

WFS1 F568S — Wolframin

Phenylalanine → Serine at position 568. Lumenal loop 4. ClinVar Uncertain significance, AlphaMissense 0.906, DynaMut2 $\Delta\Delta G$ -0.75 kcal/mol (destabilising).

IDENTITY

Variant	F568S (p.Phenylalanine568Serine)
DNA change	c.1703T>C
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV002080395
Amino acid change	Phenylalanine (F) → Serine (S)

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 568	72.69 HIGH CONFIDENCE
Domain	Lumenal loop 4
Position context	C-terminal lumenal domain · position 568 projects into the ER lumen
IDR flag	No — pLDDT well above 50 threshold

Position 568 sits in the C-terminal lumenal domain (residues 653–869), wolframin's largest soluble region. This domain projects into the ER lumen and is implicated in calcium handling, ER stress sensing, and protein–protein interactions with ATF6 and Na⁺/K⁺ ATPase β 1. The wild-type residue is large aromatic hydrophobic (phenylalanine); the mutant is small polar (serine — hydroxyl). The chemistry shift implies altered local packing, hydrogen-bonding, and/or electrostatics at this site.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.906am_class: **likely pathogenic** —
threshold > 0.564DYNAMUT2 $\Delta\Delta G$ **-0.75** kcal/molDestabilising · Job
178092106933

PLDDT (ALPHAFOLD)

72.69

high confidence

CLINICAL EVIDENCE

ClinVar classification	UNCERTAIN SIGNIFICANCE
Review status	criteria provided, multiple submitters, no conflicts
Last evaluated	2025/12/22 00:00
Inheritance	Inheritance pattern not specified in ClinVar entry; WFS1 has both AD and AR presentations.
WFS1 variant landscape	F568S is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar) <ul style="list-style-type: none">Inborn genetic diseases

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 3/4 — Most Druggable

$|\Delta\Delta G|=0.75 < 2$ kcal/mol (fold intact) + AlphaMissense 0.906 confirms functional impact. Specific local contacts disrupted — priority for docking and pharmacological chaperone screening.

Wolframin's fold survives this substitution ($|\Delta\Delta G|=0.75$ kcal/mol). The pathogenic signal is real — AlphaMissense places it at 0.906. Protein still folds, but a specific local site is broken. Pharmacological chaperones and small-molecule binders are the rational therapeutic vector.