**Supplementary Table 1**
Summary of crystallographic analysis of K1-70 Fab

| **X-ray diffraction data** | |
|---|---|
| X-ray source | Rigaku-007HF |
| Wavelength (Å) | 1.54 |
| Detector type | R-Axis IV |
| Detector distance | 175 |
| Temperature (°K) | 100 |
| Oscillation range per frame (°) | 0.5 |
| Overall rotation (°) | 125 |
| Resolution range (Å) | 30-2.22 |
| Number of observed reflections | 141074 |
| Number of unique reflections | 54304 |
| Multiplicity | 2.6 |
| Completeness (%) (overall and last shell) | 97.9 (98.1) |
| $R_{merge}$ (%) (overall and last shell) | 6.3 (34.0) |
| Mean I/sigma (overall and last shell) | 8.5 (2.5) |
| Space group | $P2_1$ |
| Unit cell parameters (Å), (°) | 70.2 62.1 131.0<br>90.0 98.3 91.0 |

| **Refinement** | |
|---|---|
| Refinement program | Refmac5 |
| Resolution range (Å) | 30-2.22 |
| Number of reflections (working/test) | 51482 (2775) |
| $R_{work}$ | 21.7% |
| $R_{free}$ | 26.4% |
| Protein residues modelled | 837 |
| Number of protein atoms modelled | 6336 |
| Number of water atoms modelled | 363 |
| RMSD Bond lengths (Å) | 0.014 |
| RMSD Bond angles (°) | 1.488 |
| Mean overall B value ($Å^2$) | 41.7 (FabA) / 38.3 (FabB) |
| Mean water B value ($Å^2$) | 43.3 |
| Ramachandran plot favored (%) | 88.8% |
| Ramachandran plot allowed (%) | 10.8% |
| Ramachandran plot generously allowed | 0.1% |
| Ramachandran plot disallowed (%) | 0.3% |