**Supporting Information Table. Data collection and structure refinement statistics**

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|  | *Entamoeba histolytica* IP6KA M85V variant |
| PDB ID code**Data collection** | 8OMI |
| Space group | I4122 |
| Cell dimensions |  |
|  *a*, *b*, *c* (Å) | 102.82, 102.82, 111.61 |
| ******(°)  | 90, 90, 90 |
| Resolution (Å) | 37.81-1.77 (1.84-1.77)\* |
| *R*merge (%) | 12.51 (251.1)  |
| < *I* / *I*) > | 8.61 (1.11) |
| Completeness (%) | 99.15 (98.25)  |
| Redundancy | 7.5 (7.6) |
|  |  |
| **Refinement** |  |
| Resolution (Å) | 1.77 |
| No. unique reflections | 29205  |
| *R*work / *R*free (%) | 23.08 / 25.36 |
| No. non-hydrogen atoms | 2233 |
|  Protein Ligands | 199945 |
|  Water | 189 |
| Average B-factor (Å²) |  |
|  Overall | 39.2 |
|  Protein Ligands | 38.649.7 |
|  Water | 42.5 |
| R.m.s deviations |  |
|  Bond lengths (Å)  | 0.002 |
|  Bond angles (º) | 0.541 |

\*Values in parenthesis are for highest resolution shell.

One single crystal was used to collect a complete dataset for structure determination.