|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Somatic Mutation | Residue | WT AA | Mutant AA | Sector | Compensating Mutation | Residue | WT AA | Mutant AA | Sector | Number of Sequences with Compensatory Mutation Pair |
| 180 | Glu | Gln | 1 | 49 | Asn | Gap | 0 | 26 |
| 200 | Asn | Gap | 1 | 56 | Thr | Asp | 0 | 25 |
| 200 | Asn | Gap | 1 | 56 | Thr | Gap | 0 | 17 |
| 200 | Asn | Gap | 1 | 59 | Asn | Thr | 0 | 23 |
| 200 | Asn | Gap | 1 | 108 | Val | Gly | 0 | 36 |
| 200 | Asn | Gap | 1 | 291 | Val | Pro | 0 | 35 |
| 220 | Tyr | His | 1 | 108 | Val | Gly | 0 | 15 |
| 220 | Tyr | His | 1 | 291 | Val | Pro | 0 | 18 |
| 235 | Asn | Ser | 1 | 100 | Val | Thr | 0 | 21 |
| 240 | Ser | Gly | 1 | 81 | Thr | Pro | 0 | 22 |
| 240 | Ser | Gly | 1 | 111 | Met | Ile | 0 | 24 |
| 270 | Phe | Val | 1 | 76 | Met | Thr | 0 | 18 |
| 270 | Phe | Val | 1 | 80 | Ser | Pro | 0 | 27 |
| 270 | Phe | Val | 1 | 81 | Thr | Pro | 0 | 27 |
| 270 | Phe | Val | 1 | 94 | Gln | Ile | 0 | 19 |
| 270 | Phe | Val | 1 | 111 | Met | Ile | 0 | 29 |
| 270 | Phe | Val | 1 | 131 | Asp | Lys | 0 | 29 |
| 363 | Arg | Lys | 5 | 73 | Cys | Ser | 0 | 17 |
| 363 | Arg | Lys | 5 | 73 | Cys | Gap | 0 | 15 |
| 363 | Arg | Lys | 5 | 76 | Met | Thr | 0 | 21 |
| 363 | Arg | Lys | 5 | 80 | Ser | Pro | 0 | 35 |
| 363 | Arg | Lys | 5 | 81 | Thr | Pro | 0 | 26 |
| 363 | Arg | Lys | 5 | 90 | Val | Met | 0 | 15 |
| 363 | Arg | Lys | 5 | 94 | Gln | Ile | 0 | 19 |
| 363 | Arg | Lys | 5 | 111 | Met | Ile | 0 | 23 |
| 363 | Arg | Lys | 5 | 111 | Met | Leu | 0 | 20 |
| 363 | Arg | Lys | 5 | 131 | Asp | Asn | 0 | 23 |
| 363 | Arg | Lys | 5 | 131 | Asp | Lys | 0 | 22 |

Table 1. **Compensatory Mutation Candidates**. This list of compensatory mutation candidates was generated from the coevolution matrix and somatic mutation list. There is no mutation in sector 2, 3, 4, or 6 that is compensated by other mutations, based on the criteria we used for screening.