

<b>Course name:</b> Genomics, Transcriptomics and Proteomics	<b>Credits:</b> 5 ECTS
<b>Class type:</b> On-line lectures + individual practice	<b>Hours per week:</b>
<b>Type of the exam:</b> Project work	
<b>Prerequisites</b> (if exist): basic biochemistry and molecular biology.	
<b>Course description:</b> Familiarity with Internet sources for genome-wide data; basic skills in using tools at these web sites; understanding how modern high-throughput methods generate sequence data and gene and protein expression data; practical skill of using genome browsers to access genome data and genome comparison data; understanding gene prediction and genome annotation pipelines; skill of performing individual gene predictions; understanding different levels of variation in human genomes; understanding basic workflows of microarray data analysis and next-generation sequencing data analysis; basic knowledge of experimental methods in proteomics and metabolomics which enables understanding data analysis in these fields; skill of identifying proteins from mass spectroscopic data.	
<b>Required reading:</b>	
<b>Recommended reading:</b> Campbell, A.M. & Heyer L.J. (2006) Discovering Genomics, Proteomics and Bioinformatics, 2nd ed.. Benjamin Cummings Press	
<b>Lecturer</b> ( <i>name, position, degree</i> ): Attila Csikász-Nagy, associate professor, PhD	
<b>Additional lecturers</b> , if exist:	