Data is stored in the MATLAB MAT file format Version 7.3 that is readable in Python with the h5py module, in R with the R.matlab library and in Julia with the MAT library.

Key to variables

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| Variable | Description | Units |
| T38 | Timepoints of measurements of Aβ38 labeled and unlabeled peaks by MS | h |
| MFL38 | Mol fraction labeled Aβ38 at timepoints in T38 | - |
| T40 | Timepoints of measurements of Aβ40 labeled and unlabeled peaks by MS | h |
| MFL40 | Mol fraction labeled Aβ40 at timepoints in T40 | - |
| T38 | Timepoints of measurements of Aβ42 labeled and unlabeled peaks by MS | h |
| MFL42 | Mol fraction labeled Aβ42 at timepoints in T42 | - |
| f | Mole fraction labeling of plasma leucine at time 0-48 h | - |
| raw38L | integration of MS peak, labeled Aβ38 | AU |
| raw38U | integration of MS peak, unlabeled Aβ38 | AU |
| raw40L | integration of MS peak, labeled Aβ40 | AU |
| raw40U | integration of MS peak, unlabeled Aβ40 | AU |
| raw42L | integration of MS peak, labeled Aβ42 | AU |
| raw42U | integration of MS peak, unlabeled Aβ42 | AU |
| Ab38conc | Aβ38 lumbar CSF concentration, t = 0 h, Xevo MS | ng/mL |
| Ab40conc | Aβ40 lumbar CSF concentration, t = 0 h, Xevo MS | ng/mL |
| Ab42conc | Aβ42 lumbar CSF concentration, t = 0 h, Xevo MS | ng/mL |
| Abtotconc | Aβ total lumbar CSF concentration, t = 0 h, Xevo MS | ng/mL |
| Brain\_thickness | Ratio of supratentorial radius minus ventricle radius to supratentorial radius | - |
| Tconcexport | Timepoints of CSF concentration measured by mass spec | h |
| CSFexport | CSF concentration measured by mass spec | ng/mL |
| TconcexportELISA | Timepoints of CSF concentration measured by ELISA | h |
| CSFexportELISA | CSF concentration measured by ELISA | ng/mL |
| ELISAonly | No mass spec concentration data if true | 0/1 |
| Time48h | Time points beyond 36 h if true | 0/1 |
| V\_ISF | Cortical volume of ISF | mL |
| Vent\_CSF | Volume of CSF in ventricles | mL |
| timespan | Length of experiment (36 or 48 h) | h |

MFL calculated from the ratio of raw\_L to raw\_U (tracer-to-tracee ratio, TTR). First, the TTR is corrected using a standard curve for the mass spec run using standards produced in vitro. Then the mean reading from time points 0-4 are subtracted from all TTR. Finally the TTR is converted to MFL; MFL = TTR/(1+TTR).