Low-resolution structural study of two human Hsp40 chaperones.

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The proteins belonging to the Hsp40 family assist the Hsp70 in many cellular functions, helping to form an essential system for cell viability. Thus, the understanding of the structural and functional characteristics of the Hsp40 family is relevant to the general knowledge of the role of the Hsp70 chaperone system in the cell. We have investigated two human Hsp40 representatives, DjA1 (Hdj2/dj2/HSDJ/Rdj1) from subfamily A and DjB4 (Hlj1/DnaJW) from subfamily B, by small angle X-ray scattering and analytical ultracentrifugation methods, and determined their quaternary structure. We have also determined low-resolution models for the structure of a C-terminal deleted mutant of DjA1, DjA1_{1-332}$, in which the dimer formation was interrupted. Our results were used in combination with the current structural information of Hsp40 C-terminal and J-domains, to generate models of the internal structural organization of DjA1 and DjB4. The characteristics of these models indicate that DjA1 and DjB4 were both dimers but with substantial differences in their quaternary structures: while DjA1 consisted of a compact dimer in which the N- and C-termini of the two monomers are facing each other, DjB4 formed a dimer where only the C-termini of the two monomers are in contact. The two proteins also differed in their capability to bind unfolded luciferase. Together, our results indicate that the representatives of subfamilies A and B of human Hsp40 have different quaternary structures and chaperone functions.

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