

# WFS1 T590M — Wolframin

Thr→Met p590 TM9 AM=0.06 ddg=+0.09 pLDDT=73. ClinVar Conflicting evidence. Atlas mechanism: see structural analysis.

## IDENTITY

|                   |                                  |
|-------------------|----------------------------------|
| Variant           | T590M (p.Threonine590Methionine) |
| DNA change        | c.1769C>T                        |
| Gene · Protein    | WFS1 · Wolframin (890 aa)        |
| UniProt           | O76024 · WFS1_HUMAN              |
| ClinVar accession | VCV000505398                     |
| Amino acid change | polar→hydrophobic                |

## STRUCTURAL CONTEXT

|                      |                                      |
|----------------------|--------------------------------------|
| AlphaFold model      | AF-O76024-F1, v6                     |
| pLDDT at residue 590 | <b>72.56</b> HIGH CONFIDENCE         |
| Domain               | TM9 (589-609), helical transmembrane |
| Position context     | TM9 (589-609)                        |
| IDR flag             | No — pLDDT well above 50 threshold   |

Position analysis: SER591 (2.5 Å), PHE589 (2.5 Å — TM9 start), ARG587 (3.8 Å — R587W/Q!). TM9 cluster + loop boundary. The Atlas's neighbor extraction surfaces this variant's contacts and connects them to the broader multi-variant target landscape.

## COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

**0.062**am\_class: **LBen** —  
threshold > 0.564

DYNAMUT2 ΔΔG

**0.09** kcal/molStabilising · Job  
177992527382

PLDDT (ALPHAFOLD)

**72.56**

high confidence

## CLINICAL EVIDENCE

ClinVar classification

**CONFLICTING CLASSIFICATIONS OF PATHOGENICITY**

Review status

criteria provided, conflicting classifications

Last evaluated

2023/04/17 00:00

Inheritance

Conflicting ClinVar classifications.

WFS1 variant landscape

T590M 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.

TM9 cluster + R587 loop boundary.