RARERESEARCH.AI · WFS1 MOLECULAR ATLAS · SYNONYMOUS

T749= — WFS1 Molecular Atlas Card

Variant type: Synonymous (silent)

Codon: position 749 (Threonine, T) — amino acid unchanged

Domain context: C-terminal ER-lumenal (calcium binding, calmodulin, chaperone)

SCHEMA CATEGORY: SILENT — SILENT — NO AMINO-ACID CHANGE

No amino-acid change (T749 is unchanged): the codon is altered but the protein sequence is identical to wild-type. No structural, stability or AlphaMissense effect applies. Synonymous variants are typically benign unless they affect splicing or regulatory elements; this one is not adjacent to an exon boundary.

CLINICAL EVIDENCE

- **Classification:** Benign
- **Review status:** criteria provided, multiple submitters, no conflicts
- **Associated conditions:** WFS1-Related Spectrum Disorders; Autosomal dominant nonsyndromic hearing loss 6; Wolfram syndrome 1
- **cDNA change:** c.2247G>A
- **ClinVar accession:** VCV000045451
- **Last evaluated:** 2026/02/01 00:00
- **Submissions:** 1

Card generated by `wolfram-atlas-batch` (synonymous pipeline) on 2026-06-08T02:56:00.598732Z.

WFS1: UniProt O76024, AlphaFold v6. Synonymous variants carry no protein-structural effect.