MS09-2-5 Identification of Potentially Bioactive Argon Binding Sites in Protein Families
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Abstract
Argon belongs to the group of chemically inert noble gases, which display a remarkable spectrum of clinically useful biological properties. In an attempt to better understand noble gases, notably argon's mechanism of action, we mined a massive noble gas modelling database which lists all possible noble gas binding sites in the proteins from the Protein Data Bank. We developed a method of analysis to identify among all predicted noble gas binding sites, the potentially relevant ones, based on their conservation, binding energy, hydrophobicity, shape and localization within structurally aligned protein families which are likely to be modulated by Ar.[1]This method allowed us to identify relevant noble gas, in particular Ar, binding sites that have potential pharmacological interest in several protein families such as Nitric Oxide Synthase (NOS), and soluble Guanylate Cyclase heme-NO and oxygen binding domain (sGC H-NOX domain). These potential Ar targets are currently undergoing crystallographic studies under Ar pressure to confirm our in-silico predictions. We have already identified a crystallographic Ar binding site under 5 MPa pressure within Thermolysin, that corresponds to a predicted noble gas binding site that meets all our suggested criteria. *In vitro* validation experiments are being performed with Ar on a few identified putative physiological targets in order to improve the understanding of its interaction mechanism of action.

References
(1) Hammami, I.; Farjot, G.; Naveau, M.; Rousseaud, A.; Prangé, T.; Katz, I.; Colloc'h, N. Method for the Identification of Potentially Bioactive Argon Binding Sites in Protein Families. J. Chem. Inf. Model. 2022. https://doi.org/10.1021/acs.jcim.2c00071.