***Table S4.*** *Number of H-bonds formed between residues (or glycans) of the RBD and chain C in the native and oxidized SARS-CoV-2 S trimer. Values represent the average count per MD frame over the last 100 ns of the simulation, where only bonds with a prevalence exceeding 10% in all frames are considered.*

|  |  |  |
| --- | --- | --- |
| **RBD-chain C** | **Native** | **Oxidized** |
| Ser375-Asp405 | 0.10 ± 0.05 | 0.27 ± 0.13 |
| Asp364-Thr478 | 0 | 0.22 ± 0.20 |
| Tyr369-Thr415 | 0.22 ± 0.08 | 0.15 ± 0.14 |
| Asn370-Lys417 | 0.12 ± 0.04 | 0 |
| N343A-Thr500 | 0.18 ± 0.09 | 0 |