**Function and inhibition of the metastasis and inflammation promoting protein, S100A4**

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High-affinity myosin peptide was evolved, amino-acid positions responsible for functional isoform differences were identified (1). Myosin variants were characterized by SPR, ITC and filament dissociation studies. NMR found shorter than 100-residue myosin fragments disordered, while those of 111 residues partly coiled-coil partly disordered (2). Ser 1942 phosphorylation was followed by NMR, and structural changes with HSQC and SOFAST. Wild-type complex formation was in silico simulated at atomic level (1). The results led to 4 conference talks, 6 posters, 3 manuscripts (under submission/writing): (1) Kiss et al.: *J. Mol. Biol.;* (2) Pálfy et al: *Chemistry;* (3) Biri et al.: *J. Biol. Chem.* We initiated a synergy enhancing popular “teatime” scientific lecture series.