Structural and functional dissection of VSG-Exclusion Protein 2 in African trypanosomes

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Structural Biology



UPF1

trypanosomatids + Bode



VEX2 depletion disturbs singular Variant Surface Glycoprotein (VSG) expression, an essential mechanism to escape immune response¹.





RecA2 Sen1 helicase KECA2 Sen1 helicase

Structural alignment of Sen1 (PDB 8FTK) and VEX2 AF2 helicase domains

VEX2 AF2 model shows strong differences with Sen1 1c subdomain, which is essential for regulatory interaction with the N-terminus in Sen1⁴.

Introduction





Hypothesis:

- 1. VEX2 is SUMOylated.
- 2. SUMOylation of VEX2 confers ESB specific localization.
- 3. SUMOylation is stage/cell cycle dependent.



Future approach to study the SUMOylation of VEX2.

Senataxin, the human orthologue of VEX2, is involved in human R-Loop metabolism⁵. R-Loops are also implicated with the induction of VSG switching in *T. brucei* ⁶.

Hypothesis:

VEX2 helicase activity is essential in regulating R-Loop levels at the active VSG expression site.



DRIP-Seq analysis of VEX2-depleted cells shows an increase in the level of R-Loops at the beginning of BES1 (where VEX2 accumulates the most, based on previous ChIP-Seq data¹) – ongoing research aims to investigate whether this is directly dependent on VEX2 helicase activity.

References

¹Faria *et al.* 2023, PMID: 38081826; ²Tammsalu *et al.* 2014, PMID: 24782567; ³Iribarren *et al.* 2015, PMID: 26258470; ⁴Appel *et al.* 2023, PMID: 37832548; ⁵Groh *et al.* 2017, PMID: 27771483; ⁶Saha *et al.* 2020, PMID: 31682833; Illustrations were created with BioRender.com