**Supplementary file 1a.** Individual chains and ligand resolvability according to Q-scores. Scores were calculated using the MapQ plugin in UCSFChimera.

|  |  |  |  |
| --- | --- | --- | --- |
| **Chain** | **Q Score** | **Expected @ 3.00** | **Estimated Resolution (Å)** |
| A | 0.69 | 0.5867 | 2.39 |
| B | 0.69 | 0.5867 | 2.41 |
| C | 0.68 | 0.5867 | 2.47 |
| D | 0.64 | 0.5867 | 2.67 |
| E | 0.65 | 0.5867 | 2.67 |
| F | 0.63 | 0.5867 | 2.77 |
| I | 0.68 | 0.5867 | 2.5 |
| J | 0.66 | 0.5867 | 2.56 |
| K | 0.58 | 0.5867 | 3.05 |
| L | 0.66 | 0.5867 | 2.61 |
| M | 0.67 | 0.5867 | 2.52 |
|  |  |  |  |
| **Average:** | 0.66 | 0.5867 | 2.62 |

**Supplementary file 1b.** Primer list used for mutant construction.

|  |  |
| --- | --- |
| Primer Name | Sequence |
| **P60\_red\_c\_Forward\_insert** | GCCGCCCATAATCCCCCCCAGGGCACCCCCTTCGGCGGCGCCTTGACCGGCGCAGGCCATACCAACCTGTAC |
| **P60\_red\_c\_Reverse\_insert** | GGCCACAGCATCAAAGAAATTCTTGCCGCCCATAATCCCCCCCA |
| **P60\_red\_c\_Forward** | aacgcagaccgttccgtggcaaagca |
| **P60\_red\_c\_Reverse** | ccgacaacgcagaccgttccgtggc |
| **PsaL\_F** | GGCGCAGTTACCCATTTCCGCTG |
| **PsaL\_R** | GAGTAACAAATCAAAATGTCCAATC |
| **Cm\_F** | GACATTTTGATTTGTTACTCCcgaataaatacctgtgacggaag |
| **Cm\_R** | AAAAATACCCCACCCGCTGGCccaggcgtttaagggcaccaataac |
| **Down\_F** | GCCAGCGGGTGGGGTATTTTTTTTGTG |
| **Down\_R** | GCCATATTATCGAAAAATTCCAGGG |
| **Backbone\_F** | GGAATTTTTCGATAATATGGCcacaattccacacattatacgag |
| **Backbone\_R** | CGGAAATGGGTAACTGCGCCatgtcatgataataatggtttc |
| **Ca\_D2L\_F** | GGGCCCGCTGCGtctgTCTGAGTAC |
| **Ca\_D2L\_R** | GTACTGGTACTCAGAcagaCGCAGC |