

# WFS1 K811R — Wolframin

Lys→Arg p811 luminal AM=0.07 ddg=-0.28 pLDDT=86. ClinVar Conflicting evidence. Atlas mechanism: see structural analysis.

## IDENTITY

Variant	K811R (p.Lysine811Arginine)
DNA change	c.2432A>G
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV001160733
Amino acid change	conservative basic-to-basic

## STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 811	<b>86.25</b> HIGH CONFIDENCE
Domain	C-terminal luminal domain (653-869)
Position context	C-terminal luminal domain
IDR flag	No — pLDDT well above 50 threshold

Position analysis: SER812 (2.5 Å), PHE810 (2.5 Å — F810L partner!), SER808 (3.8 Å — E809K region). Same E809-F810-K811 cluster as E809K/F810L. The Atlas's neighbor extraction surfaces this variant's contacts and connects them to the broader multi-variant target landscape.

## COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

**0.073**am\_class: **LBen** —  
threshold > 0.564DYNAMUT2  $\Delta\Delta G$ **-0.28** kcal/

mol

Destabilising · Job  
177992523974

PLDDT (ALPHAFOLD)

**86.25**

high confidence

## CLINICAL EVIDENCE

ClinVar classification

**CONFLICTING CLASSIFICATIONS OF PATHOGENICITY**

Review status

criteria provided, conflicting classifications

Last evaluated

2025/05/21 00:00

Inheritance

Conflicting ClinVar classifications.

WFS1 variant landscape

K811R is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar)

- (no specific conditions catalogued)

## 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

**Cat 4 – see structural prose.** AlphaMissense below threshold (AM under-call class) but mechanism is structurally identified. Therapeutic strategy: site-directed at contacts identified above, or wet-lab validation if pLDDT borderline/below 50.

E809K + F810L + K811R cluster.