**Supplementary File 10:** Average 2D-RMSDall atom of residues 25 to 315 of the structures sampled along MD trajectories.[a]

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|   | di-PlaFA[b] | di-PlaFB[b] | PlaFA[c] | t-PlaFA[d] | PlaFB[c] | t-PlaFB[d] |
| di-PlaFA[b] | 3.42 ± 0.59 | 3.96 ± 0.69 | 3.63 ± 0.58 | 3.60 ± 0.61  | 3.94 ± 0.57 | 3.91 ± 0.60 |
| di-PlaFB[b] |  | 4.01 ± 0.81 | 4.05 ± 0.68 | 4.05 ± 0.72 | 4.29 ± 0.70 | 4.23 ± 0.71 |
| PlaFA[c] |  |  | 3.59 ± 0.60 | 3.71 ± 0.63  | 4.08 ± 0.58 | 4.02 ± 0.64 |
| t-PlaFA[d] |  |  |  | 3.58 ± 0.72 | 4.05 ± 0.61 | 3.93 ± 0.65 |
| PlaFB |  |  |  |  | 4.17 ± 0.76 | 4.21 ± 0.62 |
| t-PlaFB |  |  |  |  |  | 3.99 ± 0.80 |

[a] RSMD values in Å, mean ± S.D., were computed in a pair-wise manner for respective structures sampled every ns along the MD trajectories.

[b] PlaF molecules in dimeric form starting from the crystal structure.

[c] PlaFA and PlaFB obtained from the dimeric form by removal of the opposite chain.

[d] PlaFA and PlaFB in the tilted monomeric form.