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Report:

Structure of the Stat3 β homodimer bound to DNA

STAT proteins (Signal transducers and activators of transcription) are activated in response to a large number of cytokines and growth factors. Upon activation by cell-surface receptors or associated kinases, STAT proteins become phosphorylated at a C-terminal tyrosine. Dimerization is mediated through the binding of this phosphotyrosine by the SH2-domain of its dimeric partner. Upon dimerization the STATs translocate to the nucleus and bind to specific promoter sequences of their target genes.

Seven different STAT genes have been identified thus far in mammals. The encoded proteins vary in length between 750 to 850 amino acid residues. We have crystallized a 65 kDa fragment of Stat3 β comprising the DNA-binding region and the SH2 domains in complex with its specific DNA-binding site. The Stat3 β :DNA structure was solved by multiple isomorphous replacement using three mercury, one platinum and one selenomethionine derivative. Native and derivative data were collected at the European Synchrotron Radiation Facility, Grenoble. The structure has been refined to an R-factor of 25.4% ($R_{\text{free}}=30.6\%$) using native data between 20 and 2.25 Å resolution.

The structure provides insight into the various steps by which STAT proteins deliver a response signal directly from the cell membrane to its target gene in the nucleus. It shows the domain structure of each monomer and how the dimer is bound to DNA. Furthermore, it gives a detailed view of the protein:DNA interface and explains the target site specificity of STAT proteins. It also shows how the SH2 domains form the dimer interface through the binding of the phosphotyrosine peptide of the other monomer.

The structure of the Stat3 β :DNA complex has been published as an article in Nature. Reprints will be sent to the Useroffice of the ESRF as soon as we receive them.

Reference

Becker S, Groner, B. Müller, C.W. (1998). Structure of the Stat3 β homodimer bound to DNA. Nature 394, 145- 151.