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Cell organisation and disturbance-mapping using image activated cell-profiling (CODIAC)

Protein localisation and abundance is a key mechanism to regulate cell homeostasis. Furthermore, diseases are frequently associated with aberrant protein localisation. However, high-throughput methods that monitor changes of many proteins at once are missing. Recently, image enabled cell sorting (ICS) has been demonstrated to add spatial and morphological information to classical cell sorting technology. We utilise ICS in combination with improved Cas12a PCR tagging to develop new ways to characterise proteome localisation and expression levels within complex cellular pools. Applying ICS to fluorescently tagged protein libraries and machine learning, we have devised a novel way to assess cell organisation and to map disturbances using image activated cell-profiling (CODIAC). Using image-derived measurements from ICS, we group and isolate cells with fluorescently-tagged proteins of similar visual phenotypes. Sorting cell pools in their native state as well as upon chemical perturbation, we are able to identify changes in protein localisation and abundance in a pooled fashion at a much faster pace than previously established. We hope for this method to have broad applications in the field of high content screening for the identification of novel drug targets and various medical uses.

Research type

Translational research

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