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Explore the physical mechanism of Hofmeister series on protein structural dynamics SANDIP KALEDHONKAR, LORAND KELEMEN, AIHUA XIE, Department of Physics, Oklahoma State University, Stillwater, OK 74078, XIE LAB TEAM — Hofmeister series, a classification of ions, are known to change the solubility and stability of proteins. We have found that Hofmeister series suppress functionally important structural dynamics of photoactive yellow protein (PYP). Here we investigate two possible mechanisms: (1) Hofmeister series increases the pK_a of Glu46, an active site proton donor to chromophore protonation of PYP, (2) Hofmeister series alter the energy landscape of surface exposed groups due to effective dehydration, making it difficult to change protein conformations. We will test these two hypotheses using strategic combination of protein engineering and time-resolved step-scan and rapid-scan FTIR difference spectroscopy. A variety of N-terminus tags are designed and employed to study the effect of effective dehydration of protein due to Hofmeister series. Time-resolved infrared structural biology will be used to capture light-triggered structural dynamic motions of PYP.

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