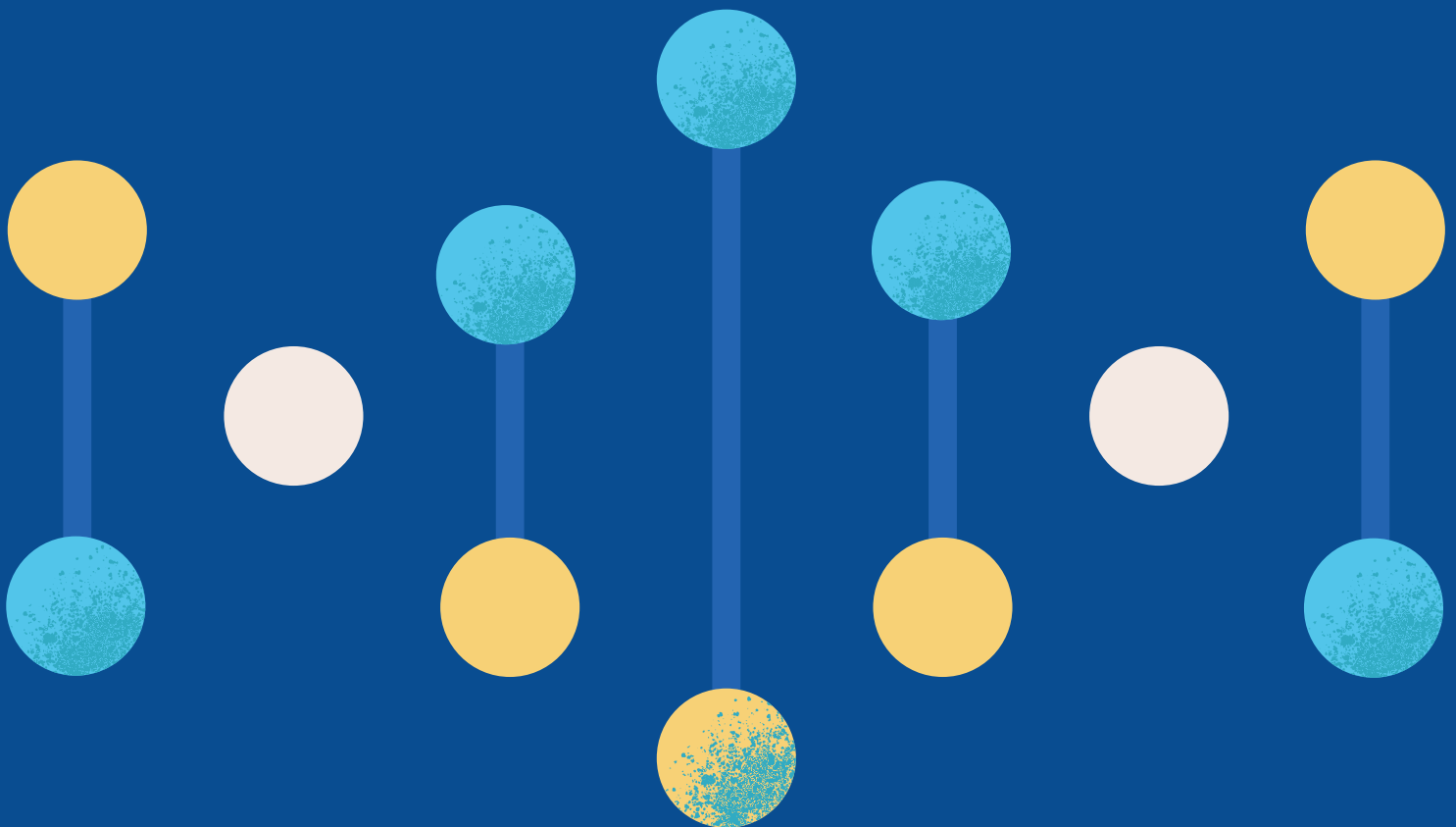


TGF-BR1 GENE COMPENDIUM

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

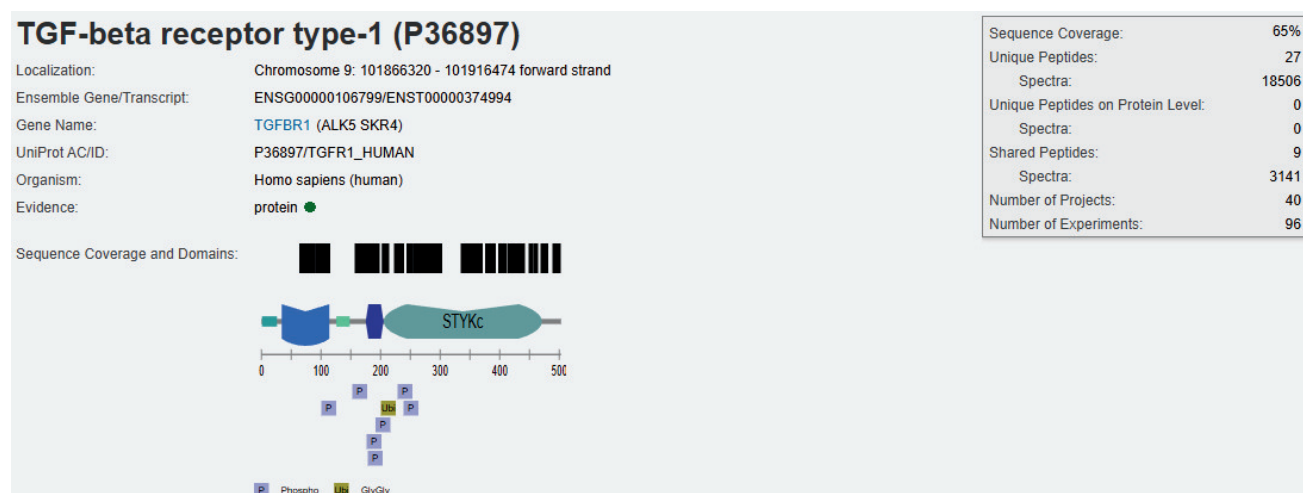
Gene MIM Number	190181
Phenotype MIM Number	609192 Loeys-Dietz syndrome ¹
Orphanet code	TAAD 91387 LDS 60030
Chromosomal Position (hg19/GRCh37)	Chr 9:101,867,395-101,916,474
Chromosomal Position (hg38/GRCh38)	Chr 9:99,105,113-99,154,192
Total Number of Amino Acids	503
MANE Transcript	NM_04612.4
Are there pseudogenes?	No
Other pitfalls (e.g. retrocopy insertion polymorphisms)?	Variation in Ala repetition in exon 1 may cause technical issues

1.2 Other phenotypes associated with TGF- β R1 with no or lower prevalence of TAAD

TGF- β R1 variants in extracellular domain leading to haplo-insufficiency are associated with Multiple self-healing squamous epithelioma (OMIM 132800).

2. Protein Structure Overview

2.1. Scheme with important domains within the protein



Source: <https://www.proteomicsdb.org/proteomicsdb/#protein/proteinDetails/55234/summary>

Table: Overview of TGF- β R1 protein with Amino Acid (AA) boundaries

Domain	From AA	To AA
Signal peptide	1	29
Extracellular	30	126
Trans-membrane	127	147
Non-specified	148	174
GS domain	175	204
Serine-Threonine Protein kinase	205	495

Source: www.umd.be/TGFBRI

2.2 List of Exon Boundaries (at cDNA Level)

MANE NM: 004612.4	Nucleotide Range	Amino Acid Range
5'UTR / Exon 1	c.-93 to 97	1 to 33
Exon 2	c.98 to 343	33 to 115

Exon 3	c.344 to 574	115 to 192
Exon 4	c.575 to 805	192 to 269
Exon 5	c.806 to 973	269 to 325
Exon 6	c.974 to 1130	325 to 377
Exon 7	c.1131 to 1255	377 to 419
Exon 8	c.1256 to 1386	419 to 462
Exon 9-3'UTR	c.1387 to *4887	463 to 503

Source: Alamut

2.3. Mutational hotspot or recurrent/founder variants

cDNA annotation	Protein annotation	Number of submissions in ClinVar
c.680AAG[1]	p.Glu228del	5
c.722C>T	p.Ser241Leu	5 VarID 213896
c.934G>A	p.Gly312Ser	7 VarID 12524
c.1459C>T	p.Arg487Trp	7 VarID 213882
c.1460G>A	p.Arg487Gln	9 VarID 12525

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

Most variants located on the Serine-Threonine Protein kinase domain (aa205- aa495) (Loeys et al. 2006).

Variants also described on the GS-domain: aa175- aa204 (Loeys et al. 2005).

No described variants in the signal peptide, extracellular or transmembrane domain associated with Loeys-Dietz syndrome (LDS) or TAAD. PTC variants in those domains are associated with Multiple self-healing squamous epithelioma (MSSE).

PTC variants in serine-threonine kinase domain should be checked for escape of NMD. Current literature suggests that only PTC variants that escape NMD cause aneurysmal phenotype (but needs further confirmation) (Goudie et al. 2011).

Clinvar database: [ClinVar - TGFBR1](#)

GnomAD database: [gnomAD.v4.1 TGFBR1](#)

Mutscore: [MutScore TGFBR1](#)

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. In one case, this was related to somatic mosaicism (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	

*PTC variants in serine-threonine kinase domain that escape NMD have been described in aneurysm phenotypes:

1. Fortugno et al 2023 described 2 different frameshift variations in exon 8 (escaping NMD).
2. In Bichat's laboratory, out of 104 MFS/TAAD probands with pathogenic variations in TGFBR1 gene, the following variations were identified:
 - Gln250* (ex4) in a proband with familial TAA (3 symptomatic carriers).
 - Leu406* (ex7) in a proband with familial TAA and some skeletal features, 9 carriers in the family (pedigree with 3 generations, 1 case of incomplete penetrance and 1 asymptomatic child).
 - Tyr476* (ex9) in a proband with TAA and mitral valve surgery (no family data).
 - c.805+1G>C (ex4) in a proband with familial TAAD (2 symptomatic carriers).

** the individual reported lacked aortic involvement (Redon et al. 2006).

*** a heterozygous deletion of exon 4 (predicted in frame) in a family with TAA, systemic features including bifid uvula (3 symptomatic carriers) was identified.

**** the individual reported lacked aortic involvement. (Breckpot et al. 2010).

5. Mode of Action of the Pathogenic Variants

Gain-of-function	No	—
Haploinsufficiency (as defined by allele that undergoes (or predicted to undergo NMD) or full gene deletion	No*	Lindsay and Dietz, 2011
Dominant-negative	Unknown**	Lindsay and Dietz, 2011
Loss-of-function (not driven by haplo-insufficiency)	Unknown*/**	Lindsay and Dietz, 2011

* the current body of evidence suggests that there must be some residual mutant protein expression necessary in order to cause an aneurysmal phenotype but that the precise mechanism of action remains under investigation.

** if mutant receptor is expressed by itself it demonstrates loss-of-function, but at the cellular membrane where it functions in a complex, the effect is more complex.

6. Additional Supportive Evidence for Pathogenicity

6.1. Clinical evidence

No features are specific for TGF- β R1.

6.2. Functional evidence

Currently, no functional tests are available that could help for missense variants interpretation in TGF- β R1. 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: [UMD-TGFBRI](#)
- LOVD: <https://databases.lovd.nl/shared/genes/TGFBRI>
- HGMD: <https://www.hgmd.cf.ac.uk/ac/gene.php?gene=TGFBRI>
- Clinvar: [TGFBRI-ClinVar](#)

7.2 Uniprot 3D protein structure

The UniProt database provides access to the 3D structure and functional annotation of TGF- β R1: <https://www.uniprot.org/uniprotkb/P36897/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 R1 cases, expert consultation is available at

Center for Medical Genetics, University Hospital Antwerp, Belgium

- Bart.loey@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

Neonatal (Yetman et al, 2007).

8.3. Youngest age of onset of aortic dissection

Three months (Williams et al, 2008).

8.4. genotype-phenotype correlation validated for this gene

A correlation was demonstrated between the severity of craniofacial involvement and the age at the first cardiovascular event, that is, surgery, dissection or death (Loeys et al, 2005; Jondeau et al, 2016).

Non-syndromic and syndromic presentations of aortic aneurysm/dissection have been associated with the identical TGF- β R1 variants (personal observation, Loeys and Dietz). In Regalado et al 2022, Arg487 substitutions confer a higher risk for aortic events than other variants. So far, this does not change the clinical management of individuals with this specific variant.

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

Yes, not specific for TGF- β R1, 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.

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