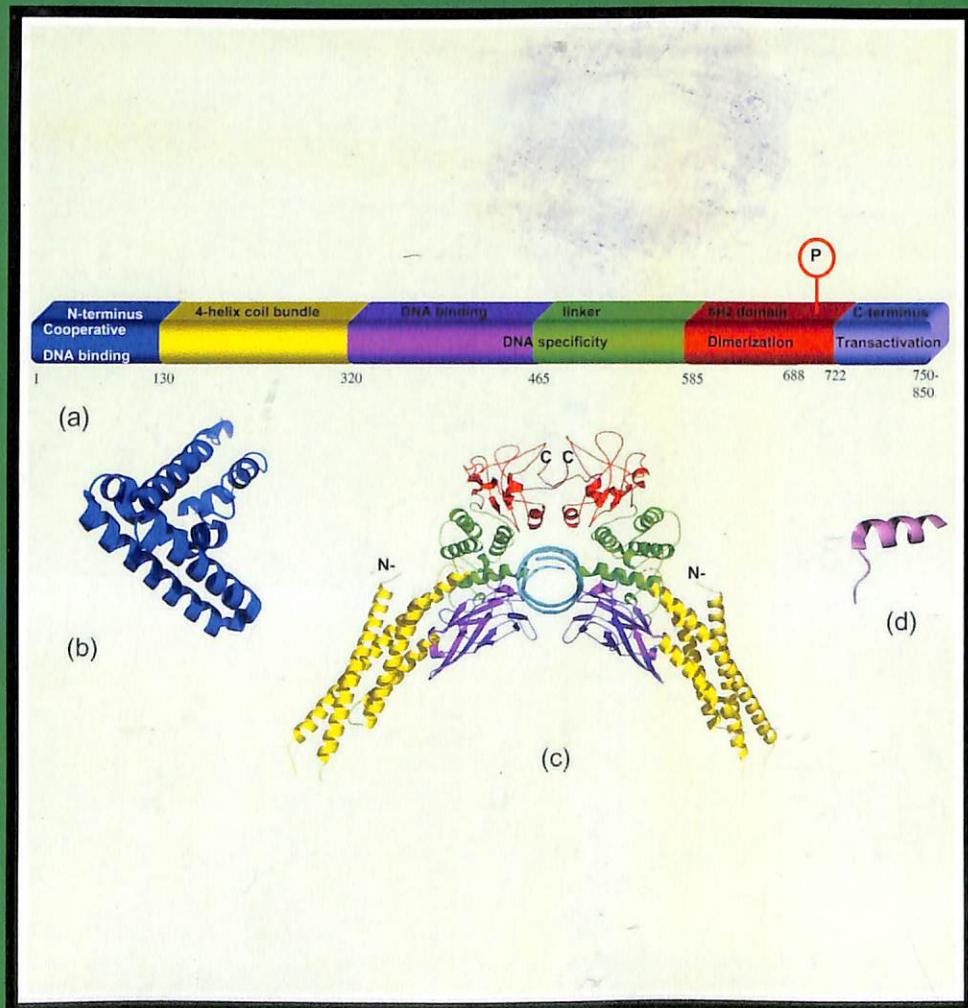


Current Cancer Drug Targets



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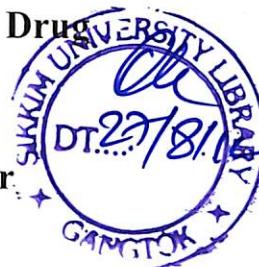
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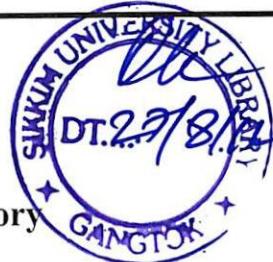
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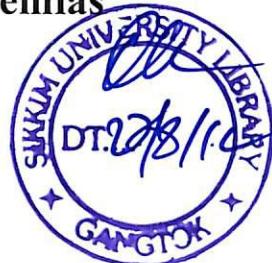
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The cover image is taken from the article by Neamati *et al.* *Current Cancer Drug Targets* 2007, 7(1), 91-107. It illustrates the structural organization of Stat proteins: (a) domain formation, (b) 8-helical N-terminus (aa1-aa123) as resolved in Stat1 (PDB 1YVL), important for cooperative DNA binding, (c) Stat3 structure (PDB 1BG1) covering residues aa136-aa716, the elongated 4-helix coil domain (aa136-aa319) is shown in yellow, the DNA binding domain (aa320-aa465) in magenta, the linker domain (aa466-aa584) in green, the SH2 domain (aa585-aa716) in red, and the bound DNA is in cyan, and (d) five-residue fragment of the C-terminal transactivation domain. The structure of the motif is taken from a complex with PAS-B domain of the nuclear receptor coactivator 1 (PDB 1OJ5).

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The cover image is taken from the article by Neamati *et al.* *Current Cancer Drug Targets* 2007, 7(1), 91-107. It illustrates the structural organization of Stat proteins: (a) domain formation, (b) 8-helical N-terminus (aa1-aa123) as resolved in Stat1 (PDB 1YVL), important for cooperative DNA binding, (c) Stat3 structure (PDB 1BG1) covering residues aa136-aa716, the elongated 4-helix coil domain (aa136-aa319) is shown in yellow, the DNA binding domain (aa320-aa465) in magenta, the linker domain (aa466-aa584) in green, the SH2 domain (aa585-aa716) in red, and the bound DNA is in cyan, and (d) five-residue fragment of the C-terminal transactivation domain. The structure of the motif is taken from a complex with PAS-B domain of the nuclear receptor coactivator 1 (PDB 1OJ5).

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The cover image is taken from the article by Tagliaferri *et al* *Current Cancer Drug Targets* 2012, 12 (7). The biogenesis and the action of miRNAs are described: miRNAs are expressed as a pri-miRNA long transcript which is then cleaved by DROSHA to a pre-miRNA hairpin that translocates in the cytoplasm following exportin 5 binding. Pre-miR DICER digestion produces miR/miR* duplex. The RISC complex incorporates one strand of the duplex, the mature miRNA, driving it to the 3'UTR of mRNA target and inducing translational repression (partial homology) or mRNA deadenylation (perfect homology). Alternatively, mature miRNAs may bind the open reading frame or the 5'UTR of target genes inducing transcription activation or may act as decoy for translation repressor ribonucleoproteins.



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Black Currant Anthocyanins Abrogate Oxidative Stress through Nrf2-Mediated Antioxidant Mechanisms in a Rat Model of Hepatocellular Carcinoma

R.J. Thoppil, D. Bhatia, K.F. Barnes, E. Háznagy-Radnai, J. Hohmann, A.S. Darvesh and A. Bishayee

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The cover image is taken from the article by Neamati *et al.* *Current Cancer Drug Targets* 2007, 7(1), 91-107. It illustrates the structural organization of Stat proteins: (a) domain formation, (b) 8-helical N-terminus (aa1-aa123) as resolved in Stat1 (PDB 1YVL), important for cooperative DNA binding, (c) Stat3 structure (PDB 1BG1) covering residues aa136-aa716, the elongated 4-helix coil domain (aa136-aa319) is shown in yellow, the DNA binding domain (aa320-aa465) in magenta, the linker domain (aa466-aa584) in green, the SH2 domain (aa585-aa716) in red, and the bound DNA is in cyan, and (d) five-residue fragment of the C-terminal transactivation domain. The structure of the motif is taken from a complex with PAS-B domain of the nuclear receptor coactivator 1 (PDB 1OJ5).