1H-NMR experiments were conducted using a Bruker 600 MHz metabolic profiler (Bruker BioSpin) operating at 600.13 MHz proton Larmor frequency and equipped with a 5 mm CPTCI 1H-13C-31P and 2H-decoupling cryoprobe including a z-axis gradient coil, an automatic tuning-matching and an automatic sample changer. A BTO 2000 thermocouple served for temperature stabilization at the level of approximately 0.1 K at the sample. Before measurement, samples were kept for at least 3 min inside the NMR probehead for temperature equilibration (310 K). Three mono‑dimensional (1D) spectra were acquired: a)  A standard Nuclear Overhauser Effect Spectroscopy (NOESY) (1) 1D presat pulse sequence (noesygppr1d.comp, Bruker BioSpin) with 98304 data points, 18028 Hz spectral width, acquisition time of 2.7 s, relaxation delay of 4 s and mixing time of 0.1 s. NOESY spectra contain 1H-NMR signals from small molecular weight metabolites as well as from high molecular weight molecules, such as lipids and lipoproteins. b)  A standard Carr-Purcell-Meiboom-Gill (CPMG) (2) pulse sequence (cpmgpr1d.comp, Bruker BioSpin) with 73728 data points, spectral width of 12019 Hz and relaxation delay of 4 s. In this NMR experiment, 1H-NMR signals of very large macromolecules are filtered out, resulting in the clearer observation of 1H-NMR signals from small molecular weight metabolites than in NOESY spectra. c)  A standard DIFFUSION-EDITED (3) pulse sequence (ledbgppr2s1d.comp; Bruker BioSpin) with 98304 data points, spectral width of 18028 Hz and relaxation delay of 4 s. In this experiment, mostly 1H-NMR signals from large molecules are observed. For all NMR spectra 64 scans were acquired.

NMR acquisition free induction decays (FIDs) were multiplied by an exponential function equivalent to 1.0 Hz line-broadening factor before applying Fourier transform, and all transformed spectra were automatically corrected for phase and baseline distortions. Moreover, NOESY and CPMG spectra were calibrated by setting the glucose doublet at 5.24 ppm (this is preferred with respect to setting the TMSP singlet at 0 ppm due to TMSP interaction with serum albumin). By the use of AMIX software (Bruker Biospin), each spectrum was divided into 0.02 ppm chemical shift bins ranging from 0.3 to 9.0 ppm, and the 4.4 to 5.0 ppm spectral region around the suppressed water 1H-NMR signal was excluded.