**STRUCTURE VALIDATION USING RAMACHANDRAN PLOT FOR BDNF GENE**

|  |  |
| --- | --- |
| **Criteria for high-resolution structure:** |  |

* The MolProbity score below 2.0
* A clash score below 5
* **Ramachandran Favoured:**>90%
* **Ramachandran outlier:** A value below 1%

**MolProbity Score - rs6265**

**MolProbity Score Summary**

| **Metric** | **Value** |
| --- | --- |
| **MolProbity Score** | 1.41 |
| **Clashscore** | 0.00 |
| **Ramachandran Favoured** | 88.98% |
| **Ramachandran Outliers** | 4.08% |
| **Rotamer Outliers** | 2.79% |

**Validation summary**

The structure is of good quality based on the MolProbity metrics. The MolProbity score (1.41) and Clashscore (0.00) are excellent, but the higher percentage of Ramachandran outliers (4.08%) suggests potential backbone conformation issues, which may require refinement for a high-resolution protein structure.

**MolProbity Score - rs1048218**

**Molprobity Summary Table**

|  |  |
| --- | --- |
| **Metric** | **Value** |
| **MolProbity Score** | 1.36 |
| **Clashscore** | 0.00 |
| **Ramachandran Favoured** | 91.02% |
| **Ramachandran Outliers** | 4.08% |

**Validation Summary**

The structure is of good quality based on the MolProbity metrics. The MolProbity score (1.36) and Clashscore (0.00) are excellent, but the higher percentage of Ramachandran outliers (4.08%) suggests potential backbone conformation issues, which may require refinement for a high-resolution protein structure.

**MolProbity Score - rs8192466-T>I**

**MolProbity Score Summary**

|  |  |
| --- | --- |
| **Metric** | **Value** |
| **MolProbity Score** | 1.30 |
| **Clashscore** | 0.00 |
| **Ramachandran Favoured** | 90.95% |
| **Ramachandran Outliers** | 4.12% |

**Validation Summary**

The structure is of good quality based on the MolProbity metrics. The MolProbity score (1.30) and Clashscore (0.00) are excellent, but the higher percentage of Ramachandran outliers (4.12%) suggests potential backbone conformation issues, which may require refinement for a high-resolution protein structure.

**MolProbity Score - rs8192466-T>N**

**MolProbity Score Summary**

| **Metric** | **Value** |
| --- | --- |
| **MolProbity Score** | 1.31 |
| **Clashscore** | 0.00 |
| **Ramachandran Favoured** | 90.61% |
| **Ramachandran Outliers** | 4.49% |

**Validation Summary**

The structure is of good quality based on the MolProbity metrics. The MolProbity score (1.31) and Clashscore (0.00) are excellent, but the higher percentage of Ramachandran outliers (4.49%) suggests potential backbone conformation issues, which may require refinement for a high-resolution protein structure.