Figure S1: Prediction plots of protein, carbohydrate and lipid content. Prediction estimates were obtained using the Leave One Out Cross Validation (LOOCV) on the PLSr models calibrated with bench-top FTIR-spectra and “wet” biochemical assays as a reference method. Each model was calibrated using three phytoplankton species (a diatom, a cyanobacterium and a green alga) grown at two temperatures (15 and 25°C). The macromolecule content is expressed as % of dry weight and the $R^2$ for each regression is also reported. The number of PLS-PCs used was 7.