|  |  |  |
| --- | --- | --- |
| MUTANT | ZoomVar prediction of mutation location | Q(SASA) value from protein hit with highest identity |
| V2F | Surface | 0.9176 |
| L21P | Surface | 0.2211 |
| L27P | Core | 0.1043 |
| H32R | Surface | 0.9865 |
| K35R | Surface | 0.9394 |
| I42N | Core | 0.1196 |
| V44M | Surface | 0.214 |
| N47S | Surface | 0.1559 |
| R48W | Surface | 0.3946 |
| P76L | Surface | 0.1535 |
| P82L | Surface | 0.6576 |
| R102Q | Surface | 0.2658 |
| R102W | Surface | 0.2658 |
| R103Q | Surface | 0.3918 |
| E112K | Core | 0.1188 |
| S113L | Core | 0.0889 |
| T123M | Surface | 0.1531 |
| T123R | Surface | 0.1531 |
|  |  |  |
| Q25R | Surface | 0.5823 |
| E41Q | Surface | 0.4961 |
| A52T | Surface | 0.5962 |
| C70R | Core | 0.1296 |
| T77I | Surface | 0.6265 |
| K93E | Surface | 0.3708 |
| Y101F | Surface | 0.3101 |
| E138K | Surface | 0.5344 |
| G141D | Surface | 0.408 |
| A144T | Surface | 0.3143 |
| I146V | Surface | 0.1802 |
| Q153R | Surface | 0.554 |