

WFS1 T490A — Wolframin

Thr→Ala p490 loop AM=0.08 ddg=-0.34 pLDDT=81. ClinVar Conflicting evidence. Atlas mechanism: see structural analysis.

IDENTITY

Variant	T490A (p.Threonine490Alanine)
DNA change	c.1468A>G
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV000505052
Amino acid change	H-bond loss + side-chain reduction

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 490	81.38 HIGH CONFIDENCE
Domain	Connecting loop
Position context	Connecting loop
IDR flag	No — pLDDT well above 50 threshold

Position analysis: VAL491 (2.5 Å), ILE489 (2.5 Å — I489M!), LEU499 (3.5 Å — L499F partner!). Multi-variant target. The Atlas's neighbor extraction surfaces this variant's contacts and connects them to the broader multi-variant target landscape.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.082am_class: **LBen** —
threshold > 0.564DYNAMUT2 $\Delta\Delta G$ **-0.34** kcal/

mol

Destabilising · Job
177992522848

PLDDT (ALPHAFOLD)

81.38

high confidence

CLINICAL EVIDENCE

ClinVar classification

CONFLICTING CLASSIFICATIONS OF PATHOGENICITY

Review status

criteria provided, conflicting classifications

Last evaluated

2016/06/02 00:00

Inheritance

Conflicting ClinVar classifications.

WFS1 variant landscape

T490A 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 3/4 — 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.

T490A + I489M + L499F cluster.