<u>MS summary</u>

Here's a quick guide on what to use for the mainstay of experiments.

MALDI: *Basement (B)* quick, dirty – good for heterogenous conjugates. Access is normally good.

Synapt: *(B)* Mainly set up for proteomics but can also do ion mobility. Brilliant but has had big gaps in 'up time' 2012 – now sorted.

LCT-A: (*1*) trained user – dedicated 24/7 to protein work. If these break these should be up and ticking asap. If not <u>go and see</u> the MS guys (do not send mail – people don't have time – if it's urgent – go see – email is useless!).

LCT-B: (*1*) trained user – 9-12am weekdays for ICL (José's group mainly). The rest of the time as for LCT-A.

LCT-P1: (*B*) trained used – also used for oligonucleotides (different LC – care!) and uses UPLC (nothing wrong with this – use it).

LCT-P2: (*G*) Open access protein MS. m/z >750. Don't become too dependent on this – get trained too.

QTOF with nanomate: (*LG*) Set-up well for native MS with ligands but very useful for whole protein and MSMS. Trained user.

Quattros x 2: (*B*) One for metabolites, one for metabolites an enzyme kinetics. Both can be used for MSn also – but due to low res might be best for lots of peptide (after a hefty manual digest) or MSn of small molecules.