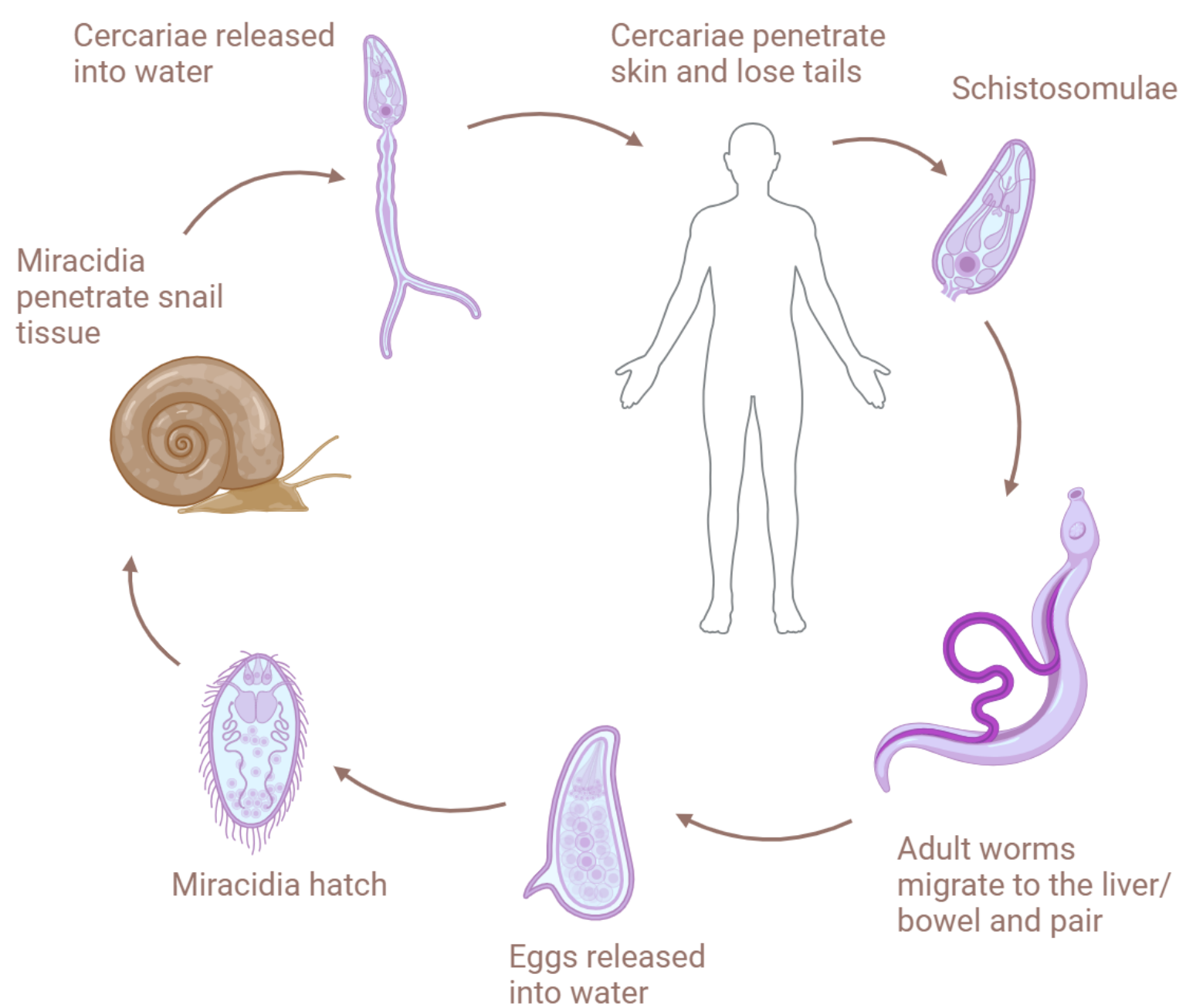


## Schistosoma mansoni Lifecycle

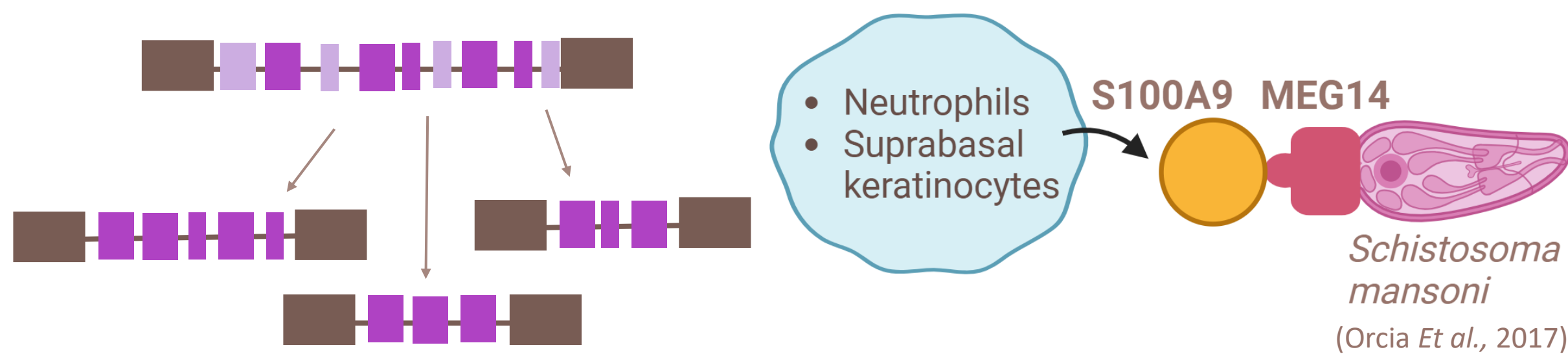


- Can survive in the host for up to 30 years
- How the parasite succeeds in avoiding immune attack is not fully understood

## Micro-Exon Genes

- Protein coding sequence comprised primarily of micro-exons
- Micro-exons have lengths that are palindromic and multiples of 3 (from 6 to 81bp) (DeMarco *Et al.*, 2010, Berriman *Et al.*, 2009)
- Very high non-synonymous/synonymous substitution rates (Philippesen *Et al.*, 2015)
- MEGs are primarily transcribed in the intramammalian stages
- Oesophageal gland is a hotspot for MEG transcription (Wilson *Et al.*, 2015, Diaz Soria *Et al.*, 2020)
- Sm-foxA knockdown blocks oesophageal gland development, knockdowns cannot establish infection in immunocompetent mice (Lee *Et al.*, 2020)

## Alternative Splicing and Immune Evasion

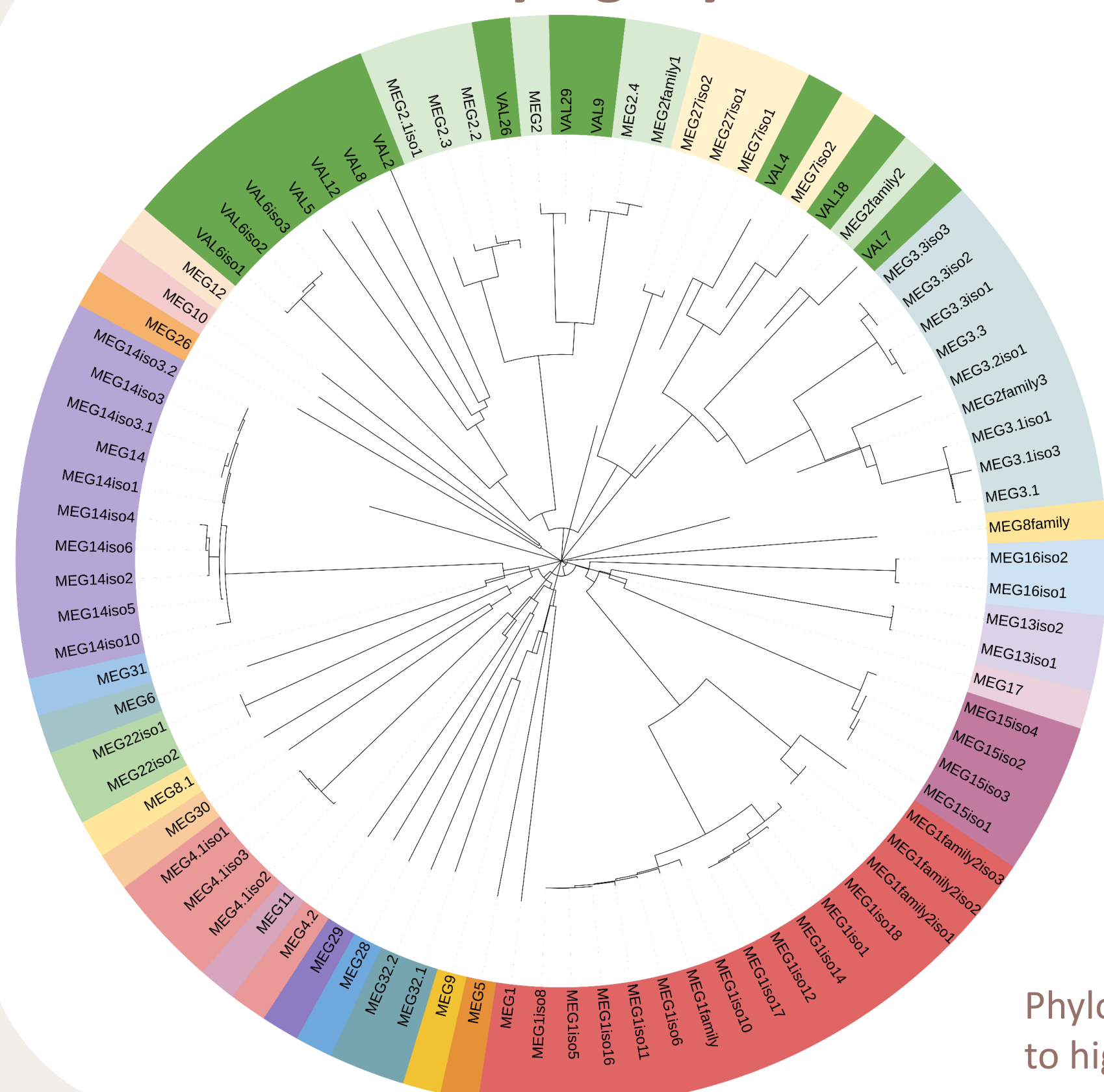


- Protein variation through alternative splicing of micro-exons
- The near endless combinations of MEGs secreted or expressed on tegument surface is believed to protect against the adaptive immune response (DeMarco *Et al.*, 2010)
- Also hypothesised that MEG interactions with human immune receptors could dampen the immune response (Orcia *Et al.*, 2017)

## My Project

- To identify new MEG alternative transcripts to create a transcriptomic dataset
- To test the binding and interaction of these MEGs to host proteins through SAVEXIS

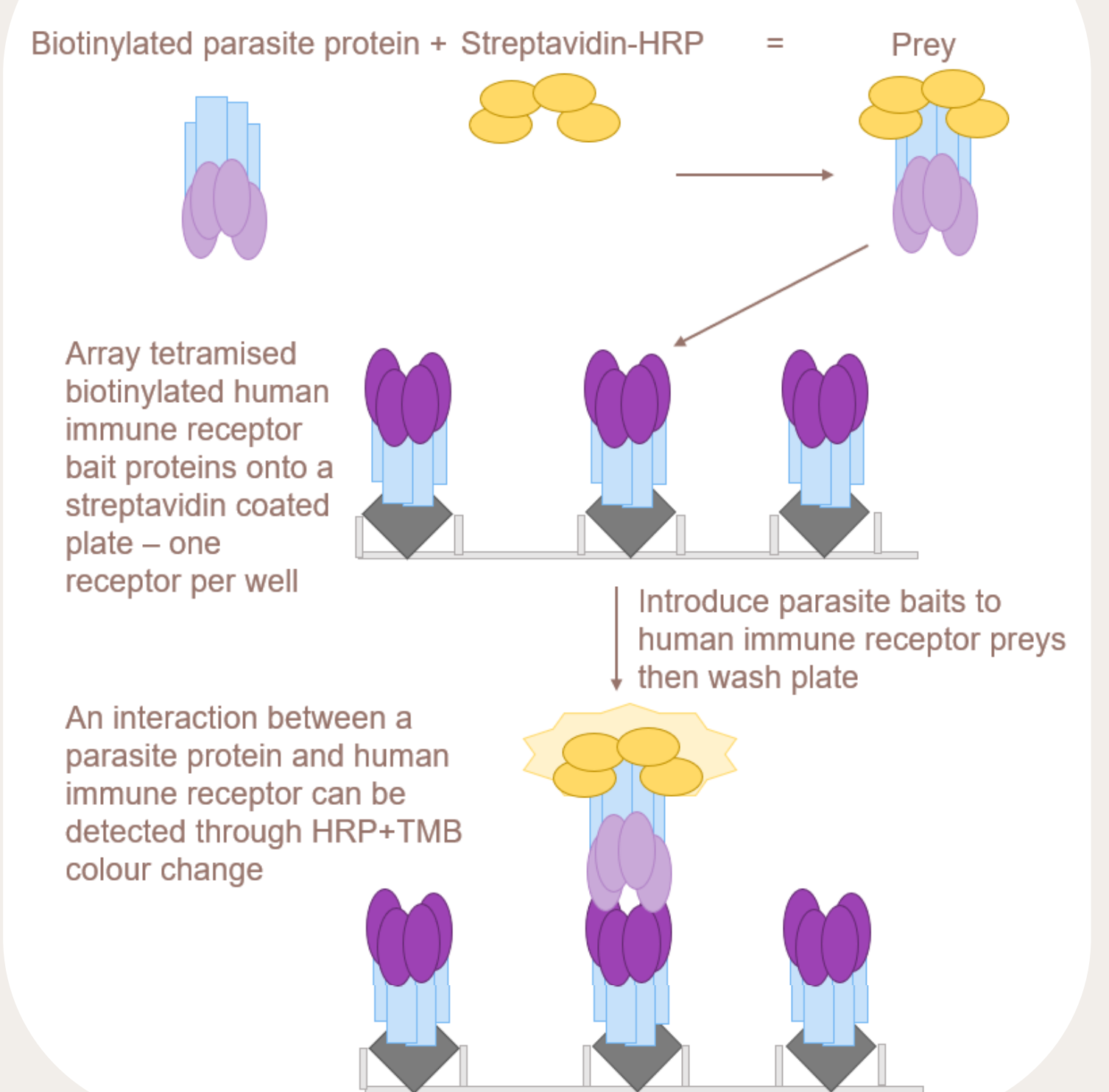
## Phylogeny of Known MEG Variants



- 35 individual MEGs identified through shotgun RNA sequencing
- 87 isoforms identified (so far!) (Nedvěďová *Et al.*, 2023)
- Long read RNA sequencing may reveal more variants

Phylogenetic tree colour coded to highlight MEG families

## SAVEXIS



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Global Health  
EDCTP3



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