**PTM ANALYSIS RESULT-APOE GENE**

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| **ID** | **Position** | **Code** | **Kinase** | **PSP** | **PSP** | **Cutoff** |
| APOE-Wildtype | 40 | S | CK1 | RQQTEWQSGQRWELA | 0.1559 | 0.0996 |

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| **ID** | **Position** | **Code** | **Kinase** | **PSP** | **PSP** | **Cutoff** |
| rs7412 | 40 | S | CK1 | RQQTEWQSGQRWELA | 0.1559 | 0.0996 |

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| **ID** | **Position** | **Code** | **Kinase** | **PSP** | **PSP** | **Cutoff** |
| rs769455 | 40 | S | CK1 | RQQTEWQSGQRWELA | 0.1559 | 0.0996 |

**CONCLUSION:**The predicted phosphorylation site at position 40 (Serine) is conserved across the wild-type and mutant protein sequences (rs7412 and rs769455).

* The mutation(s) introduced by rs7412 and rs769455 did not alter the phosphorylation site at position 40 or disrupt the Casein Kinase 1 (CK1) recognition motif.
* This suggests that the post-translational regulation of the protein at this site is likely maintained in the mutants.
* This suggests that the mutations introduced by these SNPs do not disrupt the CK1-mediated phosphorylation potential at this site.
* Therefore, the structural integrity required for CK1-mediated phosphorylation is likely preserved.