MOLECULAR ATLAS · VARIANT CARD

WFS1 K369T — Wolframin

Lysine → Threonine at position 369. Lumenal loop 1. ClinVar Uncertain significance/Uncertain risk allele, AlphaMissense 0.663, DynaMut2 ΔΔG -0.40 kcal/mol (destabilising).

IDENTITY

Variant	K369T (p.Lysine369Threonine)
DNA change	c.1106A>C
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV000215377
Amino acid change	Lysine (K) → Threonine (T)

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 369	**74.88** HIGH CONFIDENCE
Domain	Lumenal loop 1
Position context	C-terminal lumenal domain · position 369 projects into the ER lumen
IDR flag	No — pLDDT well above 50 threshold

> Position 369 sits in the C-terminal lumenal 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+/K+ ATPase β1. The wild-type residue is positively charged (lysine — primary amine); the mutant is small polar (threonine — hydroxyl). The chemistry shift implies altered local packing, hydrogen-bonding, and/or electrostatics at this site.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.663

am_class: **likely pathogenic** — threshold > 0.564

DYNAMUT2 ΔΔG

-0.4 kcal/mol

Destabilising · Job 178092127822

PLDDT (ALPHAFOLD)

74.88

high confidence

CLINICAL EVIDENCE

ClinVar classification	UNCERTAIN SIGNIFICANCE/UNCERTAIN RISK ALLELE
Review status	criteria provided, multiple submitters, no conflicts
Last evaluated	2025/07/15 00:00
Inheritance	Autosomal recessive Wolfram syndrome 1 phenotype documented.
WFS1 variant landscape	K369T is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar)

- Inborn genetic diseases
- Wolfram syndrome 1

RESEARCH PATH DECISION TREE

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ΔΔG < 2 + binding site affected → CATEGORY 3 — docking experiments ΔΔG 2–4 → CATEGORY 2 — pharmacological chaperones ΔΔG > 4 → CATEGORY 1 — gene therapy pLDDT < 50 → CATEGORY 5 — IDR, experimental only Stable fold + functional site hit → CATEGORY 4 — site-specific docking
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Category 3/4 — Most Druggable

|ΔΔG|=0.40 < 2 kcal/mol (fold intact) + AlphaMissense 0.663 confirms functional impact. Specific local contacts disrupted — priority for docking and pharmacological chaperone screening.

Wolframin's fold survives this substitution (|ΔΔG|=0.40 kcal/mol). The pathogenic signal is real — AlphaMissense places it at 0.663. Protein still folds, but a specific local site is broken. Pharmacological chaperones and small-molecule binders are the rational therapeutic vector.
