Non-perturbative single-molecule imaging of tau aggregates by genetic code expansion

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Introduction

The aberrant aggregation of tau into intracellular deposits is thought to play a key role in the pathogenesis of Alzheimer's disease and other human tauopathies. Many methods that are used to study protein aggregation in vitro and in vivo rely on the covalent attachment of a label to the protein of interest. However, amyloid proteins such as tau are highly susceptible to mutations or covalent modifications, necessitating the careful selection of an appropriate labelling strategy to maintain native protein behaviour. Here, genetic code expansion^{Ref1} is utilised to introduce a well-tolerated biotin-tag near the N-terminus of a pathological mutant of full length tau. Using a range of single-molecule methods such as cTCCD^{Ref2} and DNA-PAINT^{Ref3}, we demonstrate that this biotin-tag can be used to study different aggregates of full length human tau – such as small oligomeric nuclei or mature fibrils – with unprecedented detail

Site-specific labelling of full length P301S tau



Summary and Conclusion

- The self-assembly behaviour of full length tau is highly susceptible to covalent modifications of the protein
- Site-specific biotinylation close to the N-terminus of tau yielded an aggregation competent tau conjugate
- The biotin-tag enables the highly sensitive detection of oligomeric tau species and can be used to obtain super-resolved images of tau aggregates
- This method is a good alternative labelling approach for proteins sensitive to modifications such as amyloid proteins

References

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