
## WELCOME LETTER

Dear Colleagues and Friends,

We are thrilled to welcome you to the 54rd Annual Meeting of the Brazilian Society of Biochemistry and Molecular Biology (SBBq), at the Majestic Hotel Convention Center in Águas de Lindóia, SP, May 17 to 20, 2025.

SBBq´s annual meeting is one of Brazil's most esteemed scientific events, having been held continuously for over four decades. It is a vital forum for scientific exchange, promoting the advancement of knowledge in Biochemistry, Molecular Biology, and related fields. It also fosters discussions on scientific education and training, as well as consensus positions in the field, contributing towards public policies.

This year, the organizing committee has created an engaging interdisciplinary program that features 8 plenary lectures and 18 symposia led by world-class scientists. These sessions will highlight the latest advancements and current challenges across various research topics in Biochemistry and Molecular Biology. We are also pleased to include policy thinkers who will assess the landscape of science and technology in our country.

We eagerly anticipate your presence in Águas de Lindóia!

**Alicia J. Kowaltowski**

SBBq President



**SBBq**

Av. Prof. Lineu Prestes, 748
Bloco 3 superior, Sala 0367
05508-000 Butantã, São Paulo, SP

Telefone: (011) 3815-5798
e-mail: congress@sbbq.org.br

08606 - Sessão de Cartazes I

## D.11 - Structural Study of the Molecular Chaperone hHSP70A2

**Gustavo de Oliveira [1]**, Carlos Henrique Inácio Ramos[2], Júlio Cesar Borges[1]
[1]Universidade de São Paulo, [2]Instituto de Química, Unicamp- Instituto de Química Unicamp (São Paulo, Brasil)

INTRODUCTION: Molecular chaperones are essential functional proteins for protein quality control (PQC), mainly acting in protein synthesis, folding, and degradation. Among them, hHSP70A2 (human 70 kDa heat shock protein 2) is overexpressed under conditions of thermal and cellular stress. However, its structure and function are still poorly understood, even though it shares high sequential identity with the main inducible human Hsp70 isoform. Therefore, this study aims to obtain and evaluate the solution structure of the recombinant human hHSP70A2 OBJECTIVES: To express, purify, and characterize the recombinant hHSP70A2, a human protein poorly understood in terms of structure and function. MATERIALS AND METHODS: The hHSP70A2 protein was expressed in Escherichia coli BL21(DE3) through pET28a expression vector and purified by two chromatographic steps: nickel ion affinity chromatography and preparative size-exclusion chromatography (pSEC). Protein purity was assessed by SDS-PAGE it was quantified by UV-Vis spectroscopy. The secondary structure of the protein was determined by circular dichroism (CD), and the tertiary structure was evaluated by intrinsic tryptophan fluorescence in the absence and presence of guanidine hydrochloride, to assess whether the protein was obtained folded. DISCUSSION AND RESULTS: The protein was expressed, purified, and obtained in a folded state, as can be observed by the tryptophan intrinsic fluorescence and CD experiments. CONCLUSION: With the recombinant protein properly structurally characterized, it will be possible to have a more general understanding of its activity and its functionality as a molecular chaperone as well as to compare it to the other human Hsp70s. Therefore, future activity studies can be carried out with this recombinant protein.

**Keywords:** Chaperones molecular,, hHSP70A2., Hsp70
**Supported by:** CAPES,FAPESP,CNPq

08129 - Sessão de Cartazes II

## D.12 - Expression, Purification, and Initial Characterization of Recombinant EcTI: Insights into Its Serine Protease Inhibitory Activity

**Caio Nobrega Zanotto [1]**, Lucas Pontes Almeida[1], Daniel Pontes Herbst[1], Márcia Bonini Galo[1], Maria Luiza Vilela Oliva[1]
[1]Departamento de Bioquímica, Instituto de farmacologia e biologia molecular (São Paulo, Brasil)

INTRODUCTION: The EcTI protein has previously demonstrated promising results in blocking the proteolytic and signaling activities of various tumor cells, thereby preventing their invasion through the extracellular matrix. Additionally, this inhibitor exhibits a significant antithrombotic effect, prolonging the formation time of both arterial and venous thrombi. Given these dual actions—antitumoral and antithrombotic—evaluating the inhibitory capacity of its recombinant form is a well-founded approach. This reinforces the importance of biodiversity in developing innovative and effective therapeutic strategies for combating both cancer and thrombotic disorders. OBJECTIVES: To express, purify and test the inhibition capacity of the recombinant form of Enterolobium contortisiliquum Trypsin Inhibitor (rEcTI). MATERIALS AND METHODS: The recombinant rEcTI was obtained through heterologous expression in the Escherichia coli SHuffle strain using the pET28a plasmid. It was then purified and characterized based on its inhibitory activity against trypsin, using the BAPA substrate. This analysis was performed both in its original form and with the Histidine tag still attached to its molecular structure. DISCUSSION AND RESULTS: The expression of the recombinant form was successful, albeit with a low yield. Both rEcTI and rEcTI-His(6) effectively inhibited trypsin activity, even at low protein concentrations, demonstrating their strong inhibitory potential. CONCLUSION: Our findings demonstrate that rEcTI was successfully expressed in an active state, albeit with a low yield. The recombinant protein, both with and without the histidine tag, exhibited inhibitory capacity against trypsin even at low concentrations, similar to its natural form. Furthermore, its potential inhibition of other serine proteases and its possible effects on coagulation pathways highlight its relevance for future therapeutic applications. Further studies are needed to fully characterize its inhibitory profile and explore its potential in antithrombotic and anticancer strategies.

**Keywords:** EcTI, Inibidor, Proteases
**Supported by:** CAPES