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**Figure 1.** **(A) Sequence Conservation of *Pseudechis australis* Basic Phospholipase A2-PA5, (B) Structural Superposition of *Pseudechis australis* Basic Phospholipase A2-PA5 with Homolog, and (C) Orientation of *Pseudechis australis* Basic Phospholipase A2-PA5 in the Mammalian Membrane.**

1. Panel A displays the AlphaFold 2 model of Pseudechis australis basic phospholipase A2-PA5, colored according to sequence conservation using Consurf. The conservation scale follows the Consurf default scheme, with cyan indicating variable residues, white representing neutrally conserved residues, and magenta highlighting highly conserved residues. The orientation is set to expose the most conserved surface.

Key residues are labeled as follows (Uniprot, n.d):

* **Binding sites:** Y28, G30, G32, D49
* **Active site residues:** H48 (D92 is obscured in this view)

The multiple sequence alignment (MSA) used for this conservation analysis was curated manually rather than relying on Consurf's auto-generated alignment.

1. Panel B displays a DALI-based structural superposition of *Pseudechis australis* basic phospholipase A2-PA5 (green) with its closest structural homolog (yellow), basic phospholipase A2 PA-11 (PDB: 3v9m-A (Uniprot, n.d)). The proteins are visualized as cartoon representations, with their catalytic/active residues shown as stick models for comparison.

**Superposition details:**

* DALI Z-score (Z): 24.0
* Sequence identity (%id): 86%
* Root-mean-square deviation (RMSD): 0.8
* Aligned length (lali): 118

The 3V9M-A structure exists as a homodimer (Homo 2-mer, A2) with C2 symmetry, indicating that it forms a biologically relevant dimer composed of two identical subunits (RCSB PDB, n.d.).

1. **i) First View**

This panel illustrates the predicted orientation of *Pseudechis australis* basic phospholipase A2-PA5 in the mammalian cellular membrane, as determined using the OPM (Orientations of Proteins in Membranes) database. The membrane plane is represented by yellow transparent spheres, while the hydrophobic membrane core is shown in blue spheres.

**Labeled residue:**

* Active site residues (HIS48 and ASP92) are labeled in pink.
* Disulfide bonds are shown in yellow.
* Residues interacting with the membrane are highlighted in green.

**(ii) Second View**

This panel provides a 90-degree rotated view of the protein within the membrane plane. The active site (HIS48 and ASP92) are labeled, emphasizing the spatial arrangement of key residues relative to the membrane surface. This view highlights cysteine residues (cyan labels), disulfide bonds, and hydrophobic residues interacting with the lipid bilayer.

**References:**

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