DAVIDE CORÀ

CURRICULUM VITAE sintetico

Contatti:

Dipartimento di Medicina Traslazionale
Università degli Studi del Piemonte Orientale
Via Solaroli 17, I-28100 Novara, Italy.

CAAD - Center for translational research on Autoimmune and Allergic Disease
Via Trieste, 15/A, I-28100 Novara, Italy.

Phone: +39-0321-660631
+39-0321-660841
E-mail: davide.cora@uniupo.it
Web: http://www.to.infn.it/~cora
https://upobook.uniupo.it/davide.cora

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, 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:

- Bioinformatics and Computational Biology.
- 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.”
Cora' D., Di Cunto F., Provero P., Silengo L., Caselle M.
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2) “Ab-initio identification of putative human transcription factor binding sites by comparative genomics.”
Cora' D., Herrmann C, Dieterich C, Di Cunto F., Provero P., Caselle M.
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3) “Correlated fragile site expression allows the identification of candidate fragile genes involved in immunity and associated with carcinogenesis.”
Re A., **Cora' D**., Puliti AM., Caselle M., Sbrana I.
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4) “Identification of candidate regulatory sequences in mammalian 3' UTRs by statistical analysis of oligonucleotide frequencies.”
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5) “VRG database: a database of Vascular dysfunctions Related Genes.”
Zanivan S.*, **Cora' D.***, Caselle M., Bussolno F.
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6) “Genome-wide survey of microRNA / Transcription Factor Feed-Forward Regulatory Circuits in Human.”
Re A.*, **Cora' D.***, Taverna D., Caselle M.
Molecular Biosystems Aug;5(8):854-67, 2009.

7) “Molecular models for intrastrand DNA G-quadruplexes.”
Fogolari F., Haritha Haridas, Alessandra Corazza, Paolo Viglino, **Davide Cora'**, Michele Caselle, Gennaro Esposito and Xodo E
BMC Structural Biology 2009 Oct 7;9(1):64.

8) 8) “Nucleation dynamics in 2d cylindrical Ising models and chemotaxis.”
Bosia C., Caselle M. and **Corà D**.
Phys. Rev. E 81, 021907 (2010).

9) “Identification of functional TFAP2A and SP1 binding sites in new TFAP2A modulated genes.”
Orso F.*, **Corà D.***, Ubezio B., Provero P., Caselle M. and Taverna D.
BMC Genomics. 2010 Jun 3;11:355.

10) “CircuitsDB: a database of mixed microRNA / Transcription Factor Feed – Forward Regulatory Circuits in human and mouse.”
Friard O., Re A., Taverna D., De Bortoli M. and **Corà D**.
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11) “Identity and divergence of protein domain architectures after the Yeast Whole Genome Duplication event.”
Grassi L.,Fusco D., Sellerio A., **Corà D**., Bassetti M., Caselle M., Cosentino-Lagomarsino M.
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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.*, **Cora’ 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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15) “Mulcom: a multiple comparison statistical test for microarray data in Bioconductor.”
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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.”
Andrea Bertotti, Giorgia Migliardi, Francesco Galimi, Francesco Sassi, Davide Torti, Claudio Isella, **Davide Corà**, Federica Di Nicolantonio, Michela Buscarino, Consalvo Petti, Dario Ribero, Nadia Russolillo, Andrea Muratore, Paolo Massucco, Alberto Pisacane, Luca Molinaro, Emanuele Valtorta, Andrea Sartore-Bianchi, Mauro Risio, Lorenzo Capussotti, Marcello Gambacorta, Salvatore Siena, Enzo Medico, Anna Sapino, Silvia Marsoni, Paolo M. Comoglio, Alberto Bardelli, and Livio Trusolino.
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17) “Transcriptional hallmarks of Noonan syndrome and Noonan-like syndrome with loose anagen hair.”
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18) “Dynamic Modeling of miRNA-mediated Feed-Forward Loops.”
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19) “The role of transposable elements in shaping the combinatorial interaction of transcription factors”.
Testori A, Caizzi L, Cutrupi S, Friard O, De Bortoli M, **Cora' D*** and Caselle M.*
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20) “Gene autoregulation via intronic microRNAs and its functions.”
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24) “Association of polyalanine and polyglutamine coiled coils mediates expansion disease-related protein aggregation and dysfunction.”
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Stefania Rosano, **Davide Corà**, Sushant Parab, Claudio Isella, Roberta Porporato, Roxana Maria Hoza, Raffaele A. Calogero, Chiara Riganti, Federico Bussolino, Alessio Noghero.
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*** indica first or last authorship condivisa**