

NAME OF THE COURSE		Molecular Genetics				
Code	PMB545	Year of study	2.			
Course teacher	Ivica Šamanić, Ph.D. Assistant Professor of Faculty of Science, University of Split	Credits (ECTS)	3,5			
Associate teachers		Type of instruction (number of hours)	L	S	E	F
			30	15		
Status of the course	Obligatory	Percentage of application of e-learning	10%			
COURSE DESCRIPTION						
Course objectives	The course covers a range of basic topics of molecular genetics including the concept of the gene, transcription, translation, regulation of gene expression and replication. The course takes a genomics centered approach and covers many of the latest methodologies used in genomics analysis. The course also covers both prokaryotic and eukaryotic systems, taking a historical and methodological approach with the aim of providing insight into how understanding was obtained through experimentation and discovery.					
Course enrolment requirements and entry competences required for the course	Fundamental knowledge of molecular biology and genetics are required.					
Learning outcomes expected at the level of the course (4 to 10 learning outcomes)	<p>By the end of this course students will be able to:</p> <ul style="list-style-type: none"> <li>• explain what genes are and how they function, clarify the mechanisms of information flow, from genes to proteins, and how these processes are regulated</li> <li>• explain DNA replication in bacteria, plasmids, transposable elements, as well as eukaryotic organelles and the nucleus</li> <li>• understand the molecular mechanisms related to gene expression at the transcriptional level, with an emphasis on eukaryote</li> <li>• extract information from genomic databases and perform DNA sequence analyses using online bioinformatics tools.</li> <li>• critically examine research reports and publications dealing with molecular genomics</li> <li>• give oral presentation of scientific facts</li> </ul>					
Course content broken down in detail by weekly class schedule (syllabus)	<p><b>Lectures</b> (30 hours)</p> <ol style="list-style-type: none"> <li><b>1. Genome structure and organization;</b> genome size, introns and exons, genome structure of viruses and prokaryotes, genome organization of cellular organelles, organization of nuclear DNA in eukaryotes</li> <li><b>2. Genome Replication</b></li> <li><b>3. Operon model for the regulation of gene expression in prokaryotes</b></li> <li><b>4. Eukaryotic Transcriptional and Post-Transcriptional Gene Expression Regulation</b></li> <li><b>5. Functional diversity of RNA;</b> short non-coding RNA (snRNA, snoRNA, scaRNA, tRNA, miRNA, piRNA, siRNA), long non-coding RNA (nuclear lncRNA, cytoplasmic lncRNA)</li> <li><b>6. Functional genomics;</b> Gene expression at the biochemical, cellular and organism level, Forward Genetics, Reverse Genetics</li> <li><b>7. Translation and post-translational modifications</b></li> <li><b>8. Plasmids;</b> F plasmid conjugative DNA transfer, Ti plasmid as a vector for plant transformation</li> </ol>					

	<p><b>9. Mobile genetic elements;</b> retrotransposons and DNA transposons  <b>10. Comparative genomics;</b> gene duplication, pseudogenes and retrogenes, molecular phylogeny, Orthologous and paralogous genes  <b>11. Next-generation sequencing methods;</b> Sequencing strategies and the shotgun method, Massive parallel sequencing and its applications parallel sequencing, overview of next-generation sequencing platforms  <b>12. Mutations and DNA repair</b>  <b>13. Biological functions of site-specific recombination;</b> prophage insertion (Integration and excision of bacteriophage <math>\lambda</math>), genetic inversion  <b>14. Methods of modifying genes in eukaryotic cells;</b> Lipofection (or liposome transfection), Precise genome editing by homologous recombination, Genome editing with site-specific nucleases (zinc finger nucleases, TALEN, and CRISPR-Cas systems)  <b>15. Therapeutic genome editing strategies – genetic engineering to cure disease;</b> RNA-based therapeutic, Mitochondrial replacement therapy (MRT)</p> <p><b>Seminars</b> (15 hrs)  Reading and discussing scientific literature, writing a short essay summarizing analyzed articles in the context of the relevant genomic results. It will be additional reading from the sources that the textbook does not cover in sufficient detail since genomics is a rapidly changing field. The aim is to develop writing skills and presentation skills needed to effectively communicate the purpose, scope, and conclusions of the project.</p> <p>Practical application of computers in the analysis of biological data.</p> <p>The computational lab is an essential component of this course where students will be trained to use online tools and databases for sequence alignment, gene expression analysis and genome-scale data.</p>					
Format of instruction	<input checked="" type="checkbox"/> lectures <input checked="" type="checkbox"/> seminars and workshops <input type="checkbox"/> exercises <input type="checkbox"/> <i>on line</i> in entirety <input checked="" type="checkbox"/> partial e-learning <input type="checkbox"/> field work		<input checked="" type="checkbox"/> independent assignments <input type="checkbox"/> multimedia <input type="checkbox"/> laboratory <input type="checkbox"/> work with mentor <input checked="" type="checkbox"/> computational lab			
Student responsibilities						
Screening student work ( <i>name the proportion of ECTS credits for each activity so that the total number of ECTS credits is equal to the ECTS value of the course</i> )	Class attendance	0,5	Research		Practical training	1
	Experimental work		Report		(Other)	
	Essay		Seminar essay	1	(Other)	
	Tests		Oral exam		(Other)	
	Written exam	1	Project		(Other)	
Grading and evaluating student work in class and at the final exam	<p>Methods of Evaluation</p> <ul style="list-style-type: none"> <li>Computational tasks - Hands On: Gene Structure/Bioinformatics Project</li> </ul> <p>The evaluation of this section is carried out by a practical test at the computer lab. In this exam session, the student must perform bioinformatic analysis of genomic data using web and software based approaches; using bioinformatics tools, students analyze unknown complementary sequence of a DNA molecule (cDNA) and expected to identify the gene and organism to which it belongs. In addition,</p>					

	<p>they will demonstrate the process of aligning multiple DNA sequences using a sequence analysis tool and determine the differences in their sequence.</p> <ul style="list-style-type: none"> <li>• Research-based class seminar will be elevated.</li> </ul> <p>Students will have to prepare presentation showing background of the problem they are dealing with. The presentation will be scored according to the content of the presentation (key words, critical review of literature, presentation of scientific results), format, innovativeness and language competence as well.</p> <ul style="list-style-type: none"> <li>• Class Participation will also be part of the grade.</li> <li>• Final Lecture Exam: written examination (multiple-choice questions from the presentation material).</li> </ul> <p>Final grades will be based on each student's performance as assessed by points total.</p>		
Required literature (available in the library and via other media)	<b>Title</b>	<b>Number of copies in the library</b>	<b>Availability via other media</b>
	1. Cooper, G.M., Hausman, R.E., 2015: Stanica-molekularni pristup. Šesto izdanje, Medicinska naklada, Zagreb 2015.		
Optional literature (at the time of submission of study programme proposal)	<p>Strachan, Tom &amp; Read, Andrew - Human Molecular Genetics-Garland Science (2019)          Jocelyn E. Krebs, Elliott S. Goldstein, Stephen T. Kilpatrick - Lewin's Genes XII-Jones &amp; Bartlett (2018)</p>		
Quality assurance methods that ensure the acquisition of exit competences	Student evaluation		
Other (as the proposer wishes to add)			