

WFS1 P10S — Wolframin

Pro→Ser p10 IDR AM=0.06 ddg=-0.23 pLDDT=35. ClinVar Conflicting evidence.
Atlas mechanism: see structural analysis.

IDENTITY

Variant	P10S (p.Proline10Serine)
DNA change	c.28C>T
Gene · Protein	WFS1 · Wolframin (890 aa)
UniProt	O76024 · WFS1_HUMAN
ClinVar accession	VCV000349302
Amino acid change	proline removal

STRUCTURAL CONTEXT

AlphaFold model	AF-O76024-F1, v6
pLDDT at residue 10	35.06 BELOW IDR THRESHOLD
Domain	N-terminal intrinsically disordered region (1-86)
Position context	N-terminal IDR
IDR flag	YES — pLDDT 35.06 is below 50 threshold (route to Cat 5)

Position analysis: SER11 (2.4 Å), GLY9 (2.5 Å). pLDDT 35 deep IDR. The Atlas's neighbor extraction surfaces this variant's contacts and connects them to the broader multi-variant target landscape.

COMPUTATIONAL PREDICTIONS

ALPHAMISSENSE

0.064am_class: **LBen** —
threshold > 0.564DYNAMUT2 $\Delta\Delta G$ **-0.23** kcal/

mol

Destabilising · Job
177992526223

PLDDT (ALPHAFOLD)

35.06

BELOW IDR THRESHOLD

CLINICAL EVIDENCE

ClinVar classification

CONFLICTING CLASSIFICATIONS OF PATHOGENICITY

Review status

criteria provided, conflicting classifications

Last evaluated

2024/09/11 00:00

Inheritance

Conflicting ClinVar classifications.

WFS1 variant landscape

P10S 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 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.

Deep IDR proline removal.