**Table S3**: List of residual mutations in VP1/2 sequence of parvovirus B19V changing overall stability of the VP1/2 structure

|  |  |  |  |
| --- | --- | --- | --- |
| Mutation | Predicted ∆∆G (kcal/mol) | RSA | Destabilizing/Stabilizing |
| Val(21)Thr | -0.563 | 61 | Destabilizing |
| Ser(32)Thr | -0.396 | 45 | Destabilizing |
| Thr(122)Ala | -0.73 | 25 | Destabilizing |
| Val(128)Ile | -1.212 | 0 | Destabilizing |
| Gln(220)Glu | 0.068 | 41 | stabilizing |
| Thr(227)Ser | -0.438 | 29 | Destabilizing |
| Asp(323)Ser | -0.04 | 81 | Destabilizing |
| Ile(283)Val | -0.629 | 30 | Destabilizing |
| Met(389)Ile | -0.194 | 53 | Destabilizing |

Notes: ∆∆G, Gibbs-free energy change upon mutation, RSA: Relative solvent accessible area.