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Comparative Analysis of Contacts Between Crystal Lattice & Oligo Interface

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G proteins are molecular amplifiers. GTPases are a large family of enzymes that can bind and hydrolyze GTP. The GTP binding and hydrolysis takes place in the highly conserved G domain common to all GTPases. Protein crystal contacts are weak and generally form only under conditions designed to limit protein solubility and maximize protein-protein interactions. However, they do form with a kind of specificity, at least in the sense that only certain contacts are repeated within each unit cell of any particular crystal packing arrangement. For oligomeric proteins, amino acids at the subunit interfaces have been selected in order to maintain affinity and specificity properties. Many proteins contain highly flexible or even completely unfolded fragments that dramatically interfere with crystallization conditions. These conditions are the crystal lattice and Oligomeric interface or proteins that allow the residues to bind in such a specific way by which the crystallization of GTPase is fast. This book therefore, should be helpful for better understanding the crystallography of proteins for biologists etc. 52 pp. Englisch.



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