

# WFS1 R697G — Wolframin

Arginine → Glycine at position 697. C-terminal ER-luminal (calcium binding. ClinVar Uncertain significance, AlphaMissense 0.968, DynaMut2  $\Delta\Delta G$  -1.50 kcal/mol (destabilising).

## IDENTITY

Variant	R697G (p.Arginine697Glycine)
DNA change	c.2089A>G
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV001426730
Amino acid change	Arginine (R) → Glycine (G)

## STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 697	<b>85.00</b> HIGH CONFIDENCE
Domain	C-terminal ER-luminal (calcium binding, calmodulin, chaperone)
Position context	C-terminal luminal domain · position 697 projects into the ER lumen
IDR flag	No — pLDDT well above 50 threshold

Position 697 sits in the C-terminal luminal domain (residues 653–869), wolframin's largest soluble region. This domain projects into the ER lumen and is implicated in calcium handling, ER stress sensing, and protein–protein interactions with ATF6 and Na<sup>+</sup>/K<sup>+</sup> ATPase  $\beta$ 1. The wild-type residue is positively charged (arginine — guanidinium, strong H-bond donor); the mutant is small/flexible (glycine — backbone flexibility, no sidechain). The chemistry shift implies altered local packing, hydrogen-bonding, and/or electrostatics at this site.

## COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

**0.968**am\_class: **likely pathogenic** — threshold > 0.564DYNAMUT2  $\Delta\Delta G$ **-1.5** kcal/mol

Destabilising · Job 178092096846

PLDDT (ALPHAFOLD)

**85.00**

high confidence

## CLINICAL EVIDENCE

ClinVar classification	UNCERTAIN SIGNIFICANCE
Review status	criteria provided, multiple submitters, no conflicts
Last evaluated	2025/11/26 00:00
Inheritance	Inheritance pattern not specified in ClinVar entry; WFS1 has both AD and AR presentations.
WFS1 variant landscape	R697G is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar)
	<ul style="list-style-type: none"><li>Inborn genetic diseases</li></ul>

## RESEARCH PATH DECISION TREE

$\Delta\Delta G < 2$  + binding site affected → CATEGORY 3 – docking experiments  $\Delta\Delta G 2-4$  → CATEGORY 2 – pharmacological chaperones  $\Delta\Delta G > 4$  → CATEGORY 1 – gene therapy pLDDT < 50 → CATEGORY 5 – IDR, experimental only Stable fold + functional site hit → CATEGORY 4 – site-specific docking

### Category 3/4 — Most Druggable

$|\Delta\Delta G|=1.50 < 2$  kcal/mol (fold intact) + AlphaMissense 0.968 confirms functional impact. Specific local contacts disrupted — priority for docking and pharmacological chaperone screening.

Wolframín's fold survives this substitution ( $|\Delta\Delta G|=1.50$  kcal/mol). The pathogenic signal is real — AlphaMissense places it at 0.968. Protein still folds, but a specific local site is broken. Pharmacological chaperones and small-molecule binders are the rational therapeutic vector.