

Table SI. Docking grid parameters used for molecular docking analysis.

| Protein (PDB ID) | Target protein | Grid centre X | Grid centre Y | Grid centre Z | Size X (Å) | Size Y (Å) | Size Z (Å) |
|---------------------|---------------------------------|---------------|------------------|------------------|---------------|------------|---------------|
| 8ENQ | <i>E. coli</i> CsgA fibril | 92.5996 | 107.8450 | 25.1438 | 47.4822 | 37.8500 | 35.1224 |
| 5DFK | <i>E. coli</i> EcpB chaperone | -19.2250 | 23.0784 | -14.7058 | 55.0107 | 41.7817 | 51.5411 |
| 8FFK | <i>K. pneumoniae</i> AcrB (apo) | 174.1170 | 209.8190 | 197.3941 | 64.7269 | 97.4887 | 122.0760 |
| 9HW9 | <i>K. pneumoniae</i> MrkA | -1.2246 | 1.4784 | 1.5472 | 50.7000 | 53.6870 | 56.0285 |