

UČNI NAČRT PREDMETA / COURSE SYLLABUS

Predmet:	Proteomika
Course title:	Proteomics

Študijski program in stopnja Study programme and level	Študijska smer Study field	Letnik Academic year	Semester Semester
Nanoznanosti in nanotehnologije, 3. stopnja	Bioznanosti	1	1
Nanosciences and Nanotechnologies, 3 rd cycle	Biosciences	1	1

Vrsta predmeta / Course type Izbirni / Elective

Univerzitetna koda predmeta / University course code: NANO3-828

Predavanja Lectures	Seminar Seminar	Vaje Tutorial	Klinične vaje work	Druge oblike študija	Samost. delo Individ. work	ECTS
15	15			15	105	5

**Navedena porazdelitev ur velja, če je vpisanih vsaj 15 študentov. Drugače se obseg izvedbe kontaktnih ur sorazmerno zmanjša in prenese v samostojno delo. / This distribution of hours is valid if at least 15 students are enrolled. Otherwise the contact hours are linearly reduced and transferred to individual work.*

Nosilec predmeta / Lecturer: Prof. dr. Marko Fonović

Jeziki / Languages: **Predavanja / Lectures:** Slovenščina, angleščina/ Slovenian, English
Vaje / Tutorial: Slovenščina, angleščina/ Slovenian, English

Pogoji za vključitev v delo oz. za opravljanje študijskih obveznosti:

Poznavanje osnov biokemije in biokemijskih analitskih metod, pridobljenih na dodiplomskih študijih biokemije, kemije, biologije ali farmacije.

Prerequisites:

Knowledge of biochemistry and biochemical analytical methodology, acquired in undergraduate courses of biochemistry, chemistry, biology or pharmacy.

Vsebina:

Metode ločevanja proteinov: priprava vzorca, PAGE, 2D-PAGE, DIGE, HPLC, MudPIT, afinitetna kromatografija
Masna spektrometrija: osnove masne spektrometrije, vrste in komponente masnih spektrometrov, MALDI, ESI, CID, ETD, ECD
Kvantitativna proteomika: ICAT, SILAC, iTRAQ, absolutna kvantifikacija
Bioinformatika: statistična obdelava podatkov, proteinske in genomske podatkovne baze, algoritmi za identifikacijo MS/MS spektrov, "de novo" sekveniranje
Proteomika in reševanje bioloških problemov: "top down" in "bottom up" pristop,

Content (Syllabus outline):

Protein separation techniques: sample preparation, PAGE, 2D-PAGE, DIGE, HPLC, MudPIT, affinity chromatography.
Mass spectrometry: basic principles of mass spectrometry, types and components of mass spectrometers, MALDI, ESI, CID, ETD, ECD.
Quantitative proteomics: ICAT, SILAC, iTRAQ, absolute quantification
Bioinformatics: statistical data evaluation, protein and genomic databases, identification of MS/MS spectra, "de novo" sequencing
Proteomics and biology: "top down" and "bottom up" approach, protein posttranslational modifications, protein complexes, biomarkers.

posttranslacijske modifikacije proteinov, proteinski kompleksi, biomarkerji

Temeljni literatura in viri / Readings:

Principles of Proteomics (Advanced Text Series) [R. M. Twyman](#), BIOS Scientific Publ, 2013.

Protein analysis by shotgun/bottom-up proteomics. Y. Zhang, B.R. Fonslow, B. Shan, M.C. Baek, J.R. Yates. Chem Rev. 2013 Apr 10;113(4):2343-94.

Proteomics in Practice: A Guide to Successful Experimental Design, [R. Westermeier](#), [T. Naven](#), [H. R. Höpker](#), Wiley-VCH, 2008.

Computational Methods for Mass Spectrometry Proteomics, [I. Eidhammer](#), [K. Flikka](#), [L. Martens](#), [S. O. Mikalsen](#), Wiley-Interscience, 2008.

Cilji in kompetence:

Splošne kompetence:

- obvladanje raziskovalnih metod in postopkov, razvoj kritične in samokritične presoje,
- sposobnost uporabe znanja v praksi,
- razvoj komunikacijskih sposobnosti in spretnosti, posebej komunikacije v mednarodnem okolju,
- kooperativnost, delo v skupini (in v mednarodnem okolju)

Predmetnospecifične kompetence:

Študent se bo seznanil s teoretičnimi osnovami proteomike in z njeno uporabo v biomedicinskih raziskavah. Pri svojem delu bo uporabljal najnovejšo tujo strokovno literaturo, kar bo izboljšalo njegove sposobnosti uporabe tujega jezika in kritičnega pogleda na objavljeno raziskovalno delo.

Objectives and competences:

General Competences:

- the student will master research methods and procedures and develop skills for critical assessment of his activities,
- the student will be able to put his knowledge into practice,
- the student will develop communications skills to present research achievement in the international environment,
- training for team work (in international environment)

Course Specific Competences:

Student will learn theoretical background of proteomics and its application in biomedical research. During his study he will use the newest scientific literature, which will improve his foreign language skills and his ability to critically view the published research.

Predvideni študijski rezultati:

Osvojitev osnovnih principov proteomike in z njo povezane instrumentacije, kamor sodi poznavanje tehnik priprave vzorca, metod za separacijo proteinov in razumevanje delovanja masnih spektrometrov. Razumevanje osnovnih programskih orodij in algoritmov za statistično obdelavo masno spektroskopskih podatkov in njihovo uporabo za iskanje po proteinskih in genomskih bazah podatkov. Pregled nad različnimi pristopi k reševanju biomedicinskih raziskovalnih problemov s pomočjo proteomike.

Intended learning outcomes:

Understanding of the basic principles of proteomics, such as sample preparation, protein separation and general knowledge of mass spectrometry instrumentation. Understanding of the software tools for statistical evaluation of mass spectrometry data and its application in protein and genomic database searches. Overview of proteomic approaches toward solving of various biomedical scientific problems.

Metode poučevanja in učenja:

Predavanja/konzultacije in seminar

Learning and teaching methods:

Lectures/consultations and seminar work

Načini ocenjevanja:

- seminar
- ustni izpit

Delež (v %) /

Weight (in %)

Assessment:

- seminar
- oral exam

Reference nosilca / Lecturer's references:

VIZOVIŠEK, Matej, VIDMAR, Robert, VAN QUICKELBERGHE, Emmy, IMPENS, Francis, ANDJELKOVIĆ, Uroš, SOBOTIČ, Barbara, STOKA, Veronika, GEVAERT, Kris, TURK, Boris, FONOVIĆ, Marko. Fast profiling of protease specificity reveals similar substrate specificities for cathepsins K, L and S. *Proteomics*, ISSN 1615-9853. [Print ed.], 24 str., doi: 10.1002/pmic.201400460 .

MIKHAYLOV, Georgy, KLIMPEL, D., SCHASCHKE, Norbert, MIKAC, Urška, VIZOVIŠEK, Matej, FONOVIĆ, Marko, TURK, Vito, TURK, Boris, VASILJEVA, Olga. Selective targeting of tumor and stromal cells by a nanocarrier system displaying lipidated cathepsin B inhibitor. *Angewandte Chemie*, ISSN 1433-7851. [Print ed.], 2014, vol. 53, no. 38, str. 10077-10081, doi: 10.1002/anie.201402305.

PEČAR FONOVIĆ, Urša, JEVNIKAR, Zala, ROJNIK, Matija, DOLJAK, Bojan, FONOVIĆ, Marko, JAMNIK, Polona, KOS, Janko. Profilin 1 as a target for cathepsin X activity in tumor cells. *PLoS one*, ISSN 1932-6203, 2013, vol. 8, iss. 1, str. 1-9, e53918.

<http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0053918>, doi: 10.1371/journal.pone.0053918 .

ZHANG, Jun, FONOVIĆ, Marko, SUYAMA, Kaye, BOGYO, Matthew, SCOTT, Matthew P. Rab35 controls actin bundling by recruiting fascin as an effector protein. *Science*, ISSN 0036-8075, 2009, vol. 325, no. 5945, str. 1250-1254.

ARASTU-KAPUR, Shirin, PONDER, Elizabeth L., YEOH, Sharon, PEČAR FONOVIĆ, Urša, YUAN, Fang, FONOVIĆ, Marko, GRAINGER, Munira, PHILLIPS, Carolyn Ines, POWERS, James P., BOGYO, Matthew. Identification of proteases that regulate erythrocyte rupture by the malaria parasite Plasmodium falciparum. *Nature chemical biology*, ISSN 1552-4450, 2008, vol. 4, no. 4, str. 203-213.