**Table S2 Summary of crystallography analysis.**

| **Data set** | RGF1-RGFR1$^{LRR}$ | RGF2-RGFR1$^{LRR}$ | RGF3-RGFR1$^{LRR}$ | RGF5-RGFR1$^{LRR}$ |
|---|---|---|---|---|
| Wavelength (Å) | 1.000 | 1.000 | 1.000 | 1.000 |
| Resolution (Å) | 99.0-2.6 (2.64-2.6) | 99.0-2.55(2.59-2.55) | 99.0-2.6 (2.64-2.6) | 99.0-2.86 (2.91-2.86) |
| Space group | R3 | R3 | R3 | R3 |
| a, b, c (Å) | 182.3,182.3, 87.4 | 181.0,181.0, 88.0 | 183.5,183.5, 87.6 | 179.2,179.2, 88.4 |
| $\alpha, \beta, \gamma$ (°) | 90.0, 90.0, 120.0 | 90.0, 90.0, 120.0 | 90.0, 90.0, 120.0 | 90.0, 90.0, 120.0 |
| Unique reflections | 33,085(1,666) | 33,781(1,773) | 33,847(1,444) | 22,741(1,215) |
| Completeness | 98.8 (100.0) | 96.9% (100.0%) | 99.1%(87.8%) | 93.0%(100.0%) |
| Rsym (%) | 8.6(52.8) | 7.1(44.8) | 8.8(58.3) | 8.4(40.5) |
| redundancy | 4.7(4.7) | 5.4(5.7) | 5.2(3.9) | 5.3(5.7) |
| $I/\delta$ | 19.5(4.5) | 14.5(4.7) | 31.8(2.7) | 13.4(5.2) |
| **Statistics for refinement** | | | | |
| Resolution (Å ) | 99.0-2.6 (2.67-2.6) | 99.0-2.55 | 99.0-2.6 | 99.0-2.86 |
| | 33,048(2,752) | (2.63-2.55) | (2.67-2.6) | (2.99-2.86) |
| No. of RFs | | 33,751(2,931) | 33,780(2,629) | 22,723(3,040) |
| Completeness | 98.7% | 97.1% | 98.9% | 93.0% |
| Rwork/Rfree | 19.1 (23.3)/ | 21.9(26.2)/ | 21.7(25.2)/ | 22.9(29.4)/ |
| (%) | 24.7(35.1) | 24.2(26.3) | 26.0(32.7) | 23.6(32.5) |
| R.m.s.d | | | | |
| Bond (degree) | 1.421 | 1.485 | 1.477 | 1.485 |
| length (Å) | 0.008 | 0.008 | 0.009 | 0.008 |
| Ramachandran | Favored: 96.51% | Favored: 95.56% | Favored: 96.2% | Favored: 94.47% |
| Plot | Allowed: 3.33% | Allowed: 4.44% | Allowed: 3.8% | Allowed: 5.21% |
| | Outliers: 0.16% | Outliers: 0.0% | Outliers: 0.0% | Outliers: 0.32% |

RF: Reflection

$R_{sym} = \Sigma_h \Sigma_i | I_{h,i} - I_h | / \Sigma_h \Sigma_i I_{h,i}$, where $I_h$ is the mean intensity of the $i$ obervations of symmetry related reflections of $h$.

$R = \Sigma | F_{obs} - F_{calc} | / \Sigma F_{obs}$, where $F_{obs} = F_P$, and $F_{calc}$ is the calculated protein structure factor from the atomic model.

R.m.s.d. in bond lengths and angles are the deviations from ideal values.