## Tracking protein aggregation by intrinsic TRES

L. H. C. Chung<sup>1</sup>, A. Bella<sup>3</sup>, V. Vyshemirsky<sup>2</sup>, O. J. Rolinski<sup>1</sup>, D. J. S. Birch<sup>1</sup>, and M. G. Ryadnov<sup>3</sup>

- 1. Photophysics Research Group, Department of Physics, SUPA, University of Strathclyde, 107 Rottenrow East, Glasgow, G4 0NG
- 2. School of Mathematics and Statistics, University of Glasgow, Glasgow, G12 8QQ
- 3. Biotechnology Research, National Physical Laboratory, Hampton Road, Teddington, TW11 0LW

E-mail: <a href="mailto:chloe.chung@strath.ac.uk">chloe.chung@strath.ac.uk</a>

## Abstract

We report the use of time-resolved emission spectra (TRES) to provide an insight into selfassembly of a de novo peptide named fibrillogenesis imaging model (FiM) and insulin.

FiM is a synthetic coiled-coil trimer that was engineered to predictably self-assemble from monomers into micron-long fibres. It has been previously labelled with Alexa Fluor 488 (FiM-488) for studying with super resolution imaging [1]. In order to provide a more native approach to track self-assembly, FiM was labelled with an intrinsic fluorophore, tyrosine (FiM-Y). It is a longitudinal assembly, which may provide a better understanding of the assembly of natural protein of relevance to amyloid disease.

With this in mind, we have compared FiM-Y with the natural protein insulin that is known to readily form fibrous structures [2]. As they both contain intrinsic tyrosine fluorophores, TRES has been used to extract useful comparative information e.g. conformational changes, dielectric relaxation and the protein stability from both structures [3].

## References

[1] A.Bella, M. Shaw, S. Ray, M. G. Ryadnov, Scientific Reports. 4, 7529 (2014)

[2] I. B. Bekard and D. E. Dunstan, Biophys. J. 97, 2521 (2009)

[3] L. H. C. Chung, D. J. S. Birch, V. Vyshemirsky, M. G. Ryadnov, O. J. Rolinski, Appl. Phys. Lett. **111**, 263701 (2017)