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Title:	Synthesis, characterization, crystal structure and BSA binding studies of two novel copper(II) complexes: [trans-Cu(en)2(H2O)2](p-methoxycinnamate)2 and [trans-Cu(en)2(H2O)2](p-nitrocinnamate)2·2H2O
Authors:	Mandal, S.K. (/jspui/browse?type=author&value=Mandal%2C+S.K.) Khullar, S. (/jspui/browse?type=author&value=Khullar%2C+S.)
Keywords:	Mononuclear copper Ethylenediamine Synthesized
Issue Date:	2013
Publisher:	Elsevier
Citation:	Polyhedron,56, pp. 34-43.
Abstract:	Two mononuclear copper(II) complexes of composition [trans-Cu(en)2(H2O)2](p-methoxy cinnamate)2, 1 and [trans-Cu(en)2(H2O)2](p-nitrocinnamate)2·2H2O, 2 (where en = ethylenediamine) were synthesized by the addition of strong chelating base ethylenediamine to hydrated Cu(II) cinnamates, Cu(p-methoxy/p-nitrocinnamate)2·xH2O in methanol–water mixture. The newly synthesized complexes have been characterized by physicochemical, spectroscopic techniques and X-ray crystallography. The complex 1 crystallizes in the monoclinic crystal system with space group, P21/c and complex 2 crystallizes in the monoclinic crystal system with space group, C2/c. X-ray structure determination revealed ionic structures consisting of one complex cation [trans-Cu(en)2(H2O)2]2+, two p-methoxycinnamate anions in complex 1 while complex 2 consists of one complex cation [trans-Cu(en)2(H2O)2]2+, two p-nitrocinnamate anions and two water molecules of crystallization. The interactions of these complexes with bovine serum albumin (BSA) were investigated using fluorescence spectroscopy. The result of fluorescence titration revealed that the complexes can quench the intrinsic fluorescence of BSA through both static and collisional (dynamic) quenching mechanism. Quenching constant, association binding constant and number of binding sites were calculated by using modified Stern–Volmer and Scatchard equation. Both complexes display good binding propensity to bovine serum albumin protein with $4.07 \times 10^5$ and $1.88 \times 10^5$ M <sup>-1</sup> binding constant value for complexes 1 and 2 respectively, indicating strongest protein-binding ability in complex 1 as compared to 2.
Description:	Only IISERM authors are available in the record.
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