**S5 Table. The dynamic building units, structural units and hinge residues of an example obligomer: The homodimeric cytoplasmic domain of the serine chemotaxis receptor (1QU7 [**[**49**](#_ENREF_49)**]).**

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| --- | --- | --- |
| **Slowest mode** | ***Hinge residues*** | Chain A: HIS328/LEU329, THR450/ARG451 |
| Chain B: HIS328/LEU329, ARG451/VAL452 |
| ***Dynamic structural domains*** | A:294-328, A:451-520/B:300-328, B:452-520 |
| A:329-450/B:329-451 |
| **Second Slowest mode** | ***Hinge residues*** | Chain A: ASP353/ILE354, GLY426/LYS427, VAL483/THR484 |
| Chain B: ASP353/ILE354, GLY426/LYS427 |
| ***Dynamic structural domains*** | A:294-353, A:427-483, B:300-353, B:427-520 |
| A:354-426/B:354-426, A:484-520 |