|  |  |  |  |
| --- | --- | --- | --- |
| **SNPs&GO** | | | |
| Method | Prediction | Reliability Index | Probability |
| PhD-SNP | Check HTML | Check HTML | Check HTML |
| PANTHER | Check HTML | Check HTML | Check HTML |
| SNPs&GO | Check HTML | Check HTML | Check HTML |
| **PMut** | | | |
| Score | | Check HTML | |
| Reliability of prediction | | Check HTML | |
| Prediction | | Check HTML | |
| **HANSA** | | | |
| Prediction | | Check HTML | |
| Wild Pab | | Check HTML | |
| Mutant Pab | | Check HTML | |
| Diff. Pab | | Check HTML | |
| Wild Gab | | Check HTML | |
| Mutant Gab | | Check HTML | |
| Diff. Gab | | Check HTML | |
| Solvent accessibility | | Check HTML | |
| Secondary structure | | Check HTML | |
| BLOSUM62 | | Check HTML | |
| Diff. free energy | | Check HTML | |
| **PANTHER** | | | |
| Probability of being deleterious | | Check HTML | |
| subPSEC score | | Check HTML | |
| MSA Position | Check HTML | Pwt | Check HTML |
| Psubstituted | Check HTML | NIC | Check HTML |
| **PROVEAN** | | | |
| Score | | Check HTML | |
| Prediction | | Check HTML | |
| Number of sequences used | | Check HTML | |
| **SIFT** | | | |
| Score | | Check HTML | |
| Median Conservation Score | | Check HTML | |
| Number of sequences used | | Check HTML | |
| Prediction | | Check HTML | |
| **Mutation Assessor** | | | |
| Functional impact | | Check HTML | |
| FI score | | Check HTML | |
| **PolyPhen2** | | | |
| HumDiv (rare alleles) | | Check HTML | |
| HumDiv score | | Check HTML | |
| HumDiv sensitivity | Check HTML | HumDiv specificity | Check HTML |
| HumVar (Mendelian disease) | | Check HTML | |
| HumVar score | | Check HTML | |
| HumVar sensitivity | Check HTML | HumVar specificity | Check HTML |