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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Vaccine candidate** | **Refined model characteristics** | | | | | **ERRAT** | | **Ramachandran plot** | | | | | | | | **Structure assessment** | |
| Before refinement | | | | After refinement | | | |
| RMSD | MolProbity | Clash Score | GDT-HA | Poor Rotamer | Before refinement | After refinement | Most favored | Allowed | Generously allowed | Disallowed | Most favored | Allowed | Generously allowed | Disallowed | QMEAN Z score | QMEANDisCo Global |
| VC1 | 0.179 | 2.078 | 15.1 | 0.9987 | 0.4 | 94.1% | 88% | 81.4% | 15,1% | 1.4% | 2.1% | 87.6% | 8.1% | 1.4% | 2.1% | -1.94 | 0.39 ± 0.05 |
| VC2 | 0.216 | 2.107 | 15.8 | 0.9962 | 0.6 | 94.9% | 88% | 87.8% | 10.8% | 0.5% | 0.8% | 90.2% | 8.1% | 0.3% | 1.4% | -2.05 | 0.70 ± 0.05 |