MOLECULAR ATLAS · VARIANT CARD

WFS1 L362F — Wolframin

Leucine → Phenylalanine at position 362. Lumenal loop 1. ClinVar Uncertain significance, AlphaMissense 0.792, DynaMut2 ΔΔG -0.58 kcal/mol (destabilising).

IDENTITY

Variant	L362F (p.Leucine362Phenylalanine)
DNA change	c.1084C>T
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV002557658
Amino acid change	Leucine (L) → Phenylalanine (F)

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 362	**88.44** HIGH CONFIDENCE
Domain	Lumenal loop 1
Position context	C-terminal lumenal domain · position 362 projects into the ER lumen
IDR flag	No — pLDDT well above 50 threshold

> Position 362 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 medium hydrophobic (leucine — branched); the mutant is large aromatic hydrophobic (phenylalanine). The chemistry shift implies altered local packing, hydrogen-bonding, and/or electrostatics at this site.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.792

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

DYNAMUT2 ΔΔG

-0.58 kcal/mol

Destabilising · Job 178092150001

PLDDT (ALPHAFOLD)

88.44

high confidence

CLINICAL EVIDENCE

ClinVar classification	UNCERTAIN SIGNIFICANCE
Review status	criteria provided, single submitter
Last evaluated	2023/06/06 00:00
Inheritance	Inheritance pattern not specified in ClinVar entry; WFS1 has both AD and AR presentations.
WFS1 variant landscape	L362F is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar)

- Inborn genetic diseases

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|=0.58 < 2 kcal/mol (fold intact) + AlphaMissense 0.792 confirms functional impact. Specific local contacts disrupted — priority for docking and pharmacological chaperone screening.

Wolframin's fold survives this substitution (|ΔΔG|=0.58 kcal/mol). The pathogenic signal is real — AlphaMissense places it at 0.792. Protein still folds, but a specific local site is broken. Pharmacological chaperones and small-molecule binders are the rational therapeutic vector.

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Every assumption documented.