Supplementary Material

**Supplementary Table 7.** The 18 Features Used for Feature Selection

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| **Category** | **Feature** | **Description** |
| Conservation | Consurf\_Score | Conservative score of the mutation site, computed by Consurf server (<https://consurf.tau.ac.il/>) |
| Interaction | BSA1 | The area that the mutated residue contribute to the RPS19-18S rRNA interface, computed by PDBePISA (<https://www.ebi.ac.uk/pdbe/pisa/>) |
| rBSA1 | Percentage of BSA compared to the SASA of mutated residue, computed by PDBePISA (<https://www.ebi.ac.uk/pdbe/pisa/>) |
| HB\_Num1 | The number of hydrogen bonds between mutated residue and 18S rRNA, computed by PDBePISA (<https://www.ebi.ac.uk/pdbe/pisa/>) |
| WT\_Charge, Delta\_Charge1 | Charge of mutated residue and the difference of charge between before and after substitution |
| Structure Stability | WT\_Hydrophobicity,  Delta\_Hydrophobicity | Hydrophobicity of the mutated residue, and the difference of hydrophobicity between before and after substitution. The hydrophobicity values comes from ([PMID: 4023714](https://pubmed.ncbi.nlm.nih.gov/4023714/)). |
| DDG1 | ΔΔG, the difference of folding free energy, computed by FoldX (<http://foldxsuite.crg.eu/>) |
| WT\_Helix, Delta\_Helix1 | Helix propensity of mutated residue, and the difference of propensity between before and after mutation. The helix propensity data come from ([PMID: 4358940](https://pubmed.ncbi.nlm.nih.gov/4358940/)). |
| WT\_Volume, Delta\_Volume | Volume of mutated residue, and the difference of volume between before and after mutation. The volume data of residues come from ([PMID: 4566650](https://pubmed.ncbi.nlm.nih.gov/4566650/)). |
| Intra\_HB\_Num | The number of intramolecular hydrogen bonds formed by the mutated residue, computed by hbplus (<https://www.ebi.ac.uk/thornton-srv/software/HBPLUS/>) |
| rSASA | Relative Solvent Accessible Surface Area of mutation residue, computed by DSSP (<https://swift.cmbi.umcn.nl/gv/dssp/>) |
| Other | Blosum621 | Blosum62 substitution matrix scores |
| WT\_Disorder, Delta\_Disorder1 | Disorder score of the mutated residue, and the difference of disorder score between before and after mutation, computed by Iupred2a (<https://iupred2a.elte.hu/>) |

1 features selected for building the final prediction model