

WFS1 L592V — Wolframin

Leucine → Valine at position 592 inside TM9. ClinVar Conflicting. AlphaMissense 0.13 (below threshold) — AM under-call. DynaMut2 $\Delta\Delta G$ -0.52. pLDDT 63 borderline.

IDENTITY

Variant	L592V (p.Leucine592Valine)
DNA change	c.1774C>G
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV001320760
Amino acid change	Leucine (L) → Valine (V) — branched aliphatic to smaller branched aliphatic. Conservative volume reduction.

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 592	62.62 CONFIDENT
Domain	TM9 (589-609), helical transmembrane
Position context	TM9 (residues 589-609) · position 592 (pLDDT 63 borderline).
IDR flag	No — pLDDT well above 50 threshold

Position 592 in TM9. Neighbors: GLU593 (2.4 Å), SER591 (2.5 Å), PHE589 (4.0 Å — TM9 start). L592V conservative volume reduction in TM9. AM 0.13 under-call; Conflicting clinical evidence.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.128am_class: **LBen** —
threshold > 0.564DYNAMUT2 $\Delta\Delta G$ **-0.52** kcal/

mol

Destabilising · Job
177992508277

PLDDT (ALPHAFOLD)

62.62

confident

CLINICAL EVIDENCE

ClinVar classification

CONFLICTING CLASSIFICATIONS OF PATHOGENICITY

Review status

criteria provided, conflicting classifications

Last evaluated

2025/06/24 00:00

Inheritance

Not specified.

WFS1 variant landscape

L592V is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar)

- (no specific conditions catalogued)
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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 4 — Stable Fold, Function Disrupted (AM under-call, pLDDT borderline). $|\Delta\Delta G|$ 0.52. AlphaMissense 0.13 below threshold.

Mechanism: conservative TM9 volume reduction. Therapeutic: TM9 site-directed.

L592V is TM9 — same helix as P607L/P607R. TM9 cluster grows.
