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ARGENTOPHILICITY IN MULTIPLE SALTS OF SILVER

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The argentophilic interaction [1] promotes the aggregation of silver (I) centers into various polyhedra, as illustrated by the synthesis and X-ray analysis of a variety of double salts of the general formula $mAgY{\cdot}nAgZ{\cdot}xL$ (Y, Z = different anions; L = solvate molecule that may be present) [2]. A brief review of the subject is following by the presentation of our recent results on the designed synthesis of novel multiple salts of silver (I) that include the triple salts $AgCN{\cdot}AgF{\cdot}4AgCF_3CO_2{\cdot}2L$ (L = CH_3CN, H_2O)[3] and $Ag_2C_2{\cdot}AgF{\cdot}4AgCF_3SO_3{\cdot}RCN$ (R = CH_3, C_2H_5)[4] and the quadruple salt $2Ag_2C_2{\cdot}3AgCN{\cdot}15CF_3CO_2Ag{\cdot}2AgBF_4{\cdot}9H_2O$ [5], as well as discrete and one-dimensional silver aggregates containing embedded acetylide dianions [6, 1b].

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INDUCED FIT RECOGNITION OF M7GPPPG BY THE HUMAN NUCLEAR CAP-BINDING COMPLEX

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The hetero-dimeric nuclear cap-binding complex (CBC) binds to 5' capped polymerase II transcripts. It enhances the efficiency of several mRNA maturation steps and is essential for U snRNA nuclear export in multicellular eukaryotes. The 2Å crystal structure of human CBC shows that the large subunit, CBP80, comprises three domains each containing consecutive helical hairpins and resembling the so-called MIF4G domain found in several other proteins involved in RNA metabolism (1). The small subunit, CPB20, has a classical ribonucleoprotein (RNP) fold and associates with the second and third domains of CBP80. A 2.4 Å structure of CBC complexed with a cap analogue, m7GpppG, shows that cap binding leads to an induced fit folding of the N- and C-terminal extensions to the RNP core of CBC20. Site-directed mutagenesis of key interacting residues gives some insight to the basis of the specificity for m7G. Comparisons will be made with the two other known structures of cap-binding proteins, eIF4E and VP39 complexed with cap analogues.

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Keywords: NUCLEAR CAP BINDING COMPLEX, INDUCED FIT, RNA MATURATION,

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STRUCTURAL BIOLOGY OF EUKARYOTIC TRANSCRIPTION INITIATION

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Insights from structural studies of mRNA transcription initiation in eukaryotes will be discussed. X-ray structures of the TATA Box-binding Protein (TBP), various TBP-DNA complexes, and two ternary complexes [Transcription Factor IIB (TFIIB) recognizing a preformed TBP-DNA complex and Negative Co-factor 2 (NC2) bound to the same preformed TBP-DNA complex] will be used to explain how early, rate-limiting steps in assembly of the transcription machinery are regulated in eukaryotes.

Keywords: TRANSCRIPTION FACTORS, RNA POLYMERASE II, GENE EXPRESSION

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STRUCTURE AND FUNCTION OF THE RUV COMPLEX

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At the late stage of recombinational repair in prokaryotes, RuvA, RuvB, and RuvC proteins process the holliday junction through formation of two types of complexes, which catalyze branch migration (RuvAB) and resolution (RuvABC resolvasome), respectively. We determined the three-dimensional structures of all three protein components by x-ray crystallography. The crystal structure of the RuvA-holliday junction complex revealed that two base pairs near the crossover point are disrupted, suggesting the positive mechanistic role of RuvA in the branch migration. The crystal structure of the E. coli RuvC dimer indicated the catalytic center of this resolvase, and allowed us to build a holliday junction model bound to RuvC. The crystal structure of the thermus thermophilus RuvB protomer revealed the RuvB architecture, classified into the AAA+ family, and the environments of the ATP or ADP binding site. The X-ray structure of the RuvA-RuvB complex, determined more recently, has revealed that two RuvA tetramers form the symmetric and closed octameric shell, where four RuvA domain IIIs spring out in the two opposite directions to be individually caught by a single RuvB. The binding of domain III deforms the protruding b-hairpin in the N-terminal domain of RuvB, and thereby appears to induce a functional and less symmetric RuvB hexameric ring structure. The fitting of this complex structure into the averaged electron microscopic images of the RuvA-RuvB-junction DNA ternary complex allows the model building, which implies that the functional scheme with a fixed RuvA-RuvB interaction may be preferable to that with their rotational interaction.

Keywords: HOLLIDAY JUNCTION, HOMOLOGOUS RECOMBINATION, BRANCH MIGRATION