**Supplementary File 8 |** **Minimum Reporting Standards in MRS (MRSinMRS) checklist**

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| Site (Name or Number) | FMRIB, Wellcome Centre for Integrative Neuroimaging (University of Oxford) |
| 1. Hardware |  |
| a. Field strength [T] | 7 |
| b. Manufacturer  | Siemens |
| c. Model (software version if available) | Magnetom 7T (VB17a) |
| d. RF coils: nuclei (transmit/ receive), number of channels, type, body part | 1-channel transmit and a 32-channel receive phased-array head coil (Nova Medical Inc., USA) |
| e. Additional hardware | Two 110 × 110 × 5 mm3 Barium Titanate dielectric pads (4:1 ratio of BaTiO3:D2O, relative permittivity around 300) over occipital lobe |
| 2. Acquisition  |  |
| a. Pulse sequence  | combined fMRI-fMRS sequencefMRI: 3D EPIfMRS: semi-LASER |
| b. Volume of Interest (VOI) locations  | Visual cortex |
| c. Nominal VOI size [cm3, mm3] | 2 × 2 × 2 cm3 |
| d. Repetition Time (TR), Echo Time (TE) [ms, s] | TR = 4105 msTE = 36 ms |
| e. Total number of Excitations or acquisitions per spectrumIn time series for kinetic studies 1. Number of Averaged spectra (NA) per time-point
2. Averaging method (e.g. block-wise or moving average)
3. Total number of spectra (acquired / in time-series)
 | Average total number of spectra acquired per participant: N=457 (SD: 35.62)Between 8 and 81 spectra per condition (see Supplementary File 6). Participants with less than 8 spectra per condition (e.g. ‘remembered’ or ‘forgotten’) were not included in the analysis.Spectra were averaged according to condition (‘remembered’/‘forgotten’). |
| f. Additional sequence parameters(spectral width in Hz, number of spectral points, frequency offsets)If STEAM:, Mixing Time (TM)If MRSI: 2D or 3D, FOV in all directions, matrix size, acceleration factors, sampling method | Spectral width: 6 kHzSpectral points: 2048frequency offset: -2.0 ppm |
| g. Water Suppression Method | VAPOR |
| h. Shimming Method, reference peak, and thresholds for “acceptance of shim” chosen | 3D head shim (GRESHIM) followed by FASTESTMAP, threshold for acceptable shim was linewidth water <16 Hz |
| i. Triggering or motion correction method(respiratory, peripheral, cardiac triggering, incl. device used and delays) | N/A |
| 3. Data analysis methods and outputs |  |
| a. Analysis software | LCmodel (fitting and quantification, version 6.3-1B), MRspa (preprocessing, version 1.4) |
| b. Processing steps deviating from quoted reference or product | Residual water component was removed using Hankel Lanczos Singular Value Decomposition (HLSVD). |
| c. Output measure(e.g. absolute concentration, institutional units, ratio)Processing steps deviating from quoted reference or product | Concentrations relative to total Creatine. |
| d. Quantification references and assumptions, fitting model assumptions | The basis set included simulated model spectra of alanine, aspartate, ascorbate/vitamin C, glycerophosphocholine, phosphocholine, creatine, phosphocreatine, GABA, glucose, glutamine, glutamate, glutathione, myo-inositol, Lactate, N-acetylaspartate, N-acetylaspartylglutamate, phosphoethanolamine, scyllo-inositol, taurine and experimentally measured macromolecules.Basis set is made available on GitHub.Prior constraints that fix GABA estimates relative to more abundant neurochemicals were turned off (i.e. NRATIO set to 0). |
| 4. Data Quality  |  |
| a. Reported variables (SNR, Linewidth (with reference peaks)) | Across all spectra (Figure 4–figure supplement 3):SNR: 51.1± 2.37% (mean ± SEM)FWHM from LCModel: 9.86±0.30 Hz (mean ± SEM)Total Creatine Linewidth: 11.01±0.32Hz (mean ± SEM) |
| b. Data exclusion criteria | Subjects were excluded from an analysis if there were less than 8 spectra acquired for one or more of the conditions of interest (n=1 subject excluded for analyses concerning the question period due to less than 8 spectra in the ‘forgotten’ condition). |
| c. Quality measures of postprocessing Model fitting (e.g. CRLB, goodness of fit, SD of residual) | Across all spectra (Figure 4–figure supplement 3, mean ± SEM)):CRLB glutamate: 4.42±0.43% CRLB GABA: 11.37±0.94%Intra-subject covariance glutamate: 2.68±0.62%Intra-subject covariance GABA was 8.74±1.95%Inter-subject covariance (Supplementary File 4): glutamate: 5.69-6.71%GABA: 31.04-33.25%  |
| d. Sample Spectrum | Figure 3E |