

# c.1228del — WFS1 Molecular Atlas Card

**Variant type:** Frameshift

**Frameshift point:** residue 410

**Predicted premature stop (PTC):** residue 441

**Domain context (where the frame breaks):** Transmembrane helix 4

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## SCHEMA CATEGORY: F2 — FRAMESHIFT, NMD-ESCAPE — SCRAMBLED C-TERMINUS PRODUCED

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The premature stop falls in the last exon (exon 8), so NMD does not degrade the transcript and a protein IS produced — native sequence up to the frameshift point, then a non-native (scrambled) stretch to the new stop. The garbled C-terminus may misfold or mis-insert and can interfere with folding/membrane insertion of the upstream domains. Behavior is highly variable and typically too compromised for chaperone rescue; gene therapy is the primary path. Wet-lab validation recommended.

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## PREMATURE-STOP PREDICTION

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- **Frameshift point:** aa 410
- **Predicted PTC:** aa 441 (31 codons downstream of the frame break)
- **Method:** deterministic translation of edited NM\_006005.3 CDS (frameshift position = first changed residue, HGVS convention)
- **Confidence:** high

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## NMD PREDICTION

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- **Status:** NMD-escape
- **Confidence:** high

- **Reasoning:** Stop codon at position 441 is in the last exon (exon 8, starts ~aa 413). NMD does not target stop codons in the last exon — a truncated protein is produced.
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## PROTEIN CONSEQUENCE

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- **Native (wild-type) sequence retained:** aa 1 – 409 (46.0% of full-length protein)
- **Non-native scrambled stretch:** aa 410 – 440 (31 residues of out-of-frame sequence)
- **Lost beyond the PTC:** aa 441 – 890 (450 residues)

### Native domains retained (upstream of the frameshift)

- N-terminal cytoplasmic (intrinsically disordered) (aa 1–310)
- Transmembrane helix 1 (aa 311–331)
- Cytoplasmic loop 1 (aa 332–340)
- Transmembrane helix 2 (aa 341–361)
- Luminal loop 1 (aa 362–370)
- Transmembrane helix 3 (aa 371–391)
- Cytoplasmic loop 2 (aa 392–400)

### Domain interrupted at the frameshift point

- **Transmembrane helix 4** — native aa 401–409 retained; aa 410–421 replaced by non-native sequence

### Native domains downstream of the frameshift (lost or non-native)

- Luminal loop 2 (aa 422–431)
  - Transmembrane helix 5 (aa 432–452)
  - Cytoplasmic loop 3 (aa 453–461)
  - Transmembrane helix 6 (aa 462–482)
  - Luminal loop 3 (aa 483–496)
  - Transmembrane helix 7 (aa 497–517)
  - Cytoplasmic loop 4 (aa 518–532)
  - Transmembrane helix 8 (aa 533–553)
  - Luminal loop 4 (aa 554–573)
  - Transmembrane helix 9 (aa 574–594)
  - Cytoplasmic loop 5 / pre-luminal (aa 595–599)
  - C-terminal ER-luminal (calcium binding, calmodulin, chaperone) (aa 600–890)
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## CLINICAL EVIDENCE

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- **Classification:** Likely pathogenic
  - **Review status:** criteria provided, single submitter
  - **Associated conditions:** Wolfram syndrome 1; Autosomal dominant nonsyndromic hearing loss 6; Type 2 diabetes mellitus; Cataract 41; Wolfram-like syndrome
  - **cDNA change:** c.1228del
  - **ClinVar accession:** VCV003381937
  - **Last evaluated:** 1/01/01 00:00
  - **Submissions:** 1
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## WHY THIS VARIANT MATTERS

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Because the frame breaks late, in the last exon, the transcript escapes NMD and a protein is actually made: wild-type wolframin up to the break, then a stretch of non-native sequence to a new stop. That scrambled C-terminus is the wildcard — it can drag the upstream domains out of fold. The atlas quantifies exactly how much native protein survives and how long the non-native tail is — the data a wet-lab needs to predict behavior.

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*Card generated by `wolfram-atlas-batch` skill (v2 — frameshift pipeline) on 2026-06-08T02:15:06.190993Z.*

*NMD rule and schema definitions: `reference/nmd` `rules.md`, `reference/cardschemaextension.md` .\_\_*

*CDS reference: NM006005.3 (171..2843). WFS1 reference: UniProt O76024, AlphaFold model v6.\_\_*