

IL PRESENTE ALLEGATO COSTITUISCE UNO SCHEMA-TIPO, NEL QUALE SONO INDICATE ALCUNE VOCI A MERO TITOLO ESEMPLIFICATIVO, PERTANTO PUO' ESSERE MODIFICATO/INTEGRATO DAL CANDIDATO ADATTANDOLO ALLE PECULIARITÀ DELLA PROPRIA ATTIVITÀ SCIENTIFICO-PROFESSIONALE

ALL. B AI FINI DELLA PUBBLICAZIONE

Decreto Rettore Università di Roma "La Sapienza" n 3227/2021 del 02.12.2021

Livia Perfetto Curriculum Vitae

Education

Type	Year	Institution	Notes (Degree, Experience,...)
University graduation	2010	University of Rome 'Tor Vergata'	Master -degree (Laurea Magistrale) in Cellular and Molecular Biology with full honors (110 cum laude/110)
Post-graduate studies	2017	University of Rome 'Tor Vergata'	Level 1 Master's degree with full honors (110 cum laude/110) on "Clinical Research in Hematology and Oncology"
PhD	2015	University of Rome 'Tor Vergata'	PhD in cellular and molecular biology at the University of Rome "Tor Vergata", Thesis: "Exploiting scientific data curation to interpret biological processes: Mining and integrating literature information"

Appointments

Academic Appointments

Start	End	Institution	Position
2014	2016	University of Rome 'Tor Vergata'	Post-doc
2016	2017	University of Rome 'Tor Vergata'	Post-doc (AIRC fellow)
2017	2020	European Bioinformatic Institute (EMBL-EBI)	Staff member (senior curator and bioinformatician)

2020	Present	Fondazione Human Technopole	Scientific Consultant (SIGNOR project leader)
2020	Present	European Bioinformatic Institute (EMBL-EBI)	Visitor Scientist
2021	Present	University of Cambridge	Visitor Scientist
2021	Present	University of Rome 'Tor Vergata'	Teaching assignment

Other Appointments

Start	End	Institution	Position
2021	Present	'Frontiers in Bioinformatics' Editorial Board	Review Editor

Teaching experience

Year	Institution	Lecture/Course
2017-2020	University of Cambridge	Trainer for bioinformatics and systems biology courses.
2017-2020	European Bioinformatic Institute (EMBL-EBI)	Trainer for bioinformatics and systems biology courses.
2020-2021	University of Rome 'Tor Vergata'	Member of the exam commission for the "Systems Biology and physic-Chemistry" and for the "Systems Biology and parasitology" courses (3 CFU, MED03), for the "Bioinformatics" and "Cellular and Molecular Biology" curricula (LM6 DM-270' and LM-6 DM-270).
2021-2022	University of Rome 'Tor Vergata'	Lecturer for the "Molecular Biology" course (6 CFU, BIO/11), for the "Biotechnology" curriculum.

Society memberships, Awards and Honors

Year	Title
2016-2022	Member of the GREEKC consortium (COST action CA15205) (https://www.greekc.org/people/)
2022-Present	Member of the Elixir Systems Biology Focus Group (https://elixir-europe.org/focus-groups/systems-biology/members)
2017	Member of the ISB (International Society of Biocuration)
2010-Present	Member of the HUPO-PSI (Proteomic Standard Initiative) community

2020-Present	Member of the Variopath consortium
2010-Present	Member of the IMEx consortium
2020-Present	Member of the Disease map project
2018	Abilitazione Scientifica Nazionale alle funzioni di professore di II fascia per il Settore concorsuale 05/I1
2017	Abilitazione Scientifica Nazionale alle funzioni di professore di II fascia per il Settore concorsuale 05/F1
2011	5000.00 € Special Prize “Sebastiano and Rita Raeli” .

Funding Information [grants as PI-principal investigator or I-investigator]

Year	Title	Program	Grant value
2015	SIGNOR, a tool for patient stratification and diagnosis in personalized oncology	1 triennial fellowship Starwood Hotels & Resorts (AIRC) selected on a peer-review basis	75000 €

Research Activities

The group that I coordinate is characterized by interdisciplinarity and is made up by the strong cross-talk between a database and a bioinformatics unit. The database unit is devoted to the development, the curation and the maintenance of the SIGNOR database and its related projects to support the scientific community with high-quality and standardised information. The main area of interest of the bioinformatics unit consists in set up of algorithms and computational pipelines that use the existing knowledge annotated in SIGNOR to support a personalised medicine. I here outline current and past research activities, which are further supported by the selected list of publications.

Keywords	Brief Description
protein-protein interactions, curation, ontology development, standard development	<p>I am the coordinator for the curation of causal interactions related to signal transduction in SIGNOR database. SIGNOR is a database that captures signalling interactions between biological entities and is a tool for patient stratification and diagnosis in personalized medicine.</p> <p>I have worked as Physical Molecular interaction (PPI) curator in two of the main IMEx resource: MINT and IntAct databases.</p> <p>Beside my role as a curator in different disciplinary areas I have also pro-actively contributed to standard and ontology development in the field of PMIs and causal interactions having participated to many HUPO PSI-MI (Proteomic Standard Initiative for Molecular Interactions) meetings and been an active member of the IMEx and GREEKC (Gene Regulation Ensemble Effort for the Knowledge Commons) consortiums. I've also extensively collaborated with text miners (within the GREEKC consortium framework and the Biocreative Project), especially in the context of evaluating text mining tools that can support manual curation in a user-friendly curation environment.</p>

Biological Network Analysis, graph theory, modelling approaches	From the beginning of my research I focused on Biological Networks and on the functional insights we can gain from the understanding the networks of physical and causal relationships between proteins. I have explored strategies to extract biologically relevant information from protein interaction networks and from network of logic relationships. Also, I am currently contributing in the development of bioinformatics strategies to combine information annotated in the SIGNOR resource with -omic data (genomic, proteomic, phosphoproteomic and transcriptomic). The scope is building patient-specific models that are both mechanistic (to provide understanding) and predictive (to generate novel hypotheses). I recently applied these strategies in the study of acute myeloid leukaemia (in collaboration with Prof. Sacco, University of Rome Tor Vergata), of haematological disorders (in collaboration with Prof. Ouwehand, University of Cambridge) and in the study of neurodevelopmental diseases (in collaboration with Prof. Testa, Fondazione Human Technopole).
protein families, protein interaction domains	During my PhD, I focused on the role of protein domains in mediating PPIs and key steps in signal transduction. I especially worked in the phylogenetic characterisation of protein domains such as SH3, SPRY and PTP domains, and in the identification of protein-interaction networks mediated by these elements.

Summary of Scientific Achievements

ORCID ID: 0000-0003-4392-8725

Scopus Author ID: 35345635900

Web of Science ResearcherID: AAC-6320-2022

Product type	Number	Data Base	Start	End
Papers [international]	38	Scopus	2009	2022

Total Citations	4772 (source WoS)
Average Citations per Product	125.6 (source WoS)
Hirsch (H) index	18 (source WoS)
Normalized H index*	1.5
Average Impact factor per Publication	9.67 (source WoS)
Hirsch (H) index Last 10 years	16 (source WoS)
Total number of Publications	38 (source WoS)
Total Impact factor	358.101 (source WoS)

*H index divided by the academic seniority.

Selected Publications

De Marinis, I., Lo Surdo, P., Cesareni, G., & **Perfetto, L.**
SIGNORApp: a Cytoscape 3 application to access SIGNOR data
2021. *Bioinformatics* Vol:
10.1093/bioinformatics/btab865 Article. citations: 0; IF of 2021: 6.937

Cesareni G., Sacco F., & **Perfetto L.**
Assembling Disease Networks From Causal Interaction Resources
2021. *Frontiers in Genetics* Vol: 12
10.3389/fgene.2021.694468 Review. citations: 0; IF of 2021: 4.599

Perfetto L., Micarelli E., Iannuccelli M., Lo Surdo P., Giuliani G., Latini S., Pugliese G.M., Massacci G., Vumbaca S., Riccio F., Fuoco C., Paoluzi S., Castagnoli L., Cesareni G., Licata L., Sacco F.
A resource for the network representation of cell perturbations caused by SARS-CoV-2 infection
2021. *Genes* Vol: 12
10.3390/genes12030450 Article. citations: 1; IF of 2021: 4.096

Palma A., Iannuccelli M., Rozzo I., Licata L., **Perfetto L.**, Massacci G., Castagnoli L., Cesareni G., Sacco F.
Integrating patient-specific information into logic models of complex diseases: Application to acute myeloid leukemia
2021. *Journal of Personalized Medicine* Vol: 11
10.3390/jpm11020117 Article. citations: 4; IF of 2021: 4.945

Pugliese G.M., Latini S., Massacci G., **Perfetto L.**, Sacco F.
Combining mass spectrometry-based phosphoproteomics with a network-based approach to reveal flt3-dependent mechanisms of chemoresistance
2021. *Proteomes* Vol: 9
10.3390/proteomes9020019 Review. citations: 0; no IF

Porras P., Barrera E., Bridge A., del-Toro N., Cesareni G., Duesbury M., Hermjakob H., Iannuccelli M., Jurisica I., Kotlyar M., Licata L., Lovering R.C., Lynn D.J., Meldal B., Nanduri B., Paneerselvam K., Panni S., Pastrello C., Pellegrini M., **Perfetto L.**, Rahimzadeh N., Ratan P., Ricard-Blum S., Salwinski L., Shirodkar G., Shrivastava A., Orchard S.
Towards a unified open access dataset of molecular interactions
2020. *Nature Communications* Vol: 11
10.1038/s41467-020-19942-z Article. citations: 12; IF of 2020: 14.919

Perfetto L., Pastrello C., Del-Toro N., Duesbury M., Iannuccelli M., Kotlyar M., Licata L., Meldal B., Panneerselvam K., Panni S., Rahimzadeh N., Ricard-Blum S., Salwinski L., Shrivastava A., Cesareni G., Pellegrini M., Orchard S., Jurisica I., Hermjakob H., Porras P.
The IMEx coronavirus interactome: An evolving map of Coronaviridae-host molecular interactions
2020. *Database* Vol: 2020
10.1093/database/baaa096 Article. citations: 13; IF of 2020: 3.451

Iannuccelli M., Micarelli E., Surdo P.L., Palma A., **Perfetto L.**, Rozzo I., Castagnoli L.,

Licata L., Cesareni G.
CancerGeneNet: Linking driver genes to cancer hallmarks
2020. Nucleic Acids Research Vol: 48
10.1093/nar/gkz871 Article. citations: 7; IF of 2020: 16.971

del-Toro N., Duesbury M., Koch M., **Perfetto L.**, Shrivastava A., Ochoa D., Wagih O., Piñero J., Kotlyar M., Pastrello C., Beltrao P., Furlong L.I., Jurisica I., Hermjakob H., Orchard S., Porras P., Khadake J., Meldal B., Panni S., Thorneycroft D., van Roey K., Abbani S., Salwinski L., Pellegrini M., Iannuccelli M., Licata L., Cesareni G., Roechert B., Bridge A., Ammari M.G., McCarthy F., Broackes-Carter F., Campbell N.H., Melidoni A.N., Rodriguez-Lopez M., Lovering R.C., Jagannathan S., Chen C., Lynn D.J., Ricard-Blum S., Mahadevan U., Raghunath A., IMEx Consortium contributing authors
Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set
2019. Nature Communications Vol: 10
10.1038/s41467-018-07709-6 Article. citations: 26; IF of 2019: 12.121

Perfetto L., Acencio M.L., Bradley G., Cesareni G., Del Toro N., Fazekas D., Hermjakob H., Korcsmaros T., Kuiper M., Lægreid A., Lo Surdo P., Lovering R.C., Orchard S., Porras P., Thomas P.D., Touré V., Zabolas J., Licata L.
CausalTAB: The PSI-MITAB 2.8 updated format for signalling data representation and dissemination
2019. Bioinformatics Vol: 35
10.1093/bioinformatics/btz132 Article. citations: 11; IF of 2019: 5.61

Meldal B.H.M., Bye-A-Jee H., Gajdoš L., Hammerová Z., Horáčková A., Melicher F., **Perfetto L.**, Pokorný D., Lopez M.R., Türková A., Wong E.D., Xie Z., Casanova E.B., Del-Toro N., Koch M., Porras P., Hermjakob H., Orchard S.
Complex Portal 2018: Extended content and enhanced visualization tools for macromolecular complexes
2019. Nucleic Acids Research Vol: 47
10.1093/nar/gky1001 Article. citations: 37; IF of 2019: 11.502

Sacco F., **Perfetto L.**, Cesareni G.
Combining Phosphoproteomics Datasets and Literature Information to Reveal the Functional Connections in a Cell Phosphorylation Network
2018. Proteomics Vol: 18
10.1002/pmic.201700311 Review. citations: 12; IF of 2018: 3.106

Lo Surdo P., Calderone A., Iannuccelli M., Licata L., Peluso D., Castagnoli L., Cesareni G., **& Perfetto L.**
DISNOR: A disease network open resource
2018. Nucleic Acids Research Vol: 46
10.1093/nar/gkx876 Article. citations: 18; IF of 2018: 11.147

Surdo P.L., Calderone A., Cesareni G., **& Perfetto L.**,
SIGNOR: A database of causal relationships between biological entities-a short guide to searching and browsing
2017. Current Protocols in Bioinformatics Vol: 2017
10.1002/cpbi.28 Article. citations: 6; no IF

Perfetto L., Briganti L., Calderone A., Perpetuini A.C., Iannuccelli M., Langone F., Licata L., Marinkovic M., Mattioni A., Pavlidou T., Peluso D., Petrilli L.L., Pirró S., Posca D., Santonico E., Silvestri A., Spada F., Castagnoli L., Cesareni G.
SIGNOR: A database of causal relationships between biological entities
2016. *Nucleic Acids Research* Vol: 44
10.1093/nar/gkv1048 Article. citations: 129; IF of 2016: 10.162

Perfetto L., Gherardini P.F., Davey N.E., Diella F., Helmer-Citterich M., Cesareni G.
Exploring the diversity of SPRY/B30.2-mediated interactions
2013. *Trends in Biochemical Sciences* Vol: 38
10.1016/j.tibs.2012.10.001 Review. citations: 52; IF of 2013: 13.522

Sacco F. & **Perfetto L.**, Castagnoli L., Cesareni G.
The human phosphatase interactome: An intricate family portrait
2012. *FEBS Letters* Vol: 586
10.1016/j.febslet.2012.05.008 Review. citations: 122; IF of 2012: 3.582

Orchard S., Kerrien S., Abbani S., Aranda B., Bhate J., Bidwell S., Bridge A., Briganti L., Brinkman F., Cesareni G., Chatr-Aryamontri A., Chautard E., Chen C., Dumousseau M., Goll J., Hancock R., Hannick L.I., Jurisica I., Khadake J., Lynn D.J., Mahadevan U., **Perfetto L.**, Raghunath A., Ricard-Blum S., Roechert B., Salwinski L., Stümpflen V., Tyers M., Uetz P., Xenarios I., Hermjakob H.
Protein interaction data curation: The International Molecular Exchange (IMEx) consortium
2012. *Nature Methods* Vol: 9
10.1038/nmeth.1931 Review. citations: 334; IF of 2012: 23.565

Carducci M. & **Perfetto L.**, Briganti L., Paoluzi S., Costa S., Zerweck J., Schutkowski M., Castagnoli L., Cesareni G.
The protein interaction network mediated by human SH3 domains
2012. *Biotechnology Advances* Vol: 30
10.1016/j.biotechadv.2011.06.012 Article. citations: 37; IF of 2012: 9.599