

Structural Analysis of Protein–Aptamer complexes by X-ray crystallography

Simranjeet Singh Sekhon, 이문중, 민지호¹, 김양훈*
충북대; ¹전북대
(kyh@chungbuk.ac.kr*)

Aptamers are single-stranded DNA or RNA oligonucleotides that bind with high specificity and affinity to a wide range of target molecules including proteins, peptides, and small molecules. Despite numerous advances in the aptamer research, characterization of their specific interactions is often restricted to binding affinity. This void of understanding aptamer–protein interactions can be overcome by x-ray crystallography. Crystal structures of aptamer–target complexes can provide detailed information of their interactions, are therefore crucial for a thorough understanding of the molecular basis of aptamer–target binding mode. The use of advanced protein expression, purification, crystallization screens and powerful synchrotron radiation sources enable high-throughput structure determination, useful for functional analysis Protein–Aptamer complexes.