

Supporting Information

Development of Small-Molecule *Trypanosoma brucei* *N*-Myristoyltransferase Inhibitors: Discovery and Optimisation of a Novel Binding Mode

Daniel Spinks, Victoria Smith, Stephen Thompson, David A. Robinson, Torsten Luksch, Alasdair Smith, Leah S. Torrie, Stuart McElroy, Laste Stojanovski, Suzanne Norval, Iain T. Collie, Irene Hallyburton, Bhavya Rao, Stephen Brand, Ruth Brenk, Julie A. Frearson, Kevin D. Read, Paul G. Wyatt, and Ian H. Gilbert^{*[a]}

cmdc_201500301_sm_miscellaneous_information.pdf

SUPPORTING INFORMATION

Table. Data measurement and model refinement statistics for *Lm*NMT protein:ligand complexes described in this work.

| | LmNMT:6 | LmNMT:7 | LmNMT:13 | LmNMT:14 | LmNMT:44 |
|--|--------------------------------------|--------------------------------------|--------------------------------------|--------------------------------------|--------------------------------------|
| PDB code | 5AG5 | 5AG4 | 5AG6 | 5AG7 | 5AGE |
| Data Measurement | | | | | |
| Source | ESRF ID14eh1 | DLS I03 | Micromax 007 | ESRF ID14eh1 | Micromax 007 |
| Space Group | P2 ₁ | P2 ₁ | P2 ₁ | P2 ₁ | P2 ₁ |
| Unit Cell Dimensions (Å) | a=48.5, b=90.8, c=53.3 β=114.1 | a=48.7, b=90.9, c=53.9 β=113.5 | a=48.7, b=90.3, c=53.3 β=114.6 | a=48.2, b=91.2, c=53.2 β=113.7 | a=48.0, b=90.2, c=53.0 β=113.8 |
| Resolution (Å) ^a | 50.0-2.00 (2.07-2.00) | 20.0-2.00 (2.07-2.00) | 44.0-2.0 (2.10-2.00) | 20.0-2.60 (2.69-2.60) | 20.0-2.0 (2.03-2.00) |
| Observations | 77611 | 94047 | 84697 | 45867 | 54477 |
| Unique Observations | 28183 | 28546 | 26648 | 13076 | 25800 |
| Rmerge (%) ^a | 3.6 (12.1) | 4.5 (40.3) | 7.7 (32.3) | 7.5 (44.5) | 5.7 (35.6) |
| I/σ ^a | 33.2 (11.9) | 23.5 (1.7) | 11.4 (3.5) | 11.6 (1.9) | 21.8 (2.7) |
| Completeness (%) ^a | 98.5 (98.6) | 97.8 (84.3) | 93.4 (87.8) | 99.9 (99.9) | 92.3 (85.6) |
| Redundancy ^a | 2.8 (2.7) | 3.3 (2.7) | 3.2 (3.1) | 3.5 (3.5) | 2.1 (1.9) |
| Refinement Statistics | | | | | |
| Resolution Range (Å) | 48.7 – 2.00 | 20.0-2.00 | 40.0-2.00 | 20.0-2.60 | 19.7 – 2.00 |
| R-factor (R _{work} /R _{free}) | 16.5/21.6 | 18.2/24.6 | 17.3/23.6 | 17.4/26.7 | 17.9/24.1 |
| Number of atoms ^b | 3345/63/22/275 | 3345/63/38/125 | 3269/63/22/300 | 3345/63/17/95 | 3345/63/29/185 |
| Mean B-factor (Å ²) ^b | 28/17/22/32 | 40/31/39/44 | 19/14/19/28 | 36/29/47/35 | 31/25/34/37 |

SUPPORTING INFORMATION

| | | | | | |
|-------------------------------|-------|-------|-------|-------|-------|
| RMS bond length deviation (Å) | 0.024 | 0.024 | 0.023 | 0.016 | 0.023 |
| RMS bond angle deviation (°) | 1.981 | 2.04 | 1.99 | 1.72 | 2.01 |

^a Data for highest resolution shell in parentheses. ^b Number of atoms and mean B-factors for non-hydrogen atoms from protein, co-factor, ligand and solvent respectively.