**Table S1. Data collection and refinement statistics.**

|  |  |
| --- | --- |
|  | LILRB4-D1/Fab 128 |
| **Data collection** |  |
| Wavelength (Å) | 1.0401 |
| Space group | P 62 |
|  |  |
| Cell dimensions |  |
|  *a*, *b*, *c* (Å) | 187.28, 187.28, 183.82 |
|  (°)  | 90.00, 90.00, 120.00 |
| Resolution (Å) | 50.00-3.00 (3.11-3.00)a |
| *I* / *I* | 15.971 (2.595) |
| Completeness (%) | 99.7(100.0) |
| Redundancy | 5.1 (5.2) |
|  |  |
| **Refinement** |  |
| Resolution (Å) | 44.21-3.00 |
| No. reflections | 70146 |
| *R*work / *R*free*b* | 0.228/0.270  |
| No. atoms |  |
|  Protein | 16442 |
|  Ligand/ion | 0 |
|  Water | 0 |
| *B*-factors |  |
|  Protein | 62.5 |
|  Ligand/ion | - |
|  Water | - |
| R.m.s. deviations |  |
|  Bond lengths (Å) | 0.004 |
|  Bond angles (°) | 0.660 |
| Ramachandran plot |  |
|  Favored (%) | 96.25 |
|  Allowed (%) | 3.25 |
|  Outliers (%) | 0.00 |

a Values in parentheses are for highest-resolution shell.

b *R*work = Σ | | *F*o |－ | *F*c | | /Σ | *F*o | , where *F*o and *F*c are the structure-factor amplitudes from the data and the model, respectively. *R*free is the *R* factor for a subset (5%) of reflections that was selected prior to refinement calculations and was not included in the refinement.