

Abstract Submitted
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FT-IR Study Reveals Intrinsically Disordered Nature of Heat Shock Protein 90¹ AIHUA XIE, DAVID NETO, MAURIE BALCH, Oklahoma State University, JOHNNY HENDRIKS, Forschungszentrum Juelich GmbH, OLIVER CAUSEY, JUNPENG DENG, ROBERT MATTS, Oklahoma State University — Heat shock protein 90 (Hsp90) is a highly conserved chaperone protein that enables the proper folding of a large number of structurally diverse proteins (a.k.a., clients) in the crowded cytosolic environment and plays a key role in regulating the heat shock response. A long standing open question is how Hsp90 accommodates the structural diversity of a large cohort of client proteins? We report ATR FTIR study on structural properties of Hsp90 C-terminal domain (CTD) and their temperature dependences. Effects of temperature on Hsp90 structure are dissected into the C-terminal domain (CTD) and the N-terminal/middle domain (NTMD). One of our major findings reveals that within a narrow temperature window across the physiological temperatures (35 to 45 C), Hsp90CTD exhibits significant increases in protein aggregation and increases in unordered structures. Despite the intrinsically disordered nature of Hsp90CTD, it retains a protected hydrophobic core at 40 C. Implications of these results will be discussed in the light of the structural dynamics and client diversity of Hsp90.

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