

WFS1 T156M — Wolframin

Threonine → Methionine at position 156. N-terminal cytoplasmic (intrinsically disordered). ClinVar Uncertain significance, AlphaMissense 0.626, DynaMut2 $\Delta\Delta G$ +0.25 kcal/mol (stabilising).

IDENTITY

Variant	T156M (p.Threonine156Methionine)
DNA change	c.467C>T
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV002734642
Amino acid change	Threonine (T) → Methionine (M)

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 156	89.25 HIGH CONFIDENCE
Domain	N-terminal cytoplasmic (intrinsically disordered)
Position context	N-terminal cytoplasmic (intrinsically disordered)
IDR flag	No — pLDDT well above 50 threshold

Position 156 sits in N-terminal cytoplasmic (intrinsically disordered). The wild-type residue is small polar (threonine — hydroxyl); the mutant is hydrophobic sulfur (methionine). The chemistry shift implies altered local packing, hydrogen-bonding, and/or electrostatics at this site.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.626am_class: **likely pathogenic** —
threshold > 0.564DYNAMUT2 $\Delta\Delta G$ **0.25** kcal/mol

Stabilising · Job 178092130017

PLDDT (ALPHAFOLD)

89.25

high confidence

CLINICAL EVIDENCE

ClinVar classification

UNCERTAIN SIGNIFICANCE

Review status	criteria provided, single submitter
Last evaluated	2023/08/07 00:00
Inheritance	Inheritance pattern not specified in ClinVar entry; WFS1 has both AD and AR presentations.
WFS1 variant landscape	T156M is 1 of ~326 pathogenic-spectrum variants in WFS1 (out of 2,243 in ClinVar) <ul style="list-style-type: none">• (no 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

Category 3/4 — Most Druggable

$|\Delta\Delta G|=0.25 < 2$ kcal/mol (fold intact) + AlphaMissense 0.626 confirms functional impact. Specific local contacts disrupted — priority for docking and pharmacological chaperone screening.

Wolframins fold survives this substitution ($|\Delta\Delta G|=0.25$ kcal/mol). The pathogenic signal is real — AlphaMissense places it at 0.626. Protein still folds, but a specific local site is broken. Pharmacological chaperones and small-molecule binders are the rational therapeutic vector.