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| --- | --- | --- | --- | --- |
| WT Position | PIE12-trimer resistant Mutation | Prevalence in Q577R containing Primary Isolates | Other mutations observed at this position | Comments |
| A48 | A48**T** | 1/751 | None | * Alanine is conserved in 750/751 (99.9%) sequences at this position
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| 161-164 amino acids: ISTS | Δ161-164 | 0/751 |  | * Loss of a glycosylation site with this deletion
* 724/751 sequences have the intact glycosylation site
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| 396-400amino acids: FNSTW | Δ396-400 | 0/751 |  | * Loss of a glycosylation site with this deletion
* This region is highly variable
* 16/751 lack at least one of the V4 glycosylation sites in this region
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| Q550 | Q550**H** | 0/751 |  | * The WT Q550 is conserved in all 751 sequences. Twenty-two have the cag codon; 729 have caa.
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| V583 Codon: GTG | V583Codon: GT**A** | 28/751 | V583I, V583L and V583M (168/751) | * 583/751 sequences have V583. Of these, 28 have the gta codon.
* Only hydrophobic residues are seen at this position in this viral pool
* All variants at this position (Val, Ile, Leu and Met) have a T as the second position in the codon
* In the RRE structure, that T(U) is in a G-U pair at the end of a stem-loop—suggests this T(U) is important
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| L663 | L663**F** | 1/751 | L663W (2/751) | * 748/751 have WT L663
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| A823 | A823**V** | 0/751 | A823G (134/751) | * 617/751 have WT A823
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