Hellenic Proteomics Society

ItPA Italian Proteomics Association

SePA СРПСКО УДРУЖЕЊЕ ЗА ПРОТЕОМИКУ-SePA

XVII International Italian Proteomics Association Annual Meeting
in partnership with the Hellenic Proteomics Society and Serbian Proteomics Association

Proteomics and Metabolomics towards Global Health

Ospedale Isola Tiberina – Gemelli Isola,
ROMA, ITALY
November 29th -December 1st, 2023

Ospedale Isola Tiberina
GEMELLI ISOLA

UNIVERSITÀ CATTOLICA del Sacro Cuore

Fondazione ItPA onlus
Italian Proteomics Association

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GENERAL INFORMATION

CONFERENCE REGISTRATION FEES

Before October 13th, 2023: ItPA/EuPA member: 170 euroYPI (< 7years /PhD) ItPA/EuPA member: 150euro- After October 13th , 2023: 200 euro

CONGRESS VENUE
Ospedale Isola Tiberina – Gemelli Isola, Via di Ponte Quattro Capi, 39, Roma, Italy

OFFICIAL LANGUAGE
The Congress official language will be English

POSTER PRESENTATIONS AND AWARDS
Posters will be displayed from 30th November to 1st December 2023. During poster sessions the presence of one of the authors is required. Presentations from young corresponding authors will be candidate for poster prize competition. Awards will be supported by European Proteomics associations (EuPA), Waters S.p.A Global Services and Fondazione ItPA Onlus.

CERTIFICATE OF ATTENDANCE
Certificates of attendance and payment fee receipts will be available at the registration desk.

COFFEE BREAKS AND LUNCHES
Welcome cocktail, coffee breaks and lunches will beserved at the venue.

CONFIRMED INVITED SPEAKERS

JEAN ARMENGAUD, Université Paris-Saclay, CEA, INRAE, Département Médicaments et Technologies pour la Santé (DMTS), (Bagnols-sur-Cèze, France)

TANJA CIRKOVIC VELICKOVIC, University of Belgrade, Belgrade, Serbia

HEEYOUN HWANG, Korean Basic Science Institute, (Cheongju-si, South Corea)

JANNE LETHIO**,** Science for Life Laboratory and Department of Oncology and Pathology, Karolinska Institutet, Stockholm, Sweden.

P-30 Redox status of critical disulfides of SARS-CoV-2 receptor-binding-domain exposed to bioactive chomophore phycocyanobilin

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The emergence of the novel coronavirus SARS-CoV-2 has attracted the attention of the whole scientific community. However, as there are significant concerns regarding the effectiveness of vaccines and drugs against novel SARS-CoV-2 variants, naturally derived broad-spectrum of antivirals seems to be precious adjuvant agents to assist in combat against this disease. Phycocyanobilin (PCB) is an open-chain tetrapyrrole chromophore of phycocyanin (PC), chromoprotein derived from Spirullina, with strong anti-oxidative action. The role of disulfide bonds and thiol-disulfide balance in RBD is considered to play a significant role in the binding of S protein to ACE2 receptor. In RBD, in contrast to C480–C488 disulfide, which is thermodynamically stable, C379–C432 and C391–C525 disulfides are in dynamic equilibrium with their thiol states and, thus these two pairs of disulfides are more sensitive to changes in redox poise. Our study aimed to investigate impact of PCB on disulfide balance of RBD by redox proteomics and to investigate structural changes in the protein exposed to PCB. The effect of PCB on RBD secondary structures was examined by far-UV CD spectroscopy after titration of RBD with increasing concentrations of PCB. The presence of PCB had a pronounced effect on the spectral shape. RBD is dominantly composed of random coils and β-sheets. In the presence of PCB a slight increase of α-helical and random coils content, while the content of β-sheets and β-turns is decreased. Mapping redox-active disulfides and reactive cysteines in recombinant SARS-CoV-2 RBD was done using redox proteomics on both recombinant RBD and PCB-exposed RBD. A mass shift caused by alkylation of free Cys residues was detected on three Cys residues demonstrating disulfides C379–C432 and 432-391 to be semi-stable in both RBD and PCB-exposed RBD. Our results demonstrate that RBD exposed to PCB undergo structural changes but does not change the redox state of its critical semi-stable disulfides.
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