**Supplementary methods**

***Image acquisition***

All subjects underwent structural MRI, functional MRI (fMRI) and proton magnetic resonance spectroscopy (1H-MRS) scanning in both sessions. Images were acquired on a General Electric (Milwaukee, Wisconsin) 3.0 Tesla HDx MR system 30 mins following drug administration in a session lasting a maximum of 120 min. The present report focuses on 1H-MRS data.

*Structural MRI*

Structural images were acquired using a whole-brain three-dimensional sagittal T1-weighted scan, with parameters based on the Alzheimer’s Disease Neuroimaging Initiative (ADNI) (TE = 2.85 ms; TR = 6.98 ms; inversion time = 400 ms; flip angle = 11º; voxel size 1.0x1.0x1.2 mm; for full details see http://adni.loni.usc.edu/methods/mri-analysis/mri-acquisition/).

*1H-MRS*

1H-MRS spectra (PRESS - Point RESolved Spectroscopy; TE = 30 ms; TR = 3000 ms; 96 averages) were acquired in the left caudate head, anterior cingulate cortex (ACC), and hippocampus, as previously described by Stone (Stone, 2009). We employed the standard GE probe (proton brain examination) sequence, which uses a standardised chemically selective suppression (CHESS) water suppression routine. For each metabolite spectrum, unsuppressed water reference spectra (16 averages) were also acquired as part of the standard acquisition. Shimming and water suppression were optimised, with auto-prescan performed twice before each scan. Using standardised protocols, regions of interest (ROIs) (left caudate head, 20x20x20 mm; left ACC, 20x20x20 mm; left hippocampus, 20x20x15 mm; right-left, anterior-posterior, superior-inferior) were prescribed from the structural T1 scan.

***1H-MRS quantification***

All spectra were analysed with LCModel version 6.3-1L (Provencher, 1993) using a standard basis set of 16 metabolites (L-alanine, aspartate, creatine, phosphocreatine, GABA, glucose, glutamine, glutamate, glycerophosphocholine, glycine, myo-inositol, L-lactate, N-acetylaspartate, N-acetylaspartylglutamate, phosphocholine, and taurine), acquired with the same field strength (3 Tesla), localisation sequence (PRESS), and echo time (30 ms). Model metabolites and concentrations used in the basis set are fully detailed in the LCModel manual (http://s-provencher-.com/pages/lcmmanual.shtml). Poorly fitted metabolite peaks (Cramer-Rao minimum variance bounds of >20% as reported by LCModel) were excluded from further analysis. Values of the combined water-scaled measure of glutamate and glutamine (Glx, metabolite of interest) as well as other metabolites were corrected for the voxel tissue composition by using the formula: Mcorr = M\*[WM + (1.28\*GM) + (1.55\*CSF)] / (WM+GM), where M is the uncorrected metabolite value, and WM, GM and CSF are the white matter, grey matter and CSF fractions of the ROI, respectively (Modinos et al., 2018). These fractions were determined for each subject from the structural T1 scans, which were used to localise the spectroscopy ROIs and subsequently segmented into grey matter, white matter, and CSF using SPM8.

**References**

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