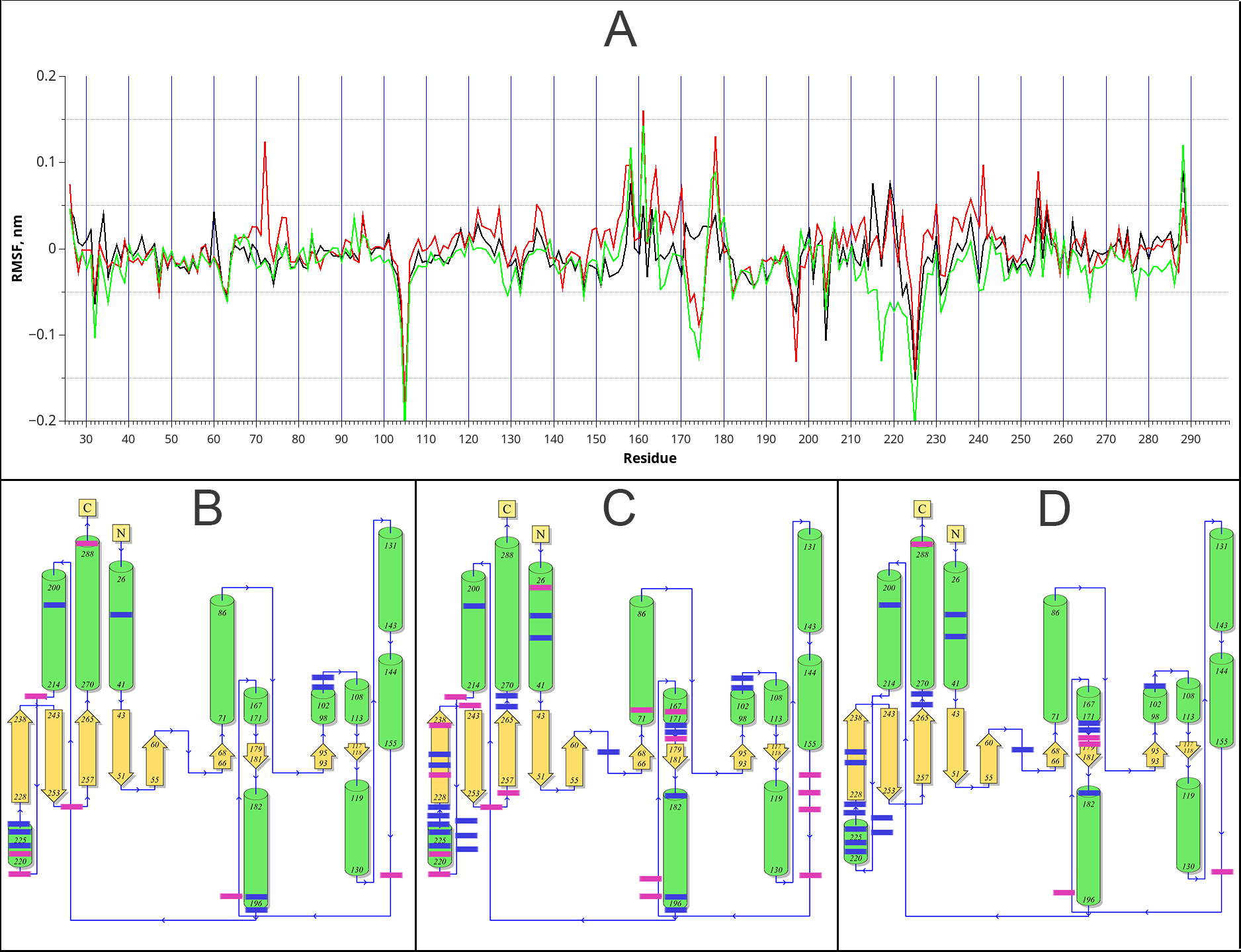


**Figure 1S**. RMSD values of TEM type β-lactamases during MD simulations at 400K. TEM-1 – black, TEM-1238,240 – green, TEM-1238,240,182 – red, TEM-1238,240,182,39 – blue.

Table 1S. The list of residues with altered values of RMSF (Å) in TEM variants in compare to TEM-1.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **TEM-1238,240 vs TEM1** | | **TEM-1238,240,182 vs TEM1** | | | **TEM-1238,240,182,39 vs TEM1** | |
| **RMSF Up** | **RMSF Down** | **RMSF Up** | **RMSF Down** | **RMSF Up** | | **RMSF Down** |
| 158 HIS | 32 LYS | 26 HIS | 32 LYS | 158 HIS | | 32 LYS |
| 161 ARG | 104 GLU | 72 PHE | 35 ASP | 161 ARG | | 35 ASP |
| 215 LYS | 105 TYR | 156 GLY | 63 GLU | 177 GLU | | 63 GLU |
| 219 PRO | 196 GLY | 157 ASP | 104 GLU | 178 ARG | | 104 GLU |
| 220 LEU | 197 GLU | 158 HIS | 105 TYR | 288 HIS | | 172 ALA |
| 254 GLY | 204 ARG | 161 ARG | 172 ALA |  | | 173 ILE |
| 288 HIS | 224 ALA | 163 ASP | 173 ILE |  | | 174 PRO |
|  | 225 LEU | 164 ARG | 174 PRO |  | | 175 ASN |
|  | 226 PRO | 170 ASN | 175 ASN |  | | 182 THR |
|  |  | 178 ARG | 182 THR |  | | 204 ARG |
|  |  | 215 LYS | 196 GLY |  | | 217 ALA |
|  |  | 219 PRO | 197 GLU |  | | 218 GLY |
|  |  | 220 LEU | 204 ARG |  | | 220 LEU |
|  |  | 230 PHE | 217 ALA |  | | 221 LEU |
|  |  | 238 SER | 218 GLY |  | | 222 ARG |
|  |  | 241 ARG | 219 PRO |  | | 223 SER |
|  |  | 254 GLY | 221 LEU |  | | 224 ALA |
|  |  | 256 PRO | 222 ARG |  | | 226 PRO |
|  |  |  | 223 SER |  | | 227 ALA |
|  |  |  | 224 ALA |  | | 231 ILE |
|  |  |  | 225 LEU |  | | 232 ALA |
|  |  |  | 226 PRO |  | | 266 GLY |
|  |  |  | 227 ALA |  | | 277 GLN |
|  |  |  | 231 ILE |  | |  |
|  |  |  | 232 ALA |  | |  |
|  |  |  | 266 GLY |  | |  |
|  |  |  | 277 GLN |  | |  |

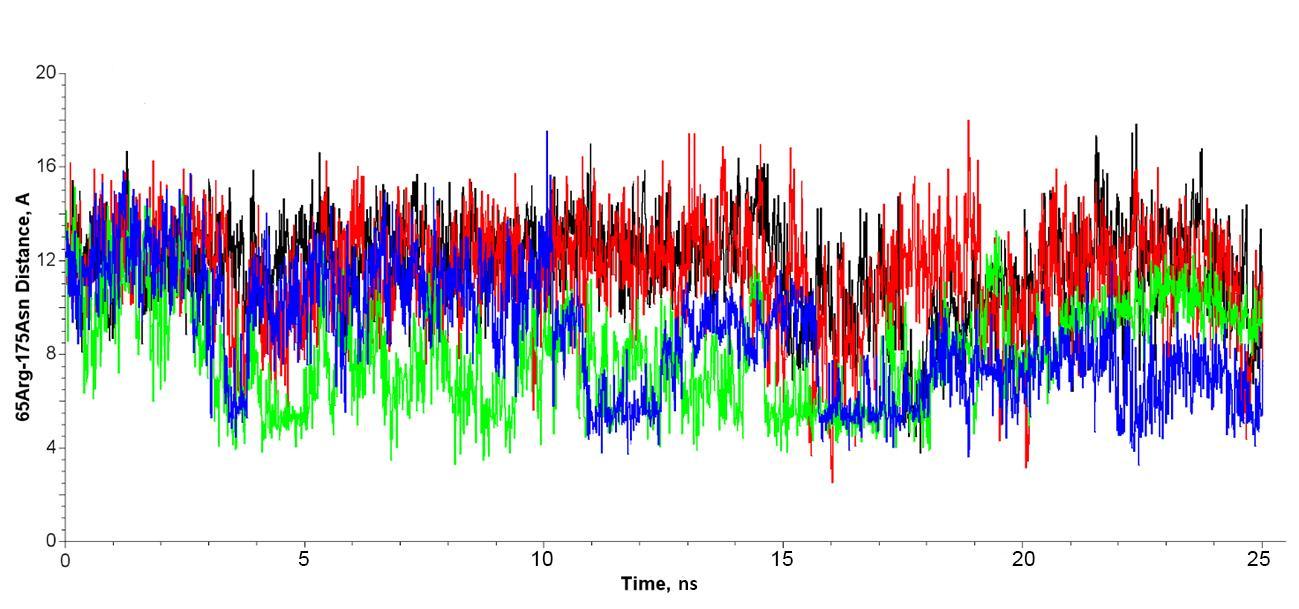


**Figure 2S** Differences in amino acid fluctuations (RMSF) during molecular dynamics.

A) Differences of values between TEM-1238,240 and TEM-1 (black), TEM-1238,240,182 and TEM-1 (red), TEM-1238,240,182,39 and TEM-1(green). See Table 1S.

Residues with significantly changed fluctuation values (difference of more than |0.5A|) are represented at PDBsum schemes: B) TEM-1238,240, C) TEM-1238,240,182 and D) TEM-1238,240,182,39

Residues with the increased RMSF values compared to the TEM-1 are represented in red, with the decreased values- blue.



**Figure 3S**. Distance between residues R65 and N175 during MD simulation of TEM type β-lactamases. TEM-1 – black, TEM-1238,240 – red, TEM-1238,240,182 – green, TEM-1238,240,182,39 – blue.