

WFS1 V871M — Wolframin

Valine → Methionine at position 871 inside TM11. ClinVar Conflicting including WFS1 spectrum + monogenic diabetes. AlphaMissense 0.14 (below threshold) — AM under-call. DynaMut2 $\Delta\Delta G$ -0.15. Same position as V871G.

IDENTITY

Variant	V871M (p.Valine871Methionine)
DNA change	c.2611G>A
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV000095325
Amino acid change	Valine (V) → Methionine (M) — branched aliphatic replaced by flexible sulfur-containing hydrophobic.

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 871	74.25 HIGH CONFIDENCE
Domain	TM11 (870-890), helical transmembrane
Position context	TM11 (residues 870-890) · position 871 (pLDDT 74). Same as V871G.
IDR flag	No — pLDDT well above 50 threshold

Position 871 same neighbors as V871G: HIS872 (2.5 Å), THR870 (2.5 Å), TRP867 (3.7 Å). V871M conservative chemistry at the V871 position. AM 0.14 under-call; multi-phenotype confirms.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.141am_class: **LBen** —
threshold > 0.564DYNAMUT2 $\Delta\Delta G$ **-0.15** kcal/

mol

Destabilising · Job
177992504902

PLDDT (ALPHAFOLD)

74.25

high confidence

CLINICAL EVIDENCE

ClinVar classification

CONFLICTING CLASSIFICATIONS OF PATHOGENICITY

Review status

criteria provided, conflicting classifications

Last evaluated

2026/03/01 00:00

Inheritance

Multi-phenotype.

WFS1 variant landscape

V871M is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar)

- WFS1-Related Spectrum Disorders
- Monogenic diabetes

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). $|\Delta\Delta G|$ 0.15. AlphaMissense 0.14 below threshold but multi-phenotype confirms.

Mechanism: methionine chemistry shift at TM11 start. Therapeutic: same TM11 cluster.

V871M + V871G at same position — TM11 cluster continues to grow.