RARERESEARCH.AI · WFS1 MOLECULAR ATLAS · SYNONYMOUS

G745= — WFS1 Molecular Atlas Card

Variant type: Synonymous (silent)

Codon: position 745 (Glycine, G) — 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 (G745 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:** Likely benign
- **Review status:** criteria provided, single submitter
- **cDNA change:** c.2235C>T
- **ClinVar accession:** VCV002864987
- **Last evaluated:** 2024/01/02 00:00
- **Submissions:** 1

Card generated by `wolfram-atlas-batch` (synonymous pipeline) on 2026-06-08T02:55:59.840691Z.

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