***Curriculum vitae*: Fran Supek.**

Researcher ID: orcid.org/0000-0002-7811-6711
Date of birth: 29/03/1981 **Citizenship:** Croatian **Residence**: Spain
Personal profiles: Google Scholar, ImpactStory, Twitter @FranSupek
Lab web site: https://www.GenomeDataLab.org/ and Twitter @GenomeDataLab
Languages: English, Croatian, Spanish. Basic knowledge of German and Catalan.

EDUCATION

2004 – 2010 PhD degree, Molecular and cellular biology program, at the Faculty of Science and Mathematics, University of Zagreb, Croatia. Supervisor: Tomislav Smuc; Laboratory for Information Systems (LIS), Rudjer Boskovic Institute (RBI), Zagreb. *LIS is a computer science group, that conducts research on applications of machine learning algorithms to the life sciences.*

1998 – 2004 BSc and Master (integrated) in Molecular Biology. Division of Biology, Univ. of Zagreb, Croatia.

Major courses: "*Science and the Web: from theory to implementation*" (MedILS, Split, Croatia, 2008). "*CRG Bio-business School*" (CRG, Barcelona, 2014). "*Leading for success in science*" (*hpf* consulting, 2017).

CURRENT POSITIONS

11/2018 – … **ICREA (Catalan Institution for Research and Advanced Studies)** Research Professor. Tenured.

04/2017 – … Group Leader, Genome Data Science lab, Cancer Science program, **Institute for Research in Biomedicine (IRB)**, Barcelona, Spain. *(promoted to senior GL in 2021)*

PREVIOUS POSITIONS

2014 – 2017 Research associate (dual affiliation, see below): permanent position. Laboratory for Information Systems, **Rudjer Boskovic Institute** (**RBI**), Zagreb, Croatia.

2013 – 2016 Postdoc (dual affiliation with RBI permanent position, see above). Genetic Systems Group, PI: Ben Lehner, EMBL/CRG Systems Biology Unit, **Centre for Genomic Regulation** (**CRG**), Bcn, Spain.

2010 – 2012 Postdoctoral fellow, joint appointment to labs: Ben Lehner, Toni Gabaldón. CRG, Barcelona, Spain

2004 – 2010 Early-stage researcher (PhD student). Group Tom Smuc; Division of Electronics, RBI, Zagreb.

FELLOWSHIPS AND AWARDS

2020 – 2024 EMBO YIP (Young Investigator Programme) member. *(acceptance rate <15%)*

2017 – 2018 *Ramon y Cajal* fellowship; tenure-track program by the Spanish government. Ranked 2nd/111 in the category 'Fundamental and Systems Biology'. *(acceptance rate <10%)* Covers 5-yr salary + general funding package. *Note: ended RyC in 2018 voluntarily, due to ICREA.*

2010 – 2012 *Marie Curie* fellowship (INTERPOD interdisciplinary postdocs, co-fund), CRG. (*) 2012 – 2013: an extension of the above M-C fellowship granted.

2008 Croatian National Science Award for Junior Researchers. Awarded by a Parliamentary committee

2004 – 2010 PhD student fellowship by the Croatian Ministry of Science and Education (*top 10% undergrad*)

2003 Award of the Dean of Faculty of Science and Mathematics (U of Zagreb) for exceptional success.

GRANTS RECEIVED

► **Acting as PI or consortium leader:**

- [PI] **ERC Starting Grant** "*HYPER-INSIGHT – Hypermutated tumors: insight into genome maintenance and cancer vulnerabilities provided by an extreme burden of somatic mutations*" (2018 – 2023)
    - 4 full-time researchers (2 postdocs, 1 student and 1 research assistant) for 5 yrs.
- [consortium leader] **CaixaResearch Health** by the charitable foundation of La Caixa, a major Spanish bank. „*POTENT-IMMUNO – Potentiating cancer immunotherapy by inhibiting the NMD quality-control pathway guided by genetic markers*". (2022–2025)
- [PI] **„Plan Estatal" grant by Spanish government**:
    - (2018–2020) salary for 1 research assistant, computer equipment and travel / 3 yrs.
    - (2021–2024) salary for 1 postdoc, 1 PhD student, computer equipment and travel / 3 yrs.
- [PI] **SGR support funding** of the Catalan government 2022-2024.

- [lead] **„iProjekti“ Information technology project**; Croatian Ministry of Science and Education – I have lead teams developing REVIGO & GORBI web tools; published as *PLOS One* & *PLOS CB* papers. (2011–'12)

► **Acting as co-PI, or work-package or task leader:**

- [workpackage leader] **H2020 RIA** "*DECIDER – Improved clinical decisions via integrating multiple data levels to overcome chemotherapy resistance in high-grade serous ovarian cancer*". (2021–2026)
- [task leader] HorizonEurope „LUCIA – Understanding Lung Cancer Related Risk Factors and Their Impact“ (2023–2027)
- [co-PI] Croatian Science Foundation "*AIGEN: Augmented intelligence for prediction, discovery and understanding in genomics and pharmacogenomics*" co-PI, w/Tom Smuc at RBI, Croatia.

► **Institutional core funding to FS:** core funding from IRB Barcelona (covers 3 persons salary+costs), 2017–2026

► **Grant applications approved, project start pending:**

- [PI] ERC Consolidator 2022 Project „*STRUCTOMATIC – Mutational processes and impact of structural variants in human somatic cells*“ (2024–2029)

TEACHING & SUPERVISION ACTIVITIES

2004 – 2006 **Lecturer at course** – Computer science lab (for mol. biology students), 8-12h/week, U of Zagreb. Designed and prepared nearly all teaching material (course started in 2014).

2007 – 2010 **Organizer** of the scientific program at the **S3++ „Summer School of Science“** for high-school students in Višnjan, Croatia. (~50 participants; 10-day program), plus team leader of week-long research workshops for students (comp. chemistry lab and microbiology lab). Volunteer work.

2017 – … **Supervision.** Thesis advisor for 8 PhD students, co-supervisor for 4. Advisor for 4 MSc students.

2014 – … **Career progression of junior researchers**. MSc/PhD students I (co)supervised: 3 have obtained assistant professor or eq. positions (Switzerland, Croatia, Netherlands). Postdocs I supervised: 2 are senior postdocs (Germany, Slovenia), 3 obtained asst. professor (US, Slovenia, Spain).

2020 – … **Serve as mentor** to colleagues via: EMBO YIP program; Max Delbrück Centre “Aspire” program.

INSTITUTIONAL RESPONSIBILITIES

2014 – … Faculty member: RBI, Zagreb, Croatia (to 2017); IRB Barcelona (2017 onwards).

2022 – … PhD student committee, regular member, IRB Barcelona.

2011 – 2013 Founding Member, the Croatian EVO Society for education and science outreach.

2005 – 2007 Department representative in the Graduate students' council (RBI Zagreb, Croatia).

ACTED AS REFEREE FOR

2009 – 2022 journals: *Nature, Nat Cancer*, *Nat Meth*, *Nat Genet*, *Nat Commun*, *Cell, Cell Genomics, PLOS Genet, Genome Biol*, *Genome Res, Mol Biol Evol, PNAS*, *Cell Res*, *NAR, Science Adv,* etc.

2013 – 2022 funding agencies: US Nat'l Science Foundation (NSF), Dutch Cancer Society, Croatian Science Foundation, Nat'l Science Centre Poland, European Research Council (ERC), UK Medical Research Council (MRC), Dutch Research Council (NWO), Worldwide Cancer Research, etc.

ACTIVE COLLABORATIONS

Universitat Pompeu Fabra (UPF), Barcelona, Spain | Centro Nacional de Investigaciones Oncologicas (CNIO), Madrid, Spain | Centre for Genomic Regulation (CRG), Barcelona, Spain | San'Raffaele hospital (HSR), Milan, Italy | Stanford University, California, USA | University of Helsinki, Finland | Ruder Boskovic Institute (RBI), Zagreb, Croatia | RARAF, Columbia University, New York, USA.

INVITED SEMINARS TO INSTITUTIONS (last 4 years)

Friedrich Mischer Institute (FMI), Basel | Ludwig Institute for Cancer Research, Oxford | UCL Genetics Institute - University College London | Center for Quantitative Biology, Peking University | Research Center for Molecular Medicine (CeMM), Vienna | Academic Medical Center, University of Amsterdam | European Oncology Institute (IEO), Milan | San Raffaele Hospital, Milan | Barcelona Supercomputing Centre (BSC) Severo Ochoa Research Seminars | LMS London Institute for Medical Sciences, UK | Gustave Roussy Cancer Institute, Paris.

OUTREACH / SCIENCE COMMUNICATION

2013 – 2015 Jury member for local/national FameLab competitions (organized by British Council)

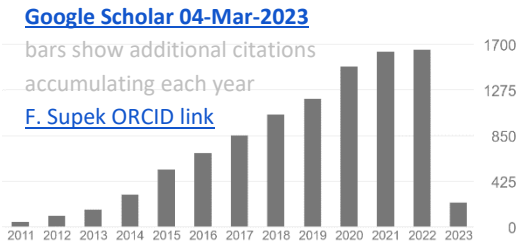
2007 Winner of the SciComm contest FameLab Croatia. Nat'l representative, Cheltenham Science Festival UK.

2007 – 2018 3 x interviews on Croatian nat'l TV (incl. prime-time news); interviews in two largest Croatian newspapers.

Fran Supek: achievement track-record.

Born 1981 (age 41), obtained PhD in 2010, group leader in 2017.

Authored 52 publications (excluding review articles and books), of that: **13** first author (❖), **21** senior or corresponding author (✱), **13** collaborative (•), and **5** consortium (•) publications.



Citations: **total 10,107** (Google Scholar); 6,842 (Scopus). **h-index=32** (Google), 27 (Scopus).

❖ **First-author publications:** 5/13 are in top-10% journals (incl. ***Cell*** [x2], ***Nature***, ***Plos G*** [x2]). Avg. IF_{2021} = 19.2

✱ **Senior-author publications:** 15/21 are in top-10% journals (incl. ***Nature Genetics*** [x3], ***Nature Commun*** [x4], ***Science Adv***, ***Nucleic Acids Res***, ***PLOS Biology***, ***Genome Biol***, ***Nature Cell Biol*** etc.) Average IF_{2021} = 16.5

- Reviews: Additionally, 4 invited review articles, and 2 book chapters. **Manuscripts:** 3 under review.

TEN HIGHLIGHTED PUBLICATIONS in the last 7 years (2016-2023)

✱ Mutational signatures are markers of drug sensitivity of cancer cells. J Levatić, M Salvadores, F Fuster, **F Supek** (2022). ***Nature Comms.*** <Altmetric.com **top 2%** by attention score, compared to articles of same age> ***16 citations, 69 bookmarks.***

We identify robust associations between certain mutational signatures and drug activity across cancer cell line panels; these are as numerous as associations with driver gene alterations. Signatures of prior exposures to DNA damaging agents associate with resistance, while deficient DNA repair tends to sensitize to therapeutics.

✱ TP53-dependent toxicity of CRISPR/Cas9 cuts is differential across genomic loci and can confound genetic screening. M Alvarez, J Biayna, **F Supek** (2022) ***Nature Comms.*** <Altmetric **top 2%**> ***5 c, 36 b***.

Cas9 gene editing involves DNA breaks, which incur a loss of cell fitness. We find Cas9 toxicity is variable depending on the local chromatin environment, with active chromatin, such as regulatory elements or transcription elongation histone marks, predicting increased toxicity. We suggest rules to improve design of CRISPR libraries.

✱ The impact of rare germline variants on human somatic mutation processes. M Vali-Pour, B Lehner*, **F Supek*** (2022) *corr. auth. ***Nature Comms.*** <Altmetric **top 2%**> <featured in Editor's Focus list for Cancer> ***3 c, 47 b***.

Rates and types of somatic mutation vary across individuals, but few inherited influences thereon are known. We perform a gene-based rare variant association study with diverse mutational processes, using ~11k cancer genomes, to identify 42 genes causal to 15 somatic mutational phenotypes incl. HR and MMR deficiencies.

✱ DNA mismatch repair promotes APOBEC3-mediated diffuse hypermutation in human cancers. D Mas-Ponte, **F Supek** (2020). ***Nature Genetics.*** <Altmetric **top 2%**> ***47 citations in Google Scholar. 93 Mendeley bookmarks.***

A novel statistical framework revealed a prevalent type of diffuse hypermutation pattern in cancer genomes, consisting of mutation pairs that likely occurred in a single mutagenic event. These are markers of activity of the APOBEC3A cytosine deaminase facilitated by activity of DNA mismatch repair.

✱ Loss of the abasic site sensor HMCES is synthetic lethal with the activity of the APOBEC3A cytosine deaminase in cancer cells. J Biayna, I Garcia-Cao, […] **F Supek***, T Stracker*. (2021) *corr auth. ***PLOS Biology.*** <Altmetric **top 3%**> ***12 c, 25 b***.

Ongoing hypermutation may present vulnerabilities particular to cancer cells. An experimental approach via CRISPR/Cas9 screens in isogenic cell lines, combined with genomic data analyses, suggested a novel vulnerability of APOBEC3A overexpressing lung cancer cells by inhibiting the HMCES protein.

✱ The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. RGH Lindeboom, M Vermeulen, B Lehner*, **F Supek*** (2019) ***Nature Genetics.*** <Altmetric.com **top 3%** > ***129 c, 260 b.*** (* corr auth)

We predicted whether NMD detects every possible nonsense variant that can occur in the human genome. This suggested that NMD aggravates phenotypes of many genetic diseases. Furthermore, NMD activity upon somatic mutations predicts response to cancer immunotherapy, suggesting benefits of inhibiting NMD.

✱ Matching cell lines with cancer type and subtype of origin via mutational, epigenomic, and transcriptomic patterns. M Salvadores, F Fuster-Tormo, **F Supek** (2020). ***Science Advances***. <Altmetric **top 11%**> ***40 c, 84 b.***

A joint analysis of cancer cell line and tumor genomes, transcriptomes and epigenomes suggests that 7% of common cancer cell lines originate from a different tissue than thought. Another 13% may have diverged substantially from the tumor-of-origin. Accounting for this improves power of drug screening to identify targets.

❖ Clustered Mutation Signatures Reveal that Error-Prone DNA Repair Targets Mutations to Active Genes. **F Supek**, B Lehner (2017) ***Cell.*** <Altmetric **top 1%**> <**f**eatured in *Cancer Discovery* journal>. ***167 c, 364 b.***

A prevalent source of mutations in human tumors is error-prone DNA repair, which employs the low-fidelity DNA polymerase eta, resulting in mutation clustering signatures. This mechanism associates with exposure to diverse mutagenic agents. Both the error-free and error-prone DNA repair are directed towards actively transcribed genes.

✱ The rules and impact of nonsense-mediated mRNA decay in human cancers. RGH Lindeboom, **F Supek***, B Lehner* (2016) ***Nature Genetics.*** (*corresponding authors) <Altmetric **top 7%**> ***344 c, 447 b.***

Matched exome and transcriptome data can systematically elucidate how the quality-control pathway NMD detects mutated transcripts in human cells. Modelling of NMD effects identifies signatures of positive and negative selection on nonsense mutations in tumor suppressor genes and oncogenes in cancer.

✱ The landscape of microbial phenotypic traits and associated genes. M Brbić, M Piškorec, V Vidulin, A Kriško, T Šmuc, **F Supek.** (2016) ***Nucl Acids Res.*** <Altmetric **top 7%** > ***85 c, 141 b.***

We demonstrated a proof-of-concept for automated, text-mining based phenomics: statistical analyses of the scientific literature and other sources such as Wikipedia can be used to systematically annotate particular species with >400 phenotypes, while also proposing the genetic determinants thereof.

MANUSCRIPTS UNDER REVIEW

✱ Prevalence, causes and impact of TP53-loss phenocopying events in human tumors. B Fito-Lopez, M Salvadores, M Alvarez, **F Supek**. (in revision in *BMC Biology*). Preprint on bioRxiv >>> link.

✱ Proton and alpha radiation-induced mutational profiles in human cells. TM Delhomme, M Buonanno, V Grilj, J Biayna, **F Supek**. (in revision in *Scientific Reports*). Preprint on bioRxiv >>> link.

✱ Cell cycle alterations associate with a redistribution of mutation rates across chromosomal domains in human cancers. M Salvadores, **F Supek**. (under review in *Nature Cancer*). Preprint on bioRxiv >>> link.

OTHER FIRST-AUTHOR (❖) OR SENIOR-AUTHOR (✱) PUBLICATIONS in the last 7 years

✱ A framework for mutational signature analysis based on DNA shape parameters.
A Karolak, J Levatić, **F Supek** (2022). ***PLOS One.*** IF = 3.8 (Q2 journal by IF_{2021})

✱ Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers.
S Park*, **F Supek***, B Lehner* (2021). *corresponding authors. ***Nature Commun.*** IF=17.7 (top 10% journal by IF_{2021})

✱ Passenger mutations accurately classify human tumors.
M Salvadores, D Mas-Ponte, **F Supek** (2019). ***PLOS Comp Biol.*** IF=4.8 (Q1)

✱ Loss of G9a preserves mutation patterns but increases chromatin accessibility, genomic instability and aggressiveness in skin tumours. A Avgustinova*, A Symeonidi […] **F Supek***, S Aznar* (2018). *corr. auth. ***Nature Cell Biol.*** IF=28.2 (top 10%)

✱ Patterns of diverse gene functions in genomic neighborhoods predict gene function and phenotype.
M Mihelcic, T Smuc, **F Supek** (2019). ***Sci Rep.*** IF=5.0 (Q2)

✱ Machine learning prioritizes synthesis of primaquine ureidoamides with high antimalarial activity and attenuated cytotoxicity. J Levatić, K Pavić, […], **F Supek***, B Zorc* (2018) ***Eur J Med Chem.*** * corr. auth. IF=8.0 (top 10%)

✱ The evolutionary signal in metagenome phyletic profiles predicts many gene functions.
V Vidulin, T Smuc, S Dzeroski, **F Supek** (2018). ***Microbiome.*** IF=16.8 (top 10%)

✱ Extensive complementarity between gene function prediction methods.
V Vidulin, T Šmuc, **F Supek** (2016) ***Bioinformatics.*** IF=6.9 (top 10%)

COLLABORATIVE PUBLICATIONS (•) in the last 7 years

• Whole genome DNA sequencing provides an atlas of somatic mutagenesis in healthy human cells and identifies a tumor-prone cell type. I Franco, H Helgadottir, A Moggio, … **F Supek**, M Eriksson (2019). ***Genome Biol*** IF=17.9 (top 10%)

• Integrated Analysis of Germline and Tumor DNA Identifies New Candidate Genes Involved in Familial Colorectal Cancer. M Diaz-Gay, S Franch-Exposito, ... **F Supek**, ..., F Balaguer, S Castellvi-Bel (2019). ***Cancers*** IF=6.6 (Q1)

• Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits.
Park S, **F Supek**, B Lehner (2018). ***Nat Commun*** IF= 17.7 (top 10%)

• Elevated rate of genome rearrangements in radiation-resistant bacteria.
J Repar, **F Supek**, T Klanjscek, T Warnecke, K Zahradka, D Zahradka. (2017) ***Genetics*** IF=4.4 (Q2)

• MUFFINN: cancer gene discovery via network analysis of somatic mutation data.
A Cho, JE Shim, E Kim, **F Supek**, B Lehner, I Lee. (2016) ***Genome Biol*** IF=17.9 (top 10%)

CONSORTIUM COLLABORATIVE PUBLICATIONS in the last 7 years

• Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours. B Rodriguez, E Alvarez†, A Baez-Ortega†, J Zamora†, **F Supek †**, […] J Tubio* (2020). († equal contrib) ***Nature Genetics*** **IF=41.3 (top 10%)**

• A synthesis of bacterial and archaeal phenotypic trait data. J Madin, … **F Supek** …, M Westoby (2020) ***Sci Data***. **IF=8.5 (Q1)**

• The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. N Zhou, Y Jiang, ... **F Supek** ... T Salakoski, D Kihara (2019) ***Genome Biol*** **IF=17.9 (top 10%)**

• An expanded evaluation of protein function prediction methods shows an improvement in accuracy.
Y Jiang, TR Oron, WT Clark … **F Supek** … I Friedberg (2016) ***Genome Biol*** **IF=17.9 (top 10%)**

ADDITIONAL PUBLICATIONS PRIOR TO 2016 (✱ ❖ •)

❖ Differential DNA mismatch repair underlies mutation rate variation across the human genome.
F Supek, B Lehner (2015) ***Nature.*** **IF = 69.5 (top 10%)** <Altmetric **top 1%** article by attention score>

✱ Global shifts in genome and proteome composition are very tightly coupled.
M Brbić, T Warnecke, A Kriško, **F Supek** (2015) ***Genome Biol Evol.*** **IF = 4.1 (Q2)**

❖ Synonymous mutations frequently act as driver mutations in human cancers. **F Supek,** […3 more], B Lehner (2014) ***Cell***.

✱ Inferring gene function from evolutionary change in signatures of translation efficiency. A Kriško, […3 more], **F Supek** (2014) ***Genome Biology***.

❖ Hydroxymethylated Cytosines Are Associated with Elevated C to G Transversion Rates. **F Supek***, B Lehner*, P Hajkova*, T Warnecke (2014) ***PLOS Genetics***. *equal contribution.

• Signatures of Conformational Stability and Oxidation Resistance in Proteomes of Pathogenic Bacteria. A Vidović, **F Supek**, A Nikolić, A Kriško (2014) ***Cell Reports***

• J Levatić, S Džeroski, **F Supek**, T Šmuc (2013) ***Informatica***

• P Radivojac, WT Clark, TR Oron, … **F Supek** … I Friedberg (2013) ***Nature Methods***

✱ J Levatić, …, **F Supek** (2013) ***J Med Chem***. **Publication highlighted in F1000Prime.**

✱ N Škunca, M Bošnjak, …, **F Supek** (2013) ***PLOS Comp Biol***

• T Warnecke, **F Supek**, B Lehner (2012) ***PLOS Comp Biol***

❖ **F Supek**, TŠ Ramljak, ... M Kralj (2011) ***Eur J Med Chem***

• K Ester, **F Supek**, ... M Kralj (2011) ***Invest New Drugs***

• Z Smole, N Nikolic, **F Supek**, T Smuc, I Sbalzarini, A Krisko (2011) ***BMC Evol Biol***

❖ **F Supek**, M Bošnjak, N Škunca, T Šmuc (2011) ***PLOS ONE***

• M Gredičak, **F Supek**, [...] Š Horvat (2010) ***Amino Acids***

❖ **F Supek**, T Šmuc (2010) ***Genetics***

❖ **F Supek**, N Škunca, J Repar, K Vlahoviček, T Šmuc (2010) ***PLOS Genetics***

❖ **F Supek**, P Peharec, M Krsnik-Rasol, T Šmuc (2008) ***Proteomics***

❖ **F Supek**, M Kralj, …, B Žinić (2008) ***Invest New Drugs***

• M Marjanović, M Kralj, **F Supek**, […], Lj Tusek-Bozic (2007) ***J Med Chem***.

• I Marinić, **F Supek**, [...], D Kozarić-Kovačić (2007) ***Croat Med J***.

❖ **F Supek**, K Vlahoviček (2005) ***BMC Bioinformatics***

❖ **F Supek**, T Smuc, B Lucic (2005) ***Periodicum Biologorum***

❖ **F Supek**, K Vlahoviček. (2004) ***Bioinformatics***

INVITED REVIEW ARTICLES & BOOK CHAPTERS in the last 7 years

- 2022: invited review article: D Mas-Ponte, M McCullough, **F Supek**. „Spectrum of DNA mismatch repair failures and implications for therapy viewed through the lens of cancer genomics“ ***Clinical Science***.
- 2020: invited review article: **F Supek**, B Lehner, R Lindeboom. „To NMD or Not To NMD: Nonsense-Mediated mRNA Decay in Cancer and Other Genetic Diseases“. ***Trends in Genetics***.
- 2019: invited review article: **F Supek**, B Lehner. „Scales and mechanisms of somatic mutation rate variation across the human genome“, in ***DNA Repair*** journal special edition: Cutting Edge Perspectives in Genomic Maintenance, volume VI.
- 2016: invited review article: **F Supek** „The Code of Silence: Widespread Associations between Synonymous Codon Biases and Gene Function“. ***J Mol Evol***.
- 2016: invited book chapter: **F Supek**, N Skunca. „Visualizing GO annotations“. In: „***The Gene Ontology Handbook***“. Eds. Nives Škunca & Christophe Dessimoz (ETH Zurich, U of Lausanne)

INVITED PRESENTATIONS AT CONFERENCES in the last 7 years

2022: **European Society for Human Genetics** conference, Vienna. | 2021: **EMBL Conference: Cancer Genomics** | 2021: **Belgrade Bioinfo. Conference 2021** (BelBI2021) | 2020: **EMBO Cancer cell signaling**, Cavtat, Croatia (postponed to 2022, due to COVID-19) | 2020: **HIBIT conference**, Istanbul, Turkey | 2019: Workshop on **Models of Evolution**, Barcelona, Spain. | 2018: **European Human Genetics Conference**, June 2018, Milan, Italy. | 2018: **Genomic Regulation 2018**, March 2018, Haute-Nendaz, Switzerland. | 2018: **NGSchool2018** – Next Generation Sequencing school, September 2018, Lublin, Poland. | 2018: **4th Croatian Genetics Congress**, Krk, Croatia. | 2017: **[BC]2 Basel Computational Biology Conference.** | 2016: **summer school** „**Mining Big and Complex Data**“, a MAESTRA event. Ohrid, FYROM. | 2015: **Computational Modelling of Gene Expression and its Evolution** (a CECAM conference). Tel-Aviv. | 2015: school „**Machine Learning and Systems Biosciences**“, JSI, Ljubljana. | 2014: **XXI Jornada de Biologia Molecular**, Barcelona.