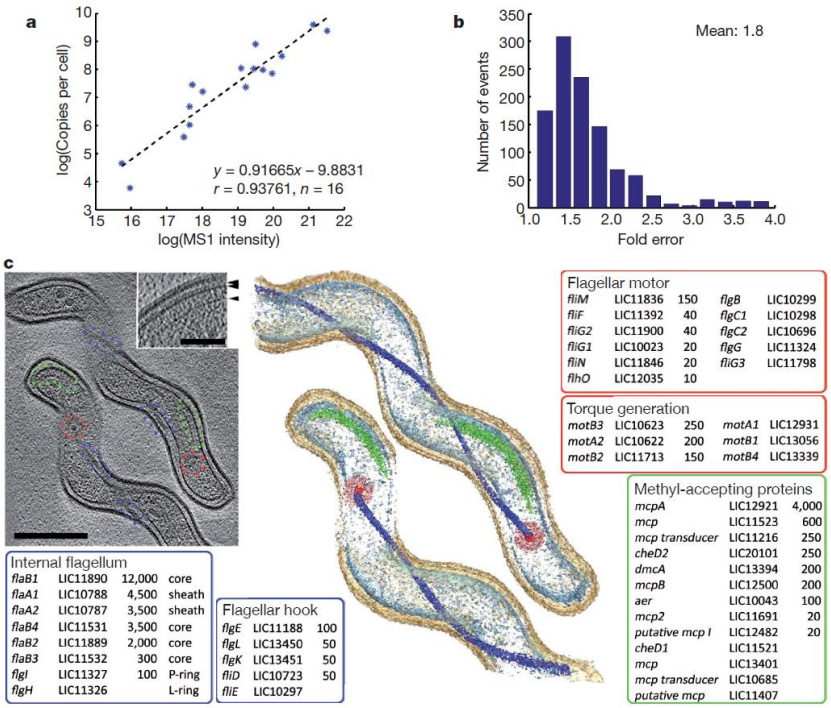


**Figure 1 | Large-scale determination of cellular protein concentrations.** **a**, Natural logarithm of extracted precursor ion intensities plotted against the natural logarithm of copies per cell for 16 proteins quantified by SRM. **b**, Distribution of error rates determined by bootstrapping. **c**, Slice through tomographic reconstruction, substructures are colour-coded as described below (scale bar, 200 nm). The inset shows a close-up of methyl-accepting proteins (scale bar, 100 nm). Arrowheads indicate the periplasmic MCP domain, plasma membrane and globular cytoplasmic MCP domain (from top). The boxes show the gene products making up the different components of methyl-accepting chemotaxis protein receptors (green), periplasmic flagella (dark blue), the flagellar stator (transparent red) and rotor (dark red). The accession numbers are from the NCBI (http://www.ncbi.nlm.nih.gov/sites/entrez), and the values represent the numbers of copies per cell.