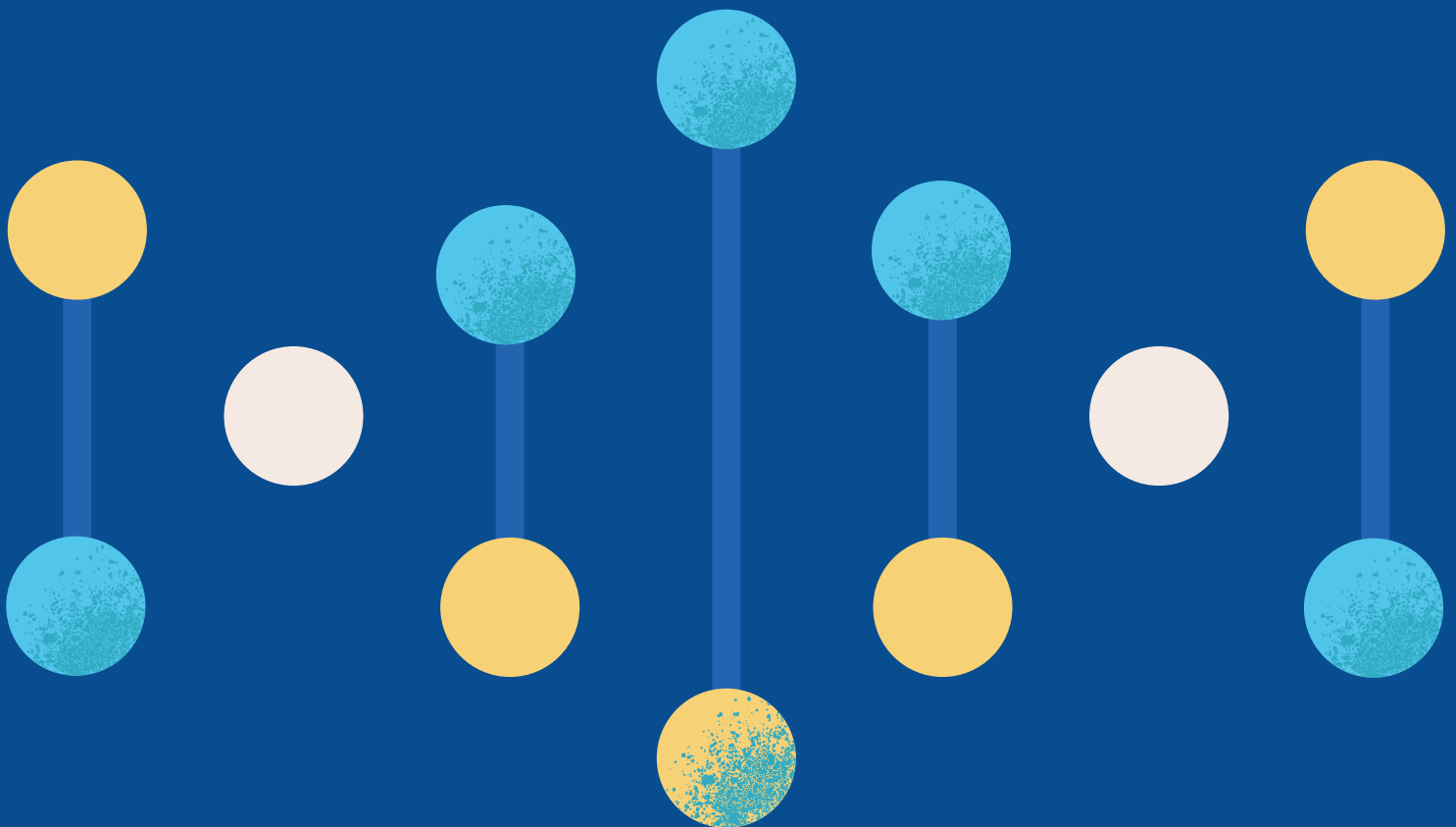


TGF-BR2 GENE COMPENDIUM

A Curated Reference for Thoracic Aortic
Aneurysm and Dissection (TAAD)



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Notices

This compendium is provided as an educational resource.

Medical and genetic knowledge evolves rapidly, and users are advised to consult up-to-date literature and clinical guidance when interpreting genetic variants.

Curators have made every effort to ensure accuracy but bear no liability for clinical or diagnostic outcomes based on this document. All variant classifications and recommendations should be considered in context and with professional clinical judgment.

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1. Basic Information for TAAD Gene

1.1 Gene Identifiers

Gene MIM Number	190182
Phenotype MIM Number	610168 Loeys-Dietz syndrome 2
Orphanet code	ORPHA: 60030 Loeys-Dietz syndrome ORPHA: 91387 Familial thoracic aortic aneurysm and aortic dissection ORPHA: 284973 Marfan syndrome type 2
Chromosomal Position (hg19/GRCh37)	NC_000003.11 (chr3:30 648 093-30 735 634)
Chromosomal Position (hg38/GRCh38)	NC_000003.12 (chr3: 30 606 601-30 694 140)
Total Number of Amino Acids	567
MANE Transcript	NM_003242.6
Are there pseudogenes?	No
Other pitfalls (e.g. retrocopy insertion polymorphisms)?	

No other condition(s) associated with this gene with no or low prevalence of aneurysm.

2. Protein Structure Overview

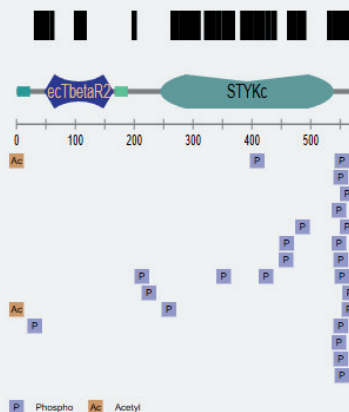
2.1. Scheme with important domains within the protein

TGF-beta receptor type-2 (P37173)

Localization: Chromosome 3: 30647994 - 30735634 forward strand
Ensemble Gene/Transcript: ENSG00000163513/ENST00000295754
Gene Name: TGFBR2
UniProt AC/ID: P37173/TGFR2_HUMAN
Organism: Homo sapiens (human)
Evidence: isoform ●

Sequence Coverage:	54%
Unique Peptides:	35
Spectra:	9228
Unique Peptides on Protein Level:	1
Spectra:	18
Shared Peptides:	0
Spectra:	18
Number of Projects:	42
Number of Experiments:	109

Sequence Coverage and Domains:



Source: <https://www.proteomicsdb.org/proteomicsdb/#protein/proteinDetails/55264/summary>

Table: Overview of TGF- β R2 protein with Amino Acid (AA) boundaries

Domain	From AA	To AA
Signal peptide	1	22
Extracellular	23	159
Trans-membrane	160	188
Cytoplasmic	189	245
Serine-Threonine Protein kinase	246	543
Cytoplasmic	544	567

Source: www.umd.be/TGFBRI

2.2 List of Exon Boundaries (at cDNA Level)

MANE transcript NM_003242.6	Nucleotide Range	Amino Acid Range
5'UTR / Exon 1	c.-283 to 94	1 to 32

Exon 2	c.95 to 263	32 to 88
Exon 3	c.264 to 454	88 to 152
Exon 4	c.455 to 1254	152 to 418
Exon 5	c.1255 to 1396	419 to 466
Exon 6	c.1397 to 1524	466 to 508
Exon 7-3'UTR	c.1525 to *2543	509 to 567

Source: Alamut

2.3. Mutational hotspot or recurrent/founder variants

Yes, amino acids Arg460, Arg528 and Arg537 appear to be highly important functionally, with different amino acids changes reported in databases and literature.

cDNA annotation	Protein annotation	Number of submissions in ClinVar	Number of Submissions in UMD
c.1336G>A	p.Asp446Asn	6 VarID 265447	5
c.1378C>A	p.Arg460Ser	1 VarID 1332770	
c.1378C>T	p.Arg460Cys	6 VarID 12514	6
c.1379G>C	p.Arg460Pro	2 VarID 1332771	
c.1379G>T	p.Arg460Leu	1 VarID 543900	1
c.1379G>A	p.Arg460His	7 VarID 12515	22
c.1483C>T	p.Arg495Ter	7 VarID 12519	7
c.1489C>T	p.Arg497Ter	8 VarID 213934	2
c.1570G>A	p.Asp524Asn	6 VarID 180541	4
c.1582C>G	p.Arg528Gly	1 VarID 1702293	

c.1582C>A	p.Arg528Ser	1 VarID 1299545	1
c.1582C>T	p.Arg528Cys	7 VarID 12512	9
c.1583G>A	p.Arg528His	5 VarID 12511	11
c.1583G>T	p.Arg528Leu		1
c.1609C>T	p.Arg537Cys	8 VarID 12507	9 personal communication Paris

2.4. Major domain(s) that involves more pathogenic variants

Almost all pathogenic variants are located in the protein kinase domain: aa246- aa544 (Loeys et al. 2006; Singh et al. 2006).

Clinvar database: [ClinVar - TGFB2](#)

GnomAD database: [gnomAD.v4.1 TGFB2](#)

Mutscore: [MutScore TGFB2](#)

3. Mode of Inheritance

Loeys-Dietz syndrome (LDS) is inherited in an autosomal dominant manner. Wide intrafamilial phenotypic variability has been documented. Rare examples of non-penetrance in LDS have been documented (Baban et al, 2018).

4. Constraint Matrices and Mutational Subtypes

pLI score	pLI=0,96 o/e= 0,35 (0.24-0.51)	gnomad v.4.1
Missense constraint	Z=3,65; o/e=0.6 (0.55-0.66)	gnomad v.4.1
Haplo-insufficiency (nonsense or out of frame splice)	No*	Goudie et al, 2011
Full gene deletion	No**	Redon et al, 2006
Multi-exon deletion	Yes***	Bichat lab
Full gene duplication	No****	Breckpot et al, 2010
Multi-exon duplication	No	

* All currently described pathogenic nonsense mutations are shown or predicted to escape NMD, so haplo-insufficiency is not believed to be a pathogenic mechanism for the

aneurysmal phenotype.

** One paper describing a full gene deletion but the patient had microcephaly, mild dysmorphic features, and global developmental delay but not LDS-aneurysmal features at the time of reporting (was a 20 month old girl) (Campbell et al, 2011).

*** Four probands with entire exon 6 deletion were identified and in one it was a de novo event (Paris, personal communication).

5. Mode of Action of the Pathogenic Variants

Gain-of-function	Unknown*	Lindsey and Dietz et al 2014. MacFarlane et al 2017.
Haploinsufficiency (as defined by allele that undergoes (or predicted to undergo NMD) or full gene deletion	No**	Lindsey and Dietz et al 2014. MacFarlane et al 2017.
Dominant-negative	Unknown*	Lindsey and Dietz et al 2014. MacFarlane et al 2017.
Loss-of-function (not driven by haplo-insufficiency)	Unknown*	Lindsey and Dietz et al 2014. MacFarlane et al 2017.

* The precise mechanism for TGF- β R2 variant is not clear. Various mechanisms have been proposed to explain how LDS mutations can result in increased TGF- β signaling in vivo, however, none of these mechanisms has been validated to date.

** All currently described pathogenic nonsense mutations are shown or predicted to escape NMD, so haplo-insufficiency is not believed to be a pathogenic mechanism for the aneurysmal phenotype.

6. Additional Supportive Evidence for Pathogenicity

6.1. Clinical evidence

No features are specific for TGF- β R2.

6.2. Functional evidence

Currently, no functional tests are available that could help for missense variants interpretation in TGF- β R2. In the case of a nonsense mutation, efforts to examine nonsense-mediated decay (NMD) should be performed to demonstrate NMD escape before concluding on pathogenicity.

7. Mutation Database or Expert

7.1. Gene-specific mutation database

- UMD: <http://www.umd.be/TGFBR2/>
- LOVD: <https://databases.lovd.nl/shared/genes/TGFBR2>
- ClinVar: <https://www.ncbi.nlm.nih.gov/clinvar/?term=TGFBR2%5bgene%5d>

7.2 Uniprot 3D protein structure

The UniProt database provides access to the 3D structure and functional annotation of TGF- β R2: <https://www.uniprot.org/uniprotkb/P37173/entry#structure>

7.3 Lab “expert” for this gene that can be contacted for advice on specific cases

For questions about specific variants or complex TGF- β R2 cases, expert consultation is available at:

Center for Medical Genetics, University Hospital Antwerp, Belgium

- Bart.loeyts@uza.be

Genetics Department, Bichat hospital, Paris, France

- pauline.arnaud@aphp.fr

8. Phenotype Characteristics

8.1. Estimated prevalence of the disease

The exact prevalence of LDS is unknown but estimated to be 1:50,000. More than 1,000 families with LDS have been described in the literature.

8.2. Youngest age of onset of aortic aneurysm

Prenatal identification of an aortic root aneurysm in a fetus of 19 week of gestation in (Viassolo et al. 2006). Also, neonatal presentation (since 2 days of life to 6 months old) with aortic root dilatation has been described in the literature (Yetman et al 2007, Baldo et al 2022, Valenzuela et al, 2017).

8.3. Youngest age of onset of aortic dissection

Aortic dissection has been reported as early as 6 months of age with aortic diameter of 4.2 cm (Williams et al. 2016).

8.4. Genotype-phenotype correlation validated for this gene

No, current data suggest there might be an early onset and more severe presentation for pathogenic variants affecting Arg528. So far, this observation does not change the clinical management of patients with this variant.

8.5. Is there any consensus on management of the disease?

Yes, not specific for TGF- β R2 but for LDS in general (Mac Carrick et al, 2014). Also consult general TAAD guidelines (Isselbacher et al 2022, Mazzolai et al, 2024, Morris et al, 2024).

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VASCERN, the European Reference Network on Rare Multisystemic Vascular Diseases, is dedicated to gathering the best expertise in Europe in order to provide accessible cross-border healthcare to patients with rare vascular diseases (an estimated 1.3 million affected). These include arterial diseases (affecting the aorta to small arteries), arterio-venous anomalies, vascular malformations, and lymphatic diseases.

VASCERN currently comprises 48 expert teams from 39 highly specialised multidisciplinary HCPs coming from 19 EU Member States, as well as various European Patient Organisations, and is coordinated in Paris, France.

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