

# c.2554dup — WFS1 Molecular Atlas Card

**Variant type:** Frameshift

**Frameshift point:** residue 852

**Predicted premature stop (PTC):** residue 891

**Domain context (where the frame breaks):** C-terminal ER-luminal (calcium binding, calmodulin, chaperone)

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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 852
- **Predicted PTC:** aa 891 (40 codons downstream of the frame break)
- **Method:** deterministic translation of edited NM\_006005.3 CDS (frameshift position = first changed residue, HGVS convention)
- **Confidence:** high

## NMD PREDICTION

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

- **Reasoning:** Stop codon at position 891 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 – 851 (95.6% of full-length protein)
- **Non-native scrambled stretch:** aa 852 – 890 (39 residues of out-of-frame sequence)
- **Lost beyond the PTC:** aa 891 – 890 (0 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)
- Transmembrane helix 4 (aa 401–421)
- 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)

### Domain interrupted at the frameshift point

- **C-terminal ER-luminal (calcium binding, calmodulin, chaperone)** — native aa 600–851 retained; aa 852–890 replaced by non-native sequence

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

*(no full native domains downstream)*

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## CLINICAL EVIDENCE

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- **Classification:** Pathogenic
- **Review status:** criteria provided, single submitter
- **Associated conditions:** Autosomal dominant nonsyndromic hearing loss 6
- **cDNA change:** c.2554dup
- **ClinVar accession:** VCV004684987
- **Last evaluated:** 2026/01/06 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 2026-06-08T02:16:42.817916Z.*

*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.\_\_*