

# WFS1 A58V — Wolframin

Ala→Val p58 IDR AM=0.09 ddg=-0.68 pLDDT=26. ClinVar Conflicting evidence.  
Atlas mechanism: see structural analysis.

## IDENTITY

Variant	A58V (p.Alanine58Valine)
DNA change	c.173C>T
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV000516852
Amino acid change	conservative volume increase

## STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 58	<b>26.17</b> <span>BELOW IDR THRESHOLD</span>
Domain	N-terminal intrinsically disordered region (1-86)
Position context	N-terminal IDR
IDR flag	YES — pLDDT 26.17 is below 50 threshold (route to Cat 5)

Position analysis: ALA59 (2.5 Å), ALA57 (2.5 Å — partner of A57S/A57T).  
pLDDT 26 deep IDR. Multiple A57 substitutions Atlas-tracked. The Atlas's neighbor extraction surfaces this variant's contacts and connects them to the broader multi-variant target landscape.

## COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

**0.087**am\_class: **LBen** —  
threshold > 0.564DYNAMUT2  $\Delta\Delta G$ **-0.68** kcal/

mol

Destabilising · Job  
177992518683

PLDDT (ALPHAFOLD)

**26.17**

BELOW IDR THRESHOLD

## CLINICAL EVIDENCE

ClinVar classification

**CONFLICTING CLASSIFICATIONS OF PATHOGENICITY**

Review status

criteria provided, conflicting classifications

Last evaluated

2026/01/07 00:00

Inheritance

Conflicting ClinVar classifications.

WFS1 variant landscape

A58V 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  $\rightarrow$  CATEGORY 3 – docking experiments  $\Delta\Delta G$  2–4  $\rightarrow$  CATEGORY 2 – pharmacological chaperones  $\Delta\Delta G > 4$   $\rightarrow$  CATEGORY 1 – gene therapy pLDDT  $< 50$   $\rightarrow$  CATEGORY 5 – IDR, experimental only Stable fold + functional site hit  $\rightarrow$  CATEGORY 4 – site-specific docking

**Cat 5 IDR — 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.

Deep IDR — multi-substitution position cluster 57-58.