

# DAVIDE CORÀ

## CURRICULUM VITAE sintetico

### Contatti:

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### Titoli:

Laurea in Fisica  
Master in Bioinformatica  
Ph.D., in “Sistemi complessi applicati alla biologia post-genomica”

### Posizione attuale:

Professore Associato (s.s.d. BIO/11 - Biologia Molecolare)  
Dipartimento di Medicina Traslazionale,  
Università del Piemonte Orientale.

## AFFILIAZIONI

- Dipartimento di Medicina Traslazionale, Università del Piemonte Orientale.
- Center for Translational Research on Autoimmune & Allergic Diseases – CAAD.
- BITS – Bioinformatics Italian Society.

## ATTIVITA' DIDATTICA FRONTALE

- Corso di “BIOLOGIA MOLECOLARE”, presso corso di Laurea in BIOTECNOLOGIE (48 ore, 6 CFU – sede di Novara).
- Corso di “BIOCHIMICA – BIOLOGIA MOLECOLARE”, presso corso di Laurea Magistrale in MEDICINA E CHIRURGIA (25 ore, 2 CFU – sede di Alessandria).
- Corso di “BIG DATA ANALYSIS”, presso Laurea Magistrale in MEDICAL BIOTECHNOLOGY (30 ore, 5 CFU – sede di Novara).
- Corso di “BIOINFORMATICA E APPROCCI DI SYSTEMS BIOLOGY”, presso Laurea Magistrale in BIOTECNOLOGIE FARMACEUTICHE (24 ore, 3 CFU – sede di Novara)
- Specialità di Genetica Medica – non medici, Scuola di Medicina (Novara).
- Specialità di Microbiologia e virologia – non medici, Scuola di Medicina (Novara).

## SINTESI INTERESSI DI RICERCA

La parte principale della mia attività di ricerca si svolge all'interno della **Bioinformatica e Biologia Computazionale**, ovvero nell'ambito di quell'insieme di studi e ricerche interdisciplinari volte alla definizione delle proprietà degli organismi viventi tramite l'uso di metodi integrati derivanti dalla biologia, matematica, fisica, informatica.

### Keywords:

- Regulatory networks, microRNAs, non-coding DNA.
- Cancer and Plant Genomics.
- Metagenomics.
- AI-driven genomics.

In questi contesti, collaboro con diversi laboratori sperimentali, fornendo competenze computazionali e di analisi dei dati.

PUBBLICAZIONI SU RIVISTE internazionali WOS / SCOPUS

- 1) "Computational identification of transcription factor binding sites by functional analysis of set of genes sharing overrepresented upstream motifs."  
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- 2) "Ab-initio identification of putative human transcription factor binding sites by comparative genomics."  
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- 3) "Correlated fragile site expression allows the identification of candidate fragile genes involved in immunity and associated with carcinogenesis."  
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- 5) "VRG database: a database of Vascular dysfunctions Related Genes."  
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- 6) "Genome-wide survey of microRNA / Transcription Factor Feed-Forward Regulatory Circuits in Human."  
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- 7) "Molecular models for intrastrand DNA G-quadruplexes."  
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- 8) 8) "Nucleation dynamics in 2d cylindrical Ising models and chemotaxis."  
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- 9) "Identification of functional TFAP2A and SP1 binding sites in new TFAP2A modulated genes."  
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- 10) "CircuitsDB: a database of mixed microRNA / Transcription Factor Feed – Forward Regulatory Circuits in human and mouse."  
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- 12) "The role of incoherent microRNA-mediated feedforward loops in noise buffering."  
Osella M., Bosia C., **Corà D.**, Caselle M.  
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- 13) "A curated database of microRNA mediated Feed-Forward loops involving MYC as master regulator."  
El-Baroudi M.\*, **Corà' D.\***, Bosia C., Osella M, Caselle M.  
*PLoS One.* 2011 Mar 3;6(3):e14742.
- 14) "Genetic and expression analysis of MET, MACC1 and HGF in liver metastases from colorectal carcinomas: assessment of response to Met inhibition in patient-derived xenografts and clinicopathological significance."  
Francesco Galimi, Davide Torti, Francesco Sassi, Claudio Isella, **Davide Corà**, Stefania Gastaldi, Dario Ribero, Andrea Muratore, Paolo Massucco, Dimitrios Siatis, Gianluca Paraluppi, Federica Gonella, Francesca Maione, Alberto Pisacane, Ezio David, Bruno Torchio, Mauro Risio, Mauro Salizzoni, Lorenzo Capussotti, Timothy Perera, Enzo Medico, Maria Flavia Di Renzo, Paolo M. Comoglio, Livio Trusolino and Andrea Bertotti.  
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- 16) "A Molecularly Annotated Platform of Patient-Derived Xenografts ("Xenopatients") Identifies HER2 as an Effective Therapeutic Target in Cetuximab-Resistant Colorectal Cancer."  
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- 22) "Molecular and morphologic characterization of superficial- and deep-subcutaneous adipose tissue subdivisions in human obesity."  
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- 23) "MiRNA/gene profiling unveils early molecular changes and NRF2 activation in a rat model recapitulating human HCC."  
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\* indica first or last authorship condivisa