Supplementary file 1. Model Refinement Statistics.

Final refinement validation for all amino acids which were modeled de novo.

| Model Refinement |
| --- |
| Total amino acids | 3,156 |
| All-atom clashscore | 13.49 |
| Ramachandran outliers | 0.00% |
| Ramachandran allowed | 5.39% |
| Ramachandran favored | 94.61% |
| Rotamer Outliers | 0.00% |
| C β Deviations | 0% |
| Cis-proline | 0% |
| Cis-general | 0.00% |
| Twisted proline | 0% |
| Twisted general | 0.00% |