SUPERPOSE from CCP4i using HFV340 (residues 382-482)

|  |  |  |  |
| --- | --- | --- | --- |
| Target | Q-Score | N-align | RMSD (Å) |
| MLV | 0.181 | 68 | 2.81 |
| HTLV | 0.176 | 71 | 3.11 |
| HIV-1 | 0.173 | 67 | 2.57 |
| JSRV | 0.149 | 63 | 2.96 |
| RSV | 0.104 | 59 | 3.30 |

E. Krissinel and K. Henrick (2004). Secondary-structure matching (SSM),

a new tool for fast protein structure alignment in three dimensions.

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