**S2 Table. X-ray crystallography: data collection and refinement statistics**

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| --- | --- |
|  | **HCBWW:hSyt I:GD1a** |
| **Data collection** |  |
| Space group | *P212121* |
| Cell dimensions |  |
|  *a*, *b*, *c* (Å) | 50.4, 78.5, 149.3 |
|  (°)  | 90.0, 90.0, 90.0 |
| Resolution (Å) | 2.4-74.5 (2.40-2.46)\* |
| No. total/unique reflections  | 248,236 / 23,939 |
| *R*merge | 0.117 (14.7) |
| *R*pim | 0.054 (0.676) |
| CC1/2  | 0.998 (0.907)\* |
| *I* / σ*I*  | 9.9 (1.2)\* |
| Completeness (%) | 100 (100)\* |
| Redundancy | 10.4 (10.5)\* |
|  |  |
| **Refinement** |  |
|  |  |
| *R*work / *R*free | 20.1 / 22.9 |
| No. atoms |  |
|  Protein / Peptide | 3,676 / 137 |
|  GD1a oligosaccharide | 88 |
|  Water | 85 |
| *B*-factors |  |
|  Protein / Peptide | 69.4 / 89.9 |
|  GD1a oligosaccharide | 101.7 |
|  Water | 54.4 |
| R.m.s. deviations |  |
|  Bond lengths (Å) | 0.008 |
|  Bond angles (°) | 1.54 |
| Ramachandran statistics (Molprobity) |  |
|  Favored (%) | 95.7 |
|  Outliers (%) | 0.0 |

\*Values in parentheses are for highest-resolution shell.