

PERSONAL INFORMATION

Name: Valencia, Alfonso

Researcher unique identifier: ORCID number 0000-0002-8937-6789

Researcher ID: [AAN-9230-2020](#)

Date of birth: August 29th 1959

Nationality: Spanish

URL for website: <https://www.bsc.es/discover-bsc/organisation/scientific-structure/computational-biology>
[@alfons_valencia](https://en.wikipedia.org/wiki/Alfonso_Valencia)

• EDUCATION

1988 Ph.D. in Biochemistry and Molecular Biology, Universidad Autónoma, Madrid, Spain
 1983 M.Sc. in Genetics, Universidad Complutense, Madrid, Spain
 1981 B.Sc. in Biological Sciences, Universidad Complutense, Madrid, Spain

• CURRENT POSITION

2017 - Present Director Life Sciences Department, Barcelona Supercomputing Centre BSC
 2017 - Present ICREA Research Professor
 2004 - Present Director of the Spanish National Bioinformatics Institute (INB-ISCIII).
 2013 - Present Head of the Spanish node of ELIXIR (European Bioinformatics Infrastructure)

• INSTITUTIONAL RESPONSABILITIES

2013 - present Head of the Spanish node of ELIXIR (European infrastructure for life-science information)
 2015 - 2018 President of the International Society for Computational Biology (ISCB), the professional association of Bioinformaticians and Computational Biologists.
 Since 2002 Director of the Master “Biology and Computational Biology” (since 2013 at ISCIII)

• PREVIOUS POSITIONS

2014 - 2017 ViceDirector basic Research CNIO.
 2006 - 2017 Director Structural Biology and Biocomputing Programme
 Spanish National Cancer research Center (CNIO), Madrid, Spain
 2002 - 2006 Group Leader and Research Professor, National Centre for Biotechnology (CNB) CSIC, Madrid, Spain
 1995 - 2002 Group Leader, National Centre for Biotechnology (CNB) CSIC, Madrid, Spain
 1990 - 1994 Tenure position at the National Centre for Biotechnology, CSIC, Spain
 1991 - 1994 Visiting scientist, EMBL Heidelberg, Chris Sander’s lab
 1989 - 1991 EMBO Post-doctoral fellow, EMBL Heidelberg, Chris Sander’s lab
 1988 - 1989 Different positions at the Instituto de Investigaciones Biomédicas CSIC, Madrid, Spain (Post-doctoral researcher, teaching assistant, responsible of the bioinformatics Service)
 1987 - 1987 Visiting scientist in the lab of Dr. Kenneth Ingham. American Red Cross, Bethesda

• RESEARCH INTERESTS

Computational biology, Bioinformatics, Natural Language Processing, Personalised Medicine, Genomics.

• SCIENTIFIC ACCOMPLISHMENTS

More than 450 papers in biological and computational journals; H-index of 130 in g-scholar, more than 86.000 citations (<https://scholar.google.com/citations?hl=en&user=4iB725QAAAAAJ>); Most cited papers include collaborations in the area of biomedicine, including collaborations in large scale international projects, and

development of original methods, some of which initiated research lines later followed by others: co-evolution based methods in structural bioinformatics, text mining in molecular biology, system for systematic genome annotation, protein interactions prediction with computational methods, disease comorbidities based on molecular data, among others.

• MEMBERSHIP TO SCIENTIFIC ADVISORY COMMITTEES

Since 2023	Member of the Scientific Advisory Committee (SAC), ELIXIR Greece
Since 2023	Chair of the ISCB Fellows Council
Since 2022	SAB of the EBI Lit Services & BioStudies
Since 2022	Member of the Europe PMC and EBI Literature Services Scientific Advisory Board
Since 2021	Member of the Data Science Committee at the Novo Nordisk Foundation
Since 2021	Panel member of the European Research Council Synergy Grants Committee
Since 2021	Member of the Scientific Advisory Board of the Barcelona Institute for Global Health (ISGlobal)
Since 2020	Member of the Scientific Advisory Board of the Institut Universitaire du Cancer de Toulouse
Since 2020	Vice-Chair of the Scientific Committee of IMI – Innovative Medicines Initiative
Since 2018	Member of the Scientific Committee of IMI – Innovative Medicines Initiative
Since 2018	Member of the Scientific Committee of the "Programmes Transversaux " set up by the "Institut National de la Santé et de la Recherche Médicale (INSERM)
Since 2018	Member of the Scientific Advisory Board of the Institute of Genetics and Development of Rennes (IGDR)
Since 2017	Member of the Turing Centre for Living Systems (CENTURI) Scientific Advisory Board
Since 2015	Member of the Institute Curie bioinformatics program Scientific Advisory Board (chair)
Since 2014	Member of SAB of the Biology Department UPF Barcelona
Since 2014	Member of SAB of the Barcelona Biomedicine Research Institute (IRB Barcelona)
Since 2008	Member of the Intepro database SAB
Since 2008	Member of the Swiss Institute of Bioinformatics SAB (Since 2014 chair)
2012 - 2019	Member of the EBI Chemical Databases SAB
2014 - 2018	Member of SourceData Scientific Board (EMBO)
2009 - 2013	Member of the Spanish Grant Evaluation Agency (ANEP)
2008 - 2014	Member of the ERC Peer Review Panels of the ERC Advanced Grant scheme
2006 - 2012	Member of the BioZentrum Basel SAC
2007 - 2013	Member of the EMBL Scientific Advisory Committee
2003 - 2006	Member of the CSIC Life sciences scientific committee
2000 - 2011	Member of the steering committee, and chair of the workshop and course committee of the ESF programme on "Functional Genomics" & "Frontiers of Functional Genomics"
1994 - 1999	External Advisor, Lion Bioscience AG

Member of EU evaluation panels in the V; VI, and VII Framework Programmes)

Referee of projects for the European Union, ESF, HFSO, Member of the Evaluation Panel of the Program Ramon Cajal and the ICREA programmes and Spanish National Grant Evaluation Agency (ANEP) - Spanish Ministry of Education and Science, Spanish Ministry of Health, Netherlands founding agency, Danish Grant agency, WellcomeTrust, MRC, German DFG, Israel Science Foundation and others.

• SCIENCE COMMUNITY SERVICES

2015 - 2019	Member of the EMBO conferences and courses committee
2007 - 2011	Member of the EMBO postdoctoral fellowship committee
2007 - 2013	Steering committee member of the ELIXIR bioinformatics EU ESFRI initiative
2004, 06, 08	Assessor of the CASP Community Challenge
2000 - 2010	Member of the steering committees and chair of the workshop and course committees of the ESF programmes on "Functional Genomics" and "Beyond Functional Genomics"
2002 - Present	Steering committee of the European Conference of Computational Biology since 2002.
1997	Founder of the International Society for Computational Biology (ISCB)

• INVOLVEMENT WITH SCIENTIFIC JOURNALS

- Since 2022 Section Editor of Molecular Oncology
- 2015-2022 Member of the Editorial Board of eLIFE
- Since 2013 Member of the Editorial Board of PeerJ
- Since 2014 Member of the Editorial Board of FEBS Letters
- Since 2004 Executive Editor of BIOINFORMATICS – OUP the main journal in the field of Bioinformatics (previously Associate Editor since 2002)

Reviewer for the main journals including Nature and Science

Former member of the Editorial Board of EMBO Journal and EMBO Reports and others

• HONORS AND AWARDS

- 2025 Honorary member of the Official College of Biologists of Catalonia
- 2024 Corresponding Member of the Academy of Medicine of Zaragoza, Spain
- 2022 Member of the Academy of Sciences of Bologna Institute
- 2010 Professor Honoris Causa of the Danish Technical University DTU
- 2009 Elected Fellow of the International Society for Computational Biology (ISCB)
- 2005 Elected member of the European Molecular Biology Organization (EMBO)
- 2003, 2004 Recognition of Achievements Spanish National Research Council (CSIC)

On-going Grants:

<i>Project Title</i>	<i>Funding source</i>	<i>Amount (Euros)</i>	<i>Period</i>	<i>Role of the PI</i>
GDI	EU-otros	40.000.000€	1.11.2022 – 30.10.2026	
CREXDATA	EU-otros	8.698.105€	1.1.2023 – 31.12.2025	
EOSC4Cancer	H2020. EC	608.450	1.9.2022 – 31.3.2025	Partner
BY-COVID – Beyond Covid	H2020, EC (INFRA-2021-EMERGENCY-01)	776.500€	1.1.2022 – 31.12.2024	Partner
Oncologies - Computational modelling and functional validation platform for personalised colorectal cancer clinical therapy decision support	H2020, EC (ERA PerMed JTC2020)	199.700€	1.1.2021 – 31.12.2023	Partner
iDATA-MP – Data Infrastructure for Personalized Medicine	Instituto de Salud Carlos III - ISCIII	150.000€	1.1.2021 – 31.12.2023	Principal Investigator / Coordinator
HPC Centre of Excellence in Personalised Medicine - PerMedCoE	H2020, EC (INFRAEDI-05-2020)	714.410€	1.10.2020 – 30.6.2023	Principal Investigator / Coordinator
Registro Español de COVID-19: The Spanish COVID-19 Data portal	Instituto de Salud Carlos III - ISCIII	105.000€	1.10.2020 – 30.9.2021	Principal Investigator / Coordinator
E4C - EXaScale smArt pLatform Against paThogEns for Corona	H2020, EC (SC1-PHE-	232.375€	1.4.2020 – 30.9.2021	Partner

Virus	CORONAVIRUS-2020)			
Integrated data and Epidemiological Observatory	Catalan Government	250.000€	1.1.2020 – 31.12.2020	Principal Investigator
Plan de impulso de la tecnología del lenguaje	Spanish Government Ministerio Asuntos Económicos y Transformación Digital	2.845.307€	1.1.2019 – 31.12.2022	Principal Investigator
eTRANSafe – Enhancing TRANslational SAFety Assessment through Integrative Knowledge Management	IMI2 – Call 9 RIA (Research and Innovation Action)	487.451€	1.9.2017- 31.8.2022	Principal Investigator for BSC
Plataforma de Recursos Biomoleculares e Informáticos - Instituto Nacional de Bioinformática	Instituto de Salud Carlos III - ISCIII	1.121.339€	1.1.2018 – 31.12.2020	Principal Investigator
EPICStemic - Extracción de perfiles de comorbilidad personalizados y de trayectorias basadas en datos multi-ómicos	Spanish Government	217.800€	1.1.2019 – 31.12.2022	Principal Investigator
INFORE – Interactive Extreme-Scale Analytics and Forecasting	H2020 , EC	502.500€	01.12.2018- 31.12.2021	Principal Investigator for BSC
iPC: individualizedPaediatricCure: Cloud-based virtual-patient models for precision paediatric oncology	H2020, EC (SC1-DTH-07-2018)	939.304€	1.1.2019 – 31.12.2022	Principal Investigator for BSC
EOSC-Life: Providing an open collaborative space for digital biology in Europe	H2020, EC (INFRAEOSC-04-2018)	43.750€	1.3.2019 – 28.2.2023	Principal Investigator for BSC
European Joint Programme on Rare Diseases	H2020, EC	291.828	1.1.2019 – 31.12.2023	Principal Investigator for BSC

Previous grants

<i>Project Title</i>	<i>Funding source</i>	<i>Amount (Euros)</i>	<i>Period</i>	<i>Role of the PI</i>
Elixir Excelerate	H20202, EC	380.000€	21.7.2017- 31.8.2019	Principal Investigator for BSC
EPIC - Patrones de Expresión en Comorbilidad Inversa	Spanish Government	176.052€	1.1.2016- 30.9.2019	Principal Investigator
Plataforma de Recursos Biomoleculares e Informáticos - Instituto Nacional de Bioinformática	Instituto de Salud Carlos III	966.130€	1.7.2017 – 31.12.2018	Principal Investigator
RD-connect	FP7	900.000€	2.11.2012 – 31.10.2018	Principal Investigator for

					CNIO/BSC
OpenMinTeD	H2020	559.875€	1.7.2016 – 31.6.2018	Principal Investigator	for CNIO/BSC
BLUEPRINT	FP7	707.000€	1.1.2012 – 30.6.2016	Principal Investigator	for CNIO
ASSET	FP7	675.600	2.11.2012 – 31.10.2018	Principal Investigator	for CNIO
ONCONET	Interreg SUDOE	189.816€	1.7.2016 – 31.6.2018	Principal Investigator	for CNIO
OpenPhacts	IMI	9.988.867€	1.3.2011 – 29.2.2016	Principal Investigator	for CNIO
eTOX	IMI	474.860€	1.1.2010 – 31.12.2016	Principal Investigator	for CNIO
GENCODE	NIH	415.913€	1.4.2013 – 31.3-2017	Principal Investigator	for CNIO
BIO2016	MINECO Spain	199.650€	1.1.2016 – 31.12.2018	Principal Investigator	

Contracts

<i>Project Title</i>	<i>Funding source</i>	<i>Amount (Euros)</i>	<i>Period</i>	<i>Role of the PI</i>
HPC technology innovation lab research agreement between BSC and Huawei	Huawei	600.000€	1.7.2020-30.6.2023	Principal Investigator
Fostering prophylactic and therapeutic strategies to fight the SARS-CoV-2 pandemic. Increasing preparedness to face further human CoV diseases	Grifols	275.300€	20.3.2020 – 19.3.2023	Principal Investigator
Collaboration Agreement between IBM and BSC	IBM	580.439€	1.3.2016 – 31.12.2019	Principal Investigator
Collaboration agreement between Lenovo and BSC	Lenovo	392.173€	1.4.2016 – 31.3.2020	Principal Investigator
Precision Medicine from Big Data to Cognitive Computing	Fundación BBVA	90.000€	1.10.2016 – 30.9.2018	Principal Investigator



Prof. Alfonso Valencia is ICREA research Professor, Director of the Life Sciences Department of the Barcelona Supercomputing Center, and Director of the Spanish National Bioinformatics Institute INB-ELIXIR-ES. His research interest is the development of Computational Biology methods and their application to biomedical problems. Some of the computational methods he developed are considered pioneering work in areas such as biological text mining, protein coevolution, disease networks and more recently modelling cellular systems (digital twins). He participates in some of the key cancer related international consortia.

In terms of community services, he is one of the initial promoters of what is now the ELIXIR infrastructure, founder of the Spanish Bioinformatics network and founder member and former president of ISCB the professional association of Bioinformaticians and the Executive Editor of the main journal in the field (Bioinformatics OUP).

Ten representative publications from the last ten years:

1. Porta-Pardo E, Ruiz-Serra V, Valentini V, **Valencia A.** (2022) The structural coverage of the human proteome before and after AlphaFold. PLoS CB 18 (1), e1009818. 42 citations.
2. Sánchez-Valle J, Tejero H, Fernández JM, Juan D, Urda-García B, Capella-Gutiérrez S, Al-Shahrour F, Tabarés-Seisdedos R, Baudot A, Pancaldi V, **Valencia A.** (2020) Interpreting molecular similarity between patients as a determinant of disease comorbidity relationships Nature communications 11 (1), 1-13. 22 citations.
3. Cirillo D, **Valencia A.** (2019) Big data analytics for personalized medicine. Current opinion in biotechnology 58, 161-167. 141 citations.
4. Tress M, Abascal F, **Valencia A.** (2017) Alternative splicing may not be the key to proteome complexity. Trends in biochemical sciences 42, 98-110. 103 citations
5. Fernández JM., de la Torre V., Richardson D., Royo R., Puiggros M., Moncunill V., Fragkogianni, S., Clarke L., Flicek P., Rico D., Torrents D., Carrillo de Santa Pau E., **Valencia A.** (2016) The BLUEPRINT Data Analysis Portal. Cell Systems 3(5)491-495.e5. 33 citations.
6. Krallinger M, Leitner F, Rabal O, Vazquez M, Oyarzabal J, **Valencia A.** (2015). CHEMDNER: The drugs and chemical names extraction challenge. Journal of cheminformatics 7, S1. 111 citations
7. Ibáñez K., Boullosa, C., Tabarés-Seisdedos R., Baudot A., **Valencia A.** (2014) Molecular Evidence for the Inverse Comorbidity between Central Nervous System Disorders and Cancers Detected by Transcriptomic Meta-analyses. PLoS Genetics 10(2). 97 citations.
8. Rojas AM, Fuentes G, Rausell A, **Valencia A.** (2012) The Ras protein superfamily: evolutionary tree and role of conserved amino acids. J cell Biol 196, 189-201 276 citations.
9. Frenkel-Morgenstern, M., Laroix V., Ezkurdia I., Levin Y., Gabashvili A., Prilusky, J., Del Pozo A., Tress M, Johnson R., Guigó R., **Valencia A.** (2012) Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. Genome Research 22(7) 1231-1242. 118 citations.
10. Glaab, E., Baudot, A., Krasnogor, N., Schneider, R., **Valencia, A.** (2012) EnrichNet: Network-based gene set enrichment analysis. Bioinformatics 28(18), i451-i457. 219 citations.

Total publications: 499; h Index: 127 (Scopus); citations: 86.704 (Scopus)

Full publication track in Annex 1: <https://orcid.org/0000-0002-8937-6789>

Google Scholar: <https://scholar.google.es/citations?user=4iB725QAAAAJ&hl=es&oi=ao>

International conferences.

More than 10 KN invited talks per year. I have delivered the main keynote in the meetings of each one of the main bioinformatics conferences, e.g. ECCB (European Conference on Computational Biology), ISMB (International Society for Computational Biology), RECOMB (Research in Computational Molecular Biology) and GIW (International Conference on Genome Informatics).

Organizer of numerous national and international conferences, including ECCB (European Conference on Computational Biology 2015 Madrid, 2020 Barcelona) and ISMB (International Society for Computational Biology as part of organizing or scientific committees/boards).

- Organizer of the ECCB2022
- Organizer of the ECCB2020
- Main organizer of various BioCreative Challenges since 2004.
- I have been the co-organizer of the Biolink Text mining workshop link to ISMB 2002 - 2015.
- Main organizer of the ESF “1st European Conference on Synthetic Biology”, 2007
- As director of the Spanish National Bioinformatics Institute and coordinator of the Spanish Bioinformatics Network, I have had a direct participation at various levels in the organization of the Annual meetings of the Spanish Bioinformaticians since they started in the year 2000.
- I was part of the organizing committee of the “Bologna Winter School” for its first ten years.
- Organizer of Barcelona NGS Conference in its three editions 2015, 16 and 17.

Open Source Software and Technological Platforms

- EPICO (Epigenomics comparative cyber-infrastructure): Using EPICO, large epigenome projects can make available their rich datasets to the community without requiring specific technical skills. EPICO can be accessed at <https://github.com/inab>
- BDAP (BLUEPRINT Data Analysis Portal): BDAP can be accessed at <http://blueprint-data.bsc.es>
- LimTox (text mining for toxicology): The LiMTox system, text-mining approach that tries to extract associations between compounds and a particular toxicological end point from public text sources (PubMed, EPAR, NDA). <http://limtox.bioinfo.cnio.es/>
- BeCalm Biomedical Annotation metasever: BeCalm is a platform to visualise, predict and benchmark biomedical entity recognition between independent automatic prediction systems. <http://www.becalm.eu/>
- APPRIS: APPRIS is a database that houses annotations of human splice isoforms, as well as the corresponding analysis and visualization tools.
- Rbbt (Ruby bioinformatics toolkit): Rbbt is a collection of tools to solve basic data-analysis problems with focus on biological data. The source code of Rbbt is published on GitHub as open software. <https://github.com/mikisvaz/rbbt>
- MelanomaMine (text mining for melanoma): Mining information related to melanoma in publicly available scientific texts from PubMed. <http://melanomamine.bioinfo.cnio.es/>
- PLAN2L (Plant annotation to literature): A web tool for integrated text mining and literature-derived bio-entity relation extraction, adapted to the needs of researches studying the model organism Arabidopsis thaliana. <http://zope.bioinfo.cnio.es/plan2l/plan2l.html>

Major contributions to the early careers of excellent researchers:

During the last 5 years, 6 former students or postdocs have positions as staff scientists and 7 as bioinformaticians in hospitals or private companies. 7 have professorships or PI positions, namely:

- Alba Lepore, Principal Scientist at Ridgeline Therapeutics, Switzerland.
- Vera Pancaldi at the Centre de Recherches en Cancérologie, Toulouse – CRCT,
- Milana Morgenstern The Azrieli Faculty of Medicine, Bar Ilan University,
- Anaïs Baudot, Centre de Génétique Médicale de Marseille,
- Eduardo Andres León, Team leader Institute of Parasitology and Biomedicine "López-Neyra",
- Martin Krallinger. Head of Text Mining Unit at BSC,
- José María Gonzalez Izarzugaza, Associate Prof. Dept of Health Technology. DTU Denmark;
- Antonio Rausell, Director of the Clinical Bioinformatics Lab Institut Imagine & Inserm, Paris.

In 2018 Alfonso Valencia started the **“Bioinfo4Women: Outstanding Young Female Bioinformaticians”** Programme, to promote the exchange of knowledge and experience of outstanding young researchers in science and technology through trainings and mentoring in areas of personalised medicine, bioinformatics and HPC. One of the activities developed within the programme is the organization of the *“Advances in Computational Biology Conference - AdvCompBio 2019”* and the conference series *“Sex and Gender Bias in Health and Artificial Intelligence”* at the la Caixa Palau Macaya in 2021.

Other merits

- Director of the Spanish Institute for Bioinformatics (Instituto Nacional de Bioinformática, INB) a Genome Spain initiative started in may 2004.
- Coordinator of the Spanish Network for Bioinformatics from 1996 to 2004, from 2004 to 2008 with Dr Roderic Guigó.
- Coordinator of the CSIC network for bioinformatics 2002-2006.
- Coordinator of the section on Theoretical Biology of the Spanish Biochemical Society (SEBBM) 2003-2008.
- Founder and Organizer of the Text Mining Interest Group associated to the ISCB.
- Assessor of the CASP protein structure competition in the 9 and 10 editions.
- Coordinator of the Biosapiens NoE outsourcing efforts, and participated in the development the GNOM science-art project.
- Member of the jury of the Elsevier Grand Challenge, 2008-2009.
- Founder member of the Science and Art “e-biolab” initiative.
- Founder of the spin-off company BioAlma in 2003.

PhD theses supervised

1. Student: Laureano Tomás Daza
PhD thesis title: “Computational framework to decipher the role of spatio-temporal epigenome organization in gene transcription”
Thesis supervisors: Biola M. Javierre, Alfonso Valencia
Universitat Autònoma de Barcelona
Date of defense: 23/10/2024
2. Student: Mónica Cabrera Pasadas
PhD thesis title: “Exploring the impact of p53 activation on spatio-temporal genome topology”
Thesis supervisors: Biola M. Javierre, Alfonso Valencia
Universitat Politècnica de Catalunya
Date of defense: 09/07/2024
3. Student: Jon Sánchez Valle
PhD thesis title: Molecular bases of comorbidities and the impact of administered drug interactions
Thesis supervisors: Alfonso Valencia, Vera Pancaldi
Universidad Autónoma de Madrid
Date of defense: 29/4/2022
4. Student: Juan Rodríguez Rivas
PhD thesis title: La coevolución en regiones de interacción entre proteínas: estudio y desarrollo de métodos computacionales
Thesis supervisors: Alfonso Valencia, Michael Tress
Universidad Autónoma de Madrid
Date of defense: 14/2/2020
5. Student: Javier Perales Patón

- PhD thesis title: Computational approaches for the identification of therapeutic targets for pancreatic ductal adenocarcinoma
Thesis supervisors: Alfonso Valencia, Fátima Al-Shahrour
Universidad Autónoma de Madrid
Date of defense: 13/12/2019
6. Student: Maria Rigau de Llobet
PhD thesis title: Analysis of the Impact of Population Copy Number Variation in Introns
Thesis supervisors: Alfonso Valencia, Daniel Rico
Universidad Autónoma de Madrid
Date of defense: 21/6/2019
 7. Student: Eduardo Andres León
PhD thesis title: Análisis computacional de las redes de regulación de la expresión génica en cáncer basadas en microARNs
Thesis supervisors: Ana Rojas, Alfonso Valencia
Universidad Autónoma de Madrid
Date of defense: 17/07/2017
 8. Student: Iakes Ezcurdia Garmendia
PhD thesis title: Proteogenómica y Splicing Alternativo
Thesis supervisors: Michael Tress, Alfonso Valencia
Universidad Autónoma de Madrid
Date of defense: 08/02/2016
 9. Student: David Alejandro de Juan Sopena
PhD thesis title: Desarrollo de métodos computacionales basados en co-evolución para la predicción de interacciones entre proteínas
Thesis supervisor: Alfonso Valencia
Universidad Autónoma de Madrid
Date of defense: 14/01/2016
 10. Student: Kristina Ibáñez Garikano
PhD thesis title: Application of machine learning methods to study the inverse comorbidity between cancer and central nervous system disorders
Universidad Complutense de Madrid
Thesis supervisors: Gonzalo Pajares, María Guijarro, Alfonso Valencia
Date of defense: Diciembre 2015
 11. Student: Simone Ecker
PhD thesis title: Epigenetic and transcriptional variability in leuk
Thesis supervisors: Daniel Rico, Alfonso Valencia
Universidad Autónoma de Madrid
Date of defense: 29/10/2015
 12. Student: Martin Krallinger
PhD thesis title: Development, application and evaluation of text-mining methods for biomedical literature processing: from document categorization to gene ranking.
Thesis supervisor: Alfonso Valencia
Universidad Autónoma de Madrid
Date of defense: 20/04/2015
 13. Student: Raquel Martínez García
PhD thesis title: Análisis transcripcional de xenoinjertos derivados de pacientes con cáncer de páncreas.
Thesis supervisors: Alfonso Valencia, Manuel Hidalgo, Daniel Rico
Universidad Autónoma de Madrid

Date of defense: 20/10/2014

14. Student: Beatriz García Jiménez
PhD thesis title: Anotación Funcional de Proteínas basada en Representación Relacional en el entorno de biología de sistemas
Thesis supervisors: María Araceli Sanchís de Miguel, Alfonso Valencia
Universidad Carlos III de Madrid
Date of defense: 04/06/2012
15. Student: José María Gonzalez Izarzugaza
PhD thesis title: Mutations in the protein kinase superfamily
Thesis supervisor: Alfonso Valencia
Universidad Autónoma de Madrid
Date of defense: 25/11/2011
16. Student: Antonio Rausell de Frías
PhD thesis title: Estudio computacional de las bases moleculares de la especificidad funcional en familias de proteínas
Thesis supervisor: Alfonso Valencia
Universidad Autónoma de Madrid
Date of defense: 13/06/2011
17. Student: Florian Leitner
PhD thesis title: Online Assessment of Protein Interaction Information Extraction Systems
Thesis supervisor: Alfonso Valencia
Entity: Universidad Autónoma de Madrid Type of entity: University
Date of defense: 01/03/2011
18. Student: Gonzalo López García
PhD thesis title: Anotación y predicción de residuos funcionales basada en información estructural de proteínas
Thesis supervisor: Alfonso Valencia
Universidad Autónoma de Madrid
Date of defense: 16/06/2009
19. Student: Parantu K Shah
PhD thesis title: Data mining from scientific literature
Thesis supervisor: Alfonso Valencia
Universidad Autónoma de Madrid
Date of defense: 21/12/2005
20. Student: Juan Carlos Oliveros Collazos
PhD thesis title: Desarrollo de sistemas informáticos para la gestión y el análisis de resultados de DNA ARRAYS. Aplicaciones al estudio de procesos biológicos en Escherichia Coli y saccharomyces Cerevisiae
Thesis supervisors: Alfonso Valencia, Esteban Montejo de Garcini
Universidad Autónoma de Madrid
Date of defense: 02/07/2004
21. Student: Christian Blaschke
PhD thesis title: Applications of information extraction techniques to molecular biology
Thesis supervisors: Alfonso Valencia, Esteban Montejo de Garcini
Universidad Autónoma de Madrid
Date of defense: 11/02/2002
22. Student: Davien Paul Devos
PhD thesis title: From genome sequence to protein function

Thesis Supervisor: Alfonso Valencia
 Universidad Autónoma de Madrid
 Date of defense: 2002

23. Student: Juan Antonio García Ranea
 PhD thesis title: Especificidad Funcional de la Superfamilia Ras: Análisis Bioinformático
 Thesis supervisor: Alfonso Valencia
 Universidad de Málaga
 Date of defense: 2001
24. Student: Florencio Pazos Cabaleiro
 PhD thesis title: Interacción entre Proteínas Técnicas Computacionales
 Universidad Autónoma de Madrid
 Thesis supervisor: Alfonso Valencia
 Date of defense: 20/07/2001
25. Student: Osvaldo Ramón Olmea Alonso
 PhD thesis title: Mutaciones correlacionadas y su uso en predicción de estructura de proteínas
 Thesis supervisor: Alfonso Valencia
 Universidad Autónoma de Madrid
 Date of defense: 14/06/2001
26. Student: Javier Tamames de la Huerta
 PhD thesis title: Desarrollo y aplicaciones de herramientas bioinformáticas para la clasificación funcional de proteínas
 Thesis supervisor: Alfonso Valencia
 Universidad Autónoma de Madrid
 Date of defense: 27/01/1999

Master theses supervised

Estrella Estivel “Reconstrucción de modelos específicos de contexto en líneas celulares de cáncer para identificar genes esenciales metabólicos y predecir nuevas dianas terapéuticas”. Master Bioinformática Instituto de Salud Carlos III (ISCIII). 2019-2020

Beatriz Urda “From comorbidities to gene expression fingerprints and back”. Universitat Pompeu Fabra. 2019-2020

Laura Jiménez “Nuclear colocalization of DNA-binding proteins through chromatin interactions”. Universitat Pompeu Fabra. 2019-2020

Gerard Pradas “PhysiBoSSa: a sustainable integration of stochastic Boolean and agent-based modelling frameworks”. Universitat Pompeu Fabra. 2019-2020

Paula López: “Characterization of nuclear condensates through DNA binding protein colocalization”

María Morales “HistTeriA: una herramienta para estudiar la relación de la organización 3D de la cromatina y sus metabolitos de marcaje”. Master Bioinformática Instituto de Salud Carlos III (ISCIII).

Annika Meert “PhysiBoSS-Drugs: A personalized multiscale simulation framework that enables predicting drug synergies in cell populations”. Universitat Pompeu Fabra 2020-2021

Hugo Bronchalo “Comprehensive comparative omics study of pediatric and adult liver cancer.”. Master Bioinformática Instituto de Salud Carlos III (ISCIII). 2020-2021

Mar Batlle – “The use of multilayer networks for the molecular characterization of hepatoblastoma”. Master Bioinformática Instituto de Salud Carlos III (ISCIII). 2021

Oumout Egkemen Moustafa “Graph-based approaches for the study of drug interactions in comorbidity relations”.

Othmane Hayoun “Implementation of cellular transport mechanisms within a multiscale simulation framework”. UPF 2021-2022

Jesús Pérez “Machine Learning approaches to improve the precision of the identification of comorbidity relationships using molecular data”. UOC

Grado

Paula Balcells “Explaining GWAS hits in CLL using Hi-C in different B-cell developmental stages”. BSC International Summer HPC Internship Programme. 2019

Annex 1. Full publication track

1. Capella-Gutierrez S, Alloza E, Rubinat-Ripoll L, ECCB2022 Organising Committee, the ECCB2022 Programme Committee, the ECCB2022 Steering Committee; Conesa A, Valencia A. ECCB2022: the 21st European Conference on Computational Biology. *Bioinformatics*. 2022 Sep 16;38(Supplement_2):ii1-ii4. doi: 10.1093/bioinformatics/btac560.
2. Joshi RS, Rigau M, García-Prieto CA, Castro de Moura M, Piñeyro D, Moran S, Davalos V, Carrión P, Ferrando-Bernal M, Olalde I, Lalueza-Fox C, Navarro A, Fernández-Tena C, Aspandi D, Sukno FM, Binefa X, Valencia A, Esteller M. Look-alike humans identified by facial recognition algorithms show genetic similarities. *Cell Rep*. 2022 Aug 23;40(8):111257. doi: 10.1016/j.celrep.2022.111257.
3. Smith M, Ponce-de-Leon M, Valencia A. Evaluating the policy of closing bars and restaurants in Cataluña and its effects on mobility and COVID19 incidence. *Sci Rep*. 2022 Jun 7;12(1):9132. doi: 10.1038/s41598-022-11531-y.
4. Harms RL, Ferrari A, Meier IB, Martinkova J, Santus E, Marino N, Cirillo D, Mellino S, Catuara Solarz S, Tarnanas I, Szoek C, Hort J, Valencia A, Ferretti MT, Seixas A, Santuccione Chadha A. Digital biomarkers and sex impacts in Alzheimer's disease management - potential utility for innovative 3P medicine approach. *EPMA J*. 2022 Jun 6;13(2):299-313. doi: 10.1007/s13167-022-00284-3. eCollection 2022 Jun.
5. Tarrés-Freixas F, Trinité B, Pons-Grífols A, Romero-Durana M, Riveira-Muñoz E, Ávila-Nieto C, Pérez M, Garcia-Vidal E, Perez-Zsolt D, Muñoz-Basagoiti J, Raich-Regué D, Izquierdo-Useros N, Andrés C, Antón A, Pumarola T, Blanco I, Noguera-Julian M, Guallar V, Lepore R, Valencia A, Urrea V, Vergara-Alert J, Clotet B, Ballana E, Carrillo J, Segalés J, Blanco J. Heterogeneous Infectivity and Pathogenesis of SARS-CoV-2 Variants Beta, Delta and Omicron in Transgenic K18-hACE2 and Wildtype Mice. *Front Microbiol*. 2022 May 4;13:840757. doi: 10.3389/fmicb.2022.840757. eCollection 2022.
6. Garcia-Prieto CA, Martínez-Jiménez F, Valencia A, Porta-Pardo E. Detection of oncogenic and clinically actionable mutations in cancer genomes critically depends on variant calling tools. *Bioinformatics*. 2022 May 5;btac306. doi: 10.1093/bioinformatics/btac306.
7. Catalá-López F, Driver JA, Page MJ, Hutton B, Ridao M, Berrozpe-Villabona C, Alonso-Arroyo A, Fraga-Medín CA, Bernal-Delgado E, Valencia A, Tabarés-Seisdedos R. Design and methodological characteristics of studies using observational routinely collected health data for investigating the link between cancer and neurodegenerative diseases: protocol for a meta-research study. *BMJ Open*. 2022 Apr 29;12(4):e058738. doi: 10.1136/bmjopen-2021-058738.
8. Ponce-de-Leon M, Montagud A, Akasiadis C, Schreiber J, Ntiniakou T, Valencia A. Optimizing Dosage-Specific Treatments in a Multi-Scale Model of a Tumor Growth. *Front Mol Biosci*. 2022 Apr 6;9:836794. doi: 10.3389/fmolb.2022.836794. eCollection 2022.

9. Akasiadis C, Ponce-de-Leon M, Montagud A, Michelioudakis E, Atsidakou A, Alevizos E, Artikis A, Valencia A, Paliouras, G. Parallel model exploration for tumor treatment simulations. *Computational Intelligence*. 2022 Mar 19. doi: 10.1111/coin.1251
10. Pradenas E, Trinité B, Urrea V, Marfil S, Tarrés-Freixas F, Ortiz R, Roviroso C, Rodon J, Vergara-Alert J, Segalés J, Guallar V, Valencia A, Izquierdo-Useros N, Noguera-Julian M, Carrillo J, Paredes R, Mateu L, Chamorro A, Toledo R, Massanella M, Clotet B, Blanco J. Clinical course impacts early kinetics, magnitude, and amplitude of SARS-CoV-2 neutralizing antibodies beyond 1 year after infection. *Cell Rep Med*. 2022 Jan 24;3(2):100523. doi: 10.1016/j.xcrm.2022.100523.
11. Montagud A, Béal J, Tobalina L, Traynard P, Subramanian V, Szalai B, Alföldi R, Puskás L, Valencia A, Barillot E, Saez-Rodriguez J, Calzone L. Patient-specific Boolean models of signalling networks guide personalised treatments. *Elife*. 2022 Feb 15;11:e72626. doi: 10.7554/eLife.72626.
12. Catalá-López F, Hutton B, Page MJ, Driver JA, Ridao M, Alonso-Arroyo A, Valencia A, Macías Saint-Gerons D, Tabarés-Seisdedos R. Mortality in Persons With Autism Spectrum Disorder or Attention-Deficit/Hyperactivity Disorder: A Systematic Review and Meta-analysis. *JAMA Pediatr*. 2022 Feb 14;e216401. doi: 10.1001/jamapediatrics.2021.6401.
13. Porta-Pardo E, Ruiz-Serra V, Valentini S, Valencia A. The structural coverage of the human proteome before and after AlphaFold. *PLoS Comput Biol*. 2022 Jan 24;18(1):e1009818. doi: 10.1371/journal.pcbi.1009818.
14. Vazquez M, Krallinger M, Leitner F, Kuiper M, Valencia A, Laegreid A. ExTRI: Extraction of transcription regulation interactions from literature. *Biochim Biophys Acta Gene Regul Mech*. 2021 Dec 4;194778. doi: 10.1016/j.bbagr.2021.194778. Online ahead of print.
15. Ponce-de-Leon M, Del Valle J, Fernandez JM, Bernardo M, Cirillo D, Sanchez-Valle J, Smith M, Capella-Gutierrez S, Gullón T, Valencia A. COVID-19 Flow-Maps an open geographic information system on COVID-19 and human mobility for Spain. *Sci Data*. 2021 Nov 30;8(1):310. doi: 10.1038/s41597-021-01093-5.
16. Rehm HL, Page AJH, Smith L. et al. GA4GH: International policies and standards for data sharing across genomic research and healthcare. *Cell Genom*. 2021 Nov 10;1(2):100029. doi: 10.1016/j.xgen.2021.100029.
17. Werutsky G, Barrios CH, Cardona AF, Albergaria A, Valencia A, Ferreira CG, Rolfo C, Azambuja E, Rabinovich GA, Sposetti G, Arrieta O, Dienstmann R, Rebelatto TF, Denninghoff V, Aran V, Cazap E. Perspectives on emerging technologies, personalised medicine, and clinical research for cancer control in Latin America and the Caribbean. *Lancet Oncol*. 2021 Nov;22(11):e488-e500. doi: 10.1016/S1470-2045(21)00523-4.
18. Kuiper M, Bonello J, Fernández-Breis JT, Bucher P, Futschik ME, Gaudet P, Kulakovskiy IV, Licata L, Logie C, Lovering RC, Makeev VJ, Orchard S, Panni S, Perfetto L, Sant D, Schulz S, Zerbino DR, Lægreid A, GRECO Consortium. The Gene Regulation Knowledge Commons: The action area of GREEKC. *Biochim Biophys Acta Gene Regul Mech*. 2021 Oct 29;194768. doi: 10.1016/j.bbagr.2021.194768.

19. Richart R, Lapi E, Pancaldi V, Cuenca-Ardura M, Carrillo-de-Santa Pau E, Madrid-Mencía M, Neyret-Kahn H, Radvanyi F, Rodríguez JA, Cuartero Y, Serra F, Le Dily F, Valencia A, Marti-Renom MA, Real FX. STAG2 loss-of-function affects short-range genomic contacts and modulates the basal-luminal transcriptional program of bladder cancer cells. *Nucleic Acids Res.* 2021 Oct 14;gkab864. doi: 10.1093/nar/gkab864.
20. Ostaszewski M, et al. , Reinhard Schneider 1 , COVID-19 Disease Map Community. COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. *Mol Syst Biol.* 2021 Oct;17(10):e10387. doi: 10.15252/msb.202110387.
21. Ruiz-Serra V , Pontes C, Milanetti E, Kryshtafovych A, Lepore R, Valencia A. Assessing the accuracy of contact and distance predictions in CASP14. *Proteins.* 2021 Oct 1. doi: 10.1002/prot.26248. Online ahead of print.
22. Llabata P, Torres-Diz M, Gomez A, Tomas-Daza L, Romero OA, Grego-Bessa J, Llinas-Arias P, Valencia A, Esteller M, Javierre BM, Zhang X, Sanchez-Cespedes M. MAX mutant small-cell lung cancers exhibit impaired activities of MGA-dependent noncanonical polycomb repressive complex. *Proc Natl Acad Sci U S A.* 2021 Sep 14;118(37):e2024824118. doi: 10.1073/pnas.2024824118
23. Mukherjee S, Detroja R, Balamurali D, Matveishina E, Medvedeva YA, Valencia A, Gorohovski A , Frenkel-Morgenstern M. Computational analysis of sense-antisense chimeric transcripts reveals their potential regulatory features and the landscape of expression in human cells. *NAR Genom Bioinform.* 2021 Aug 25;3(3):lqab074. doi: 10.1093/nargab/lqab074. eCollection 2021 Sep.
24. Walsh I, Fishman D , Garcia-Gasulla D, Titma T, Pollastri G, ELIXIR Machine Learning Focus Group; Harrow J, Psomopoulos FE, Tosatto SCE. DOME: recommendations for supervised machine learning validation in biology. *Nat Methods.* 2021 Jul 27. doi: 10.1038/s41592-021-01205-4.
25. Vergara-Alert J, Rodon J, Carrillo J, Te N, Izquierdo-Useros N, Rodríguez de la Concepción ML, Ávila-Nieto C, Guallar V, Valencia A, Cantero G Blanco J, Clotet B, Bensaid A, Segalés J. Pigs are not susceptible to SARS-CoV-2 infection but are a model for viral immunogenicity studies. *Transbound Emerg Dis .* 2021 Jul;68(4):1721-1725. doi: 10.1111/tbed.13861. Epub 2020 Oct 23.
26. Forés-Martos J, Boullosa C, Rodrigo-Domínguez D, Sánchez-Valle J, Suay-García B, Climent J, Falcó A, Valencia A, Puig-Butillé JA, Puig S, Tabarés-Seisdedos R. Transcriptomic and Genetic Associations between Alzheimer's Disease, Parkinson's Disease, and Cancer. *Cancers (Basel).* 2021 Jun 15;13(12):2990. doi: 10.3390/cancers13122990.
27. Hübschmann D, Kleinheinz K, Wagener R, Bernhart SH , López C, Toprak UH, Sungalee S, Ishaque N , Kretzmer H , Kreuz M , Waszak SM, Paramasivam N, Ammerpohl O , Aukema SM, Beekman R, Bergmann AK, Bieg M, Binder H, Borkhardt A, Borst C, Brors B, Bruns P, Carrillo de Santa Pau E , Claviez A , Doose G , Haake A, Karsch D, Haas S, Hansmann ML, Hoell JI, Hovestadt V, Huang B , Hummel M , Jäger-Schmidt C, Kerssemakers JNA, Korbel JO, Kube D, Lawerenz C, Lenze D, Martens JHA, Ott G, Radlwimmer B , Reisinger E, Richter J, Rico D, Rosenstiel P, Rosenwald A, Schillhabel M, Stilgenbauer S , Stadler PF , Martín-Subero JI, Szczepanowski M, Warsaw G, Weniger MA , Zapatka M, Valencia A, Stunnenberg HG, Lichter P, Möller P, Loeffler M, Eils R, Klapper W, Hoffmann S , Trümper L, ICGC MMML-Seq consortium; ICGC DE-Mining consortium; BLUEPRINT

- consortium; Küppers R, Schlesner M, Siebert R. Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. *Leukemia*. 2021 May 5. doi: 10.1038/s41375-021-01251-z.
28. Brustolin M, Rodon J, Rodríguez de la Concepción ML, Ávila-Nieto C, Cantero G, Pérez M, Te N, Noguera-Julian M, Guallar V, Valencia A, Roca N, Izquierdo-Useros N, Blanco J, Clotet B, Bensaid A, Carrillo J, Vergara-Alert J, Segalés J. Protection against reinfection with D614- or G614-SARS-CoV-2 isolates in golden Syrian hamster. *Emerg Microbes Infect*. 2021 Apr 7;1-36. doi: 10.1080/22221751.2021.1913974.
 29. Núñez-Carpintero I, Petrizzelli M, Zinovyev A, Cirillo D, Valencia A. The multilayer community structure of medulloblastoma. *iScience*. 2021 Mar 26;24(4):102365. doi: 10.1016/j.isci.2021.102365. eCollection 2021 Apr 23.
 30. Rodon J, Muñoz-Basagoiti J, Perez-Zsolt D, Noguera-Julian M, Paredes R, Mateu L, Quiñones C, Perez C, Erkizia I, Blanco I, Valencia A, Guallar V, Carrillo J, Blanco J, Segalés J, Clotet B, Vergara-Alert J, Izquierdo-Useros N. Identification of Plitidepsin as Potent Inhibitor of SARS-CoV-2-Induced Cytopathic Effect After a Drug Repurposing Screen. *Front Pharmacol*. 2021 Mar 25;12:646676. doi: 10.3389/fphar.2021.646676. eCollection 2021.
 31. Rajewsky N, Almouzni G, Gorski SA, Aerts S, Amit S, Bertero MG, Bock C, Bredenoord AL, Cavalli G, Chiocca S, Clevers H, De Strooper B, Eggert A, Ellenberg J, Fernández XM, Figlerowicz M, Gasser SM, Hubner N, Kjems J, Knoblich JA, Krabbe G, Lichter P, Linnarsson S, Marine JC, Marioni J, Marti-Renom MA, Netea MG, Nickel D, Nollmann M, Novak HR, Parkinson H, Piccolo S, Pinheiro I, Pombo A, Popp C, Reik W, Roman-Roman S, Rosenstiel P, Schultze JL, Stegle O, Tanay A, Testa G, Thanos D, Theis FJ, Torres-Padilla ME, Valencia A, Vallot C, van Oudenaarden A, Vidal M, Voet T, LifeTime Community. Publisher correction: LifeTime and improving European healthcare through cell-based interceptive medicine. *Nature*. 2021 Mar 17. doi: 10.1038/s41586-021-03287-8.
 32. Santus E, Marino N, Cirillo D, Chersoni E, Montagud A, Santuccione Chada A, Valencia A, Hughes K, Lindvall C. AI-aided Precision Medicine against COVID-19: Strategic Areas of Research and Development. *J Med Internet Res*. 2021 Mar 12. doi: 10.2196/22453
 33. Pognan F, Steger-Hartmann T, Díaz C, Blomberg N, Bringezu F, Briggs K, Callegaro G, Capella-Gutierrez S, Centeno E, Corvi J, Drew P, Drewe WC, Fernández JM, Furlong LI, Guney E, Kors JA, Mayer MA, Pastor M, Piñero J, Ramírez-Anguita JM, Ronzano F, Rowell P, Sánchez-Pitarch J, Valencia A, van de Water B, van der Lei J, van Mulligen E, Sanz F. The eTRANSAFE Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. *Pharmaceuticals (Basel)* 2021 Mar 8;14(3):237. doi: 10.3390/ph14030237.
 34. Delso G, Cirillo D, Kaggie JD, Valencia A, Metser U, Veit-Haibach P. How to Design AI-Driven Clinical Trials in Nuclear Medicine. *Semin Nucl Med* . 2021 Mar;51(2):112-119. doi: 10.1053/j.semnuclmed.2020.09.003.
 35. Harrow J, Hancock J, ELIXIR-EXCELERATE Community; Blomberg N. ELIXIR-EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. *EMBO J* 2021 Feb 9;e107409. doi: 10.15252/embj.2020107409.

36. Cirillo D, Nuñez-Carpintero I, Valencia A. Artificial Intelligence in Cancer Research: learning at different levels of data granularity. *Molecular Oncology* 2021 Feb 3. doi: 10.1002/1878-0261.12920.
37. Pradenas E, Trinité B, Urrea V, Marfil S, Ávila-Nieto C, Rodríguez de la Concepción ML, Tarrés-Freixas F, Pérez-Yanes S, Rovirosa C, Ainsua-Enrich E, Rodon J, Vergara-Alert J, Segalés J, Guallar V, Valencia A, Izquierdo-Useros N, Paredes R, Mateu L, Chamorro A, Massanella M, Carrillo J, Clotet B, Blanco J. Stable neutralizing antibody levels six months after mild and severe COVID-19 episode. *Med (N Y)*. 2021 Jan 31. doi: 10.1016/j.medj.2021.01.005.
38. Ferrari A, Santus E, Cirillo D, Ponce-de-Leon M, Marino N, Ferretti MT, Santuccione Chadha A, Mavridis N, Valencia A. Simulating SARS-CoV-2 epidemics by region-specific variables and modeling contact tracing app containment. *npj Digital Medicine*. 2021 Jan 14;4(1):9. doi: 10.1038/s41746-020-00374-4.
39. Ehrhart F, Jacobsen A, Rigau M, Bosio M, Kaliyaperumal R, Laros J, Willighagen EL, Valencia A, Roos M, Capella-Gutierrez S, Curfs LMG, Evelo CT. A catalogue of 863 Rett-syndrome-causing MECP2 mutations and lessons learned from data integration. *Sci Data*. 2021 Jan 15;8(1):10. doi: 10.1038/s41597-020-00794-7.
40. Trinité B, Tarrés-Freixas F, Rodon J, Pradenas E, Urrea V, Marfil S, Rodríguez de la Concepción ML, Ávila-Nieto C, Aguilar-Gurrieri C, Barajas A, Ortiz R, Paredes R, Mateu L, Valencia A, Guallar V, Ruiz L, Grau E, Massanella M, Puig J, Chamorro A, Izquierdo-Useros N, Segalés J, Clotet B, Carrillo J, Vergara-Alert J, Blanco J. SARS-CoV-2 infection elicits a rapid neutralizing antibody response that correlates with disease severity. *Sci Rep* 2021 Jan 28;11(1):2608. doi: 10.1038/s41598-021-81862-9.
41. Pontes C, Ruiz-Serra V, Lepore R, Valencia A. Unraveling the molecular basis of host cell receptor usage in SARS-CoV-2 and other human pathogenic β -CoVs. *Computational and Structural Biotechnology Journal*. 2021;19:759-766. doi: 10.1016/j.csbj.2021.01.006. Epub 2021 Jan 12.
42. Capella-Gutierrez S, Alloza E, Gallastegui E, Kavakiotis I, Harrow J, Langtry A, ECCB2020 Steering Committee; Valencia A. ECCB2020: the 19th European Conference on Computational Biology. *Bioinformatics*. 2020 Dec 30;36(Suppl_2):i569-i572. doi: 10.1093/bioinformatics/btaa979.
43. Porta-Pardo E, Valencia A, Godzik A. Understanding oncogenicity of cancer driver genes and mutations in the cancer genomics era. *FEBS Letters*. 2020 Dec;594(24):4233-4246. doi: 10.1002/1873-3468.13781.
44. Gaudelot T, Malod-Dognin N, Sánchez-Valle J, Pancaldi V, Valencia A, Pržulj N. Unveiling new disease, pathway, and gene associations via multi-scale neural network. *PLoS One* 15(4): e0231059.2020. <https://doi.org/10.1371/journal.pone.0231059>.
45. Josep-Fabregó M, Teruel X, Gimenez-Abalos V, Cirillo D, Garcia Gasulla D, Alvarez-Napagao S, García-Gasulla M, Ayguadé E, Valencia A. GOPHER, an HPC Framework for Large Scale Graph Exploration and Inference. In *High Performance Computing*, Springer, 2020. ISBN: 978-3-030-59851-8.

46. Delso G, Cirillo D, Kaggie JD, Valencia A, Metser U, Veit-Haibach P. How to Design AI-Driven Clinical Trials in Nuclear Medicine. *Semin Nucl Med* 2021 Mar;51(2):112-119. doi: 10.1053/j.semnuclmed.2020.09.003.
47. Rajewsky N, Almouzni G, Gorski SA, Aerts S, Amit S, Bertero MG, Bock C, Bredenoord AL, Cavalli G, Chiocca S, Clevers H, De Strooper B, Eggert A, Ellenberg J, Fernández XM, Figlerowicz M, Gasser SM, Hubner N, Kjems J, Knoblich JA, Krabbe G, Lichter P, Linnarsson S, Marine JC, Marioni J, Marti-Renom MA, Netea MG, Nickel D, Nollmann M, Novak HR, Parkinson H, Piccolo S, Pinheiro I, Pombo A, Popp C, Reik W, Roman-Roman S, Rosenstiel P, Schultze JL, Stegle O, Tanay A, Testa G, Thanos D, Theis FJ, Torres-Padilla ME, Valencia A, Vallot C, van Oudenaarden A, Vidal M, Voet T, LifeTime Community. LifeTime and improving European healthcare through cell-based interceptive medicine. *Nature*. Septiembre 2020. doi: 10.1038/s41586-020-2715-9.
48. Malod-Dognin N, Pancaldi V, Valencia A, Pržulj N. Chromatin network markers of leukemia. *Bioinformatics*. 2020 Jul 1;36(Suppl_1):i455-i463. doi: 10.1093/bioinformatics/btaa445.
49. Constance H, Prokopec SD, Sun RX, Yousif F, Schmitz N, PCAWG Tumour Subtypes and Clinical Translation; Boutros PC, PCAWG Consortium. Sex differences in oncogenic mutational processes. *Proc Natl Acad Sci U S A*. 2021 Sep 14;118(37):e2024824118. doi: 10.1073/pnas.2024824118.
50. Salgado D, Armean IM, Baudis M, Beltran S, Capella-Gutierrez S, Carvalho-Silva D, Dominguez Del Angel V, Dopazo J, Furlong LI, Gao B, Garcia L, Gerloff D, Gut I, Gyenesi A, Habermann N, Hancock JM, Hanauer M, Hovig E, Johansson LF, Keane T, Korbel J, Lauer KB, Laurie S, Leskošek B, Lloyd D, Marques-Bonet T, Mei H, Monostory K, Piñero J, Poterlowicz K, Rath A, Samarakoon P, Sanz F, Saunders G, Sie D, Swertz MA, Tsukanov K, Valencia A, Vidak M, González CY, Ylstra B, Bérout C. The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. *F1000Res*. 2020 Oct 13;9:ELIXIR-1229. doi: 10.12688/f1000research.24887.1. eCollection 2020.
51. Ostaszewski M, Mazein A, Gillespie ME, Kuperstein I, Niarakis A, Hermjakob H, Pico AR, Willighagen EL, Evelo CT, Hasenauer J, Schreiber F, Dräger A, Demir E, Wolkenhauer O, Furlong LI, Barillot E, Dopazo J, Orta-Resendiz A, Messina F, Valencia A, Funahashi A, Kitano H, Auffray C, Balling R, Schneider R. Author Correction: COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. *Scientific Data* 7(1):247. 17 de julio de 2020. doi: 10.1038/s41597-020-00589-w.
52. Goldman MJ, Zhang J, Fonseca NA, Cortés-Ciriano I, Xiang Q, Craft B, Piñeiro-Yáñez E, O'Connor BD, Bazant W, Barrera E, Muñoz-Pomer A, Petryszak R, Füllgrabe A, Al-Shahrour F, Keays M, Haussler D, Weinstein JN, Huber W, Valencia A, Park PJ, Papatheodorou I, Zhu J, Ferretti V, Vazquez M. A user guide for the online exploration and visualization of PCAWG data. *Nature Communications* 11(1):3400. 7 de julio de 2020. doi: 10.1038/s41467-020-16785-6.
53. Sánchez-Valle J, Tejero H, Fernández JM, Juan D, Urda-García B, Capella-Gutiérrez S, Al-Shahrour F, Tabarés-Seisdedos R, Baudot A, Pancaldi V, Valencia A. Interpreting molecular

- similarity between patients as a determinant of disease comorbidity relationships. *Nature Communications*. 5 de junio de 2020; 11, 2854.
54. Cirillo D, Catuara-Solarz S, Morey C, Guney E, Subirats L, Mellino S, Gigante A, Valencia A, Rementeria MJ, Santucci Chadha A, Mavridis N. Sex and gender differences and biases in artificial intelligence for biomedicine and healthcare. *npj Digital Medicine*. 1 de junio de 2020; 3,81.
 55. Ostaszewski M, Mazein A, Gillespie ME, Kuperstein I, Niarakis A, Hermjakob H, Pico AR, Willighagen EL, Evelo CT, Hasenauer J, Schreiber F, Dräger A, Demir E, Wolkenhauer O, Furlong LI, Barillot E, Dopazo J, Orta-Resendiz A, Messina F, Valencia A, Funahashi A, Kitano H, Auffray C, Balling R, Schneider R. COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. *Scientific Data* 7(1):136. 5 de mayo de 2020. doi: 10.1038/s41597-020-0477-8.
 56. Reyna MA, Haan D, Paczkowska M, Verbeke LPC, Vazquez M, Kahraman A, et al. Pathway and network analysis of more than 2500 whole cancer genomes. *Nat Commun*. 5 de febrero de 2020;11(1):729.
 57. Wren JD, Valencia A, Kelso J. Reviewer-coerced citation: case report, update on journal policy and suggestions for future prevention. *Bioinformatics*. 15 de septiembre de 2019;35(18):3217-8.
 58. Vazquez M, Valencia A. Patient Dossier: Healthcare queries over distributed resources. *PLoS Comput Biol*. 2019;15(10):e1007291.
 59. Saunders G, Baudis M, Becker R, Beltran S, Bérout C, Birney E, et al. Leveraging European infrastructures to access 1 million human genomes by 2022. *Nat Rev Genet*. 2019;20(11):693-701.
 60. Saunders G, Baudis M, Becker R, Beltran S, Bérout C, Birney E, et al. Author Correction: Leveraging European infrastructures to access 1 million human genomes by 2022. *Nat Rev Genet*. noviembre de 2019;20(11):702.
 61. Rigau M, Juan D, Valencia A, Rico D. Intronic CNVs and gene expression variation in human populations. *PLoS Genet*. 2019;15(1):e1007902.
 62. Pérez-Pérez M, Pérez-Rodríguez G, Blanco-Míguez A, Fdez-Riverola F, Valencia A, Krallinger M, et al. Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. *J Cheminform*. 24 de junio de 2019;11(1):42.
 63. Perales-Patón J, Di Domenico T, Fustero-Torre C, Piñeiro-Yáñez E, Carretero-Puche C, Tejero H, et al. vulcanSpot: a tool to prioritize therapeutic vulnerabilities in cancer. *Bioinformatics*. 1 de noviembre de 2019;35(22):4846-8.
 64. Ison J, Ienasescu H, Chmura P, Rydzka E, Ménager H, Kalaš M, et al. The bio.tools registry of software tools and data resources for the life sciences. *Genome Biol*. 12 de 2019;20(1):164.

65. Greco A, Sanchez Valle J, Pancaldi V, Baudot A, Barillot E, Caselle M, et al. Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. *Int J Mol Sci.* 26 de junio de 2019;20(13).
66. Gómez-López G, Dopazo J, Cigudosa JC, Valencia A, Al-Shahrour F. Precision medicine needs pioneering clinical bioinformaticians. *Brief Bioinformatics.* 2019;20(3):752-66.
67. Giatrakos N, Ponce De Leon M, Gaetano Tartaglia G, Valencia A, Zissis D, Katzouris N, et al. Interactive Extreme-Scale Analytics: Towards Battling Cancer. *IEEE Technol Soc Mag.* junio de 2019;38(2):54-61.
68. Forés-Martos J, Catalá-López F, Sánchez-Valle J, Ibáñez K, Tejero H, Palma-Gudiel H, et al. Transcriptomic metaanalyses of autistic brains reveals shared gene expression and biological pathway abnormalities with cancer. *Mol Autism.* 2019;10:17.
69. Cirillo D, Valencia A. Big data analytics for personalized medicine. *Curr Opin Biotechnol.* 2019;58:161-7.
70. Catalá-López F, Forés-Martos J, Driver JA, Page MJ, Hutton B, Ridao M, et al. Association of Anorexia Nervosa With Risk of Cancer: A Systematic Review and Meta-analysis. *JAMA Netw Open.* 05 de 2019;2(6):e195313.
71. Bergmann AK, Fataccioli V, Castellano G, Martin-Garcia N, Pelletier L, Ammerpohl O, et al. DNA methylation profiling of hepatosplenic T-cell lymphoma. *Haematologica.* 2019;104(3):e104-7.
72. Bazaga A, Valencia A, JoséRementeria M-. BIOLITMAP: a web-based geolocated, temporal and thematic visualization of the evolution of bioinformatics publications. *Bioinformatics.* 15 de julio de 2019;35(14):2518-20.
73. Rodriguez JM, Rodriguez-Rivas J, Di Domenico T, Vázquez J, Valencia A, Tress ML. APPRIS 2017: principal isoforms for multiple gene sets. *Nucleic Acids Res.* 04 de 2018;46(D1):D213-7.
74. Piñeiro-Yáñez E, Reboiro-Jato M, Gómez-López G, Perales-Patón J, Troulé K, Rodríguez JM, et al. PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. *Genome Med.* 31 de 2018;10(1):41.
75. Mur P, Jemth A-S, Bevc L, Amaral N, Navarro M, Valdés-Mas R, et al. Germline variation in the oxidative DNA repair genes NUDT1 and OGG1 is not associated with hereditary colorectal cancer or polyposis. *Hum Mutat.* 2018;39(9):1214-25.
76. Mur P, De Voer RM, Olivera-Salguero R, Rodríguez-Perales S, Pons T, Setién F, et al. Germline mutations in the spindle assembly checkpoint genes BUB1 and BUB3 are infrequent in familial colorectal cancer and polyposis. *Mol Cancer.* 15 de 2018;17(1):23.
77. Grassi L, Pourfarzad F, Ullrich S, Merkel A, Were F, Carrillo-de-Santa-Pau E, et al. Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. *Cell Rep.* 04 de 2018;24(10):2784-94.
78. Ecker S, Pancaldi V, Valencia A, Beck S, Paul DS. Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. *Bioessays.* 2018;40(2).

79. Bellido F, Sowada N, Mur P, Lázaro C, Pons T, Valdés-Mas R, et al. Association Between Germline Mutations in BRF1, a Subunit of the RNA Polymerase III Transcription Complex, and Hereditary Colorectal Cancer. *Gastroenterology*. 2018;154(1):181-194.e20.
80. Vargas-Parra GM, González-Acosta M, Thompson BA, Gómez C, Fernández A, Dámaso E, et al. Elucidating the molecular basis of MSH2-deficient tumors by combined germline and somatic analysis. *Int J Cancer*. 01 de 2017;141(7):1365-80.
81. Tress ML, Abascal F, Valencia A. Most Alternative Isoforms Are Not Functionally Important. *Trends Biochem Sci*. 2017;42(6):408-10.
82. Tress ML, Abascal F, Valencia A. Alternative Splicing May Not Be the Key to Proteome Complexity. *Trends Biochem Sci*. 2017;42(2):98-110.
83. Thornton JM, Valencia A, Schwede T. Anna Tramontano 1957-2017. *Nat Struct Mol Biol*. 04 de 2017;24(5):431-2.
84. Sanz F, Pognan F, Steger-Hartmann T, Díaz C, eTOX, Cases M, et al. Legacy data sharing to improve drug safety assessment: the eTOX project. *Nat Rev Drug Discov*. diciembre de 2017;16(12):811-2.
85. Sánchez-Valle J, Tejero H, Ibáñez K, Portero JL, Krallinger M, Al-Shahrour F, et al. A molecular hypothesis to explain direct and inverse co-morbidities between Alzheimer's Disease, Glioblastoma and Lung cancer. *Sci Rep*. 30 de 2017;7(1):4474.
86. Porta-Pardo E, Kamburov A, Tamborero D, Pons T, Grases D, Valencia A, et al. Comparison of algorithms for the detection of cancer drivers at subgene resolution. *Nat Methods*. agosto de 2017;14(8):782-8.
87. Piccolo P, Attanasio S, Secco I, Sangermano R, Strisciuglio C, Limongelli G, et al. MIB2 variants altering NOTCH signalling result in left ventricle hypertrabeculation/non-compaction and are associated with Ménétrier-like gastropathy. *Hum Mol Genet*. 01 de 2017;26(1):33-43.
88. Krallinger M, Rabal O, Lourenço A, Oyarzabal J, Valencia A. Information Retrieval and Text Mining Technologies for Chemistry. *Chem Rev*. 28 de junio de 2017;117(12):7673-761.
89. Intxaurrenondo A, Perez-Perez M, Perez-Rodriguez G, Lopez-Martin JA, Santamaria J, Villegas M, et al. The Biomedical Abbreviation Recognition and Resolution (BARR) track: benchmarking, evaluation and importance of abbreviation recognition systems applied to Spanish biomedical abstracts. *CEUR workshop proceedings*. 2017;
90. Frenkel-Morgenstern M, Gorohovski A, Tagore S, Sekar V, Vazquez M, Valencia A. ChiPPI: a novel method for mapping chimeric protein-protein interactions uncovers selection principles of protein fusion events in cancer. *Nucleic Acids Res*. 7 de julio de 2017;45(12):7094-105.
91. Flobak Å, Vazquez M, Lægreid A, Valencia A. Clmbinator: a web-based tool for drug synergy analysis in small- and large-scale datasets. *Bioinformatics*. 1 de agosto de 2017;33(15):2410-2.

92. Ecker S, Chen L, Pancaldi V, Bagger FO, Fernández JM, Carrillo de Santa Pau E, et al. Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. *Genome Biol.* 26 de 2017;18(1):18.
93. Catalá-López F, Hutton B, Page MJ, Ridao M, Driver JA, Alonso-Arroyo A, et al. Risk of mortality among children, adolescents, and adults with autism spectrum disorder or attention deficit hyperactivity disorder and their first-degree relatives: a protocol for a systematic review and meta-analysis of observational studies. *Syst Rev.* 15 de 2017;6(1):189.
94. Catalá-López F, Hutton B, Driver JA, Page MJ, Ridao M, Valderas JM, et al. Cancer and central nervous system disorders: protocol for an umbrella review of systematic reviews and updated meta-analyses of observational studies. *Syst Rev.* 04 de 2017;6(1):69.
95. Catalá-López F, Hutton B, Driver JA, Ridao M, Valderas JM, Gènova-Maleras R, et al. Anorexia nervosa and cancer: a protocol for a systematic review and meta-analysis of observational studies. *Syst Rev.* 11 de 2017;6(1):137.
96. Carrillo-de-Santa-Pau E, Juan D, Pancaldi V, Were F, Martin-Subero I, Rico D, et al. Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. *Nucleic Acids Res.* 19 de septiembre de 2017;45(16):9244-59.
97. Cañada A, Capella-Gutierrez S, Rabal O, Oyarzabal J, Valencia A, Krallinger M. LimTox: a web tool for applied text mining of adverse event and toxicity associations of compounds, drugs and genes. *Nucleic Acids Res.* 03 de 2017;45(W1):W484-9.
98. Berger B, Gaasterland T, Lengauer T, Orengo CA, Gaeta B, Markel S, et al. ISCB's initial reaction to New England Journal of Medicine editorial on data sharing. *Bioinformatics.* 15 de 2017;33(18):2968.
99. Vazquez M, Pons T, Brunak S, Valencia A, Izarzugaza JMG. wKinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. *Hum Mutat.* enero de 2016;37(1):36-42.
100. Valencia A, Markel S, Gaeta B, Gaasterland T, Lengauer T, Berger B, et al. ISCB's initial reaction to New England Journal of Medicine editorial on data sharing. *F1000Res.* 2016;5.
101. Toll A, Fernández LC, Pons T, Groesser L, Sagrera A, Carrillo-de Santa Pau E, et al. Somatic Embryonic FGFR2 Mutations in Keratinocytic Epidermal Nevi. *J Invest Dermatol.* 2016;136(8):1718-21.
102. Stunnenberg HG, International Human Epigenome Consortium, Hirst M. The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell.* 17 de noviembre de 2016;167(5):1145-9.
103. Rodríguez-Rivas J, Marsili S, Juan D, Valencia A. Conservation of coevolving protein interfaces bridges prokaryote-eukaryote homologies in the twilight zone. *Proc Natl Acad Sci USA.* 27 de 2016;113(52):15018-23.

104. Pons T, Vazquez M, Matey-Hernandez ML, Brunak S, Valencia A, Izarzugaza JM. KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. *BMC Genomics*. 23 de 2016;17 Suppl 2:396.
105. Pérez-Pérez M, Pérez-Rodríguez G, Rabal O, Vazquez M, Oyarzabal J, Fdez-Riverola F, et al. The Markyt visualisation, prediction and benchmark platform for chemical and gene entity recognition at BioCreative/CHEMDNER challenge. *Database (Oxford)*. 2016;2016.
106. Pancaldi V, Carrillo-de-Santa-Pau E, Javierre BM, Juan D, Fraser P, Spivakov M, et al. Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. *Genome Biol*. 08 de 2016;17(1):152.
107. Juan D, Perner J, Carrillo de Santa Pau E, Marsili S, Ochoa D, Chung H-R, et al. Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. *Cell Rep*. 9 de febrero de 2016;14(5):1246-57.
108. Jiang Y, Oron TR, Clark WT, Bankapur AR, D'Andrea D, Lepore R, et al. An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biol*. 07 de 2016;17(1):184.
109. Ibáñez K, Guijarro M, Pajares G, Valencia A. A computational approach inspired by simulated annealing to study the stability of protein interaction networks in cancer and neurological disorders. *Data Min Knowl Disc*. enero de 2016;30(1):226-42.
110. Gurard-Levin ZA, Wilson LOW, Pancaldi V, Postel-Vinay S, Sousa FG, Reyes C, et al. Chromatin Regulators as a Guide for Cancer Treatment Choice. *Mol Cancer Ther*. 2016;15(7):1768-77.
111. Galindo-Albarrán AO, López-Portales OH, Gutiérrez-Reyna DY, Rodríguez-Jorge O, Sánchez-Villanueva JA, Ramírez-Pliego O, et al. CD8+ T Cells from Human Neonates Are Biased toward an Innate Immune Response. *Cell Rep*. 15 de 2016;17(8):2151-60.
112. Fernández JM, de la Torre V, Richardson D, Royo R, Puiggròs M, Moncunill V, et al. The BLUEPRINT Data Analysis Portal. *Cell Syst*. 23 de 2016;3(5):491-495.e5.
113. Earl J, Rico D, Carrillo-de-Santa-Pau E, Rodríguez-Santiago B, Méndez-Pertuz M, Auer H, et al. Erratum to: The UBC-40 Urothelial Bladder Cancer cell line index: a genomic resource for functional studies. *BMC Genomics*. 25 de 2016;17(1):829.
114. Durinx C, McEntyre J, Appel R, Apweiler R, Barlow M, Blomberg N, et al. Identifying ELIXIR Core Data Resources. *F1000Res*. 2016;5.
115. Chen L, Ge B, Casale FP, Vasquez L, Kwan T, Garrido-Martín D, et al. Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. *Cell*. 17 de 2016;167(5):1398-1414.e24.
116. Camilla Sammartino J, Krallinger M, Valencia A. Annotation process, guidelines and text corpus of small non-coding RNAmolecules: the MiNCor for microRNA annotations. *CEUR workshop proceedings*. 2016;

117. Berger B, Gaasterland T, Lengauer T, Oren C, Gaeta B, Markel S, et al. ISCB's Initial Reaction to The New England Journal of Medicine Editorial on Data Sharing. *PLoS Comput Biol.* marzo de 2016;12(3):e1004816.
118. Bellido F, Pineda M, Aiza G, Valdés-Mas R, Navarro M, Puente DA, et al. POLE and POLD1 mutations in 529 kindred with familial colorectal cancer and/or polyposis: review of reported cases and recommendations for genetic testing and surveillance. *Genet Med.* abril de 2016;18(4):325-32.
119. Astle WJ, Elding H, Jiang T, Allen D, Ruklisa D, Mann AL, et al. The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. *Cell.* 17 de 2016;167(5):1415-1429.e19.
120. Abascal F, Corvelo A, Cruz F, Villanueva-Cañas JL, Vlasova A, Marcet-Houben M, et al. Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. *Genome Biol.* 14 de 2016;17(1):251.
121. Verspoor K, Shatkay H, Hirschman L, Blaschke C, Valencia A. Summary of the BioLINK SIG 2013 meeting at ISMB/ECCB 2013. *Bioinformatics.* 15 de enero de 2015;31(2):297-8.
122. Vázquez M, Valencia A, Pons T. Structure-PPI: a module for the annotation of cancer-related single-nucleotide variants at protein-protein interfaces. *Bioinformatics.* 15 de julio de 2015;31(14):2397-9.
123. Sutto L, Marsili S, Valencia A, Gervasio FL. From residue coevolution to protein conformational ensembles and functional dynamics. *Proc Natl Acad Sci USA.* 3 de noviembre de 2015;112(44):13567-72.
124. Seguí N, Mina LB, Lázaro C, Sanz-Pamplona R, Pons T, Navarro M, et al. Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. *Gastroenterology.* septiembre de 2015;149(3):563-6.
125. Rodríguez JM, Carro A, Valencia A, Tress ML. APPRIS WebServer and WebServices. *Nucleic Acids Res.* 1 de julio de 2015;43(W1):W455-459.
126. Puente XS, Beà S, Valdés-Mas R, Villamor N, Gutiérrez-Abril J, Martín-Subero JJ, et al. Non-coding recurrent mutations in chronic lymphocytic leukaemia. *Nature.* 22 de octubre de 2015;526(7574):519-24.
127. Ochoa D, Juan D, Valencia A, Pazos F. Detection of significant protein coevolution. *Bioinformatics.* 1 de julio de 2015;31(13):2166-73.
128. Maraver A, Fernandez-Marcos PJ, Cash TP, Mendez-Pertuz M, Dueñas M, Maietta P, et al. NOTCH pathway inactivation promotes bladder cancer progression. *J Clin Invest.* febrero de 2015;125(2):824-30.
129. Lees JG, Hériché J-K, Morilla I, Fernández JM, Adler P, Krallinger M, et al. FUN-L: gene prioritization for RNAi screens. *Bioinformatics.* 15 de junio de 2015;31(12):2052-3.

130. Kulis M, Merkel A, Heath S, Queirós AC, Schuyler RP, Castellano G, et al. Whole-genome fingerprint of the DNA methylome during human B cell differentiation. *Nat Genet.* julio de 2015;47(7):746-56.
131. Krallinger M, Rabal O, Leitner F, Vazquez M, Salgado D, Lu Z, et al. The CHEMDNER corpus of chemicals and drugs and its annotation principles. *J Cheminform.* 2015;7(Suppl 1 Text mining for chemistry and the CHEMDNER track):S2.
132. Krallinger M, Leitner F, Rabal O, Vazquez M, Oyarzabal J, Valencia A. CHEMDNER: The drugs and chemical names extraction challenge. *J Cheminform.* 2015;7(Suppl 1 Text mining for chemistry and the CHEMDNER track):S1.
133. Frenkel-Morgenstern M, Gorohovski A, Vucenovic D, Maestre L, Valencia A. ChiTaRS 2.1--an improved database of the chimeric transcripts and RNA-seq data with novel sense-antisense chimeric RNA transcripts. *Nucleic Acids Res.* enero de 2015;43(Database issue):D68-75.
134. Ezkurdia I, Vázquez J, Valencia A, Tress M. Correction to «Analyzing the first drafts of the human proteome». *J Proteome Res.* 3 de abril de 2015;14(4):1991.
135. Ezkurdia I, Rodriguez JM, Carrillo-de Santa Pau E, Vázquez J, Valencia A, Tress ML. Most highly expressed protein-coding genes have a single dominant isoform. *J Proteome Res.* 3 de abril de 2015;14(4):1880-7.
136. Ezkurdia I, Calvo E, Del Pozo A, Vázquez J, Valencia A, Tress ML. The potential clinical impact of the release of two drafts of the human proteome. *Expert Rev Proteomics.* 2015;12(6):579-93.
137. Ecker S, Pancaldi V, Rico D, Valencia A. Higher gene expression variability in the more aggressive subtype of chronic lymphocytic leukemia. *Genome Med.* 2015;7(1):8.
138. Earl J, Rico D, Carrillo-de-Santa-Pau E, Rodríguez-Santiago B, Méndez-Pertuz M, Auer H, et al. The UBC-40 Urothelial Bladder Cancer cell line index: a genomic resource for functional studies. *BMC Genomics.* 22 de 2015;16:403.
139. Earl J, Rico D, Carrillo-de-Santa-Pau E, Rodríguez-Santiago B, Méndez-Pertuz M, Auer H, et al. Erratum to: The UBC-40 Urothelial Bladder Cancer Cell Line Index: a genomic resource for functional studies. *BMC Genomics.* 30 de noviembre de 2015;16(1):1019.
140. Creixell P, Reimand J, Haider S, Wu G, Shibata T, Vazquez M, et al. Pathway and network analysis of cancer genomes. *Nat Methods.* julio de 2015;12(7):615-21.
141. Abascal F, Tress ML, Valencia A. The evolutionary fate of alternatively spliced homologous exons after gene duplication. *Genome Biol Evol.* 29 de abril de 2015;7(6):1392-403.
142. Abascal F, Tress ML, Valencia A. Alternative splicing and co-option of transposable elements: the case of TMPO/LAP2 α and ZNF451 in mammals. *Bioinformatics.* 15 de julio de 2015;31(14):2257-61.

143. Abascal F, Ezkurdia I, Rodriguez-Rivas J, Rodriguez JM, del Pozo A, Vázquez J, et al. Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. *PLoS Comput Biol.* junio de 2015;11(6):e1004325.
144. Usié A, Alves R, Solsona F, Vázquez M, Valencia A. CheNER: chemical named entity recognizer. *Bioinformatics.* 1 de abril de 2014;30(7):1039-40.
145. Santa Pau E, Real FX, Valencia A. Bioinformatics analysis of pancreas cancer genome in high-throughput genomic technologies. En: *Molecular diagnostics and treatment of pancreatic cancer* [Internet]. 2014. p. 93-131. Disponible en: <https://doi.org/10.1016/C2012-0-06759-2>
146. Rojas AM, Valencia A. Evolution of the ras superfamily of GTPases. En: *Ras superfamily small G proteins: Biology and mechanisms 1: General features.* 2014.
147. Pons T, Paramonov I, Boullosa C, Ibáñez K, Rojas AM, Valencia A. A common structural scaffold in CTD phosphatases that supports distinct catalytic mechanisms. *Proteins.* enero de 2014;82(1):103-18.
148. Martinez-Garcia R, Lopez-Casas PP, Rico D, Valencia A, Hidalgo M. Colorectal cancer classification based on gene expression is not associated with FOLFIRI response. *Nat Med.* noviembre de 2014;20(11):1230-1.
149. Martinez-Garcia R, Juan D, Rausell A, Muñoz M, Baños N, Menéndez C, et al. Transcriptional dissection of pancreatic tumors engrafted in mice. *Genome Med.* 2014;6(4):27.
150. Maietta P, Lopez G, Carro A, Pingilley BJ, Leon LG, Valencia A, et al. FireDB: a compendium of biological and pharmacologically relevant ligands. *Nucleic Acids Res.* enero de 2014;42(Database issue):D267-272.
151. Krallinger M, Leitner F, Vazquez M, Valencia A. Text Mining. En: *Comprehensive Biomedical Physics.* 2014.
152. Krallinger M, Leitner F, Valencia A. Retrieval and Discovery of Cell Cycle Literature and Proteins by Means of Machine Learning, Text Mining and Network Analysis. 8th International Conference on Practical Applications of Computational Biology & Bioinformatics (PACBB 2014). 2014;285-92.
153. Juan D, Rico D, Marques-Bonet T, Fernández-Capetillo O, Valencia A. Late-replicating CNVs as a source of new genes. *Biol Open.* 15 de 2014;3(3).
154. Ibáñez K, Boullosa C, Tabarés-Seisdedos R, Baudot A, Valencia A. Molecular evidence for the inverse comorbidity between central nervous system disorders and cancers detected by transcriptomic meta-analyses. *PLoS Genet.* febrero de 2014;10(2):e1004173.
155. Hériché J-K, Lees JG, Morilla I, Walter T, Petrova B, Roberti MJ, et al. Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. *Mol Biol Cell.* 15 de agosto de 2014;25(16):2522-36.

156. Garralda E, Paz K, López-Casas PP, Jones S, Katz A, Kann LM, et al. Integrated next-generation sequencing and avatar mouse models for personalized cancer treatment. *Clin Cancer Res.* 1 de mayo de 2014;20(9):2476-84.
157. García-Jiménez B, Pons T, Sanchis A, Valencia A. Predicting Protein Relationships to Human Pathways through a Relational Learning Approach Based on Simple Sequence Features. *IEEE/ACM Trans Comput Biol Bioinform.* agosto de 2014;11(4):753-65.
158. Ferreira PG, Jares P, Rico D, Gómez-López G, Martínez-Trillos A, Villamor N, et al. Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. *Genome Res.* febrero de 2014;24(2):212-26.
159. Ezkurdia I, Vázquez J, Valencia A, Tress M. Analyzing the first drafts of the human proteome. *J Proteome Res.* 1 de agosto de 2014;13(8):3854-5.
160. Ezkurdia I, Juan D, Rodriguez JM, Frankish A, Diekhans M, Harrow J, et al. Multiple evidence strands suggest that there may be as few as 19,000 human protein-coding genes. *Hum Mol Genet.* 15 de noviembre de 2014;23(22):5866-78.
161. Catalá-López F, Suárez-Pinilla M, Suárez-Pinilla P, Valderas JM, Gómez-Beneyto M, Martinez S, et al. Inverse and direct cancer comorbidity in people with central nervous system disorders: a meta-analysis of cancer incidence in 577,013 participants of 50 observational studies. *Psychother Psychosom.* 2014;83(2):89-105.
162. Catalá-López F, Crespo-Facorro B, Vieta E, Valderas JM, Valencia A, Tabarés-Seisdedos R. Alzheimer's disease and cancer: current epidemiological evidence for a mutual protection. *Neuroepidemiology.* 2014;42(2):121-2.
163. Basilico F, Maffini S, Weir JR, Prumbaum D, Rojas AM, Zimniak T, et al. The pseudo GTPase CENP-M drives human kinetochore assembly. *Elife.* 8 de julio de 2014;3:e02978.
164. Arighi CN, Wu CH, Cohen KB, Hirschman L, Krallinger M, Valencia A, et al. BioCreative-IV virtual issue. *Database (Oxford).* 2014;2014.
165. Rubio-Camarillo M, Gómez-López G, Fernández JM, Valencia A, Pisano DG. RUBioSeq: a suite of parallelized pipelines to automate exome variation and bisulfite-seq analyses. *Bioinformatics.* 1 de julio de 2013;29(13):1687-9.
166. Rodriguez JM, Maietta P, Ezkurdia I, Pietrelli A, Wesselink J-J, Lopez G, et al. APPRIS: annotation of principal and alternative splice isoforms. *Nucleic Acids Res.* enero de 2013;41(Database issue):D110-117.
167. Ochoa D, García-Gutiérrez P, Juan D, Valencia A, Pazos F. Incorporating information on predicted solvent accessibility to the co-evolution-based study of protein interactions. *Mol Biosyst.* 27 de enero de 2013;9(1):70-6.
168. Mosca R, Pons T, Céol A, Valencia A, Aloy P. Towards a detailed atlas of protein-protein interactions. *Curr Opin Struct Biol.* diciembre de 2013;23(6):929-40.

169. Morante R, Krallinger M, Valencia A, Daelemans W. Machine reading of biomedical texts about alzheimer's disease. *CEUR workshop proceedings*. 2013;
170. Landa I, Boullosa C, Inglada-Pérez L, Sastre-Perona A, Pastor S, Velázquez A, et al. An epistatic interaction between the PAX8 and STK17B genes in papillary thyroid cancer susceptibility. *PLoS ONE*. 2013;8(9):e74765.
171. Juan D, Rico D, Marques-Bonet T, Fernández-Capetillo O, Valencia A. Late-replicating CNVs as a source of new genes. *Biol Open*. 15 de diciembre de 2013;2(12):1402-11.
172. Izarzugaza JMG, Vazquez M, del Pozo A, Valencia A. wKinMut: an integrated tool for the analysis and interpretation of mutations in human protein kinases. *BMC Bioinformatics*. 29 de noviembre de 2013;14:345.
173. Gonzalez-Perez A, Mustonen V, Reva B, Ritchie GRS, Creixell P, Karchin R, et al. Computational approaches to identify functional genetic variants in cancer genomes. *Nat Methods*. agosto de 2013;10(8):723-9.
174. Frenkel-Morgenstern M, Gorohovski A, Lacroix V, Rogers M, Ibanez K, Boullosa C, et al. ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. *Nucleic Acids Res*. enero de 2013;41(Database issue):D142-151.
175. de Juan D, Pazos F, Valencia A. Emerging methods in protein co-evolution. *Nat Rev Genet*. abril de 2013;14(4):249-61.
176. Comeau DC, Islamaj Doğan R, Ciccarese P, Cohen KB, Krallinger M, Leitner F, et al. BioC: a minimalist approach to interoperability for biomedical text processing. *Database (Oxford)*. 2013;2013:bat064.
177. Cases M, Furlong LI, Albanell J, Altman RB, Bellazzi R, Boyer S, et al. Improving data and knowledge management to better integrate health care and research. *J Intern Med*. octubre de 2013;274(4):321-8.
178. Blaschke C, Valencia A. The Functional Genomics Network in the evolution of biological text mining over the past decade. *N Biotechnol*. 25 de marzo de 2013;30(3):278-85.
179. Balbás-Martínez C, Sagrera A, Carrillo-de-Santa-Pau E, Earl J, Márquez M, Vazquez M, et al. Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. *Nat Genet*. diciembre de 2013;45(12):1464-9.
180. Abascal F, Corpet A, Gurard-Levin ZA, Juan D, Ochsenbein F, Rico D, et al. Subfunctionalization via adaptive evolution influenced by genomic context: the case of histone chaperones ASF1a and ASF1b. *Mol Biol Evol*. agosto de 2013;30(8):1853-66.
181. Wu CH, Arighi CN, Cohen KB, Hirschman L, Krallinger M, Lu Z, et al. BioCreative-2012 virtual issue. *Database (Oxford)*. 2012;2012:bas049.
182. Wu CH, Arighi CN, Cohen KB, Hirschman L, Krallinger M, Lu Z, et al. BioCreative-2012 virtual issue. *Database (Oxford)*. 2012;2012:bas049.

183. Vazquez M, de la Torre V, Valencia A. Chapter 14: Cancer genome analysis. *PLoS Comput Biol.* 2012;8(12):e1002824.
184. Valencia A, Hidalgo M. Getting personalized cancer genome analysis into the clinic: the challenges in bioinformatics. *Genome Med.* 2012;4(7):61.
185. Salgado D, Krallinger M, Depaule M, Drula E, Tendulkar AV, Leitner F, et al. MyMiner: a web application for computer-assisted biocuration and text annotation. *Bioinformatics.* 1 de septiembre de 2012;28(17):2285-7.
186. Ruiz-Llrente S, Carrillo Santa de Pau E, Sastre-Perona A, Montero-Conde C, Gómez-López G, Fagin JA, et al. Genome-wide analysis of Pax8 binding provides new insights into thyroid functions. *BMC Genomics.* 24 de abril de 2012;13:147.
187. Rojas AM, Fuentes G, Rausell A, Valencia A. The Ras protein superfamily: evolutionary tree and role of conserved amino acids. *J Cell Biol.* 23 de enero de 2012;196(2):189-201.
188. Rojas AM, Santamaria A, Malik R, Jensen TS, Körner R, Morilla I, et al. Uncovering the molecular machinery of the human spindle--an integration of wet and dry systems biology. *PLoS ONE.* 2012;7(3):e31813.
189. Peng H, Bateman A, Valencia A, Wren JD. Bioimage informatics: a new category in Bioinformatics. *Bioinformatics.* 15 de abril de 2012;28(8):1057.
190. Muth T, García-Martín JA, Rausell A, Juan D, Valencia A, Pazos F. JDet: interactive calculation and visualization of function-related conservation patterns in multiple sequence alignments and structures. *Bioinformatics.* 15 de febrero de 2012;28(4):584-6.
191. Kulis M, Heath S, Bibikova M, Queirós AC, Navarro A, Clot G, et al. Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. *Nat Genet.* noviembre de 2012;44(11):1236-42.
192. Krallinger M, Leitner F, Vazquez M, Salgado D, Marcelle C, Tyers M, et al. How to link ontologies and protein-protein interactions to literature: text-mining approaches and the BioCreative experience. *Database (Oxford).* 2012;2012:bas017.
193. Izarzugaza JMG, Krallinger M, Valencia A. Interpretation of the consequences of mutations in protein kinases: combined use of bioinformatics and text mining. *Front Physiol.* 2012;3:323.
194. Izarzugaza JMG, del Pozo A, Vazquez M, Valencia A. Prioritization of pathogenic mutations in the protein kinase superfamily. *BMC Genomics.* 18 de junio de 2012;13 Suppl 4:S3.
195. Izarzugaza J, Vazquez M, Del Pozo A, Valencia A. WKinMut: An integrated tool for the analysis and interpretation of mutations in human protein kinases. *CEUR workshop proceedings.* 2012;
196. Hirschman L, Burns GAPC, Krallinger M, Arighi C, Cohen KB, Valencia A, et al. Text mining for the biocuration workflow. *Database (Oxford).* 2012;2012:bas020.

197. Heyn H, Li N, Ferreira HJ, Moran S, Pisano DG, Gomez A, et al. Distinct DNA methylomes of newborns and centenarians. *Proc Natl Acad Sci USA*. 26 de junio de 2012;109(26):10522-7.
198. Harrow J, Frankish A, Gonzalez JM, Tapanari E, Diekhans M, Kokocinski F, et al. GENCODE: the reference human genome annotation for The ENCODE Project. *Genome Res*. septiembre de 2012;22(9):1760-74.
199. Hajirasouliha I, Schönhuth A, de Juan D, Valencia A, Sahinalp SC. Mirroring co-evolving trees in the light of their topologies. *Bioinformatics*. 1 de mayo de 2012;28(9):1202-8.
200. Glaab E, Baudot A, Krasnogor N, Schneider R, Valencia A. EnrichNet: network-based gene set enrichment analysis. *Bioinformatics*. 15 de septiembre de 2012;28(18):i451-7.
201. Frenkel-Morgenstern M, Valencia A. Novel domain combinations in proteins encoded by chimeric transcripts. *Bioinformatics*. 15 de junio de 2012;28(12):i67-74.
202. Frenkel-Morgenstern M, Lacroix V, Ezkurdia I, Levin Y, Gabashvili A, Prilusky J, et al. Chimeras taking shape: potential functions of proteins encoded by chimeric RNA transcripts. *Genome Res*. julio de 2012;22(7):1231-42.
203. Ezkurdia I, del Pozo A, Frankish A, Rodriguez JM, Harrow J, Ashman K, et al. Comparative proteomics reveals a significant bias toward alternative protein isoforms with conserved structure and function. *Mol Biol Evol*. septiembre de 2012;29(9):2265-83.
204. ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome. *Nature*. 6 de septiembre de 2012;489(7414):57-74.
205. Djebali S, Lagarde J, Kapranov P, Lacroix V, Borel C, Mudge JM, et al. Evidence for transcript networks composed of chimeric RNAs in human cells. *PLoS ONE*. 2012;7(1):e28213.
206. Adams D, Altucci L, Antonarakis SE, Ballesteros J, Beck S, Bird A, et al. BLUEPRINT to decode the epigenetic signature written in blood. *Nat Biotechnol*. 7 de marzo de 2012;30(3):224-6.
207. Wass MN, Fuentes G, Pons C, Pazos F, Valencia A. Towards the prediction of protein interaction partners using physical docking. *Mol Syst Biol*. 15 de febrero de 2011;7:469.
208. Vazquez M, Krallinger M, Leitner F, Valencia A. Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications. *Mol Inform*. junio de 2011;30(6-7):506-19.
209. Tabarés-Seisdedos R, Dumont N, Baudot A, Valderas JM, Climent J, Valencia A, et al. No paradox, no progress: inverse cancer comorbidity in people with other complex diseases. *Lancet Oncol*. junio de 2011;12(6):604-8.

210. Quesada V, Conde L, Villamor N, Ordóñez GR, Jares P, Bassaganyas L, et al. Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. *Nat Genet.* 11 de diciembre de 2011;44(1):47-52.
211. Puente XS, Pinyol M, Quesada V, Conde L, Ordóñez GR, Villamor N, et al. Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. *Nature.* 5 de junio de 2011;475(7354):101-5.
212. Palczewska M, Casafont I, Ghimire K, Rojas AM, Valencia A, Lafarga M, et al. Sumoylation regulates nuclear localization of repressor DREAM. *Biochim Biophys Acta.* mayo de 2011;1813(5):1050-8.
213. Marenne G, Rodríguez-Santiago B, Closas MG, Pérez-Jurado L, Rothman N, Rico D, et al. Assessment of copy number variation using the Illumina Infinium 1M SNP-array: a comparison of methodological approaches in the Spanish Bladder Cancer/EPICURO study. *Hum Mutat.* febrero de 2011;32(2):240-8.
214. Lopez G, Maietta P, Rodriguez JM, Valencia A, Tress ML. firestar--advances in the prediction of functionally important residues. *Nucleic Acids Res.* julio de 2011;39(Web Server issue):W235-241.
215. Krallinger M, Vazquez M, Leitner F, Salgado D, Chatr-Aryamontri A, Winter A, et al. The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. *BMC Bioinformatics.* 3 de octubre de 2011;12 Suppl 8:S3.
216. Kallioniemi O, Wessels L, Valencia A. On the organization of bioinformatics core services in biology-based research institutes. *Bioinformatics.* 15 de mayo de 2011;27(10):1345.
217. Javierre BM, Rodriguez-Ubreva J, Al-Shahrour F, Corominas M, Graña O, Ciudad L, et al. Long-range epigenetic silencing associates with deregulation of Ikaros targets in colorectal cancer cells. *Mol Cancer Res.* agosto de 2011;9(8):1139-51.
218. Izarzugaza JMG, Hopcroft LEM, Baresic A, Orengo CA, Martin ACR, Valencia A. Characterization of pathogenic germline mutations in human protein kinases. *BMC Bioinformatics.* 2011;12 Suppl 4:S1.
219. Herman D, Ochoa D, Juan D, Lopez D, Valencia A, Pazos F. Selection of organisms for the co-evolution-based study of protein interactions. *BMC Bioinformatics.* 12 de septiembre de 2011;12:363.
220. ENCODE Project Consortium. A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biol.* abril de 2011;9(4):e1001046.
221. Arighi CN, Lu Z, Krallinger M, Cohen KB, Wilbur WJ, Valencia A, et al. Overview of the BioCreative III Workshop. *BMC Bioinformatics.* 3 de octubre de 2011;12 Suppl 8:S1.
222. Tress ML, Valencia A. Predicted residue-residue contacts can help the scoring of 3D models. *Proteins.* junio de 2010;78(8):1980-91.

223. Tendulkar AV, Krallinger M, de la Torre V, López G, Wangikar PP, Valencia A. FragKB: structural and literature annotation resource of conserved peptide fragments and residues. PLoS ONE. 18 de marzo de 2010;5(3):e9679.
224. Rodríguez-Santiago B, Malats N, Rothman N, Armengol L, Garcia-Closas M, Kogevinas M, et al. Mosaic uniparental disomies and aneuploidies as large structural variants of the human genome. Am J Hum Genet. 9 de julio de 2010;87(1):129-38.
225. Rausell A, Juan D, Pazos F, Valencia A. Protein interactions and ligand binding: from protein subfamilies to functional specificity. Proc Natl Acad Sci USA. 2 de febrero de 2010;107(5):1995-2000.
226. Leitner F, Mardis SA, Krallinger M, Cesareni G, Hirschman LA, Valencia A. An Overview of BioCreative II.5. IEEE/ACM Trans Comput Biol Bioinform. septiembre de 2010;7(3):385-99.
227. Leitner F, Krallinger M, Cesareni G, Valencia A. The FEBS Letters SDA corpus: a collection of protein interaction articles with high quality annotations for the BioCreative II.5 online challenge and the text mining community. FEBS Lett. 8 de octubre de 2010;584(19):4129-30.
228. Leitner F, Chatr-aryamontri A, Mardis SA, Ceol A, Krallinger M, Licata L, et al. The FEBS Letters/BioCreative II.5 experiment: making biological information accessible. Nat Biotechnol. septiembre de 2010;28(9):897-9.
229. Krallinger M, Leitner F, Valencia A. Analysis of biological processes and diseases using text mining approaches. Methods Mol Biol. 2010;593:341-82.
230. International Cancer Genome Consortium, Hudson TJ, Anderson W, Artez A, Barker AD, Bell C, et al. International network of cancer genome projects. Nature. 15 de abril de 2010;464(7291):993-8.
231. Glaab E, Baudot A, Krasnogor N, Valencia A. TopoGSA: network topological gene set analysis. Bioinformatics. 1 de mayo de 2010;26(9):1271-2.
232. Glaab E, Baudot A, Krasnogor N, Valencia A. Extending pathways and processes using molecular interaction networks to analyse cancer genome data. BMC Bioinformatics. 13 de diciembre de 2010;11:597.
233. García-Jiménez B, Juan D, Ezkurdia I, Andrés-León E, Valencia A. Inference of functional relations in predicted protein networks with a machine learning approach. PLoS ONE. 1 de abril de 2010;5(4):e9969.
234. Fernandez JM, Valencia A. Bioinformatic Software Developments in Spain. En: Statistical Significance for NGS Reads Similarities. 2010. p. 108-20.
235. Carilla-Latorre S, Gallardo ME, Annesley SJ, Calvo-Garrido J, Graña O, Accari SL, et al. MidA is a putative methyltransferase that is required for mitochondrial complex I function. J Cell Sci. 15 de mayo de 2010;123(Pt 10):1674-83.
236. Blaschke C, Hirschman L, Shatkay H, Valencia A. Overview of the Ninth Annual Meeting of the BioLINK SIG at ISMB: Linking Literature, Information and Knowledge for

- Biology. En: Linking Literature, Information, and Knowledge for Biology Lecture Notes in Computer Science [Internet]. Springer, Berlin, Heidelberg; 2010. Disponible en: https://doi.org/10.1007/978-3-642-13131-8_1
237. Baudot A, de la Torre V, Valencia A. Mutated genes, pathways and processes in tumours. *EMBO Rep.* octubre de 2010;11(10):805-10.
238. Trigo A, Valencia A, Cases I. Systemic approaches to biodegradation. *FEMS Microbiol Rev.* enero de 2009;33(1):98-108.
239. Starlinger J, Leitner F, Valencia A, Leser U. SOA-based Integration of Text Mining Services. En: *SERVICES 2009 - 5th 2009 world congress on services*. 2009.
240. Leitner F, Hoffmann R, Valencia A. Biological knowledge extraction a case study of ihop and other language processing systems. En: *Bioinformatics for systems biology*. 2009.
241. Krallinger M, Rojas AM, Valencia A. Creating reference datasets for systems biology applications using text mining. *Ann N Y Acad Sci.* marzo de 2009;1158:14-28.
242. Krallinger M, Rodriguez-Penagos C, Tendulkar A, Valencia A. PLAN2L: a web tool for integrated text mining and literature-based bioentity relation extraction. *Nucleic Acids Res.* julio de 2009;37(Web Server issue):W160-165.
243. Krallinger M, Izarzugaza JMG, Rodriguez-Penagos C, Valencia A. Extraction of human kinase mutations from literature, databases and genotyping studies. *BMC Bioinformatics.* 27 de agosto de 2009;10 Suppl 8:S1.
244. Juncker AS, Jensen LJ, Pierleoni A, Bernsel A, Tress ML, Bork P, et al. Sequence-based feature prediction and annotation of proteins. *Genome Biol.* 2 de febrero de 2009;10(2):206.
245. Izarzugaza JMG, Redfern OC, Orengo CA, Valencia A. Cancer-associated mutations are preferentially distributed in protein kinase functional sites. *Proteins.* diciembre de 2009;77(4):892-903.
246. Izarzugaza JMG, Baresic A, McMillan LEM, Yeats C, Clegg AB, Orengo CA, et al. An integrated approach to the interpretation of single amino acid polymorphisms within the framework of CATH and Gene3D. *BMC Bioinformatics.* 27 de agosto de 2009;10 Suppl 8:S5.
247. Fuentes G, Valencia A. Ras classical effectors: new tales from in silico complexes. *Trends Biochem Sci.* noviembre de 2009;34(11):533-9.
248. Fernandez-Ballester G, Beltrao P, Gonzalez JM, Song Y-H, Wilmanns M, Valencia A, et al. Structure-based prediction of the *Saccharomyces cerevisiae* SH3-ligand interactions. *J Mol Biol.* 15 de mayo de 2009;388(4):902-16.
249. Fernandez AF, Rosales C, Lopez-Nieva P, Graña O, Ballestar E, Ropero S, et al. The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. *Genome Res.* marzo de 2009;19(3):438-51.

250. Ezkurdia I, Bartoli L, Fariselli P, Casadio R, Valencia A, Tress ML. Progress and challenges in predicting protein-protein interaction sites. *Brief Bioinformatics*. mayo de 2009;10(3):233-46.
251. Carbajosa G, Trigo A, Valencia A, Cases I. Bionemo: molecular information on biodegradation metabolism. *Nucleic Acids Res*. enero de 2009;37(Database issue):D598-602.
252. Baudot A, Real FX, Izarzugaza JMG, Valencia A. From cancer genomes to cancer models: bridging the gaps. *EMBO Rep*. abril de 2009;10(4):359-66.
253. Baudot A, Gómez-López G, Valencia A. Translational disease interpretation with molecular networks. *Genome Biol*. 2009;10(6):221.
254. Bacardit J, Stout M, Hirst JD, Valencia A, Smith RE, Krasnogor N. Automated alphabet reduction for protein datasets. *BMC Bioinformatics*. 6 de enero de 2009;10:6.
255. Andres Leon E, Ezkurdia I, García B, Valencia A, Juan D. EcID. A database for the inference of functional interactions in *E. coli*. *Nucleic Acids Res*. enero de 2009;37(Database issue):D629-635.
256. Yeats C, Orengo CA, Veuthey A-L, Boeckmann B, Jensen LJ, Valencia A, et al. Modern genome annotation: the BioSapiens network. En: *Modern genome annotation: the BioSapiens network* [Internet]. Vienna: Springer-Verlag Wien; 2008. p. 213-38. Disponible en: [10.1007/978-3-211-75123-7](https://doi.org/10.1007/978-3-211-75123-7)
257. Watson JD, Thornton JM, Tress ML, Lopez G, Valencia A, Redfern OC, et al. Structure to function. En: *Modern genome annotation: The biosapiens network* [Internet]. Vienna: Springer-Verlag Wien; 2008. p. 239-62. Disponible en: [10.1007/978-3-211-75123-7](https://doi.org/10.1007/978-3-211-75123-7)
258. Valiente PA, Batista PR, Pupo A, Pons T, Valencia A, Pascutti PG. Predicting functional residues in *Plasmodium falciparum* plasmepsins by combining sequence and structural analysis with molecular dynamics simulations. *Proteins*. 1 de noviembre de 2008;73(2):440-57.
259. Valencia A. ProLINK: A framework for linking text mining with ontology and systems biology. En 2008.
260. Tress ML, Wesselink J-J, Frankish A, López G, Goldman N, Löytynoja A, et al. Determination and validation of principal gene products. *Bioinformatics*. 1 de enero de 2008;24(1):11-7.
261. Tress ML, Casadio R, Giorgetti A, Fischer Hallin P, Juncker AS, Kulberkyte E, et al. Alternative splicing in the ENCODE protein complement. En: *Modern Genome Annotation: The Biosapiens Network*. 2008. p. 453-80.
262. Tress ML, Bodenmiller B, Aebersold R, Valencia A. Proteomics studies confirm the presence of alternative protein isoforms on a large scale. *Genome Biol*. 2008;9(11):R162.

263. Tress M, Bujnicki J, Lopez G, Valencia A. Integrating prediction of structure, function, and interactions. En: Prediction of Protein Structures, Functions, and Interactions. 2008.
264. Pazos F, Valencia A. Protein co-evolution, co-adaptation and interactions. EMBO J. 22 de octubre de 2008;27(20):2648-55.
265. Pazos F, Juan D, Izarzugaza JMG, Leon E, Valencia A. Prediction of protein interaction based on similarity of phylogenetic trees. Methods Mol Biol. 2008;484:523-35.
266. Leitner F, Valencia A. A text-mining perspective on the requirements for electronically annotated abstracts. FEBS Lett. 9 de abril de 2008;582(8):1178-81.
267. Leitner F, Krallinger M, Rodriguez-Penagos C, Hakenberg J, Plake C, Kuo C-J, et al. Introducing meta-services for biomedical information extraction. Genome Biol. 2008;9 Suppl 2:S6.
268. Krallinger M, Valencia A, Hirschman L. Linking genes to literature: text mining, information extraction, and retrieval applications for biology. Genome Biol. 2008;9 Suppl 2:S8.
269. Krallinger M, Valencia A. Text mining methods as computational biology tools. En 2008.
270. Krallinger M, Morgan A, Smith L, Leitner F, Tanabe L, Wilbur J, et al. Evaluation of text-mining systems for biology: overview of the Second BioCreative community challenge. Genome Biol. 2008;9 Suppl 2:S1.
271. Krallinger M, Leitner F, Rodriguez-Penagos C, Valencia A. Overview of the protein-protein interaction annotation extraction task of BioCreative II. Genome Biol. 2008;9 Suppl 2:S4.
272. Juan D, Pazos F, Valencia A. High-confidence prediction of global interactomes based on genome-wide coevolutionary networks. Proc Natl Acad Sci USA. 22 de enero de 2008;105(3):934-9.
273. Juan D, Pazos F, Valencia A. Co-evolution and co-adaptation in protein networks. FEBS Lett. 9 de abril de 2008;582(8):1225-30.
274. Izarzugaza JMG, Juan D, Pons C, Pazos F, Valencia A. Enhancing the prediction of protein pairings between interacting families using orthology information. BMC Bioinformatics. 23 de enero de 2008;9:35.
275. Gómez-López G, Valencia A. Bioinformatics and cancer research: building bridges for translational research. Clin Transl Oncol. febrero de 2008;10(2):85-95.
276. Frishman D, Valencia A, editores. Modern Genome Annotation The Biosapiens Network [Internet]. Vienna: Springer-Verlag Wien; 2008. Disponible en: [10.1007/978-3-211-75123-7](https://doi.org/10.1007/978-3-211-75123-7)
277. Frishman D, Albrecht, Mario, Blankenburg H, Bork P, Harrington ED, Hermjakob H, et al. Protein-protein interactions: analysis and prediction. En: Modern genome

- annotation: The biosapiens network [Internet]. Springer-Verlag Wien. 2008. p. 353-410. Disponible en: [10.1007/978-3-211-75123-7](https://doi.org/10.1007/978-3-211-75123-7)
278. del Pozo A, Pazos F, Valencia A. Defining functional distances over gene ontology. *BMC Bioinformatics*. 25 de enero de 2008;9:50.
279. BioMoby Consortium, Wilkinson MD, Senger M, Kavas E, Bruskiewich R, Gouzy J, et al. Interoperability with Moby 1.0--it's better than sharing your toothbrush! *Brief Bioinformatics*. mayo de 2008;9(3):220-31.
280. Altman RB, Bergman CM, Blake J, Blaschke C, Cohen A, Gannon F, et al. Text mining for biology--the way forward: opinions from leading scientists. *Genome Biol*. 2008;9 Suppl 2:S7.
281. Tress ML, Martelli PL, Frankish A, Reeves GA, Wesselink JJ, Yeats C, et al. The implications of alternative splicing in the ENCODE protein complement. *Proc Natl Acad Sci USA*. 27 de marzo de 2007;104(13):5495-500.
282. Tamames J, Moya A, Valencia A. Modular organization in the reductive evolution of protein-protein interaction networks. *Genome Biol*. 2007;8(5):R94.
283. Sanchez-Pulido L, Valencia A, Rojas AM. Are promyelocytic leukaemia protein nuclear bodies a scaffold for caspase-2 programmed cell death? *Trends Biochem Sci*. septiembre de 2007;32(9):400-6.
284. López G, Valencia A, Tress ML. firestar--prediction of functionally important residues using structural templates and alignment reliability. *Nucleic Acids Res*. julio de 2007;35(Web Server issue):W573-577.
285. Lopez G, Valencia A, Tress M. FireDB--a database of functionally important residues from proteins of known structure. *Nucleic Acids Res*. enero de 2007;35(Database issue):D219-223.
286. López G, Rojas A, Tress M, Valencia A. Assessment of predictions submitted for the CASP7 function prediction category. *Proteins*. 2007;69 Suppl 8:165-74.
287. Krallinger M, Valencia A. Mining information on protein function from text. En: *Bioinformatics-from genomes to therapies* [Internet]. 2007. p. 1253-95. Disponible en: <https://doi.org/10.1002/9783527619368.ch34>
288. Jiménez-Baranda S, Gómez-Moutón C, Rojas A, Martínez-Prats L, Mira E, Ana Lacalle R, et al. Filamin-A regulates actin-dependent clustering of HIV receptors. *Nat Cell Biol*. julio de 2007;9(7):838-46.
289. Izarzugaza JMG, Graña O, Tress ML, Valencia A, Clarke ND. Assessment of intramolecular contact predictions for CASP7. *Proteins*. 2007;69 Suppl 8:152-8.
290. Hirschman L, Hayes W, Valencia A. Knowledge Acquisition from the Biomedical Literature. En: *Semantic web: Revolutionizing knowledge discovery in the life sciences* [Internet]. Springer US; 2007. p. 53-81. Disponible en: [10.1007/978-0-387-48438-9](https://doi.org/10.1007/978-0-387-48438-9)

291. Gómez MJ, Pazos F, Guijarro FJ, de Lorenzo V, Valencia A. The environmental fate of organic pollutants through the global microbial metabolism. *Mol Syst Biol.* 2007;3:114.
292. Fernández JM, Hoffmann R, Valencia A. iHOP web services. *Nucleic Acids Res.* julio de 2007;35(Web Server issue):W21-26.
293. ENCODE Project Consortium, Birney E, Stamatoyannopoulos JA, Dutta A, Guigó R, Gingeras TR, et al. Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature.* 14 de junio de 2007;447(7146):799-816.
294. Cases I, Pisano DG, Andres E, Carro A, Fernández JM, Gómez-López G, et al. CARGO: a web portal to integrate customized biological information. *Nucleic Acids Res.* julio de 2007;35(Web Server issue):W16-20.
295. Valencia A, Bateman A. Software patents in Bioinformatics. *Bioinformatics.* 15 de junio de 2006;22(12):1415-1415.
296. Tress ML, Cozzetto D, Tramontano A, Valencia A. An analysis of the Sargasso Sea resource and the consequences for database composition. *BMC Bioinformatics.* 19 de abril de 2006;7:213.
297. Tamames J, Valencia A. The success (or not) of HUGO nomenclature. *Genome Biol.* 2006;7(5):402.
298. Pazos F, Rausell A, Valencia A. Phylogeny-independent detection of functional residues. *Bioinformatics.* 15 de junio de 2006;22(12):1440-8.
299. Llorca O, Betti M, González JM, Valencia A, Márquez AJ, Valpuesta JM. The three-dimensional structure of an eukaryotic glutamine synthetase: functional implications of its oligomeric structure. *J Struct Biol.* diciembre de 2006;156(3):469-79.
300. Krallinger M, Malik R, Valencia A. Text mining and protein annotations: the construction and use of protein description sentences. *Genome Inform.* 2006;17(2):121-30.
301. Izarzugaza JMG, Juan D, Pons C, Ranea JAG, Valencia A, Pazos F. TSEMA: interactive prediction of protein pairings between interacting families. *Nucleic Acids Res.* 1 de julio de 2006;34(Web Server issue):W315-319.
302. Ideker T, Valencia A. Bioinformatics in the human interactome project. *Bioinformatics.* 15 de diciembre de 2006;22(24):2973-4.
303. Hahn U, Valencia A. Semantic Mining in Biomedicine (Introduction to the papers selected from the SMBM 2005 Symposium, Hinxton, U.K., April 2005). *Bioinformatics.* 15 de marzo de 2006;22(6):643-4.
304. de Lorenzo V, Serrano L, Valencia A. Synthetic biology: challenges ahead. *Bioinformatics.* 15 de enero de 2006;22(2):127-8.
305. Carro A, Tress M, de Juan D, Pazos F, Lopez-Romero P, del Sol A, et al. TreeDet: a web server to explore sequence space. *Nucleic Acids Res.* 1 de julio de 2006;34(Web Server issue):W110-115.

306. Cabrera JR, Sanchez-Pulido L, Rojas AM, Valencia A, Mañes S, Naranjo JR, et al. Gas1 is related to the glial cell-derived neurotrophic factor family receptors alpha and regulates Ret signaling. *J Biol Chem*. 19 de mayo de 2006;281(20):14330-9.
307. Bateman A, Valencia A. Structural genomics meets computational biology. *Bioinformatics*. 1 de octubre de 2006;22(19):2319.
308. Valencia A, Pazos F. Prediction of Protein-Protein Interactions from Evolutionary Information. En: Bourne PE, Weissig H, editores. *Methods of Biochemical Analysis* [Internet]. Hoboken, NJ, USA: John Wiley & Sons, Inc.; 2005 [citado 17 de abril de 2020]. p. 409-26. Disponible en: <http://doi.wiley.com/10.1002/0471721204.ch20>
309. Valencia A. Protein refinement: a new challenge for CASP in its 10th anniversary. *Bioinformatics*. 1 de febrero de 2005;21(3):277.
310. Valencia A. Automatic annotation of protein function. *Curr Opin Struct Biol*. junio de 2005;15(3):267-74.
311. Valencia A, Bateman A. INCREASING THE IMPACT OF BIOINFORMATICS. *Bioinformatics*. 1 de enero de 2005;21(1):1-1.
312. Tress M, Tai C-H, Wang G, Ezkurdia I, López G, Valencia A, et al. Domain definition and target classification for CASP6. *Proteins*. 2005;61 Suppl 7:8-18.
313. Tress M, Ezkurdia I, Graña O, López G, Valencia A. Assessment of predictions submitted for the CASP6 comparative modeling category. *Proteins*. 2005;61 Suppl 7:27-45.
314. Tress M, de Juan D, Graña O, Gómez MJ, Gómez-Puertas P, González JM, et al. Scoring docking models with evolutionary information. *Proteins*. 1 de agosto de 2005;60(2):275-80.
315. Rojas AM, Sanchez-Pulido L, Fütterer A, van Wely KHM, Martinez-A C, Valencia A. Death inducer obliterator protein 1 in the context of DNA regulation. Sequence analyses of distant homologues point to a novel functional role. *FEBS J*. julio de 2005;272(14):3505-11.
316. Pazos F, Guijas D, Valencia A, De Lorenzo V. MetaRouter: bioinformatics for bioremediation. *Nucleic Acids Res*. 1 de enero de 2005;33(Database issue):D588-592.
317. Pazos F, Guijas D, Gomez MJ, Trigo A, de Lorenzo V, Valencia A. The Biodegradation Network, a New Scenario for Computational Systems Biology Research. En: Danos V, Schachter V, editores. *Computational Methods in Systems Biology* [Internet]. Berlin, Heidelberg: Springer Berlin Heidelberg; 2005 [citado 17 de abril de 2020]. p. 252-6. (Lecture Notes in Computer Science; vol. 3082). Disponible en: http://link.springer.com/10.1007/978-3-540-25974-9_23
318. Krallinger M, Valencia A. Text-mining and information-retrieval services for molecular biology. *Genome Biol*. 2005;6(7):224.
319. Krallinger M, Valencia A. Applications of Text Mining in Molecular Biology, from Name Recognition to Protein Interaction Maps. En: Azuaje F, Dopazo J, editores. *Data Analysis and Visualization in Genomics and Proteomics* [Internet]. Chichester, UK: John

- Wiley & Sons, Ltd; 2005 [citado 17 de abril de 2020]. p. 41-59. Disponible en: <http://doi.wiley.com/10.1002/0470094419.ch4>
320. Krallinger M, Padron M, Valencia A. A sentence sliding window approach to extract protein annotations from biomedical articles. *BMC Bioinformatics*. 2005;6 Suppl 1:S19.
 321. Krallinger M, Erhardt RA-A, Valencia A. Text-mining approaches in molecular biology and biomedicine. *Drug Discov Today*. 15 de marzo de 2005;10(6):439-45.
 322. Hoffmann R, Valencia A. Implementing the iHOP concept for navigation of biomedical literature. *Bioinformatics*. 1 de septiembre de 2005;21 Suppl 2:ii252-258.
 323. Hoffmann R, Krallinger M, Andres E, Tamames J, Blaschke C, Valencia A. Text mining for metabolic pathways, signaling cascades, and protein networks. *Sci STKE*. 10 de mayo de 2005;2005(283):pe21.
 324. Hoffmann R, Dopazo J, Cigudosa JC, Valencia A. HCAD, closing the gap between breakpoints and genes. *Nucleic Acids Res*. 1 de enero de 2005;33(Database issue):D511-513.
 325. Hirschman L, Yeh A, Blaschke C, Valencia A. Overview of BioCreAtIvE: critical assessment of information extraction for biology. *BMC Bioinformatics*. 2005;6 Suppl 1:S1.
 326. Hirschman L, Blaschke C, Valencia A. The BioLink SIG Workshop at ISMB2004. *Comp Funct Genomics*. 2005;6(1-2):58-60.
 327. Guigo R, Moran F, Valencia A, Abril JF. ECCB/JBI 2005. *Bioinformatics*. 1 de septiembre de 2005;21(Suppl 2):ii1-2.
 328. Graña O, Eyrych VA, Pazos F, Rost B, Valencia A. EVAcon: a protein contact prediction evaluation service. *Nucleic Acids Res*. 1 de julio de 2005;33(Web Server issue):W347-351.
 329. Graña O, Baker D, MacCallum RM, Meiler J, Punta M, Rost B, et al. CASP6 assessment of contact prediction. *Proteins*. 2005;61 Suppl 7:214-24.
 330. Gómez M, Alonso-Allende R, Pazos F, Graña O, Juan D, Valencia A. Accessible Protein Interaction Data for Network Modeling. *Structure of the Information and Available Repositories*. En: Priami C, editor. *Transactions on Computational Systems Biology I* [Internet]. Berlin, Heidelberg: Springer Berlin Heidelberg; 2005 [citado 17 de abril de 2020]. p. 1-13. (Hutchison D, Kanade T, Kittler J, Kleinberg JM, Mattern F, Mitchell JC, et al. *Lecture Notes in Computer Science*; vol. 3380). Disponible en: http://link.springer.com/10.1007/978-3-540-32126-2_1
 331. de Juan D, Mellado M, Rodríguez-Frade JM, Hernanz-Falcón P, Serrano A, del Sol A, et al. A framework for computational and experimental methods: identifying dimerization residues in CCR chemokine receptors. *Bioinformatics*. 1 de septiembre de 2005;21 Suppl 2:ii13-18.
 332. Contreras-Moreira B, Ezkurdia I, Tress ML, Valencia A. Empirical limits for template-based protein structure prediction: the CASP5 example. *FEBS Lett*. 14 de febrero de 2005;579(5):1203-7.

333. Blaschke C, Yeh A, Camon E, Colosimo M, Apweiler R, Hirschman L, et al. Do you do text? *Bioinformatics*. 1 de diciembre de 2005;21(23):4199-200.
334. Blaschke C, Leon EA, Krallinger M, Valencia A. Evaluation of BioCreAtIvE assessment of task 2. *BMC Bioinformatics*. 2005;6 Suppl 1:S16.
335. BioSapiens Network of Excellence. Research networks: BioSapiens: a European network for integrated genome annotation. *Eur J Hum Genet*. septiembre de 2005;13(9):994-7.
336. Bateman A, Valencia A. An update from the Bioinformatics Editors. *Bioinformatics*. 15 de diciembre de 2005;21(24):4319-4319.
337. Agirrezabala X, Martín-Benito J, Valle M, González JM, Valencia A, Valpuesta JM, et al. Structure of the connector of bacteriophage T7 at 8Å resolution: structural homologies of a basic component of a DNA translocating machinery. *J Mol Biol*. 15 de abril de 2005;347(5):895-902.
338. Vargiu P, De Abajo R, Garcia-Ranea JA, Valencia A, Santisteban P, Crespo P, et al. The small GTP-binding protein, Rhes, regulates signal transduction from G protein-coupled receptors. *Oncogene*. 15 de enero de 2004;23(2):559-68.
339. Tress ML, Graña O, Valencia A. SQUARE--determining reliable regions in sequence alignments. *Bioinformatics*. 12 de abril de 2004;20(6):974-5.
340. Sánchez-Pulido L, Rojas AM, van Wely KH, Martínez-A C, Valencia A. SPOC: a widely distributed domain associated with cancer, apoptosis and transcription. *BMC Bioinformatics*. 7 de julio de 2004;5:91.
341. Sanchez-Pulido L, Rojas AM, Valencia A, Martínez-A C, Andrade MA. ACRATA: a novel electron transfer domain associated to apoptosis and cancer. *BMC Cancer*. 29 de diciembre de 2004;4:98.
342. Morillas M, López-Viñas E, Valencia A, Serra D, Gómez-Puertas P, Hegardt FG, et al. Structural model of carnitine palmitoyltransferase I based on the carnitine acetyltransferase crystal. *Biochem J*. 1 de mayo de 2004;379(Pt 3):777-84.
343. Hoffmann R, Valencia A. A gene network for navigating the literature. *Nat Genet*. julio de 2004;36(7):664.
344. Hernanz-Falcón P, Rodríguez-Frade JM, Serrano A, Juan D, del Sol A, Soriano SF, et al. Identification of amino acid residues crucial for chemokine receptor dimerization. *Nat Immunol*. febrero de 2004;5(2):216-23.
345. Hermjakob H, Montecchi-Palazzi L, Lewington C, Mudali S, Kerrien S, Orchard S, et al. IntAct: an open source molecular interaction database. *Nucleic Acids Res*. 1 de enero de 2004;32(Database issue):D452-455.
346. Fernández JM, Valencia A. YAdumper: extracting and translating large information volumes from relational databases to structured flat files. *Bioinformatics*. 12 de octubre de 2004;20(15):2455-7.

347. Blanco FJ, Yee A, Campos-Olivas R, Ortiz AR, Devos D, Valencia A, et al. Solution structure of the hypothetical protein Mth677 from *Methanobacterium thermoautotrophicum*: a novel alpha+beta fold. *Protein Sci.* junio de 2004;13(6):1458-65.
348. van Ham RCHJ, Kamerbeek J, Palacios C, Rausell C, Abascal F, Bastolla U, et al. Reductive genome evolution in *Buchnera aphidicola*. *Proc Natl Acad Sci USA.* 21 de enero de 2003;100(2):581-6.
349. Valencia A, Pazos F. Prediction of protein-protein interactions from evolutionary information. *Methods Biochem Anal.* 2003;44:411-26.
350. Valencia A. Multiple sequence alignments as tools for protein structure and function prediction. *Comp Funct Genomics.* 2003;4(4):424-7.
351. Valencia A. Meta, Meta(N) and cyber servers. *Bioinformatics.* 1 de mayo de 2003;19(7):795.
352. Tress ML, Jones D, Valencia A. Predicting reliable regions in protein alignments from sequence profiles. *J Mol Biol.* 18 de julio de 2003;330(4):705-18.
353. Sarnago S, Roca R, de Blasi A, Valencia A, Mayor F, Murga C. Involvement of intramolecular interactions in the regulation of G protein-coupled receptor kinase 2. *Mol Pharmacol.* septiembre de 2003;64(3):629-39.
354. Sánchez-Pulido L, Devos D, Genevrois S, Vicente M, Valencia A. POTRA: a conserved domain in the FtsQ family and a class of beta-barrel outer membrane proteins. *Trends Biochem Sci.* octubre de 2003;28(10):523-6.
355. Pons T, Gómez R, Chinae G, Valencia A. Beta-propellers: associated functions and their role in human diseases. *Curr Med Chem.* marzo de 2003;10(6):505-24.
356. Pazos F, Valencia A, De Lorenzo V. The organization of the microbial biodegradation network from a systems-biology perspective. *EMBO Rep.* octubre de 2003;4(10):994-9.
357. Ouzounis CA, Valencia A. Early bioinformatics: the birth of a discipline--a personal view. *Bioinformatics.* 22 de noviembre de 2003;19(17):2176-90.
358. Morillas M, Gómez-Puertas P, Bentebibel A, Sellés E, Casals N, Valencia A, et al. Identification of conserved amino acid residues in rat liver carnitine palmitoyltransferase I critical for malonyl-CoA inhibition. Mutation of methionine 593 abolishes malonyl-CoA inhibition. *J Biol Chem.* 14 de marzo de 2003;278(11):9058-63.
359. Koh IYY, Eyrich VA, Marti-Renom MA, Przybylski D, Madhusudhan MS, Eswar N, et al. EVA: Evaluation of protein structure prediction servers. *Nucleic Acids Res.* 1 de julio de 2003;31(13):3311-5.
360. Juan D, Graña O, Pazos F, Fariselli P, Casadio R, Valencia A. A neural network approach to evaluate fold recognition results. *Proteins.* 1 de marzo de 2003;50(4):600-8.

361. Iliopoulos I, Tsoka S, Andrade MA, Enright AJ, Carroll M, Pouillet P, et al. Evaluation of annotation strategies using an entire genome sequence. *Bioinformatics*. 12 de abril de 2003;19(6):717-26.
362. Hoffmann R, Valencia A. Protein interaction: same network, different hubs. *Trends Genet*. diciembre de 2003;19(12):681-3.
363. Hoffmann R, Valencia A. Life cycles of successful genes. *Trends Genet*. febrero de 2003;19(2):79-81.
364. Gomez-Puertas P, Valencia A. ESF Programme on «Integrated Approaches for Functional Genomics» Workshop on «Modelling of Molecular Networks». *Comp Funct Genomics*. 2003;4(1):144-7.
365. Eyrich VA, Przybylski D, Koh IYY, Grana O, Pazos F, Valencia A, et al. CAFASP3 in the spotlight of EVA. *Proteins*. 2003;53 Suppl 6:548-60.
366. del Sol A, del Sol Mesa A, Pazos F, Valencia A. Automatic methods for predicting functionally important residues. *J Mol Biol*. 28 de febrero de 2003;326(4):1289-302.
367. Casals N, Gómez-Puertas P, Pié J, Mir C, Roca R, Puisac B, et al. Structural (betaalpha)8 TIM barrel model of 3-hydroxy-3-methylglutaryl-coenzyme A lyase. *J Biol Chem*. 1 de agosto de 2003;278(31):29016-23.
368. Carettoni D, Gómez-Puertas P, Yim L, Mingorance J, Massidda O, Vicente M, et al. Phage-display and correlated mutations identify an essential region of subdomain 1C involved in homodimerization of Escherichia coli FtsA. *Proteins*. 1 de febrero de 2003;50(2):192-206.
369. Blaschke C, Yeh A, Hirschman L, Valencia A. ISMB 2003 Text Mining SIG Meeting Report. *Comp Funct Genomics*. 2003;4(6):667-73.
370. Blaschke C, Valencia A. Automatic classification of protein functions from the literature. *Comp Funct Genomics*. 2003;4(1):75-9.
371. Blaschke C, Hirschman L, Yeh A, Valencia A. Critical assessment of information extraction systems in biology. *Comp Funct Genomics*. 2003;4(6):674-7.
372. Balsera M, Arellano JB, Pazos F, Devos D, Valencia A, De Las Rivas J. The single tryptophan of the PsbQ protein of photosystem II is at the end of a 4-alpha-helical bundle domain. *Eur J Biochem*. octubre de 2003;270(19):3916-27.
373. Abascal F, Valencia A. Automatic annotation of protein function based on family identification. *Proteins*. 15 de noviembre de 2003;53(3):683-92.
374. Valencia A, Pazos F. Computational methods for the prediction of protein interactions. *Curr Opin Struct Biol*. junio de 2002;12(3):368-73.
375. Valencia A. Search and retrieve. Large-scale data generation is becoming increasingly important in biological research. But how good are the tools to make sense of the data? *EMBO Rep*. mayo de 2002;3(5):396-400.

376. Valencia A. Bioinformatics: biology by other means. *Bioinformatics*. diciembre de 2002;18(12):1551-2.
377. Valencia A. Bioinformatics and Computational Biology at the crossroads of post-genomic technology. *Phytochemistry Reviews*. mayo de 2002;1(2):209-14.
378. Tamames J, Clark D, Herrero J, Dopazo J, Blaschke C, Fernández JM, et al. Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. *J Biotechnol*. 25 de septiembre de 2002;98(2-3):269-83.
379. Sánchez-Pulido L, Martín-Belmonte F, Valencia A, Alonso MA. MARVEL: a conserved domain involved in membrane apposition events. *Trends Biochem Sci*. diciembre de 2002;27(12):599-601.
380. Sánchez-Pulido L, Devos D, Valencia A. BRICHOS: a conserved domain in proteins associated with dementia, respiratory distress and cancer. *Trends Biochem Sci*. julio de 2002;27(7):329-32.
381. Rost B, Honig B, Valencia A. Bioinformatics in structural genomics. *Bioinformatics*. julio de 2002;18(7):897-8.
382. Pazos F, Valencia A. In silico two-hybrid system for the selection of physically interacting protein pairs. *Proteins*. 1 de mayo de 2002;47(2):219-27.
383. Paz-Ares J, Regia Consortium. REGIA, an EU project on functional genomics of transcription factors from *Arabidopsis Thaliana*. *Comp Funct Genomics*. 2002;3(2):102-8.
384. Morillas M, Gómez-Puertas P, Rubí B, Clotet J, Ariño J, Valencia A, et al. Structural model of a malonyl-CoA-binding site of carnitine octanoyltransferase and carnitine palmitoyltransferase I: mutational analysis of a malonyl-CoA affinity domain. *J Biol Chem*. 29 de marzo de 2002;277(13):11473-80.
385. Ligos JM, de Lera TL, Hinderlich S, Guinea B, Sánchez L, Roca R, et al. Functional interaction between the Ser/Thr kinase PKL12 and N-acetylglucosamine kinase, a prominent enzyme implicated in the salvage pathway for GlcNAc recycling. *J Biol Chem*. 22 de febrero de 2002;277(8):6333-43.
386. Jensen LJ, Gupta R, Blom N, Devos D, Tamames J, Kesmir C, et al. Prediction of human protein function from post-translational modifications and localization features. *J Mol Biol*. 21 de junio de 2002;319(5):1257-65.
387. Garcia-Ranea JA, Mirey G, Camonis J, Valencia A. p23 and HSP20/alpha-crystallin proteins define a conserved sequence domain present in other eukaryotic protein families. *FEBS Lett*. 9 de octubre de 2002;529(2-3):162-7.
388. Fariselli P, Pazos F, Valencia A, Casadio R. Prediction of protein--protein interaction sites in heterocomplexes with neural networks. *Eur J Biochem*. marzo de 2002;269(5):1356-61.
389. Devos D, Garmendia J, de Lorenzo V, Valencia A. Deciphering the action of aromatic effectors on the prokaryotic enhancer-binding protein XylR: a structural model of its N-terminal domain. *Environ Microbiol*. enero de 2002;4(1):29-41.

390. de Daruvar A, Collado-Vides J, Valencia A. Analysis of the cellular functions of *Escherichia coli* operons and their conservation in *Bacillus subtilis*. *J Mol Evol.* agosto de 2002;55(2):211-21.
391. Blaschke C, Valencia A. Molecular biology nomenclature thwarts information-extraction progress. *IEEE Intell Syst their Appl.* mayo de 2002;17(3).
392. Blaschke C, Valencia A. Automatic ontology construction from the literature. *Genome Inform.* 2002;13:201-13.
393. Blaschke C, Hirschman L, Valencia A. Information extraction in molecular biology. *Brief Bioinformatics.* junio de 2002;3(2):154-65.
394. Blaschke C, Valencia A. The frame-based module of the SUISEKI information extraction system. *IEEE Intell Syst.* marzo de 2002;17(2):14-20.
395. Asturias JA, Gómez-Bayón N, Arilla MC, Sánchez-Pulido L, Valencia A, Martínez A. Molecular and structural analysis of the panallergen profilin B cell epitopes defined by monoclonal antibodies. *Int Immunol.* septiembre de 2002;14(9):993-1001.
396. Alonso-Allende R, Fernández-González JM, Graña O, Valencia A. The REGIA database (RegiaDB): status, limitations and future developments. *Comp Funct Genomics.* 2002;3(2):109-14.
397. Abascal F, Valencia A. Clustering of proximal sequence space for the identification of protein families. *Bioinformatics.* julio de 2002;18(7):908-21.
398. Torán JL, Sánchez-Pulido L, Kremer L, del Real G, Valencia A, Martínez-A C. Improvement in affinity and HIV-1 neutralization by somatic mutation in the heavy chain first complementarity-determining region of antibodies triggered by HIV-1 infection. *Eur J Immunol.* enero de 2001;31(1):128-37.
399. Tamames J, González-Moreno M, Mingorance J, Valencia A, Vicente M. Bringing gene order into bacterial shape. *Trends Genet.* marzo de 2001;17(3):124-6.
400. Pazos F, Valencia A. Similarity of phylogenetic trees as indicator of protein-protein interaction. *Protein Eng.* septiembre de 2001;14(9):609-14.
401. Pazos F, Heredia P, Valencia A, de las Rivas J. Threading structural model of the manganese-stabilizing protein PsbO reveals presence of two possible beta-sandwich domains. *Proteins.* 1 de diciembre de 2001;45(4):372-81.
402. Morillas M, Gómez-Puertas P, Roca R, Serra D, Asins G, Valencia A, et al. Structural model of the catalytic core of carnitine palmitoyltransferase I and carnitine octanoyltransferase (COT): mutation of CPT I histidine 473 and alanine 381 and COT alanine 238 impairs the catalytic activity. *J Biol Chem.* 30 de noviembre de 2001;276(48):45001-8.
403. Mingorance J, Rueda S, Gómez-Puertas P, Valencia A, Vicente M. *Escherichia coli* FtsZ polymers contain mostly GTP and have a high nucleotide turnover. *Mol Microbiol.* julio de 2001;41(1):83-91.

404. Iliopoulos I, Tsoka S, Andrade MA, Janssen P, Audit B, Tramontano A, et al. Genome sequences and great expectations. *Genome Biol.* 2001;2(1):INTERACTIONS0001.
405. Herrero J, Valencia A, Dopazo J. A hierarchical unsupervised growing neural network for clustering gene expression patterns. *Bioinformatics.* febrero de 2001;17(2):126-36.
406. Garmendia J, Devos D, Valencia A, de Lorenzo V. A la carte transcriptional regulators: unlocking responses of the prokaryotic enhancer-binding protein XylR to non-natural effectors. *Mol Microbiol.* octubre de 2001;42(1):47-59.
407. Fischer D, Elofsson A, Rychlewski L, Pazos F, Valencia A, Rost B, et al. CAFASP2: the second critical assessment of fully automated structure prediction methods. *Proteins.* 2001;Suppl 5:171-83.
408. Fariselli P, Olmea O, Valencia A, Casadio R. Progress in predicting inter-residue contacts of proteins with neural networks and correlated mutations. *Proteins.* 2001;Suppl 5:157-62.
409. Fariselli P, Olmea O, Valencia A, Casadio R. Prediction of contact maps with neural networks and correlated mutations. *Protein Eng.* noviembre de 2001;14(11):835-43.
410. Eyrich VA, Martí-Renom MA, Przybylski D, Madhusudhan MS, Fiser A, Pazos F, et al. EVA: continuous automatic evaluation of protein structure prediction servers. *Bioinformatics.* diciembre de 2001;17(12):1242-3.
411. Devos D, Valencia A. Intrinsic errors in genome annotation. *Trends Genet.* agosto de 2001;17(8):429-31.
412. Chillarón J, Roca R, Valencia A, Zorzano A, Palacín M. Heteromeric amino acid transporters: biochemistry, genetics, and physiology. *Am J Physiol Renal Physiol.* diciembre de 2001;281(6):F995-1018.
413. Blaschke C, Valencia A. The potential use of SUISEKI as a protein interaction discovery tool. *Genome Inform.* 2001;12:123-34.
414. Blaschke C, Valencia A. Can bibliographic pointers for known biological data be found automatically? Protein interactions as a case study. *Comp Funct Genomics.* 2001;2(4):196-206.
415. Blaschke C, Oliveros JC, Valencia A. Mining functional information associated with expression arrays. *Funct Integr Genomics.* marzo de 2001;1(4):256-68.
416. Blaschke C, Hoffmann R, Oliveros JC, Valencia A. Extracting information automatically from biological literature. *Comp Funct Genomics.* 2001;2(5):310-3.
417. Via A, Ferrè F, Brannetti B, Valencia A, Helmer-Citterich M. Three-dimensional view of the surface motif associated with the P-loop structure: cis and trans cases of convergent evolution. *J Mol Biol.* 3 de noviembre de 2000;303(4):455-65.

418. Oliveros JC, Blaschke C, Herrero J, Dopazo J, Valencia A. Expression profiles and biological function. *Genome Inform Ser Workshop Genome Inform.* 2000;11:106-17.
419. Devos D, Valencia A. Practical limits of function prediction. *Proteins.* 1 de octubre de 2000;41(1):98-107.
420. Torán JL, Kremer L, Sánchez-Pulido L, de Alborán IM, del Real G, Llorente M, et al. Molecular analysis of HIV-1 gp120 antibody response using isotype IgM and IgG phage display libraries from a long-term non-progressor HIV-1-infected individual. *Eur J Immunol.* 1999;29(9):2666-75.
421. Pazos F, Rost B, Valencia A. A platform for integrating threading results with protein family analyses. *Bioinformatics.* diciembre de 1999;15(12):1062-3.
422. Olmea O, Rost B, Valencia A. Effective use of sequence correlation and conservation in fold recognition. *J Mol Biol.* 12 de noviembre de 1999;293(5):1221-39.
423. Blaschke C, Andrade MA, Ouzounis C, Valencia A. Automatic extraction of biological information from scientific text: protein-protein interactions. *Proc Int Conf Intell Syst Mol Biol.* 1999;60-7.
424. Bauer B, Mirey G, Vetter IR, García-Ranea JA, Valencia A, Wittinghofer A, et al. Effector recognition by the small GTP-binding proteins Ras and Ral. *J Biol Chem.* 18 de junio de 1999;274(25):17763-70.
425. Azuma Y, Renault L, García-Ranea JA, Valencia A, Nishimoto T, Wittinghofer A. Model of the ran-RCC1 interaction using biochemical and docking experiments. *J Mol Biol.* 18 de junio de 1999;289(4):1119-30.
426. Andrade MA, Ouzounis C, Sander C, Tamames J, Valencia A. Functional classes in the three domains of life. *J Mol Evol.* noviembre de 1999;49(5):551-7.
427. Andrade MA, Brown NP, Leroy C, Hoersch S, de Daruvar A, Reich C, et al. Automated genome sequence analysis and annotation. *Bioinformatics.* mayo de 1999;15(5):391-412.
428. Alvarez-Dolado M, González-Moreno M, Valencia A, Zenke M, Bernal J, Muñoz A. Identification of a mammalian homologue of the fungal Tom70 mitochondrial precursor protein import receptor as a thyroid hormone-regulated gene in specific brain regions. *J Neurochem.* diciembre de 1999;73(6):2240-9.
429. Uez OC, Knez V, Fernández Pascua CA, Gutiérrez ML, Sánchez-Pulido L, Valencia A, et al. Influenza virus epidemiological surveillance in Argentina, 1987-1993, with molecular characterization of 1990 and 1993 isolates. *Rev Panam Salud Publica.* diciembre de 1998;4(6):405-10.
430. Trelles O, Andrade MA, Valencia A, Zapata EL, Carazo JM. Computational space reduction and parallelization of a new clustering approach for large groups of sequences. *Bioinformatics.* junio de 1998;14(5):439-51.

431. Tamames J, Ouzounis C, Casari G, Sander C, Valencia A. EUCLID: automatic classification of proteins in functional classes by their database annotations. *Bioinformatics*. 1998;14(6):542-3.
432. Sancho E, Vilá MR, Sánchez-Pulido L, Lozano JJ, Paciucci R, Nadal M, et al. Role of UEV-1, an inactive variant of the E2 ubiquitin-conjugating enzymes, in in vitro differentiation and cell cycle behavior of HT-29-M6 intestinal mucosecretory cells. *Mol Cell Biol*. enero de 1998;18(1):576-89.
433. Pons T, Olmea O, Chinae G, Beldarraín A, Márquez G, Acosta N, et al. Structural model for family 32 of glycosyl-hydrolase enzymes. *Proteins*. 15 de noviembre de 1998;33(3):383-95.
434. Pons T, Chinae G, Olmea O, Beldarraín A, Roca H, Padrón G, et al. Structural model of Dex protein from *Penicillium minioluteum* and its implications in the mechanism of catalysis. *Proteins*. 1 de junio de 1998;31(4):345-54.
435. Ouzounis C, Pérez-Irratxeta C, Sander C, Valencia A. Are binding residues conserved? *Pac Symp Biocomput*. 1998;401-12.
436. Ouzounis C, Pérez-Irratxeta C, Sander C, Valencia A. Are binding residues conserved? *Pac Symp Biocomput*. 1998;401-12.
437. Gässler CS, Buchberger A, Laufen T, Mayer MP, Schröder H, Valencia A, et al. Mutations in the DnaK chaperone affecting interaction with the DnaJ cochaperone. *Proc Natl Acad Sci USA*. 22 de diciembre de 1998;95(26):15229-34.
438. Garcia-Ranea JA, Valencia A. Distribution and functional diversification of the ras superfamily in *Saccharomyces cerevisiae*. *FEBS Lett*. 4 de septiembre de 1998;434(3):219-25.
439. Atrian S, Sánchez-Pulido L, González-Duarte R, Valencia A. Shaping of *Drosophila* alcohol dehydrogenase through evolution: relationship with enzyme functionality. *J Mol Evol*. agosto de 1998;47(2):211-21.
440. Andrade MA, Valencia A. Automatic extraction of keywords from scientific text: application to the knowledge domain of protein families. *Bioinformatics*. 1998;14(7):600-7.
441. Andrade MA, Sander C, Valencia A. Updated catalogue of homologues to human disease-related proteins in the yeast genome. *FEBS Lett*. 10 de abril de 1998;426(1):7-16.
442. Voss H, Benes V, Andrade MA, Valencia A, Rechmann S, Teodoru C, et al. DNA sequencing and analysis of 130 kb from yeast chromosome XV. *Yeast*. 15 de junio de 1997;13(7):655-72.
443. Tamames J, Casari G, Ouzounis C, Valencia A. Conserved clusters of functionally related genes in two bacterial genomes. *J Mol Evol*. enero de 1997;44(1):66-73.
444. Solano R, Fuertes A, Sánchez-Pulido L, Valencia A, Paz-Ares J. A single residue substitution causes a switch from the dual DNA binding specificity of plant transcription factor MYB.Ph3 to the animal c-MYB specificity. *J Biol Chem*. 31 de enero de 1997;272(5):2889-95.

- 445. Pazos F, Olmea O, Valencia A. A graphical interface for correlated mutations and other protein structure prediction methods. *Comput Appl Biosci.* junio de 1997;13(3):319-21.
- 446. Pazos F, Helmer-Citterich M, Ausiello G, Valencia A. Correlated mutations contain information about protein-protein interaction. *J Mol Biol.* 29 de agosto de 1997;271(4):511-23.
- 447. Olmea O, Valencia A. Improving contact predictions by the combination of correlated mutations and other sources of sequence information. *Fold Des.* 1997;2(3):S25-32.
- 448. Kato Z, Fukuda S, Tomatsu S, Vega H, Yasunaga T, Yamagishi A, et al. A novel common missense mutation G301C in the N-acetylgalactosamine-6-sulfate sulfatase gene in mucopolysaccharidosis IVA. *Hum Genet.* noviembre de 1997;101(1):97-101.
- 449. Espeso EA, Tilburn J, Sánchez-Pulido L, Brown CV, Valencia A, Arst HN, et al. Specific DNA recognition by the *Aspergillus nidulans* three zinc finger transcription factor PacC. *J Mol Biol.* 12 de diciembre de 1997;274(4):466-80.
- 450. Andrade M, Casari G, de Daruvar A, Sander C, Schneider R, Tamames J, et al. Sequence analysis of the *Methanococcus jannaschii* genome and the prediction of protein function. *Comput Appl Biosci.* agosto de 1997;13(4):481-3.
- 451. Andrade MA, Valencia A. Automatic annotation for biological sequences by extraction of keywords from MEDLINE abstracts. Development of a prototype system. *Proc Int Conf Intell Syst Mol Biol.* 1997;5:25-32.
- 452. Andrade MA, Casari G, Sander C, Valencia A. Classification of protein families and detection of the determinant residues with an improved self-organizing map. *Biol Cybern.* junio de 1997;76(6):441-50.
- 453. Tamames J, Ouzounis C, Sander C, Valencia A. Genomes with distinct function composition. *FEBS Lett.* 24 de junio de 1996;389(1):96-101.
- 454. Rost B, Valencia A. Pitfalls of protein sequence analysis. *Curr Opin Biotechnol.* agosto de 1996;7(4):457-61.
- 455. Ouzounis C, Casari G, Valencia A, Sander C. Novelties from the complete genome of *Mycoplasma genitalium*. *Mol Microbiol.* mayo de 1996;20(4):898-900.
- 456. Ouzounis C, Casari G, Sander C, Tamames J, Valencia A. Computational comparisons of model genomes. *Trends Biotechnol.* agosto de 1996;14(8):280-5.
- 457. Martín-Gallardo A, Moratilla M, Funes JM, Agromayor M, Nuñez A, Varas AJ, et al. Sequence analysis of a *Molluscum contagiosum* virus DNA region which includes the gene encoding protein kinase 2 and other genes with unique organization. *Virus Genes.* 1996;13(1):19-29.

458. Feussner G, Albanese M, Valencia A. Three-dimensional structure of the LDL receptor-binding domain of the human apolipoprotein E2 (Arg136-->Cys) variant. *Atherosclerosis*. 25 de octubre de 1996;126(2):177-84.
459. Feussner G, Albanese M, Mann WA, Valencia A, Schuster H. Apolipoprotein E2 (Arg-136-->Cys), a variant of apolipoprotein E associated with late-onset dominance of type III hyperlipoproteinaemia. *Eur J Clin Invest*. enero de 1996;26(1):13-23.
460. Voss H, Tamames J, Teodoru C, Valencia A, Sensen C, Wiemann S, et al. Nucleotide sequence and analysis of the centromeric region of yeast chromosome IX. *Yeast*. enero de 1995;11(1):61-78.
461. Valencia A, Hubbard TJ, Muga A, Bañuelos S, Llorca O, Carrascosa JL, et al. Prediction of the structure of GroES and its interaction with GroEL. *Proteins*. julio de 1995;22(3):199-209.
462. Ouzounis C, Valencia A, Tamames J, Bork P, Sander C. The functional composition of living machines as a design principle for artificial organisms. En: Morán F, Moreno A, Merelo JJ, Chacón P, editores. *Advances in Artificial Life* [Internet]. Berlin, Heidelberg: Springer Berlin Heidelberg; 1995 [citado 20 de abril de 2020]. p. 841-51. (Goos G, Hartmanis J, Leeuwen J, Carbonell JG, Siekmann J. *Lecture Notes in Computer Science*; vol. 929). Disponible en: http://link.springer.com/10.1007/3-540-59496-5_347
463. Casari G, Sander C, Valencia A. A method to predict functional residues in proteins. *Nat Struct Biol*. febrero de 1995;2(2):171-8.
464. Casari G, Andrade MA, Bork P, Boyle J, Daruvar A, Ouzounis C, et al. Challenging times for bioinformatics. *Nature*. 24 de agosto de 1995;376(6542):647-8.
465. Albo C, Valencia A, Portela A. Identification of an RNA binding region within the N-terminal third of the influenza A virus nucleoprotein. *J Virol*. junio de 1995;69(6):3799-806.
466. Stenmark H, Valencia A, Martinez O, Ullrich O, Goud B, Zerial M. Distinct structural elements of rab5 define its functional specificity. *EMBO J*. 1 de febrero de 1994;13(3):575-83.
467. Scharf M, Schneider R, Casari G, Bork P, Valencia A, Ouzounis C, et al. GeneQuiz: a workbench for sequence analysis. *Proc Int Conf Intell Syst Mol Biol*. 1994;2:348-53.
468. Sánchez M, Valencia A, Ferrándiz MJ, Sander C, Vicente M. Correlation between the structure and biochemical activities of FtsA, an essential cell division protein of the actin family. *EMBO J*. 17 de octubre de 1994;13(20):4919-25.
469. Lütcke A, Parton RG, Murphy C, Olkkonen VM, Dupree P, Valencia A, et al. Cloning and subcellular localization of novel rab proteins reveals polarized and cell type-specific expression. *J Cell Sci*. diciembre de 1994;107 (Pt 12):3437-48.
470. Koonin EV, Mushegian AR, Tatusov RL, Altschul SF, Bryant SH, Bork P, et al. Eukaryotic translation elongation factor 1 gamma contains a glutathione transferase domain--study of a diverse, ancient protein superfamily using motif search and structural modeling. *Protein Sci*. noviembre de 1994;3(11):2045-54.

471. Göbel U, Sander C, Schneider R, Valencia A. Correlated mutations and residue contacts in proteins. *Proteins*. abril de 1994;18(4):309-17.
472. Buchberger A, Valencia A, McMacken R, Sander C, Bukau B. The chaperone function of DnaK requires the coupling of ATPase activity with substrate binding through residue E171. *EMBO J*. 1 de abril de 1994;13(7):1687-95.
473. Buchberger A, Schröder H, Büttner M, Valencia A, Bukau B. A conserved loop in the ATPase domain of the DnaK chaperone is essential for stable binding of GrpE. *Nat Struct Biol*. febrero de 1994;1(2):95-101.
474. Stouten PF, Sander C, Wittinghofer A, Valencia A. How does the switch II region of G-domains work? *FEBS Lett*. 29 de marzo de 1993;320(1):1-6.
475. Lütcke A, Jansson S, Parton RG, Chavrier P, Valencia A, Huber LA, et al. Rab17, a novel small GTPase, is specific for epithelial cells and is induced during cell polarization. *J Cell Biol*. mayo de 1993;121(3):553-64.
476. Holmes KC, Sander C, Valencia A. A new ATP-binding fold in actin, hexokinase and Hsc70. *Trends Cell Biol*. febrero de 1993;3(2):53-9.
477. Bork P, Sander C, Valencia A. Convergent evolution of similar enzymatic function on different protein folds: the hexokinase, ribokinase, and galactokinase families of sugar kinases. *Protein Sci*. enero de 1993;2(1):31-40.
478. Bork P, Sander C, Valencia A. An ATPase domain common to prokaryotic cell cycle proteins, sugar kinases, actin, and hsp70 heat shock proteins. *Proc Natl Acad Sci USA*. 15 de agosto de 1992;89(16):7290-4.
479. Bork P, Sander C, Valencia A, Bukau B. A module of the DnaJ heat shock proteins found in malaria parasites. *Trends Biochem Sci*. abril de 1992;17(4):129.
480. Valencia A, Kjeldgaard M, Pai EF, Sander C. GTPase domains of ras p21 oncogene protein and elongation factor Tu: analysis of three-dimensional structures, sequence families, and functional sites. *Proc Natl Acad Sci USA*. 15 de junio de 1991;88(12):5443-7.
481. Valencia A, Chardin P, Wittinghofer A, Sander C. The ras protein family: evolutionary tree and role of conserved amino acids. *Biochemistry*. 14 de mayo de 1991;30(19):4637-48.
482. Valencia A, Pestaña A, Cano A. Spectroscopical studies on the structural organization of the lectin discoidin I: analysis of sugar- and calcium-binding activities. *Biochim Biophys Acta*. 27 de enero de 1989;990(1):93-7.
483. Valencia A, Serrano L, Caballero R, Anderson PS, Lacal JC. Conformational alterations detected by circular dichroism induced in the normal ras p21 protein by activating point mutations at position 12, 59, or 61. *Eur J Biochem*. 1 de julio de 1988;174(4):621-7.

484. Valencia A, Pestaña A, Cano A. Developmental changes in the structural organization of the lectin discoidin I detected by limited proteolysis. *Biochem Biophys Res Commun.* 16 de mayo de 1988;152(3):1332-8.
485. Valencia A, Cano A, Caballero R, Pestaña A. Spectroscopic studies on the structural organization of the lectin discoidin I: homologies with fibronectin. *Biochim Biophys Acta.* 5 de enero de 1987;911(1):11-8.
486. Serrano L, Valencia A, Caballero R, Avila J. Localization of the high affinity calcium-binding site on tubulin molecule. *J Biol Chem.* 25 de mayo de 1986;261(15):7076-81.
487. García Prieto, Carlos A. Martínez-Jiménez, Francisco. Valencia, Alfonso. Porta-Pardo, Eduard. Detection of oncogenic and clinically actionable mutations in cancer genomes critically depends on variant calling tools. *Bioinformatics* 2022 Nov 3;14(21):4645. doi: 10.3390/nu14214645.
488. Akdel, Mehmet, E V Pires, Douglas, Porta Pardo, Eduard, Jänes, Jürgen, Zalevsky, Arthur O., Mészáros, Bálint, Bryant, Patrick, L Good, Lydia L., Laskowski, Roman A., Pozzati, Gabriele, Shenoy, Aditi, Zhu, Wensi, Kundrotas, Petras, Ruiz Serra, Victoria, Rodrigues, Carlos H.M., S Dunham, Alistair, Burke, David, Borkakoti, Neera, Velankar, Sameer, Frost, Adam, Basquin, Jérôme, Lindorff-Larsen, Kresten, Bateman, Alex, Andrey V Kajava, Andrey, Valencia, Alfonso, Ovchinnikov, Serge , Durairaj, Janani, Ascher, David B., Thornton, Janet M., Davey, Norman E., Stein Amelie , Elofsson, Arne, Croll, Tristan I. Beltrao, Pedro. A structural biology community assessment of AlphaFold2 applications. *Nat Struct Mol Biol.* 2022 Nov 7. doi: 10.1038/s41594-022-00849-w.
489. Karolina Jodkowska, Vera Pancaldi , Maria Rigau, Ricardo Almeida, José M Fernández-Justel, Osvaldo Graña-Castro, Sara Rodríguez-Acebes, Miriam Rubio-Camarillo, Enrique Carrillo-de Santa Pau, David Pisano, Fátima Al-Shahrour, Alfonso Valencia, María Gómez, Juan Méndez. 3D chromatin connectivity underlies replication origin efficiency in mouse embryonic stem cells. *Nucleic Acids Research*, 2022 Nov 28;50(21):12149-12165. doi: 10.1093/nar/gkac1111.
490. Marta Villegas , Aitor Gonzalez-Agirre , Asier Gutiérrez-Fandiño, Jordi Armengol-Estapé, Casimiro Pio Carrino , David Pérez-Fernández, Felipe Soares, Pablo Serrano, Miguel Pedrera, Noelia García, Alfonso Valencia. Predicting the evolution of COVID-19 mortality risk: A Recurrent Neural Network approach. *Computer Methods and Programs in Biomedecine Update.* 2022 Dec. 29.
491. Laureano Tomás-Daza, Llorenç Rovirosa, Paula López-Martí, Andrea Nieto-Aliseda, François Serra, Ainoa Planas-Riverola, Oscar Molina, Rebecca McDonald, Cedric Ghevaert, Esther Cuatrecasas, Dolors Costa, Mireia Camós, Clara Bueno, Pablo Menéndez, Alfonso Valencia & Biola M. Javierre. "Low input capture Hi-C (liCHi-C) identifies promoter-enhancer interactions at high-resolution". *Nature communications* 14, article nr. 268. 2023 Jan 17th.
492. Jon Sánchez-Valle, Rion Brattig Correia, Marta Camacho-Artacho, Rosalba Lepore, Mauro M Mattos, Luis M Rocha, Alfonso Valencia. "Analysis of electronic health records

- from three distinct and large populations reveals high prevalence and biases in the co-administration of drugs known to interact". National Library of Medicine, 2023, Feb. 8.
493. Michael Baumann , Julio Celis , Ulrik Ringborg , Manuel Heitor , Anton Berns , Tit Albrecht , Jeliazko Arabadjiev , Michael Boutros , Mario Brandenburg , Helena Canhao , Fatima Carneiro, Christine Chomienne , Francesco De Lorenzo , Alexander M M Eggermont , Angel Font , Elena Garralda , Margarida Goulart , Rui Henrique , Mark Lawler , Lena Maier-Hein , Francoise Meunier , Simon Oberst , Pedro Oliveira , Maria Papatriantafyllou , Joachim Schüz Eric Solary , Alfonso Valencia , Rosalia Vargas , Elisabete Weiderpass , Nils Wilking. "Engaging European society at the forefront of cancer research and care. How discussions at the 5th Gago Conference on European Science policy led to the Heidelberg Manifesto". Molecular Oncology, 2023 March 20th.
 494. Llorenç Roviro , Laureano Tomás-Daza , Blanca Urmeneta , Alfonso Valencia, Biola M Javierre. "An Integrated Workflow to Study the Promoter-Centric Spatio-Temporal Genome Architecture in Scarce Cell Populations". National Library of Medicine, April 21st, 2023.
 495. Baumann M, Celis J, Ringborg U, Heitor M, Berns A, Albrecht T, Arabadjiev J, Boutros M, Brandenburg M, Canhao H, Carneiro F, Chomienne C, De Lorenzo F, Eggermont AMM, Font A, Garralda E, Goulart M, Henrique R, Lawler M, Maier-Hein L, Meunier F, Oberst S, Oliveira P, Papatriantafyllou M, Schüz J, Solary E, Valencia A, Vargas R, Weiderpass E, Wilking N. "Engaging European society at the forefront of cancer research and care: How discussions at the 5th Gago Conference on European Science policy led to the Heidelberg Manifesto: How discussions at the 5th Gago Conference on European Science policy led to the Heidelberg Manifesto". Molecular Oncology, Vol. 17, issue 6, March 20th, 2023.
 496. Sanz F, Pognan F, Steger-Hartmann T, Díaz C, Asakura S, Amberg A, Bécourt-Lhote N, Blomberg N, Bosc N, Briggs K, Bringezu F, Brulle-Wohlhueter C, Brunak S, Bueters R, Callegaro G, Capella-Gutierrez S, Centeno E, Corvi J, Cronin MTD, Drew P, Duchateau-Nguyen G, Ecker GF, Escher S, Felix E, Ferreira M, Frericks M, Furlong LI, Geiger R, George C, Grandits M, Ivanov-Draganov D, Kilgour-Christie J, Kiziloren T, Kors JA, Koyama N, Kreuchwig A, Leach AR, Mayer MA, Monecke P, Muster W, Nakazawa CM, Nicholson G, Parry R, Pastor M, Piñero J, Oberhauser N, Ramírez-Anguaita JM, Rodrigo A, Smajic A, Schaefer M, Schieferdecker S, Soininen I, Terricabras E, Trairatphisan P, Turner SC, Valencia A, van de Water B, van der Lei JL, van Mulligen EM, Vock E, Wilkinson D. "eTRANSAFE: data science to empower translational safety assessment". Nature Reviews Drug Discovery, June 14th 2023.
 497. Sánchez-Valle, Jon; Alfonso Valencia. "Molecular bases of comorbidities: present and future perspectives". Trends in genetics, October 2023, Vol. 39, No. 10.
 498. Ferran Sanz, François Pognan, Thomas Steger-Hartmann, Carlos Díaz, Shoji Asakura, Alexander Amberg, Nathalie Bécourt-Lhote, Niklas Blomberg, Nicolas Bosc, Katharine Briggs, Frank Bringezu, Claire Brulle-Wohlhueter, Søren Brunak, Ruud Bueters, Giulia Callegaro, Salvador Capella-Gutierrez, Emilio Centeno, Javier Corvi, Mark T D Cronin, Philip Drew, Guillemette Duchateau-Nguyen, Gerhard F Ecker, Sylvia Escher, Eloy Felix, Miguel Ferreira, Markus Frericks, Laura I Furlong, Robert Geiger, Catherine George, Melanie Grandits, Dragomir Ivanov-Draganov, Jean Kilgour-Christie, Tevfik Kiziloren, Jan A Kors, Naoki Koyama, Annika Kreuchwig, Andrew R Leach, Miguel-Angel Mayer, Peter Monecke, Wolfgang Muster, Chihiro Miyamoto Nakazawa, Gavin Nicholson, Rowan Parry, Manuel Pastor, Janet Piñero, Nils Oberhauser, Juan Manuel Ramírez-Anguaita, Adrián Rodrigo, Aljosa Smajic, Markus Schaefer, Sebastian Schieferdecker, Inari Soininen, Emma Terricabras, Panuwat Trairatphisan, Sean C Turner, Alfonso Valencia, Bob van de Water,

- Johan L van der Lei, Erik M van Mulligen, Esther Vock, David Wilkinson. “eTRANSAFE: data science to empower translational safety assessment”. *Nature Reviews Drug Discovery*, June 14, 2023.
499. Carlos Ávila-Nieto, Júlia Vergara-Alert, Pep Amengual-Rigo, Erola Ainsua-Enrich, Marco Brustolin, María Luisa Rodríguez de la Concepción, Núria Pedreño-Lopez, Jordi Rodon, Victor Urrea, Edwards Pradenas, Silvia Marfil, Ester Ballana, Eva Riveira-Muñoz, Mònica Pérez, Núria Roca, Ferran Tarrés-Freixas, Julieta Carabelli, Guillermo Cantero, Anna Pons-Grífols, Carla Roviroso, Carmen Aguilar-Gurrieri, Raquel Ortiz, Ana Barajas, Benjamin Trinité, Rosalba Lepore, Jordana Muñoz-Basagoiti, Daniel Perez-Zsolt, Nuria Izquierdo-Useros, Alfonso Valencia, Julià Blanco, Bonaventura Clotet, Victor Guallar, Joaquim Segalés, Jorge Carrillo. “Novel Spike-stabilized trimers with improved production protect K18-hACE2 mice and golden Syrian hamsters from the highly pathogenic SARS-CoV-2 Beta variant”. *Frontiers in Immunology*, Dec. 4th, 2023, Volume 14.
 500. Miguel Ponce-de-Leon, Arnau Montagud, Vincent Noël, Annika Meert, Gerard Pradas, Emmanuel Barillot, Laurence Calzone & Alfonso Valencia. “PhysiBoSS 2.0: a sustainable integration of stochastic Boolean and agent-based modelling frameworks”. *Nature magazine, NPJ Syst. Biol. Appl.*, October 30th, 2023.
 501. Antonio Miranda-Escalada, Farrokh Mehryary, Jouni Luoma, Darryl Estrada-Zavala, Luis Gasco, Sampo Pyysalo, Alfonso Valencia, Martin Krallinger. “Overview of DrugProt task at BioCreative VII: data and methods for large-scale text mining and knowledge graph generation of heterogenous chemical-protein relations”. *Database Journal*, vol. 2023, Nov. 28, 2023.
 502. Alexandros Armaos, François Serra, Iker Núñez-Carpintero, Ji-Heui Seo, Sylvan C Baca, Stefano Gustinich, Alfonso Valencia, Matthew L Freedman, Davide Cirillo, Claudia Giambartolomei, Gian Gaetano Tartaglia. “The PENGUIN approach to reconstruct protein interactions at enhancer-promoter regions and its application to prostate cancer”. *Nature* nr. 14, art. 8084. Dec. 6th, 2023.
 503. Ana Barajas, Pep Amengual-Rigo, Anna Pons-Grífols, Raquel Ortiz, Oriol Gracia Carmona, Victor Urrea, Nuria de la Iglesia, Juan Blanco-Heredia, Carla Anjos-Souza, Ismael Varela, Benjamin Trinité, Ferran Tarrés-Freixas, Carla Roviroso, Rosalba Lepore, Miguel Vázquez, Leticia de Mattos-Arruda, Alfonso Valencia, Bonaventura Clotet, Carmen Aguilar-Gurrieri, Victor Guallar, Jorge Carrillo, Julià Blanco “Virus-like particle-mediated delivery of structure-selected neoantigens demonstrates immunogenicity and antitumoral activity in mice”. *Journal of Translational Medicine* 22, Article nr. 14, January 3, 2024.
 504. Michael Boutros, Michael Baumann, Anna Bigas, Linda Chaabane, Julien Guérin, Jens K Habermann, Aurélien Jobard, Pier Giuseppe Pelicci, Oliver Stegle, Giovanni Tonon, Alfonso Valencia, Eva C Winkler, Patricia Blanc, Ruggero De Maria, Rene H Medema, Peter Nagy, Josep Tabernero, Eric Solary. “UNCAN.eu: Toward a European Federated Cancer Research Data Hub”. *Cancer Discovery*, Vol. 14, issue 1. Jan. 12, 2024.
 505. Anna Niarakis, Marek Ostaszewski, Alexander Mazein, Inna Kuperstein, Martina Kutmon, Marc E Gillespie, Akira Funahashi, Marcio Luis Acencio, Ahmed Hemedan, Michael Aiche, Karsten Klein, Tobias Czauderna, Felicia Burtscher, Takahiro G Yamada, Yusuke Hiki, Noriko F Hiroi, Finterly Hu, Nhung Pham, Friederike Ehrhart, Egon L Willighagen, Alberto Valdeolivas, Aurelien Dugourd, Francesco Messina, Marina Esteban-Medina, Maria Peña-Chilet, Kinza Rian, Sylvain Soliman, Sara

- Sadat Aghamiri , Bhanwar Lal Puniya , Aurélien Naldi , Tomáš Helikar , Vidisha Singh, Marco Fariñas Fernández , Viviam Bermudez, Eirini Tsirvouli , Arnau Montagud , Vincent Noël , Miguel Ponce-de-Leon , Dieter Maier , Angela Bauch , Benjamin M, John A Bachman, Augustin Luna , Janet Piñero , Laura I Furlong , Irina Balaur , Adrien Rougny , Yohan Jarosz , Rupert W Overall , Robert Phair, Livia Perfetto , Lisa Matthews , Devasahayam Arokia Balaya Rex , Marija Orlic-Milacic , Luis Cristobal Monraz Gomez , Bertrand De Meulder , Jean Marie Ravel , Bijay Jassal 8 , Venkata Satagopam, Guanming Wu , Martin Golebiewski , Piotr Gawron , Laurence Calzone , Jacques S Beckmann , Chris T Evelo , Peter D'Eustachio , Falk Schreiber , Julio Saez-Rodriguez, Joaquin Dopazo , Martin Kuiper, Alfonso Valencia , Olaf Wolkenhauer , Hiroaki Kitano , Emmanuel Barillot, Charles Auffray , Rudi Balling , Reinhard Schneider. “Drug-target identification in COVID-19 disease mechanisms using computational systems biology approaches”. *Frontiers in Immunology*, 13 February 2024, Vol. 14.
506. Iker Núñez-Carpintero, Maria Rigau, Mattia Bosio, Emily O'Connor, Sally Spendiff, Yoshiteru Azuma, Ana Topf, Rachel Thompson, Peter A C 't Hoen, Teodora Chamova, Ivailo Tournev, Velina Guergueltcheva, Steven Laurie, Sergi Beltran, Salvador Capella-Gutiérrez, Davide Cirillo, Hanns Lochmüller, Alfonso Valencia. “Rare disease research workflow using multilayer networks elucidates the molecular determinants of severity in Congenital Myasthenic Syndromes”. *Nature Communications* 15 Article number: 1227 (2024), 28 February 2024.
507. Carlos Ávila-Nieto, Júlia Vergara-Alert, Pep Amengual-Rigo , Erola Ainsua-Enrich, Marco Brustolin, María Luisa Rodríguez de la Concepción, Núria Pedreño-Lopez, Jordi Rodon , Victor Urrea, Edwards Pradenas, Silvia Marfil, Ester Ballana, Eva Riveira-Muñoz, Mónica Pérez , Núria Roca, Ferran Tarrés-Freixas, Guillermo Cantero, Anna Pons-Grífols, Carla Roviroso, Carmen Aguilar-Gurreri, Raquel Ortiz, Ana Barajas, Benjamin Trinité, Rosalba Lepore, Jordana Muñoz-Basagoiti, Daniel Perez-Zsolt, Nuria Izquierdo-Useros, Alfonso Valencia, Julià Blanco, Victor Guallar, Bonaventura Clotet, Joaquim Segalés, Jorge Carrillo. “Immunization with V987H-stabilized Spike glycoprotein protects K18-hACE2 mice and golden Syrian hamsters upon SARS-CoV-2 infection”. *Nature Communications* 15, Article nr.: 2349 (2024), 21 March 2024.
508. Victoria Ruiz-Serra, Samuel Valentini, Sergi Madroñero, Alfonso Valencia, Eduard Porta-Pardo. “3Dmapper: a command line tool for BioBank-scale mapping of variants to protein structures”. *Bioinformatics*, Vol. 40, Issue 4, 2 April, 2024.
509. François Serra, Andrea Nieto-Aliseda, Lucía Fanlo-Escudero, Llorenç Roviroso, Mónica Cabrera-Pasadas, Aleksey Lazarenkov, Blanca Urmeneta, Alvaro Alcalde-Merino, Emanuele M Nola, Andrei L Okorokov, Peter Fraser, Mariona Graupera, Sandra D Castillo, Jose L Sardina, Alfonso Valencia, Biola M Javierre. “p53 rapidly restructures 3D chromatin organization to trigger a transcriptional response”. *Nature Communications* nr. 15, Article nr. 2821. 1 April 2024.
510. Macha Nikolski, Eivind Hovig, Fatima Al-Shahrour, Niklas Blomberg, Serena Scollen, Alfonso Valencia, Gary Saunders. “Roadmap for a European cancer data management and precision medicine infrastructure”. *Nature Cancer* nr. 5, page 367-372. & February 2024.
511. R Gonzalo Parra, Maria I Freiburger, Miriam Poley-Gil, Miguel Fernandez-Martin, Leandro G Radusky, Victoria Ruiz-Serra, Peter G Wolynes, Diego U Ferreira, Alfonso Valencia. “Frustraevo: a web server to localize and quantify the conservation of local

- energetic frustration in protein families". *Nucleic Acids Research*, July 5, 2024; 52(W1):W233-W237.
512. Michela Riba, Cinzia Sala, Aedin C Culhane, Åsmund Flobak , Attila Patocs , Kjetil Boye, Karla Plevova, Šárka Pospíšilová , Giorgia Gandolfi, Marco J Morelli , Gabriele Bucci, Anders Edsjö, Ulrik Lassen , Fátima Al-Shahrour , Nuria Lopez-Bigas , Randi Hovland, Edwin Cuppen, Alfonso Valencia , Helene A Poirel , Richard Rosenquist, Serena Scollen, Juan Arenas Marquez , Jeroen Belien, Arcangela De Nicolo, Ruggero De Maria, David Torrents , Giovanni Tonon. "The 1+Million Genomes Minimal Dataset for Cancer". *Nature Genetics*, May 3rd. 2024.
 513. Nuria Olvera, Jon Sánchez-Valle, Iker Núñez-Carpintero, Joselyn Rojas-Quintero, Guillaume Noell, Sandra Casas-Recasens, Alen Faiz, Philip Hansbro , Angela Guirao, Rosalba Lepore, Davide Cirillo, Alvar Agustí, Francesca Polverino , Alfonso Valencia, Rosa FanerRosa Faner. "Lung Tissue Multi-Layer Network Analysis Uncovers the Molecular Heterogeneity of Chronic Obstructive Pulmonary Disease". *ATS Journals -American Journal of Respiratory and Critical Care Medicine-*, November 15th, 2024.
 514. Ferrán Catalá-López, Laura Tejedor-Romero, Jane A. Driver, Brian Hutton, Joan Vicent Sánchez-Ortí, Manuel Ridao, Adolfo Alonso-Arroyo, Patricia Correa-Ghisays, Jaume Forés-Martos, Vicent Balanzá-Martínez, Alfonso Valencia, Inmaculada Cobos & Rafael Tabarés-Seisdedos "Risk of cancer development associated with disease-modifying therapies for multiple sclerosis: study protocol for a systematic review and meta-analysis of randomised and non-randomised studies". *Systematic Reviews* nr. 13, article 263, October 18th 2024.
 515. Victoria Ruiz-Serra, Nataly Buslón, Olivier R. Philippe, Diego Saby, María Morales, Camila Pontes, Alejandro Muñoz Andirkó, Gemma L. Holliday, Aina Jené, Mauricio Moldes, Jordi Rambla, Alfonso Valencia, María José Rementería, Atia Cortés, Davide Cirillo. "Analyzing sex imbalance in EGA and dbGaP biological databases: Recommendations for better practices". *iScience*, October 18th, 2024, Vol. 27, nr. 10.
 516. Anna Niarakis, Reinhard Laubenbacher , Gary An, Yaron Ilan, Jasmin Fisher, Åsmund Flobak, Kristin Reich, María Rodríguez Martínez, Liesbet Geris, Luiz Ladeira, Lorenzo Veschini, Michael L Blinov, Francesco Messina, Luis L Fonseca, Sandra Ferreira, Arnau Montagud, Vincent Noël, Malvina Marku, Eirini Tsirvouli, Marcella M Torres, Leonard A Harris, T J Sego, Chase Cockrell, Amanda E Shick, Hasan Balci, Albin Salazar, Kinza Rian , Ahmed Abdelmonem Hemedan , Marina Esteban-Medina , Bernard Staumont, Esteban Hernandez-Vargas, Shiny Martis B , Alejandro Madrid-Valiente , Panagiotis Karampelesis , Luis Sordo Vieira, Pradyumna Harlapur , Alexander Kulesza , Niloofar Nikaein, Winston Garira, Rahuman S Malik Sheriff , Juilee Thakar , Van Du T Tran , Jose Carbonell-Caballero, Soroush Safaei, Alfonso Valencia, Andrei Zinovyev, James A Glazier. "Immune digital twins for complex human pathologies: applications, limitations, and challenges". *NPJ Systems Biology and applications*, November 30th 2024, vol. 10, chapter 1, p.141.
 517. Javier Corvi, Nicolás Díaz-Roussel, José M. Fernández, Francesco Ronzano, Emilio Centeno, Pablo Accuosto, Celine Ibrahim, Shoji Asakura, Frank Bringezu, Mirjam Fröhlicher, Annika Kreuchwig, Yoko Nogami, Jeong Rih, Raul Rodriguez-Esteban, Nicolas Sajot, Joerg Wichard, Heng-Yi Michael Wu, Philip Drew, Thomas Steger-Hartmann, Alfonso Valencia, Laura I. Furlong & Salvador Capella-Gutierrez. "PretoxTM: a text mining system for extracting treatment-related findings from preclinical toxicology reports". *Journal of Cheminformatics*, February 3rd, 2025. Vol. 17, nr. 1, page 15.

518. Jon Sánchez-Valle, María Flores-Rodero, Felipe Xavier Costa, Jose Carbonell-Caballero, Iker Núñez-Carpintero, Rafael Tabarés-Seisdedos, Luis Mateus Rocha, Davide Cirillo, Alfonso Valencia. “Sex-specific transcriptome similarity networks elucidate comorbidity relationships”. *bioRxiv*, January 24th, 2025.
519. Rion Brattig Correia, Jordan C Rozum, Leonard Cross , Jack Felag , Michael Gallant, Ziqi Guo, Bruce W Herr, Aehong Min, Jon Sanchez-Valle, Deborah Stungis Rocha, Alfonso Valencia, Xuan Wang, Katy Börner, Wendy Miller, Luis M Rocha. “myAURA: a personalized health library for epilepsy management via knowledge graph sparsification and visualization”. Oxford University Press, January 31st, 2025.
520. Teresa D’Altri, Mallory Ann Freeberg, Amy J. Curwin, Ana Alonso, Ana T. Freitas, Salvador Capella-Gutierrez, Luiz Gadelha, Anna Hagwall, Eivind Hovig, Giselle Kerry, Koray Kirli, Krzysztof Kochel, Oliver Kohlbacher, Jan O. Korbel, Jaakko Leinonen, Blazej Marciniak, Jorge S. Oliveira, Kjell Petersen, Mário J. Silva, Oliver Stegle, Alfonso Valencia, Johan Viklund, Roderic Guigo, Helen Parkinson, Arcadi Navarro, Jordi Rambla & Thomas M. Keane. “The Federated European Genome–Phenome Archive as a global network for sharing human genomics data”. *Nature Genetics*, March 3rd, 2025.
521. Alfonso Valencia. “Decentralized databases in biomedical research: lessons from recent events : The recent shutdown of critical health databases by the US CDC is a wake-up call for the research community about the vulnerability of centralised databases”. *EMBO Reports*, EMBO Press, March 18th, 2025.
522. Mihai Pop, Teresa K Attwood, Judith A Blake, Philip E Bourne, Ana Conesa, Terry Gaasterland, Lawrence Hunter, Carl Kingsford, Oliver Kohlbacher, Thomas Lengauer, Scott Marke, Yves Moreau, William S Noble, Christine Orengo, B F Francis Ouellette , Laxmi Parida, Natasa Przulj, Teresa M Przytycka , Shoba Ranganathan , Russell Schwartz, Alfonso Valencia, Tandy Warnow. “Biological databases in the age of generative artificial intelligence”. *Bioinformatics Advances*, Volume 5, Issue 1, March 20th, 2025, vbaf044.
523. Sofya Marchenko, Niklas Goernitz, Wiebke Alina Zoern, Maria Joosten, Inga Hoffmann, Jalid Sehoul, Gerald Niedobitek, Carsten Denkert, Bruno V Sinn, Svenja Kolb, José Carbonell-Caballero, Alfonso Valencia, Mihnea P Dragomir, Wolfgang D Schmitt, David Horst, Ioana I Braicu, Christine Sers, Jonathan Pohl, Eliane T Taube. “Transcriptome Analysis of Matched Cohorts of Long- and Short-term Survivors in Advanced High-Grade Serous Tubo-ovarian Cancer”. *Clinical Cancer Research*, AACR Journals, Volume 31, Issue 18, September 15th, 2025.
524. Alejandro Navarro-Martínez, Meriem Hajji, Jan Mateu Armengol, Albert Soret, Miguel Ponce-de-León, Alfonso Valencia. “The effect of recurrent mobility on air pollution exposure and mortality burden in Catalonia”. *International Journal of Health Geographics*, nr- 24, article 19. July 28th, 2025.
525. Miguel Ponce-de-Leon, Camila Pontes, Alex Arenas, Alfonso Valencia. “Assessing the impact of interregional mobility on COVID19 spread in Spain using transfer entropy”. *Scientific Reports* 15, Article number: 31504. 26 August 2025.

526. Anna Oncins, Roser Zaurin, Houyem Toukabri, Kimberly Quililan, José R Hernández Mora, Magdalena A Karpinska, Erik Wernersson, Alastair Smith, Agostina Bianchi, Leone Albinati, Luca Cozzuto, Andrea Rivero, Chloe Gulliver, Jessica Velten, Johanna Denkena, François Serra, Raúl Gómez, Cristina López, Silvia Beà, Jonas Paulsen, Nadia Halidi, Alfonso Valencia, Magda Bienko, A Marieke Oudelaar, Renée Beekman. “Translocations can drive expression changes of multiple genes in regulons covering entire chromosome arms”. *Nucleic Acids Research*, Volume 53, Issue 15, 28 August 2025.
527. Beatriz Urda-García, Jon Sánchez-Valle, Rosalba Lepore, Alfonso Valencia. “Patient stratification reveals the molecular basis of disease co-occurrences”. *PNAS*, August 29th, 2025.
528. Romina Royo, Eva Garcia, Irene Schlünder, Christina Hilmarsen, Mette Kielsholm Thomsen, Emilie Cauët, Simon Kok Jensen, Simona Giardina, Aline Hebrant, Gordana Raicevic Tounouz, Marc Van Den Bulcke, Juan Arenas, Christian Fynbo Christiansen, Eivind Hovig, Petr Holub, Alfonso Valencia, Salvador Capella-Gutierrez. “Genomic data sharing in research across Europe: legal challenges and upcoming opportunities within the European Health Data Space”. *European Journal of Public Health*, Volume 35, Issue Supplement 3, September 2025, Pages iii25–iii31.
529. Xavier Benedicto, Åsmund Flobak, Miguel Ponce-de-Leon, Alfonso Valencia. “Constraint based modeling of drug induced metabolic changes in a cancer cell line”. *NPJ, Systems Biology and Applications*, nr. 11, article 111. October 6th, 2025.