|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Protein** | **Normalized DOPE** | **C-score** | **Predicted TM-score$** | **Predicted RMSD** |
| V | **2.09**, 1.70, 1.99, 1.23, 1.27 | **-0.79**, -1.82, -0.32, -3.56, -2.69 | 0.61 | 8.9 |
| W | **1.45**, 0.77, 0.75, 1.56, 0.80 | **-1.42**, -1.73, -3.07, -4.34, -3.30 | 0.54 | 10.4 |
| C | **0.49**, -0.08, -1.53, -0.33, -0.88 | **-3.68**, -3.67, -3.29, -4.16, -4.09 | 0.31 | 13.6 |
| L# (14 - 1177) | **0.29**, 0.31, -0.04, 0.01, -0.16 | **0.07**, -0.30, -1.87, -1.05, -0.83 | 0.72 | 9.1 |
| L# (1191 - 1435) | **0.52** | **1.1** | 0.86 | 3.6 |
| L# (1553 - 1859) | **0.21**, 0.82, 0.95, 2.69, 0.44 | **-2.61**, -4.24, -4.52, -4.76, -5.00 | 0.41 | 12.4 |

#The protein was built domain wise because I-TASSER has a maximum size limit of 1500 residues.

$Although models built for V, W proteins and two of the Polymerase L domains had a TM-scores greater than 0.5, none of these models had a Normalized DOPE score less than or equal to zero and therefore were not used further in the study.