

c.2385_2390del — WFS1 Molecular Atlas Card

Variant type: In-frame indel

Change: 2 residue(s) deleted in frame at position 795

Domain context: C-terminal ER-luminal (calcium binding, calmodulin, chaperone)

SCHEMA CATEGORY: I3 — MULTI-RESIDUE IN-FRAME INDEL — LIKELY MAJOR STRUCTURAL DISRUPTION

2 residues removed in frame around position 795 (C-terminal ER-luminal (calcium binding, calmodulin, chaperone)). A change this size usually perturbs local packing and can propagate to the fold. Gene therapy is the primary path unless an AlphaFold prediction of the modified sequence shows a surprisingly intact fold. Predicted structure pending (ColabFold).

STRUCTURAL PREDICTION

- **Reading frame:** preserved (in-frame) — no premature stop, NMD does not apply.
- **Affected domain:** C-terminal ER-luminal (calcium binding, calmodulin, chaperone)
- **Predicted modified structure:** _pending — AlphaFold/ColabFold prediction of the

modified sequence and backbone-RMSD vs wild-type backfill here (Wave 2)._

CLINICAL EVIDENCE

Not found in the cached WFS1 ClinVar set ([reference/WFS1clinvarvariants.csv](#))._

Schema: `reference/card schemaextension.md` (I1–I3). WFS1: UniProt O76024, AlphaFold v6.