

# WFS1 G789S — Wolframin

Gly→Ser p789 IDR AM=0.07 ddg=-0.11 pLDDT=43. ClinVar Conflicting evidence. Atlas mechanism: see structural analysis.

## IDENTITY

Variant	G789S (p.Glycine789Serine)
DNA change	c.2365G>A
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV001419650
Amino acid change	glycine flexibility lost

## STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 789	<b>43.34</b> <span>BELOW IDR THRESHOLD</span>
Domain	C-terminal luminal domain (653-869)
Position context	C-terminal luminal IDR
IDR flag	YES — pLDDT 43.34 is below 50 threshold (route to Cat 5)

Position analysis: SER790 (2.5 Å — partner of S790W/L), ASP788 (2.5 Å), ALA787 (4.5 Å — A787T). pLDDT 43 IDR boundary. Position 789 adjacent to multi-substitution 790. The Atlas's neighbor extraction surfaces this variant's contacts and connects them to the broader multi-variant target landscape.

## COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

**0.069**am\_class: **LBen** —  
threshold > 0.564DYNAMUT2  $\Delta\Delta G$ **-0.11** kcal/

mol

Destabilising · Job  
177992523646

PLDDT (ALPHAFOLD)

**43.34**

BELOW IDR THRESHOLD

## CLINICAL EVIDENCE

ClinVar classification

**CONFLICTING CLASSIFICATIONS OF PATHOGENICITY**

Review status

criteria provided, conflicting classifications

Last evaluated

2025/08/30 00:00

Inheritance

Conflicting ClinVar classifications.

WFS1 variant landscape

G789S 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.

IDR boundary near S790 cluster.