

WFS1 P420L — Wolframin

Proline → Leucine at position 420. Transmembrane helix 4. ClinVar Uncertain significance, AlphaMissense 0.907, DynaMut2 $\Delta\Delta G$ -0.19 kcal/mol (destabilising).

IDENTITY

Variant	P420L (p.Proline420Leucine)
DNA change	c.1259C>T
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV003981553
Amino acid change	Proline (P) → Leucine (L)

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 420	87.56 HIGH CONFIDENCE
Domain	Transmembrane helix 4
Position context	Inside Transmembrane helix 4 · position 420 is bilayer-embedded
IDR flag	No — pLDDT well above 50 threshold

Position 420 sits in a transmembrane helix (Transmembrane helix 4). 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 rigid/helix-breaking (proline — kinks backbone); the mutant is medium hydrophobic (leucine — branched). The chemistry shift implies altered local packing, hydrogen-bonding, and/or electrostatics at this site.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.907am_class: **likely pathogenic** —
threshold > 0.564DYNAMUT2 $\Delta\Delta G$ **-0.19** kcal/molDestabilising · Job
178092106346

PLDDT (ALPHAFOLD)

87.56

high confidence

CLINICAL EVIDENCE

ClinVar classification	UNCERTAIN SIGNIFICANCE
Review status	criteria provided, single submitter
Last evaluated	2025/06/12 00:00
Inheritance	Inheritance pattern not specified in ClinVar entry; WFS1 has both AD and AR presentations.
WFS1 variant landscape	P420L is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar)
	<ul style="list-style-type: none">Inborn genetic diseases

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

$|\Delta\Delta G|=0.19 < 2$ kcal/mol (fold intact) + AlphaMissense 0.907 confirms functional impact. Specific local contacts disrupted — priority for docking and pharmacological chaperone screening.

Wolframín's fold survives this substitution ($|\Delta\Delta G|=0.19$ kcal/mol). The pathogenic signal is real — AlphaMissense places it at 0.907. Protein still folds, but a specific local site is broken. Pharmacological chaperones and small-molecule binders are the rational therapeutic vector.