>
<a href="#">Amigo</a>	<a href="#">DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest</a>
<a href="#">Amigo</a>	<a href="#">cell cycle arrest</a>
<a href="#">Amigo</a>	<a href="#">cell aging</a>
<a href="#">Amigo</a>	<a href="#">zinc ion binding</a>
<a href="#">Amigo</a>	<a href="#">zinc ion binding</a>
<a href="#">Amigo</a>	<a href="#">nuclear matrix</a>
<a href="#">Amigo</a>	<a href="#">transcriptional repressor activity</a>
<a href="#">Amigo</a>	<a href="#">PML body</a>
<a href="#">Amigo</a>	<a href="#">PML body</a>
<a href="#">Amigo</a>	<a href="#">negative regulation of cell growth</a>
<a href="#">Amigo</a>	<a href="#">negative regulation of cell growth</a>
<a href="#">Amigo</a>	<a href="#">positive regulation of histone deacetylation</a>
<a href="#">Amigo</a>	<a href="#">DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis</a>
<a href="#">Amigo</a>	<a href="#">metal ion binding</a>
<a href="#">Amigo</a>	<a href="#">protein heterodimerization activity</a>
<a href="#">BIOCARTA</a>	<a href="#">Regulation of transcriptional activity by PML</a> [Genes]
<a href="#">PubGene</a>	<a href="#">PML</a>
<b>Other databases</b>	
Other database	<a href="#">PML at 15q22 in normal cells (Bari)</a>
<b>Probes</b>	
<a href="#">Probe</a>	<a href="#">PML Related clones (RZPD - Berlin)</a>

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Medline [99252073](#)

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Medline [20268213](#)

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