

**UČNI NAČRT PREDMETA / COURSE SYLLABUS**

<b>Predmet:</b>	Sodobne računalniške metode v biokemiji
<b>Course Title:</b>	Contemporary computational methods in biochemistry

Študijski program in stopnja Study Programme and Level	Študijska smer Study Field	Letnik Academic Year	Semester Semester
UŠP Kemijske znanosti, 3. stopnja	Biokemija	1.	1. in 2.
USP Chemical sciences, 3 <sup>rd</sup> Cycle	Biochemistry	1 <sup>st</sup>	1 <sup>st</sup> and 2 <sup>nd</sup>

**Vrsta predmeta / Course Type:** izbirni predmet/elective course

**Univerzitetna koda predmeta / University Course Code:** KZ324

Predavanja Lectures	Seminar Seminar	Vaje Tutorial	Klinične vaje Work	Druge oblike študija	Samost. delo Individual Work	ECTS
15	30			60	45	5

**Nosilec predmeta / Lecturer:** izr. prof. dr. Marko Novinec / Dr. Marko Novinec,  
Associate Professor

**Jeziki / Languages:** **Predavanja / Lectures:** slovenski / Slovenian  
**Vaje / Tutorial:** slovenski / Slovenian

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

Študent oz. kandidat mora imeti predmet opredeljen kot študijsko obveznost.

**Prerequisites:**

The course has to be assigned to the student.

**Vsebina:**

Predmet obravnava sodobne metode in pristope za računalniško analizo proteinov, nukleinskih kislin, molekularne evolucije in interakcij med biološkimi molekulami. Vključene so tako metode za bioinformatično analizo baz podatkov kot metode za analizo eksperimentalnih podatkov. Poudarek je zlasti na najsodobnejših in naprednih metodah, ki so bile razvite v zadnjih letih oz. se še intenzivno razvijajo in zato še niso vključene v učbenike ali v predmetnike nižjih stopenj. Študenti bodo spoznali teoretične podlage metod, preko individualnega projektnega dela pa tudi njihovo uporabo.

**Content (Syllabus outline):**

The course discusses contemporary methods and approaches used for computational analysis of proteins, nucleic acids, molecular evolution and biomolecular interactions. It focuses on bioinformatics methods for database analyses as well as computational methods for the analysis of experimental data. The major focus is on novel and advanced methods developed in the past several years and methods that are still under intensive development and are therefore not included in standard textbooks or undergraduate courses. Students will learn the theoretical background of these methods and learn to use them through individual project work.

**Temeljna literatura in viri / Readings:**

Ustrezna znanstvena literatura s področja vsebine predmeta, ki se vsako leto posodobi. /  
Appropriate scientific literature related to the course syllabus, updated annually.

**Cilji in kompetence:**

Študenti bodo spoznali sodobne računalniške metode za analizo biokemijskih podatkov in bodo znali te metode uporabiti pri svojem raziskovalnem delu.

**Objectives and Competences:**

Students will become familiar with contemporary computational methods for the analysis of biochemical data and will learn to use them in their own research work.

**Predvideni študijski rezultati:**Znanje in razumevanje

Študenti bodo spoznali teoretične podlage novih metod in se naučili kdaj in kako posamezno metodo uporabiti ter kako interpretirati podatke.

Uporaba

Poznavanje najsodobnejših metod bo študentom omogočilo njihovo uporabo pri svojem raziskovalnem delu.

Refleksija

Osvojeno znanje bodo znali povezati s predhodno pridobljenim, predvsem z znanjem vezanim na lastno raziskovalno delo.

Prenosljive spretnosti

Uporaba računalnika in računalniških metod, interpretacija rezultatov, iskanje po bazah podatkov in literature.

**Intended Learning Outcomes:**Knowledge and Comprehension

Students will learn the theoretical background of novel methods and learn when and how to use these methods and how to interpret the results.

Application

Students will be able to apply contemporary computational methods in their research work.

Analysis

Students integrate new knowledge with prior knowledge, especially in the light of their own research work.

Skill-transference Ability

Use of computers and computational methods, interpretation of results, database and literature mining .

**Metode poučevanja in učenja:**

Predavanja, konzultacije, seminarske naloge

**Learning and Teaching Methods:**

Lectures, consultations, seminar work

Delež (v %) /

**Načini ocenjevanja:**

Weight (in %) **Assessment:**

Projektno delo	<b>50</b>	Project work
Seminarska naloga	<b>50</b>	Seminar work

**Reference nosilca / Lecturer's references:**

NOVINEC, Marko, KORENČ, Matevž, CAFLISCH, Amedeo, RANGANATHAN, Rama, LENARČIČ, Brigita, BAICI, Antonio. A novel allosteric mechanism in the cysteine peptidase cathepsin K discovered by computational methods. Nature communications, ISSN 2041-1723, feb. 2014, vol. 5, art. no. 3287 (str. 1-10) [COBISS.SI-ID 1678895]  
NOVINEC, Marko, LENARČIČ, Brigita, BAICI, Antonio. Probing the activity modification space of the cysteine peptidase cathepsin K with novel allosteric modifiers. PloS one, ISSN 1932-6203, 2014, vol. 9, no. 9, art. no. e106642 (str. 1-11 [COBISS.SI-ID 1767215]

NOVINEC, Marko, KORDIŠ, Dušan, TURK, Vito, LENARČIČ, Brigita. Diversity and evolution of the thyroglobulin type-1 domain superfamily. *Molecular biology and evolution*, ISSN 0737-4038, 2006, vol. 23, str. 744-755. [COBISS.SI-ID 19851815]