Supporting Information

for

Biochemical and structural characterisation of the second oxidative crosslinking step during the biosynthesis of the glycopeptide antibiotic A47934

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HPLC–MS analysis of StaF turnover activity of Tei7-L-Hpg7 (a) and Act7-rac-Hpg7 (b) bound to MBP-PCP-X_{tei}

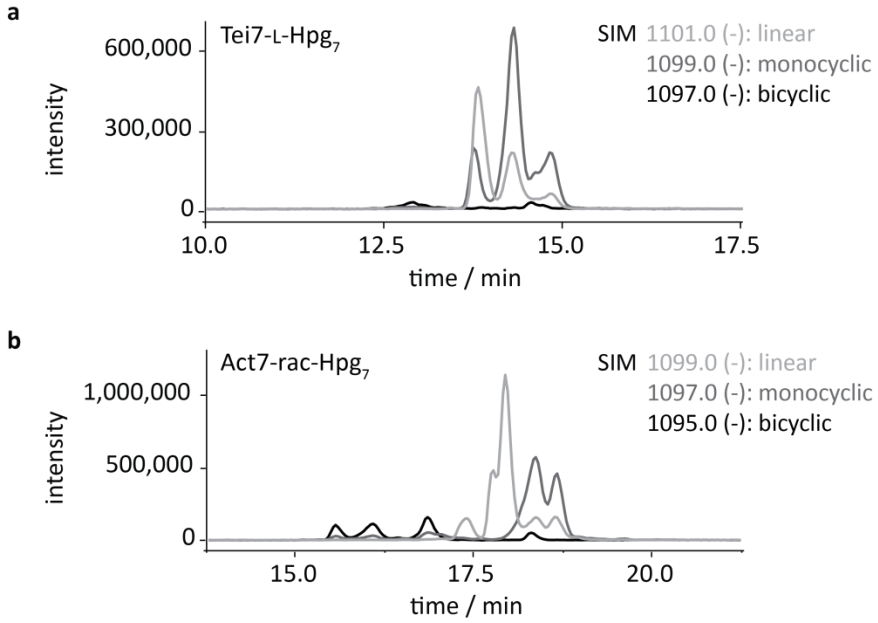

Figure S1: HPLC-MS analysis of StaF turnover activity of Tei7-L-Hpg_7 (a) and Act7-rac-Hpg_7 (b) bound to MBP-PCP-X_{tei}. a) Ions corresponding to singly charged, linear (methylamine *m*/*z* 1101.0; depicted in light grey), monocyclic (methylamine *m*/*z* 1099.0; depicted in grey) and bicyclic Tei7-L-Hpg_7 (methylamine *m*/*z* 1097.0; depicted in black) were recorded using single-ion monitoring (SIM) in negative mode. The minor peak of the monocyclic peptide represents Tei7-D-Hpg_7, which could not be separated completely from Tei7-L-Hpg_7 by preparative HPLC during peptide synthesis. b) Ions corresponding to singly charged, linear (methylamine *m*/*z* 1099.0; depicted in light grey), monocyclic (methylamine *m*/*z* 1097.0; depicted in grey) and bicyclic Act7-rac-Hpg_7 (methylamine *m*/*z* 1095.0; depicted in black) were recorded using single-ion monitoring (SIM) in negative mode. Major peaks for each *m*/*z* represent diastereomers due to racemisation of Hpg_7. a) and b) Smaller peaks are caused through overlapping mass signal detection.