MS10 Protein-carbohydrate interactions

MS10-01
Integrative methods in structural glycobiology
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Abstract
The introduction of intuitive graphical software (Potterton et al., 2018) has enabled structural biologists who are not experts in crystallography to build complete protein or nucleic acid models rapidly. In contrast, up until recently carbohydrates were in a completely different situation: scant automation existed, and users building models manually frequently tripped over legacy issues such as incorrect dictionaries or non-standard atom naming, which evidenced a historical lack of methodological support for carbohydrates (Agirre, 2017). Sugars are stereochemically complex and, as pyranose rings, have clear conformational preferences. And despite this, all refinement programs produced high-energy conformations at medium to low resolution, without any support from the electron density (Atanasova et al., 2020); this problem rendered the affected structures unusable in glyco-chemical terms. More recently, the AlphaFold revolution has delivered glycan-less but generally accurate structures of glycoproteins, once again enlarging the gap between protein and carbohydrates (Bagdonas et al., 2021). Bringing structural glycobiology up to 'protein standards' is requiring a total methodological overhaul. Time is of the essence, as the community is steadily increasing the production rate of glycoproteins, and electron cryo- microscopy is imaging them in the resolution range where crystallographic methods falter most. In this talk, I will introduce our latest methodological developments, which integrate prior knowledge from multiple techniques to streamline and automate hitherto error-prone processes (Bagdonas et al., 2020), helping structural biologists to produce correct atomic models with confidence.

References
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