Supplementary Table 1: 33-fold FliF Cryo-EM data collection, refinement and validation statistics

|                      | 33-fold FliF Whole map (EMD-10143) | 33-fold FliF RBM3/β-collar (EMD-10145) | 33-fold FliF RBM2inner (EMD-10146) |
|----------------------|----------------------------------|----------------------------------------|-----------------------------------|
|                      | (PDB-6SCN)                       | (PDB-6SD1)                             | (PDB-6SD2)                        |
| **Data collection and processing** |                                  |                                        |                                   |
| Magnification        | 165,000                          | 165,000                                | 165,000                           |
| Voltage (kV)         | 300                              | 300                                    | 300                               |
| Electron exposure (e−/Å²) | 48                              | 48                                     | 48                                |
| Defocus range (μm)   | 0.5–4                            | 0.5–4                                  | 0.5–4                             |
| Pixel size (Å)       | 0.822                            | 0.822                                  | 0.822                             |
| Symmetry imposed     | C3                               | C33                                    | C21                               |
| Initial particle images (no.) | 449142                          | 449142                                 | 449142                            |
| Final particle images (no.) | 175233                          | 77849                                  | 84797                            |
| Map resolution (Å)   | 3.1                              | 2.6                                    | 2.9                               |
| FSC threshold        | 0.143                            | 0.143                                  | 0.143                             |
| Map resolution range (Å) | 2.9–5.0                          |                                        |                                   |
| **Refinement**       |                                  |                                        |                                   |
| Initial model used (PDB code) | Ab initio              | Ab initio                             | Ab initio                         |
| Model resolution (Å) | 3.1                              | 2.6                                    | 2.9                               |
| FSC threshold        | 0.143                            | 0.143                                  | 0.143                             |
| Model resolution range (Å) | -72                            | -62                                    | -104                              |
| Map sharpening B factor (Å²) |                        |                                        |                                   |
| Model composition    |                                  |                                        |                                   |
| Non-hydrogen atoms   | 60582                            | 39377                                  | 13566                             |
| Protein residues     | 7875                             | 4984                                   | 1848                              |
| Ligands              | 0                                | 0                                      | 0                                 |
| B factors (Å²)       |                                  |                                        |                                   |
| Protein              | 130                              | 53                                     | 59                                |
| Ligand               | N/A                              | N/A                                    | N/A                               |
| R.m.s. deviations    |                                  |                                        |                                   |
| Bond lengths (Å)     | 0.007                            | 0.003                                  | 0.009                             |
| Bond angles (°)      | 0.817                            | 0.442                                  | 0.770                             |
| **Validation**       |                                  |                                        |                                   |
| MolProbity score     | 2.0                              | 1.7                                    | 2.4                               |
| Clashscore           | 13.0                             | 7.1                                     | 6.7                               |
| Poor rotamers (%)    | 0.8                              | 0.0                                     | 5.6                               |
| Ramachandran plot    |                                  |                                        |                                   |
| Favored (%)          | 94.3                             | 95.7                                    | 92.7                              |
| Allowed (%)          | 4.9                              | 4.3                                     | 7.3                               |
| Disallowed (%)       | 0.8                              | 0.0                                     | 0.0                               |
### Supplementary Table 2: 34-fold FlIF Cryo-EM data collection, refinement and validation statistics

|                      | 34-fold FlIF Whole map (EMD-10147) | 34-fold FlIF RBM3/β-collar (EMD-10148) | 34-fold FlIF RBM2inner (EMD-10149) |
|----------------------|-----------------------------------|--------------------------------------|-----------------------------------|
|                      | (PDB-6SD3)                        | (PDB-6SD4)                           | (PDB-6SD5)                        |
| **Data collection and processing** |                                   |                                      |                                   |
| Magnification        | 165,000                           | 165,000                              | 165,000                           |
| Voltage (kV)         | 300                               | 300                                  | 300                               |
| Electron exposure (e−/Å²) | 48                                 | 48                                  | 48                                |
| Defocus range (μm)   | 0.5–4                             | 0.5–4                                | 0.5–4                             |
| Pixel size (Å)       | 0.822                             | 0.822                                | 0.822                             |
| Symmetry imposed     | C2                                | C34                                  | C22                               |
| Initial particle images (no.)* | 449142                            | 449142                              | 449142                           |
| Final particle images (no.) | 140606                            | 140606                              | 87107                             |
| Map resolution (Å)   | 3.3                               | 2.8                                  | 3.1                               |
| FSC threshold        | 0.143                             | 0.143                                | 0.143                             |
| Map resolution range (Å) | 3.1-7.4                         | 2.7-3.6                              | 3.0-3.9                           |
| **Refinement**       |                                   |                                      |                                   |
| Initial model used (PDB code) | EMD-10143                        | EMD-10143                            | EMD-10143                        |
| Model resolution (Å) | 3.3                               | 2.8                                  | 3.1                               |
| FSC threshold        | 0.143                             | 0.143                                | 0.143                             |
| Model resolution range (Å) | -67                              | -85                                  | -103                              |
| Map sharpening B factor (Å²) | -67                              | -85                                  | -103                              |
| Model composition    |                                   |                                      |                                   |
| Non-hydrogen atoms   | 63144                             | 40562                                | 14212                             |
| Protein residues     | 8212                              | 5134                                 | 1936                              |
| Ligands              | 0                                 | 0                                    | 0                                 |
| B factors (Å²)       |                                   |                                      |                                   |
| Protein             | 139                               | 41                                   | 51                                |
| Ligand              | N/A                               | N/A                                  | N/A                               |
| R.m.s. deviations    |                                   |                                      |                                   |
| Bond lengths (Å)     | 0.008                             | 0.009                                | 0.006                             |
| Bond angles (°)      | 0.824                             | 0.657                                | 0.617                             |
| Validation           |                                   |                                      |                                   |
| MolProbity score     | 2.3                               | 1.9                                  | 2.0                               |
| Clashscore           | 12.3                              | 5.7                                  | 7.1                               |
| Poor rotamers (%)    | 1.2                               | 0.8                                  | 1.4                               |
| Ramachandran plot    |                                   |                                      |                                   |
| Favored (%)          | 88.5                              | 89.7                                 | 91.7                              |
| Allowed (%)          | 10.8                              | 9.6                                  | 8.3                               |
| Disallowed (%)       | 0.7                               | 0.7                                  | 0.0                               |

* Particle numbers quoted are post-2D clean-up
Supplementary Table 3: 32-fold and 35-fold FliF Cryo-EM data collection, refinement and validation statistics

|                        | 32-fold FliF RBM3/β-collar (EMD-10560) | 35-fold FliF RBM3/β-collar (EMD-10561) |
|------------------------|----------------------------------------|----------------------------------------|
| **Data collection and processing** |                                        |                                        |
| Magnification          | 165,000                                | 165,000                                |
| Voltage (kV)           | 300                                    | 300                                    |
| Electron exposure (e−/Å²) | 48                                      | 48                                      |
| Defocus range (μm)     | 0.5–4                                  | 0.5–4                                  |
| Pixel size (Å)         | 0.822                                  | 0.822                                  |
| Symmetry imposed       | C32                                    | C35                                    |
| Initial particle images (no.) * | 449142                                 | 449142                                 |
| Final particle images (no.) | 33026                                  | 42165                                  |
| Map resolution (Å)     | 3.3                                    | 4.5                                    |
| FSC threshold          | 0.143                                  | 0.143                                  |
| Map resolution range (Å) | 3.2-6.0                                | 4.1-6.6                                |
| **Refinement**         |                                        |                                        |
| Initial model used (PDB code) | EMD-10143                             |                                        |
| Model resolution (Å)   | 3.3                                    |                                        |
| FSC threshold          | 0.143                                  |                                        |
| Model resolution range (Å) |                                       |                                        |
| Map sharpening B factor (Å²) | -106                                   |                                        |
| Model composition      |                                        |                                        |
| Non-hydrogen atoms     | 38176                                  |                                        |
| Protein residues       | 4832                                   |                                        |
| Ligands                | 0                                      |                                        |
| **B factors (Å²)**     |                                        |                                        |
| Protein                | 70                                     |                                        |
| Ligand                 | N/A                                    |                                        |
| R.m.s. deviations      |                                        |                                        |
| Bond lengths (Å)       | 0.009                                  |                                        |
| Bond angles (°)        | 0.87                                   |                                        |
| **Validation**         |                                        |                                        |
| MolProbity score       | 3.1                                    |                                        |
| Clashscore             | 18.4                                   |                                        |
| Poor rotamers (%)      | 11.3                                   |                                        |
| Ramachandran plot      |                                        |                                        |
| Favored (%)            | 89.7                                   |                                        |
| Allowed (%)            | 10.3                                   |                                        |
| Disallowed (%)         | 0.0                                    |                                        |

* Particle numbers quoted are post-2D clean-up
