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Structural maturation of HIV-1 reverse transcriptase

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The genome of RNA viruses such as HIV is subject to severe size limitations that result from the chemical instability of the RNA polymer and from biological instability attributed to reliance on low fidelity polymerases. The average size of the RNA virus is only about 9 kB. Genome compression is achieved by reliance on strategies that minimize the size of both the genome and the viral proteome. HIV-1 reverse transcriptase (RT), a critical enzyme of the viral life cycle, undergoes a complex maturation process, required so that a pair of p66 precursor proteins can develop conformationally along different pathways, one evolving to form active polymerase and ribonuclease H (RH) domains, while the second forms a non-functional polymerase and a proteolyzed RH domain. These parallel maturation pathways rely on the structural ambiguity of a metamorphic polymerase domain, for which the sequence-structure relationship is not unique. This strategy thus allows formation of two alternate structures, each fulfilling a different function, from a single gene sequence. Alternate strategies more commonly encountered involve utilization of symmetric multimers, as in the case of HIV-1 protease, and reliance on multi-functional proteins, also true of RT. Recent progress toward unraveling the general features of the maturation pathway has been made using a combination of crystallographic, nuclear magnetic resonance, and molecular modeling approaches. The structure of the monomeric p66 precursor was obtained by deletion of a loop required for the metamorphic conversion, in effect introducing an isomerization-restriction mutation. Structural maturation involves three major steps: Domain rearrangement; dimerization and; subunit-selective RH domain proteolysis. I will summarize the major structural changes that occur during the maturation process, and describe how mutations, often viewed within the context of the mature RT heterodimer, can exert a major influence on maturation and dimerization. Several steps in the RT maturation pathway may provide attractive targets for future drug development.

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Framework structure of porous crystalline materials

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A great interest has been raised during the last years concerning gas storage in porous crystalline materials. Consequently, the synthesis of metal organic frameworks (MOFs), Prussian blue analogues (PBAs), nitroprussides (NPs), perovskites (PEs) and other porous crystalline materials along with their structural characterization and the investigation of their adsorption properties became a significant field in materials science. In this regard, metal-organic frameworks (MOFs) are materials consisting of metal nodes and organic spacers, showing permanent porosity while, transition metal cyanides display structures assembled with transition metals, attached through the linear cyanide, the basic component of the structure of PBAs is the linear, $-M' - C \equiv N - M - N \equiv C - M' -$ chain; NPs are a group of metal cyanides, consisting of micro porous frameworks that assembled from [Fe(CN)5NO]2- units, bridged through M2+ cations by means of the CN- ligands. Finally, PEs are oxides possessing analogous structures with a general formula ABO3, where A is a cation larger in size than B, both enclosed in a close-packed perovskite cubic structure, in which the center of the cube is occupied by the A cation. Hence, the key question reported in this talk is how the structure of these materials is elucidated? To carry out this task these materials were studied with SEM, EDAX, IR and Raman spectrometry, TGA, X-ray diffraction, magnetic measurements and low and high pressure carbon dioxide adsorption. As a result, using the XRD data along with the Pawley and Rietveld methods and using the Bruker DIFFRACplus TOPAS™ software package, the structures were elucidated, taking into account the literature information provided for similar compounds, and the atomic positions, Wyckoff sites and occupancy factors reported in the international tables for crystallography for the corresponding space group. Finally, the unit cell representation and the corresponding simulated XRD profile corresponding to the tested materials was generated with the software PowderCell-2.4

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