Structures and dynamics of S100 proteins

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The dynamical properties of S100A2, S100A5, S100A16 and S100P have been investigated by NMR. The analysis of the R_1, R_2 and NOE values indicates for each protein the regions experiencing a large flexibility. In particular the hinge loop region is characterized by a mobility faster than protein tumbling. The interaction of members of the S100 family with RAGE, and the structural and dynamic properties of the complex have been characterized to obtain information on the molecular species responsible for RAGE activation by extracellular S100 proteins.