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unveiling the complexity of antigen-antibody interactions of antivenoms

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High-throughput epitope profiling of snake venom toxins – unveiling the complexity of antigen-antibody interactions of antivenoms

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Introduction
Insight into the molecular details of polyclonal antivenom antibody specificity is a prerequisite for accurate prediction of cross-reactivity and can provide a basis for design of novel antivenoms. In this work, a high-throughput approach was applied to characterize linear epitopes in venom toxins from four African mamba and three neurotoxic cobra snakes obtained from public databases.

Studying linear epitopes using peptide microarrays

High number of epitopes recognized by SAIMR antivenom

Key residues for antivenom toxin recognition

Antivenoms antibodies bind to functional sites of toxins

Conclusions

Perspectives

Affiliations

References

Acknowledgement