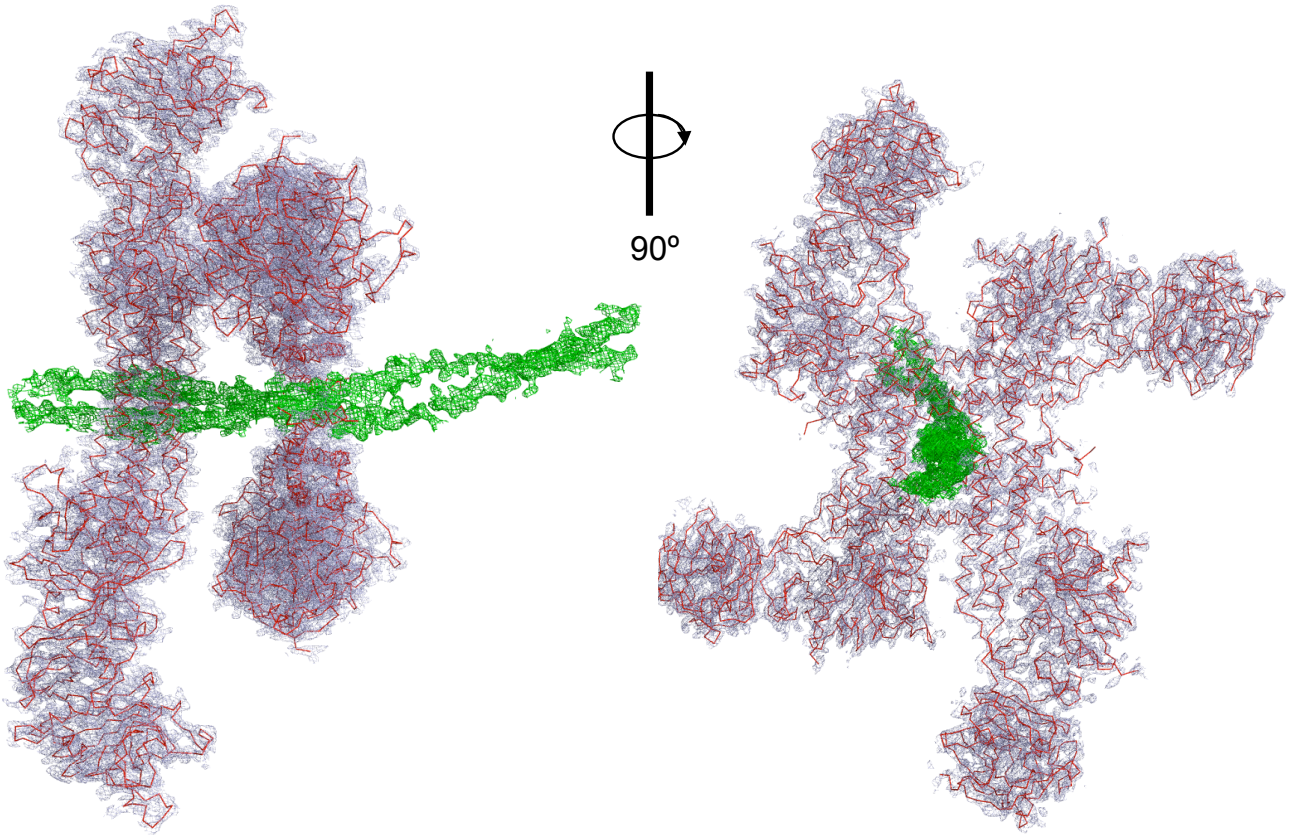
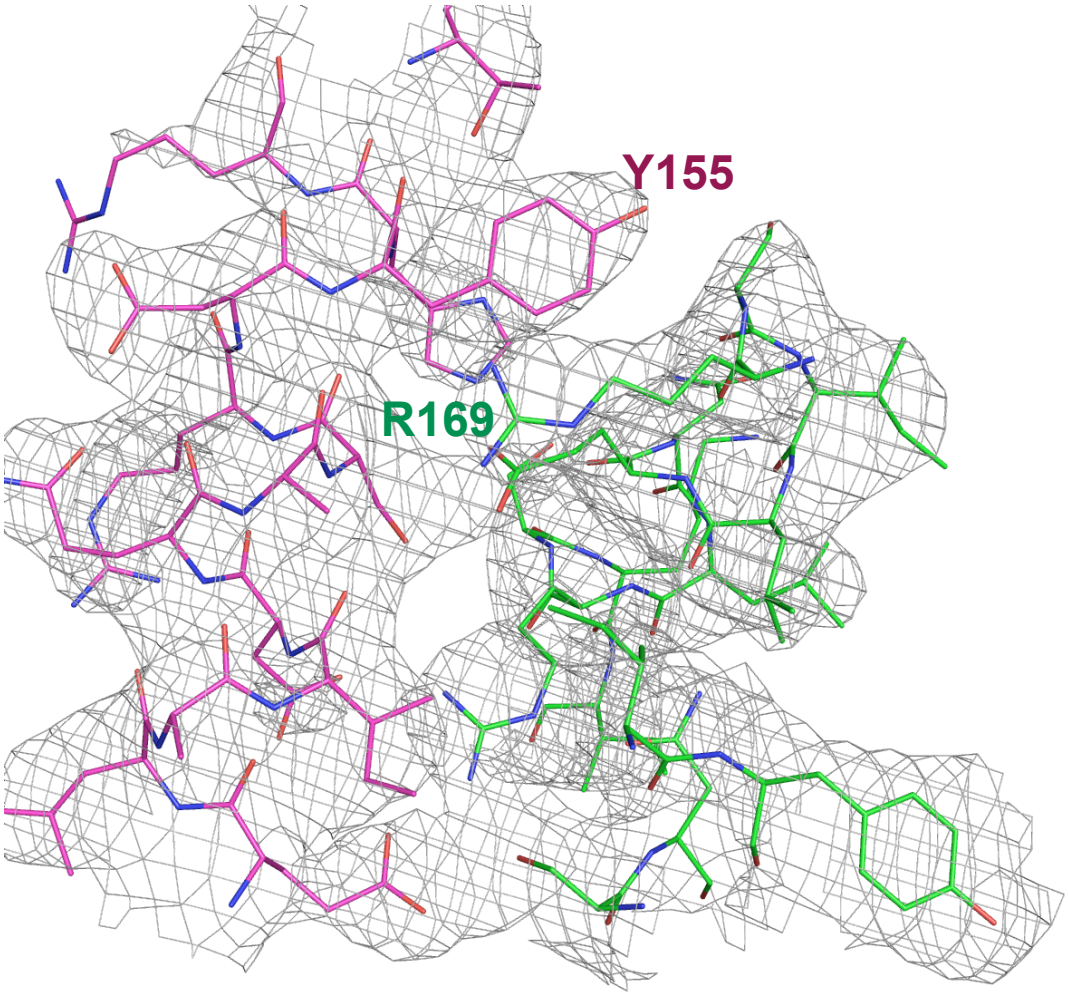
**Supplementary Table 1** Data collection and refinement statistics

| | **$M1^{BC1}$-FgD** | **$M1^{BC1}$(I148M)-FgD SeMet** | **$M1^{A}$-FgD** |
|---|---|---|---|
| **Data collection** | | | |
| Space group | $P2_1$ | $P2_1$ | $P3_221$ |
| Cell dimensions | | | |
| *a*, *b*, *c* (Å) | 112.7, 216.8, 140.8 | 110.7, 215.3, 139.3 | 165.7, 165.7, 289.6 |
| $\alpha, \beta, \gamma$ (°) | 90.0, 102.5, 90.0 | 90.0, 101.5, 90.0 | 90.0, 90.0, 120.0 |
| Resolution (Å) | 116.30-3.30 (3.48-3.30)* | 40.00-4.50 (4.60-4.50) | 142.08-7.50 (7.70-7.50) |
| $R_{merge}$ | 11.0 (50.4) | 15.2 (40.2) | 19.6 (33.0) |
| $I/\sigma I$ | 5.8 (1.4) | 21.1 (5.8) | 7.7 (1.8) |
| Completeness (%) | 96.7 (91.5) | 97.4 (89.1) | 92.1 (56.3) |
| Redundancy | 2.6 (2.4) | 16.6 (13.7) | 4.0 (2.3) |
| | | | |
| **Refinement** | | | |
| Resolution (Å) | 3.30 | | |
| No. reflections | 90,704 | | |
| $R_{work/}$ $R_{free}$ | 27.7/ 32.5 | | |
| No. atoms | | | |
| Protein | 23,867 | | |
| Ligand/ion | None | | |
| Water | None | | |
| B-factors | | | |
| Protein | 77.95 | | |
| Ligand/ion | None | | |
| Water | None | | |
| R.m.s deviations | | | |
| Bond lengths (Å) | 0.008 | | |
| Bond angles (°) | 1.153 | | |

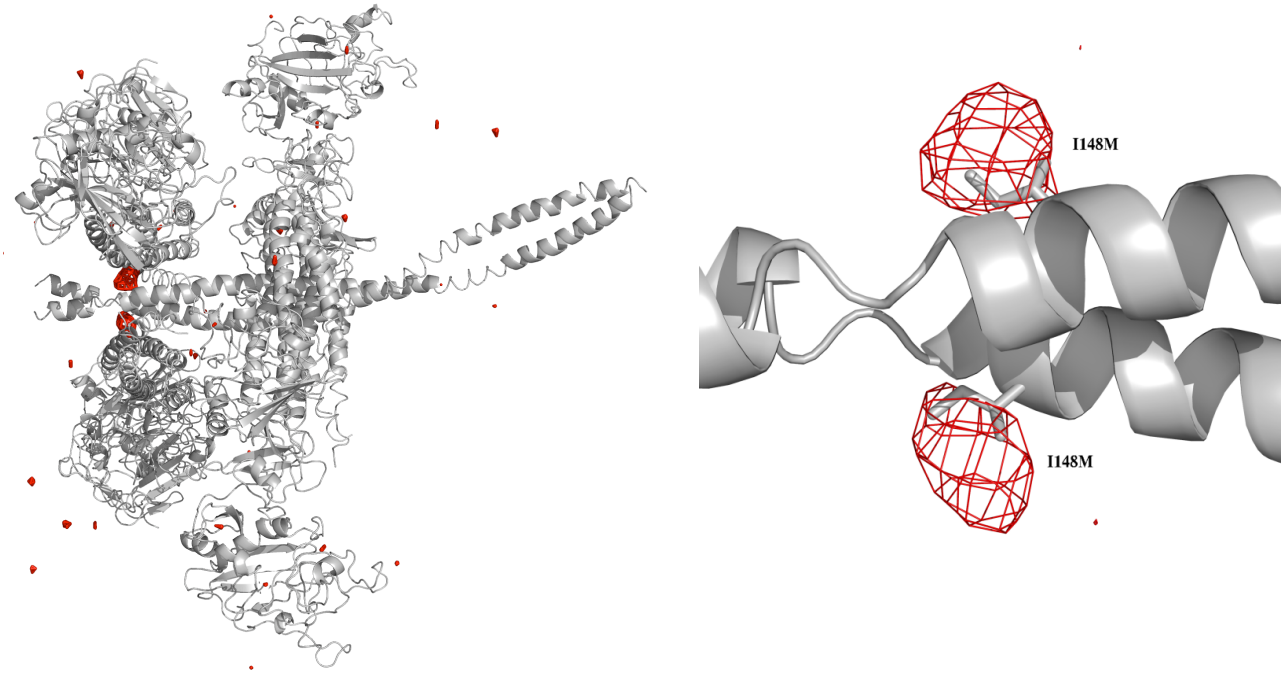
Each data set was collected from one crystal.
*Highest resolution shell is shown in parenthesis.



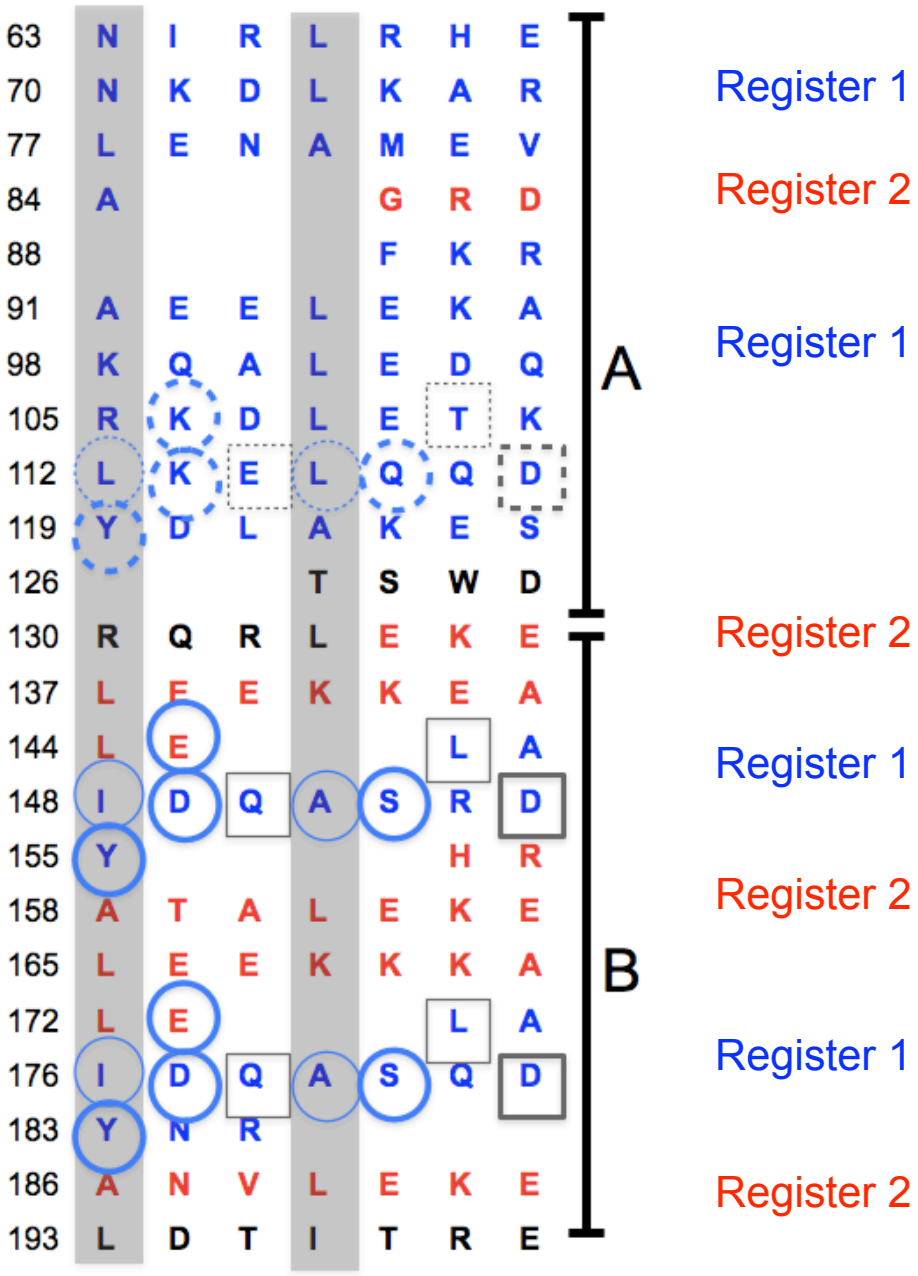

**Supplementary Figure 1a. Electron density for M1$^{BC1}$-FgD**
2Fo-Fc density (contoured at 1σ) from the molecular replacement solution of M1$^{BC1}$-FgD without further refinement, except for rigid body refinement of FgD. FgD (red) is represented as a Cα chain trace and the electron density corresponding to FgD is gray. The green electron density corresponds to M1$^{BC1}$.




**Supplementary Figure 1b. Electron density for M1$^{BC1}$-FgD**
Simulated annealing 2Fo-Fc omit map (contoured at 1σ). Residues FgD β168-179, FgD γ109-121, and M1$^{BC1}$ 144-159 (chain 1) were excluded along with a 3.5 Å sphere around these residues, prior to performing simulated annealing (2500 K). The final model is overlaid in bonds representation. M1 has pink carbon bonds, and FgD green carbon bonds; nitrogen and oxygen bonds are blue and red, respectively, for both.



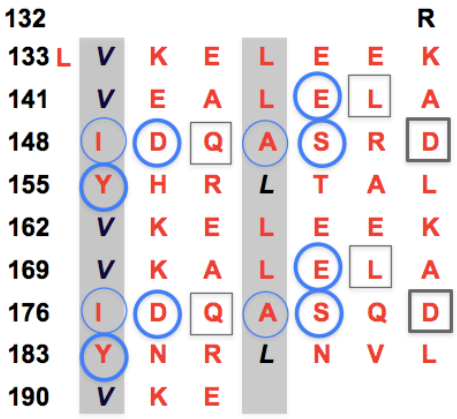

**Supplementary Figure 2. Position of residue M1$^{BC1}$ 148** Anomalous difference map contoured at 4σ showing the position of selenomethionine-substituted M1$^{BC1}$(I148M). The left panel shows the density (in red) superimposed on the M1$^{BC1}$-FgD structure. The right panel shows an enlarged view.



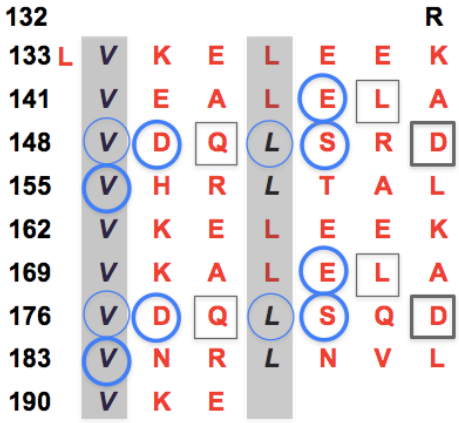

**Supplementary Figure 3. Heptad register propensity of M1 A-region and B-repeats**
Heptad register propensity for the A-region and B-repeats, colored blue for register 1 and red for register 2. The *a* and *d* heptad positions are shaded gray. Residues in black were observed to have dimeric α-helical contacts in register 2, but did not have regular coiled-coil packing. Residues that contact FgD in the B-repeats are in circles for one helix of the coiled coil and in boxes for the opposing helix. Heavy lines denote polar contacts, and light vdW contacts. Residues in the putative Fg-binding site in the A-region are demarcated by dashed circles and boxes.

## Register 1

M1*-R




M1*

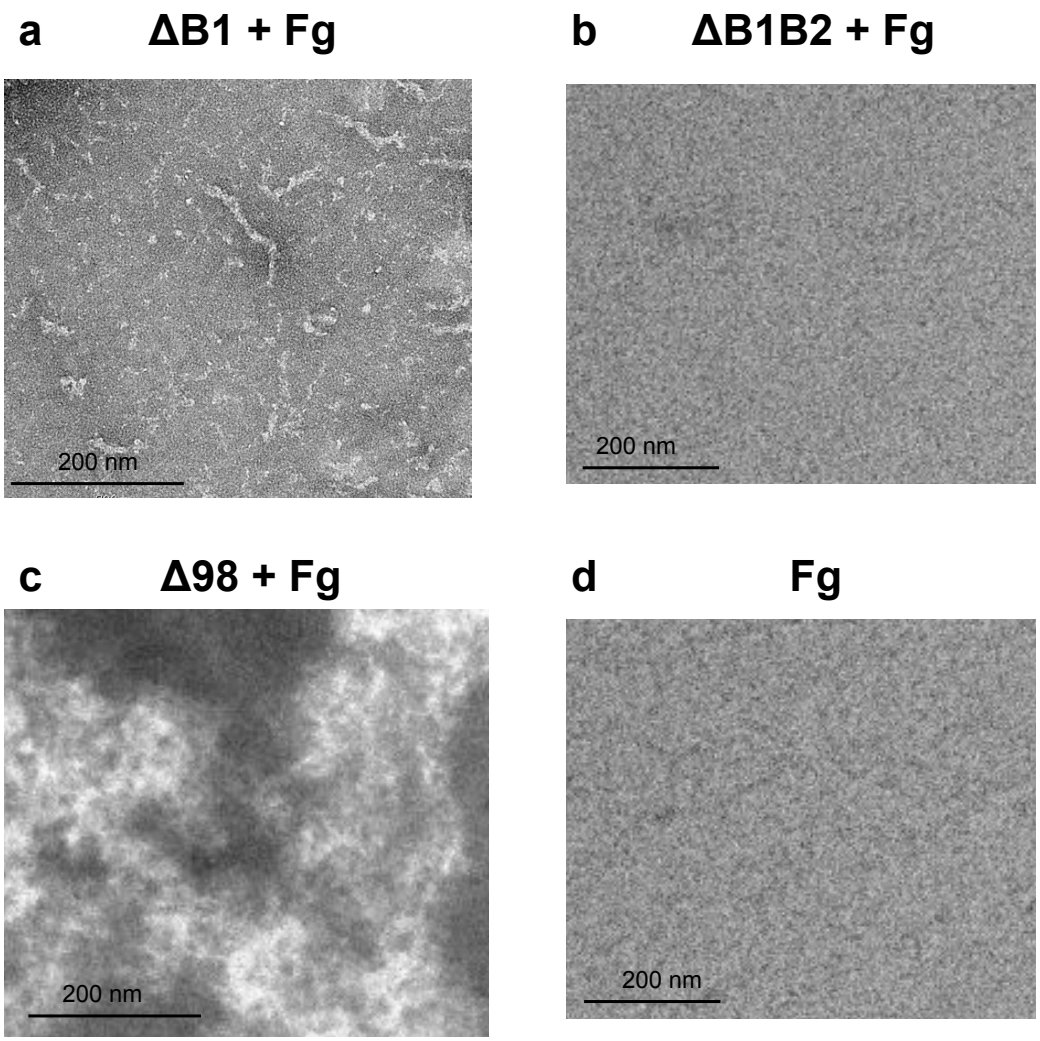



## Register 2

M1*-R


M1*


**Supplementary Figure 4. M1*-R and M1***
Sequence of M1*-R and M1* shown in register 1 at top, and in register 2 at bottom. Valine and leucine substitutions are in black italics. The gray shading, circles, and boxes are as in Supplementary Figure 3.




**Supplementary Figure 5. Electron microscopic visualization of M1 mutants mixed with Fg**

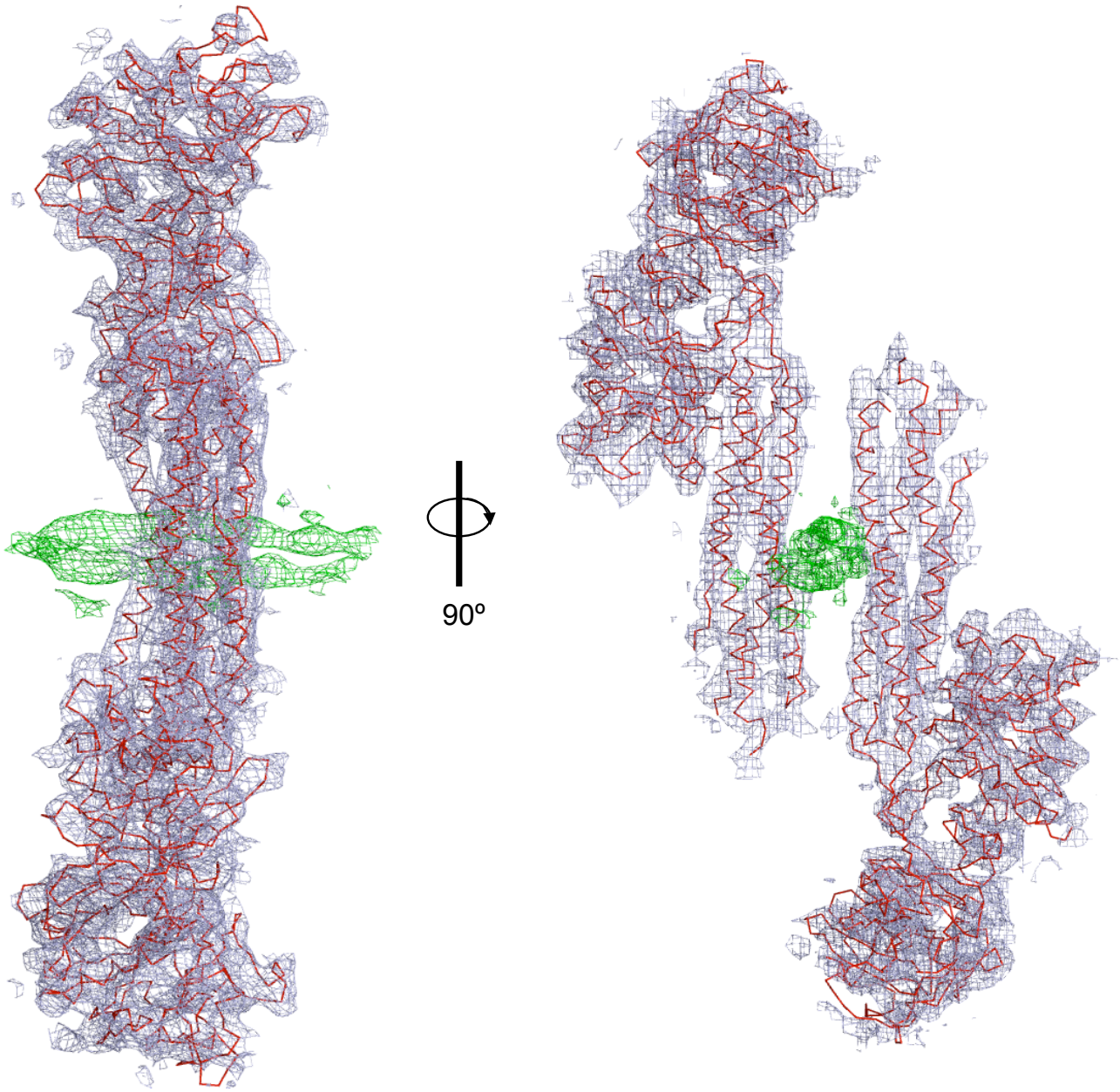
**a,** Fibers formed by mixing ΔB1 and Fg.

**b,** ΔB1B2 mixed with Fg. No networks or fibers were apparent.

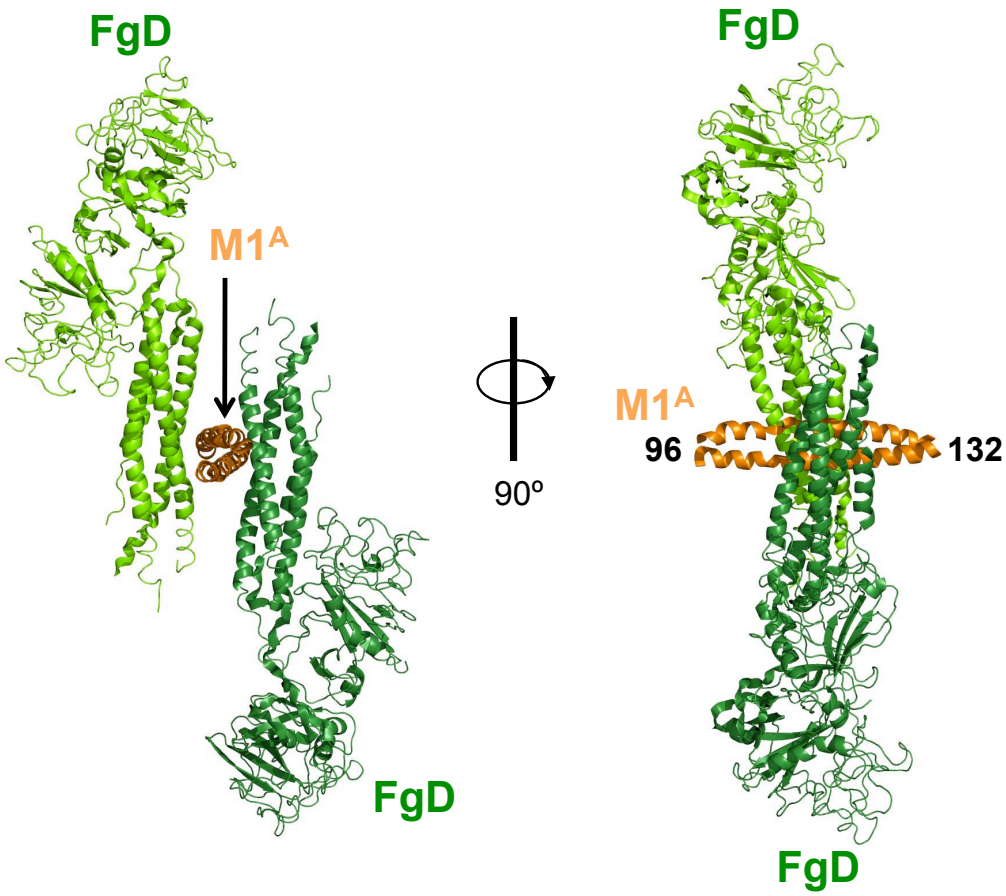
**c,** Networks formed by mixing Δ98 and Fg.

**d,** Fg alone.

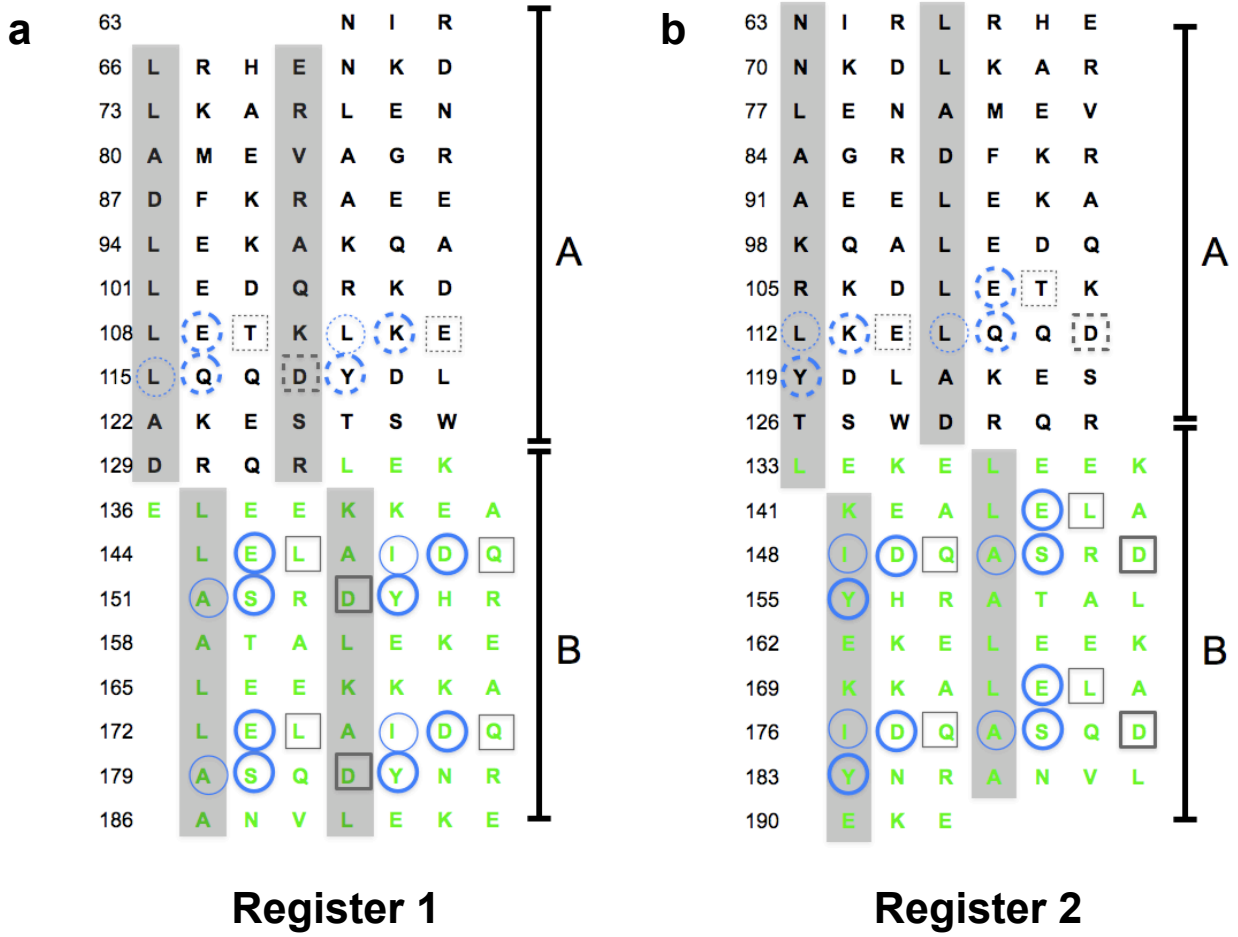
**e,** M1 alone.




**Supplementary Figure 6a. Structure of M1$^{A}$-FgD**
2Fo-Fc density (contoured at 1σ) from the molecular replacement solution of M1$^{A}$-FgD without further refinement except for rigid body refinement of FgD. FgD (red) is represented as a Cα chain trace and the electron density corresponding to FgD is gray. The green electron density corresponds to M1$^{A}$.




**Supplementary Figure 6b. Structure of $M1^A$-FgD**
Ribbon representation for the molecular replacement solution of $M1^A$-FgD. The A-region of M1 (gold) was modeled into the green electron density from panel a; FgD is in green.




**Supplementary Figure 7. Cryptic Fg-binding site in the A-region**

**a,** The M1 A-region and the B-repeats in register 1. Shaded boxes indicate *a* and *d* positions. This register was directly observed in the structure of $M1^{AB}$. The gray shading, circles, and boxes are as in Supplementary Figure 3.

**b,** The M1 A-region and B-repeats in register 2. The B-repeats were observed to have this register in the structure of $M1^{BC1}$-FgD.