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A Study of the Binding of Dansylated Amino Acids to Human Serum Albumin Ali Ryan, Jamie Ghuman, Patricia A. Zunszain and Stephen Curry *Biophysics Section, Blackett Laboratory, Imperial College London, SW7 2AZ, UK*. E-mail: ali.ryan00@imperial.ac.uk

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Human serum albumin (HSA) is the most abundant protein in the blood where it acts to transport a wide variety of both endogenous compounds such as fatty acids and hemin, as well as many common drugs [1]. HSA has two major drug binding sites which were originally identified via displacement of fluorescent markers including dansylated amino acids [2]. In recent years the structures of several drugs bound to HSA have been published [3] which have improved the understanding of how compounds bind to these sites. The structures of HSA complexed with dansylated amino acids either in the presence or absence of fatty acids will be presented here. These new structures allow comparisons to be made within a set of molecules whose core is the same. This allows a more systematic determination of the factors that determine whether a compound binds primarily to drug site 1 or 2. It helps to explain much of the previously published binding data and will allow these compounds to be used with much greater precision as drug site markers on HSA.

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