MOLECULAR ATLAS · VARIANT CARD

WFS1 E462A — Wolframin

Glutamic acid → Alanine at position 462. Transmembrane helix 6. ClinVar Uncertain significance, AlphaMissense 0.662, DynaMut2 ΔΔG -0.01 kcal/mol (destabilising).

IDENTITY

Variant	E462A (p.Glutamic acid462Alanine)
DNA change	c.1385A>C
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV002579941
Amino acid change	Glutamic acid (E) → Alanine (A)

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 462	**84.75** HIGH CONFIDENCE
Domain	Transmembrane helix 6
Position context	Inside Transmembrane helix 6 · position 462 is bilayer-embedded
IDR flag	No — pLDDT well above 50 threshold

Position 462 sits in a transmembrane helix (Transmembrane helix 6). Wolframin has eleven such helices anchoring it in the ER membrane; substitutions inside the bilayer-embedded segments can disrupt helix packing, lipid contacts, and the overall ER topology of the protein. The wild-type residue is negatively charged (glutamate — carboxylate); the mutant is small/hydrophobic (alanine — methyl sidechain). The chemistry shift implies altered local packing, hydrogen-bonding, and/or electrostatics at this site.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.662

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

DYNAMUT2 ΔΔG

-0.01 kcal/mol

Destabilising · Job 178092128171

PLDDT (ALPHAFOLD)

84.75

high confidence

CLINICAL EVIDENCE

ClinVar classification	UNCERTAIN SIGNIFICANCE
Review status	criteria provided, multiple submitters, no conflicts
Last evaluated	2024/02/09 00:00
Inheritance	Autosomal dominant pattern indicated by associated DFNA6/14/38 (WFS1 hearing loss 6).
WFS1 variant landscape	E462A is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar)

- Autosomal dominant nonsyndromic hearing loss 6
- Type 2 diabetes mellitus
- Wolfram syndrome 1
- Cataract 41
- Wolfram-like syndrome

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|=0.01 < 2 kcal/mol (fold intact) + AlphaMissense 0.662 confirms functional impact. Specific local contacts disrupted — priority for docking and pharmacological chaperone screening.

Wolframin's fold survives this substitution (|ΔΔG|=0.01 kcal/mol). The pathogenic signal is real — AlphaMissense places it at 0.662. Protein still folds, but a specific local site is broken. Pharmacological chaperones and small-molecule binders are the rational therapeutic vector.
