Small-angle X-ray scattering studies of tryptophan synthase from E. coli and its subunits.

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Tryptophan synthase (EC 4.2.1.20) isolated from E. coli is an $\alpha_2\beta_2$ bienzyme complex with interesting heterologous subunit interactions. By small-angle X-ray scattering we studied size and shape of the native $\alpha_2\beta_2$ complex as well as of the α and β_2 subunits. Radius of gyration (R), maximum particle dimension (D), and volume (V) were determined as follows:

	α	β_2	$\alpha_2\beta_2$
R (nm)	1.95	3.01	4.01
D (nm)	5.8	10.5	13.5
V (nm^3)	60	160	270

Models for the subunits and their possible arrangement in the $\alpha_2\beta_2$ complex will be discussed by comparing experimental and theoretical data in reciprocal (scattering curves) and real space (distance distribution functions).

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