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PLP1 proteolipid protein 1 [Homo sapiens (human)]

Gene ID: 5354, updated on 12-Sep-2024

Summarv

Official Symbol PLP1 provided by HGNC

Official Full Name proteolipid protein 1 provided by HGNC

Primary source HGNC:HGNC:9086

See related Ensembl:ENSG00000123560 MIM:300401; AllianceGenome:HGNC:9086

Gene type protein coding
RefSeq status REVIEWED
Organism Homo sapiens

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

Also known as PLP; PMD; HLD1; MMPL; SPG2; GPM6C; PLP/DM20

Summary This gene encodes a transmembrane proteolipid protein that is the predominant component of myelin. The encoded protein may play a role in the compaction,

stabilization, and maintenance of myelin sheaths, as well as in oligodendrocyte development and axonal survival. Mutations in this gene cause Pelizaeus-

Merzbacher disease and spastic paraplegia type 2. Alternatively splicing results in multiple transcript variants, including the DM20 splice variant. [provided by

RefSeq, Feb 2015]

Expression Restricted expression toward brain (RPKM 1259.3) See more

Orthologs mouse all

Try the new Gene table

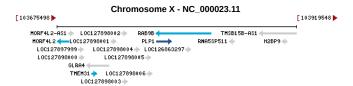
Try the new Transcript table

Genomic context

Location: Xq22.2

Exon count: 8

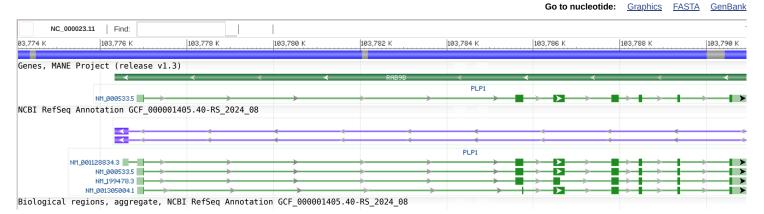
Annotation release	Status	Assembly	Chr	Location
RS_2024_08	current	GRCh38.p14 (GCF_000001405.40)	Х	NC_000023.11 (103776506103792619)
RS_2024_08	current	T2T-CHM13v2.0 (GCF_009914755.1)	Χ	NC_060947.1 (102223463102239585)
RS_2024_09	previous assembly	GRCh37.p13 (GCF_000001405.25)	Х	NC_000023.10 (103031434103047548)



Genomic regions, transcripts, and products

Go to reference sequence details

Genomic Sequence: NC_000023.11 Chromosome X Reference GRCh38.p14 Primary Assembly ▼



Expression

HPA RNA-seq normal tissues

NC_000023.11: 104M..104M (20,948 nt)

See details

103,790 K

- Project title: HPA RNA-seq normal tissues HPA RNA-seq normal tissues
- Description: RNA-seq was performed of tissue samples from 95 human individuals representing 27 different tissues in order to determine tissue-specificity of all protein-coding genes

103,782 K

19198

103,786 K

103,784 K

5<u>591</u> 17<u>8</u>09

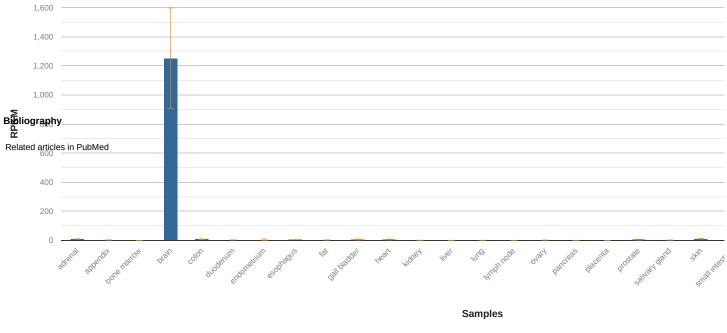
103,788 K

21573

103,780 K

- BioProject: PRJEB4337
- Publication: <u>PMID 24309898</u>
- Analysis date: Wed Apr 4 07:08:55 2018

103,776 K



GeneRIFs: Gene References Into Functions

What's a GeneRIF?

- 1. Microdeletion in distal PLP1 enhancers causes hereditary spastic paraplegia 2.
- 2. PLP1 gene mutations cause spastic paraplegia type 2 in three families.
- 3. Identifying oligodendrocyte enhancers governing Plp1 expression.
- 4. Novel Insight into the Potential Pathogenicity of Mitochondrial Dysfunction Resulting from PLP1 Duplication Mutations in Patients with Pelizaeus-Merzbacher Disease.
- 5. Correlation Between Anti-Myelin Proteolipid Protein (PLP) Antibodies and Disease Severity in Multiple Sclerosis Patients With PLP Response-Permissive HLA Types.
- 6. These findings support the assumption that genetic variation in PLP1 affects white matter myelination in the healthy human brain.
- $7. \ \underline{\text{demonstrate for the first time that the wmN1 enhancer region: } \underline{\text{(1)}} \ \underline{\text{is functional in hPLP1}}$
- 8. PLP1 mutation is associated with hereditary spastic paraplegia.
- 9. Findings suggest that PLP1 and CNTN1 gene variations modulate specific aspects of callosal microstructure that are in line with their gene function.
- 10. three single nucleotide polymorphisms in PLP1 that were associated with interhemispheric integration via the corpus callosum in a previous study also are relevant for functional hemispheric asymmetries.

Submit: New GeneRIF Correction See all GeneRIFs (82)

Phenotypes

BioGRID CRISPR Screen Phenotypes (21 hits/885 screens)

Find tests for this gene in the NIH Genetic Testing Registry (GTR)

Review eQTL and phenotype association data in this region using PheGenI

Associated conditions

Description	Tests
Hereditary spastic paraplegia 2 MedGen: C1839264, OMIM: 312920, GeneReviews: PLP1 Disorders	Compare labs
Pelizaeus-Merzbacher disease MedGen: C0205711, OMIM: 312080, GeneReviews: PLP1 Disorders	Compare labs

Copy number response

Description

Copy number response

Haploinsufficency

Sufficient evidence for dosage pathogenicity (Last evaluated 2021-04-12)

ClinGen Genome Curation Page, PubMed

Triplosensitivity

Sufficient evidence for dosage pathogenicity (Last evaluated 2021-04-12)

ClinGen Genome Curation Page, PubMed

Variation

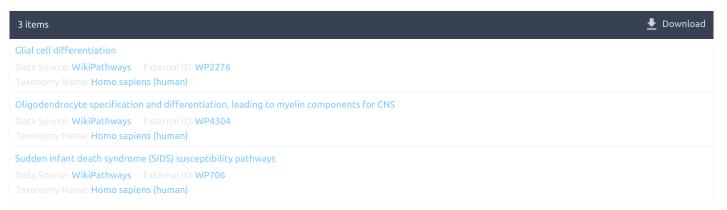
See variants in ClinVar

See studies and variants in dbVar

See Variation Viewer (GRCh37.p13)

See Variation Viewer (GRCh38)

Pathways from PubChem



▶ PubChem

Interactions

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Products	Interactant	Other Gene	Complex	Source	Pubs	Description
P60201	<u>P27797</u>	CALR	_	HPRD	PubMed	
P60201	P27824	CANX	_	<u>HPRD</u>	PubMed	
P60201	<u>P06756</u>	<u>ITGAV</u>	-	<u>HPRD</u>	<u>PubMed</u>	
P60201	P20916	MAG	_	<u>HPRD</u>	PubMed	
P60201	P02686	MBP	-	<u>HPRD</u>	<u>PubMed</u>	
BioGRID:111368	BioGRID:128799	ADGRG3	_	<u>BioGRID</u>	<u>PubMed</u>	Two-hybrid
BioGRID:111368	BioGRID:106710	AKT1	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:106848	<u>APP</u>	_	<u>BioGRID</u>	PubMed	Affinity Capture-Western; Two-hybrid
BioGRID:111368	BioGRID:124627	AQP10	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:106859	AQP6	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:128353	ARL13B	-	BioGRID	<u>PubMed</u>	Two-hybrid
BioGRID:111368	BioGRID:117285	BCL2L13	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:107107	<u>BIK</u>	-	BioGRID	<u>PubMed</u>	Two-hybrid
BioGRID:111368	BioGRID:123732	CALN1	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:107262	CALR	_	<u>BioGRID</u>	PubMed	Affinity Capture-Western
BioGRID:111368	BioGRID:107396	<u>CD40</u>	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:107410	<u>CD74</u>	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:115692	<u>CDIPT</u>	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:114532	CLDN2	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:119070	CLDN20	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:118886	CLEC2D	_	BioGRID	PubMed	Two-hybrid
BioGRID:111368	BioGRID:108369	CLN8	_	BioGRID	PubMed	Two-hybrid
BioGRID:111368	BioGRID:115751	CREB3	_	<u>BioGRID</u>	PubMed	Two-hybrid
BioGRID:111368	BioGRID:124786	CREB3L1	_	BioGRID	PubMed	Two-hybrid
BioGRID:111368	BioGRID:107889	CTSD	-	BioGRID	PubMed	Co-localization
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General gene information

Markers

Homology

NCBI Orthologs Orthologs from OrthoDB

Gene Ontology Provided by GOA

Function	Evidence Code	Pubs
enables protein binding	<u>IPI</u>	<u>PubMed</u>
enables protein-containing complex binding	<u>IEA</u>	
enables structural constituent of myelin sheath	<u>IBA</u>	
enables structural molecule activity	<u>TAS</u>	<u>PubMed</u>

Process	Evidence Code	Pubs
involved_in AMPA selective glutamate receptor signaling_pathway	<u>IEA</u>	
involved_in astrocyte development	<u>IEA</u>	
involved_in axon development	<u>IBA</u>	
involved_in axon ensheathment	TAS	PubMed
involved_in central nervous system myelination	<u>IBA</u>	
involved_in chemical synaptic transmission	TAS	PubMed
involved_in inflammatory response	<u>IEA</u>	
involved_in long-chain fatty acid biosynthetic process	<u>IEA</u>	
involved_in positive regulation of calcium ion transmembrane transport	<u>IEA</u>	
involved_in_positive regulation of cell migration	<u>IEA</u>	
involved_in positive regulation of gene expression	<u>IEA</u>	
involved_in substantia nigra development	HEP	PubMed

Component	Evidence Code	Pubs
part_of integrin alphav-beta3 complex	<u>IEA</u>	
is active in myelin sheath	<u>IBA</u>	
is_active_in_plasma_membrane	<u>IBA</u>	
located_in_plasma_membrane	<u>IDA</u>	<u>PubMed</u>
located in synapse	<u>IEA</u>	

General protein information

Preferred Names

myelin proteolipid protein

Names

lipophilin

major myelin proteolipid protein

NCBI Reference Sequences (RefSeq)

 ${\scriptsize \mathsf{NEW}} \quad \textbf{Try the new } \underline{\textbf{Transcript table}}$

RefSeqs maintained independently of Annotated Genomes

These reference sequences exist independently of genome builds. Explain

Genomic

1. NG_008863.2 RefSeqGene

Range	533021109
Download	GenBank, FASTA, Sequence Viewer (Graphics)

mRNA and Protein(s)

1. NM 000533.5 \rightarrow NP 000524.3 myelin proteolipid protein isoform 1

See identical proteins and their annotated locations for NP 000524.3

Status: REVIEWED

Description Transcript Variant: This variant (1, also known as PLP) encodes the longest isoform (1). Variants 1 and 3 encode the same isoform (1). Source sequence(s)

Consensus CDS CCDS14513.1

2. NM 001128834.3 \rightarrow NP 001122306.1 myelin proteolipid protein isoform 1

See identical proteins and their annotated locations for NP 001122306.1

Status: REVIEWED

Description
Source sequence(s)
Consensus CDS
UniProtKB/Swiss-Prot
UniProtKB/TrEMBL
Related
Conserved Domains (1) Summary

Transcript Variant: This variant (3) differs in the 5' UTR compared to variant 1. Variants 1 and 3 encode the same isoform (1).

AK292728, BC095452, DC342197
CCDS14513.1
P04400, P06905, P60201, Q502Y1, Q6FHZ6
A8K91.3, B4D121, E7EMV6
ENSP0000481006.1, ENST00000612423.4

Conserved Domains (1) Summary

Myelin_PLP; Myelin proteolipid protein (PLP or lipophilin)
Location: 5 – 273

Myelin_PLP; Myelin proteolipid protein (PLP or lipophilin)

3. NM 001305004.1 \rightarrow NP 001291933.1 myelin proteolipid protein isoform 3

See identical proteins and their annotated locations for NP 001291933.1

Status: REVIEWED

Description	Transcript Variant: This variant (4) has a shorter 5' UTR and uses an alternate in-frame acceptor site compared to variant 1. It encodes a shorter isoform (3) than isoform 1.			
Source sequence(s)	AK292728, AK295388, BC09	AK292728, AK295388, BC095452, DC342996		
UniProtKB/TrEMBL	B4DI30			
Conserved Domains (1) su	Conserved Domains (1) <u>summary</u>			
	<u>pfam01275</u>	Myelin_PLP; Myelin proteolipid protein (PLP or lipophilin)		
	Location:2 → 218			

4. NM 199478.3 \rightarrow NP 955772.1 myelin proteolipid protein isoform 2

See identical proteins and their annotated locations for NP 955772.1

Status: REVIEWED

Description	Transcript Variant: This variant (2, also known as DM20) uses an alternate in-frame donor splice site compared to variant 1. It encodes a shorter isoform (2) than isoform 1.			
Source sequence(s)	AK292728, BC095452, DA299940	AK292728, BC095452, DA299940		
Consensus CDS	CCDS14514.1	CCDS14514.1		
UniProtKB/TrEMBL	A0A0S2Z4D4, Q5U0F2, Q5U0F3			
Related	ENSP0000477619.1, ENST00000619236.1			
Conserved Domains (1) su	Conserved Domains (1) <u>summary</u>			
	pfam01275 Location:5 → 238 Myelin_PLP; Myelin proteolipid protein (PLP or lipophilin)			

RefSeqs of Annotated Genomes: GCF_000001405.40-RS_2024_08

The following sections contain reference sequences that belong to a specific genome build. $\underline{\text{Explain}}$

Reference GRCh38.p14 Primary Assembly

Genomic

1. NC_000023.11 Reference GRCh38.p14 Primary Assembly

Range	103776506103792619
Download	GenBank, FASTA, Sequence Viewer (Graphics)

Alternate T2T-CHM13v2.0

Genomic

1. NC_060947.1 Alternate T2T-CHM13v2.0

Range	102223463102239585
Download	GenBank, FASTA, Sequence Viewer (Graphics)

Related sequences

Items 1 - 25 of 43 < Prev Page 1 of 2 Next >

Nucleotide		Protein
Heading	Accession and Version	Protein
genomic	AH002975.2	AAA60350.1
genomic	AJ006976.1	CAA07364.1
genomic	CH471190.2	EAW54690.1
		EAW54691.1
		EAW54692.1
		EAW54693.1
		EAW54694.1
genomic	<u>CP068255.2</u> (102223463102239585)	None
genomic	<u>D13320.1</u>	BAA02577.1
genomic	<u>D16830.1</u>	BAA04110.1
genomic	<u>KF510145.1</u>	None
genomic	<u>KF510147.1</u>	None
genomic	<u>KF510609.1</u>	None
genomic	<u>M27111.1</u> (12721307)	None
genomic	<u>M95057.1</u> (40397)	None
genomic	<u>\$55837.1</u>	AAD13880.1
genomic	<u>\$62086.1</u>	AAB26927.2
genomic	<u>\$62117.1</u>	AAB26928.1
genomic	<u>X66420.1</u>	<u>CAA47050.1</u>
genomic	<u>773964.2</u> (607222181)	None
mRNA	<u>Al205189.1</u>	None
mRNA	AK128782.1	None
mRNA	AK292728.1	BAF85417.1
mRNA	<u>AK295374.1</u>	BAG58333.1
mRNA	AK295388.1	BAG58342.1
mRNA	AK308966.1	None
mRNA	AK309239.1	None
mRNA	AK312340.1	BAG35261.1
mRNA	AV731932.2	None
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Protein Accession	Links	
	GenPept Link	UniProtKB Link
P60201.2	<u>GenPept</u>	UniProtKB/Swiss-Prot:P60201

Additional links

Locus-specific Databases

PLP1 @ LOVD

Gene LinkOut