

Generating potent and selective inhibitors of Kv1.3 ion channels by fusing venom derived mini proteins into peripheral CDR loops of antibodies

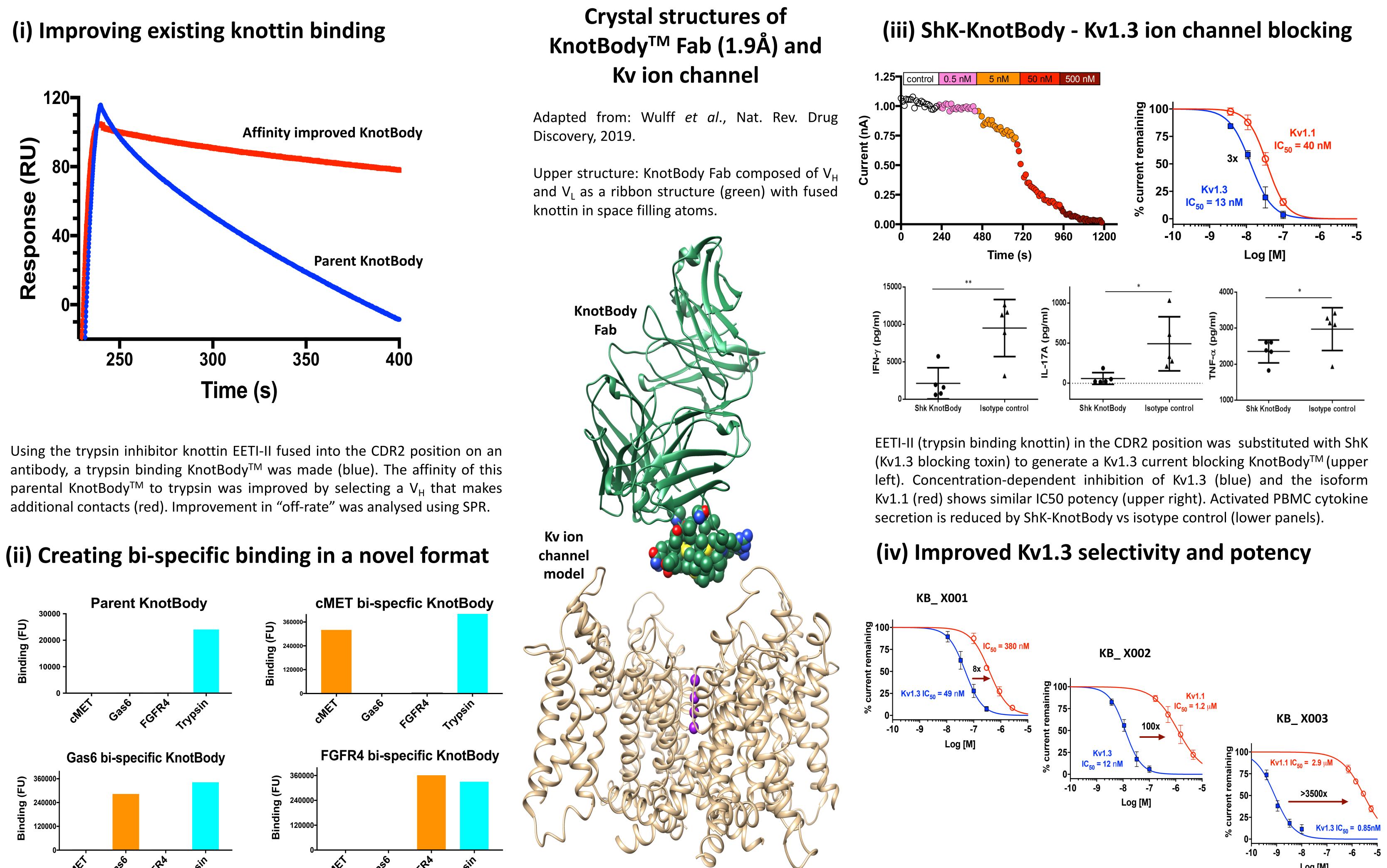
A.Karatt-Vellatt, D. C. Bell, S. Surade, P. A. Slavny, T. Luetkens, E. Masters & J. McCafferty

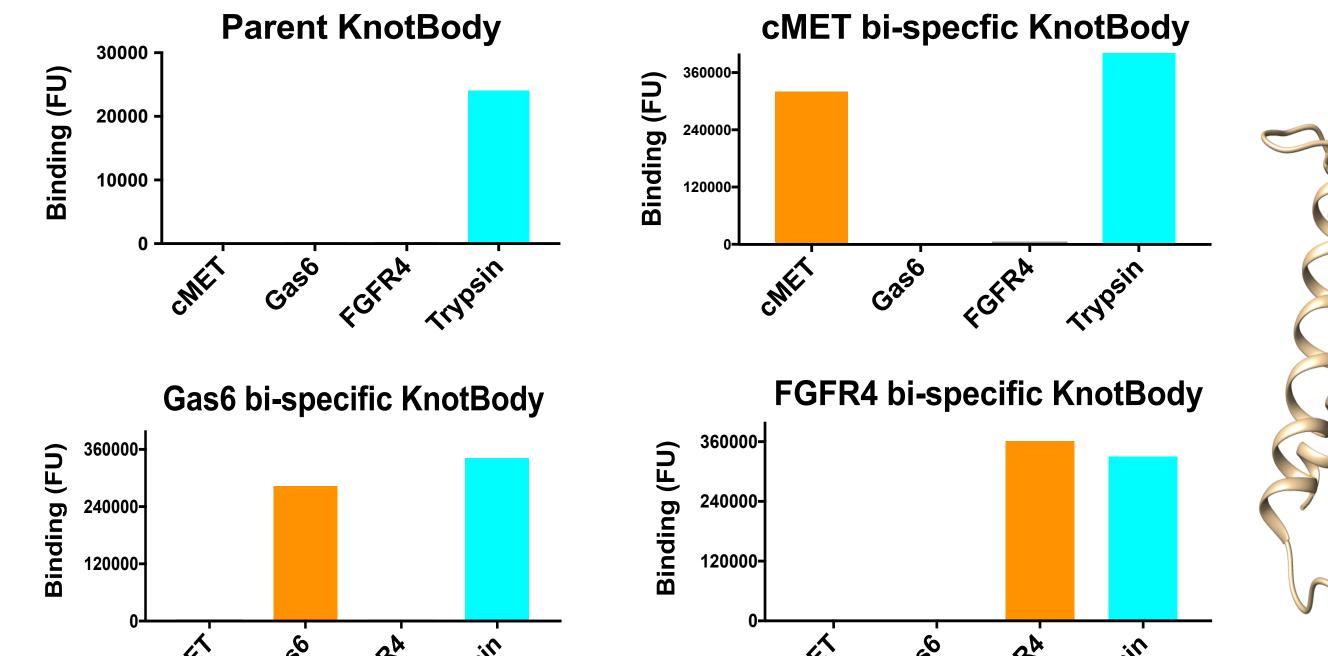
IONTAS Ltd, Cambridge, UK

Background

Pathogenic T cell effector memory (TEM) cells drive many autoimmune disorders and are uniquely dependent on the Kv1.3 channel. A number of venom derived knottin (cysteine-rich mini-protein) inhibitors of Kv1.3 are being developed as potential drug candidates, but can suffer from manufacturing difficulties, short half-lives and a lack of specificity. We have developed a novel molecular format wherein a peripheral CDR loop of an antibody has been replaced by a knottin. In this novel KnotBodyTM format, the knottin benefits from the improved therapeutic functionality of an antibody gains additional diversity by the addition of a scaffold which is pre-disposed to blockade of ion channels.

A proof-of-concept fusion protein of one structural domain within another was initially achieved by inserting a trypsin inhibiting knottin (EETI-II) flanked by diverse repertoire of short linker sequences into the CDR2 position of naïve antibody light chain sequences. Functional KnotBodyTM molecules were selected from this library using phage display technology on the basis of retained trypsin binding, with the correct folding of both domains confirmed using X-ray crystallography. To further demonstrate the benefits of this novel format, the modular nature of the KnotBodyTM binding surface was exploited to: (i) improve existing knottin binding by introducing additional V_H contacts; (ii) create a bispecific molecule by introducing a V_H chain that binds to a different target; (iii) substitute the proof-of-concept knottin (EETI-II, a trypsin inhibitor) with ShK, a Kv1.3 ion channel blocking toxin; (iv) develop a panel of low-nM Kv1.3 inhibitors with selectivity exceeding 3000-fold over the Kv1.1 channel, a closely related Kv family member.





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Bi-specific KnotBody[™] molecules were selected against cMET, Gas6 and FGFR4 from a phage display library created by shuffling the "Parent KnotBody" light chain (with trypsin binding knottin EETI-II at V₁ CDR2 position) with a repertoire of naïve heavy chains.

Lower structure: Kv ion channel ribbon structure (gold) with K⁺ ions in selectivity filter (purple). Atomic coordinates from the Kv1.2/2.1 chimaera crystal structure (Long et al., Nature, 2007).

By inserting alternative Kv1.3 blocking knottins and/or via modifications in the 'linker' residues a second generation of KnotBody[™] molecules were generated. These KnotBody[™] molecules showed improved Kv1.3 channel selective inhibition (blue) over Kv1.1 (red), a closely related isoform - the most improved KnotBody[™] showed over 3500x selectivity for Kv1.3.

Summary

- IONTAS have invented a novel molecular format that encapsulates the benefits of antibodies and naturally occurring knottins: •
 - Antibodies gain the functional diversity of the knottin, whilst the knottin gains the improved therapeutic functionality (e.g. longer half life) of an antibody.
 - Both knottin and antibody CDR loops can be further engineered using phage display technology to increase affinity and specificity.
- Due to the modular nature of the KnotBodyTM binding surface, this format can be used to create bi-specifics. •
- Functional ion channel blocking KnotBodyTM molecules were generated by substituting trypsin binding knottin at V₁ CDR2 position with Kv1.3 blocking knottins. **
 - Nav1.7 (a chronic pain target) and ASIC1a (stroke) ion channel blocking KnotBodyTM molecules have also been generated data not shown.
- This technology unlocks new possibilities for the blockade of ion channels using "engineerable" antibody based drugs. •