| Branch | Population | Pairwise RMSD (Å) | % α-helical | % β-sheet | Aligned residues |
|--------|------------|-------------------|-------------|-----------|-----------------|
| 0      | 29         | 2.35 ± 0.34       | 25.0 ± 3.2  | 43.7 ± 2.7 | 1–56            |
| 1010   | 11         | 7.78 ± 2.04       | 20.3 ± 6.1  | 34.1 ± 4.0 | 2–41            |
| 1011   | 22         | 9.63 ± 2.27       | 17.5 ± 7.7  | 31.1 ± 5.6 | 10–40           |
| 110    | 20         | 11.95 ± 1.96      | 4.0 ± 4.1   | 36.1 ± 6.9 | 8–24            |
| 1110   | 13         | 12.01 ± 2.14      | 5.2 ± 8.4   | 32.1 ± 5.9 | 1–39            |
| 11110  | 11         | 12.06 ± 1.93      | 24.0 ± 10.4 | 5.7 ± 8.9  | 29–45           |
| 111110 | 10         | 11.29 ± 1.85      | 8.7 ± 7.0   | 32.0 ± 10.8| 11–37           |
| 1111110| 12         | 10.59 ± 2.11      | 12.9 ± 6.3  | 33.0 ± 10.8| 1–35            |
| 1111111| 47         | 11.28 ± 2.40      | 14.1 ± 8.6  | 28.7 ± 10.2| 1–37            |
| Total  | 175        | 10.76 ± 2.85      | 15.1 ± 9.9  | 31.9 ± 11.3| -               |