

CURRICULUM VITAE

INFORMAZIONI PERSONALI

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Qualifica	Associate Professor of Systems Biology
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TITOLI DI STUDIO E PROFESSIONALI ED ESPERIENZE LAVORATIVE

Titolo di studio (anno di conseguimento; nome e tipo di istituto di istruzione o formazione)	PhD, 2003, Biochemistry, Ruhr-University Bochum, Germany & Max-Planck Institute for Molecular Physiology Dortmund, Germany
Altri titoli di studio e professionali	National Scientific qualification as full professor in the Italian higher education system, 2023, Ministero dell'Università e della Ricerca, Rome, Italy
Esperienze professionali (incarichi ricoperti; data; tipo di azienda o settore; principali mansioni o responsabilità)	<ul style="list-style-type: none"> • Since 2021: Associate Professor of Systems Biology, University of Pavia, Italy • 2017-2021: Principal Investigator, Associate Professor, Systems Biology Ireland & Charles Institute of Dermatology, School of Medicine, University College Dublin, Ireland • 2006-2017: Staff Scientist, Department of Systems Biology, Centre for Genomic Regulation (CRG) Barcelona, Spain • 2003-2006: Postdoctoral Researcher, Department of Structural and Computational Biology, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
Capacità linguistiche	German, English
Capacità nell'uso delle tecnologie	
Altro (partecipazione a convegni e seminari, pubblicazioni, collaborazione a riviste, ecc., ed ogni altra informazione che il compilante ritiene di dover pubblicare)	<p><u>Publications in peer-reviewed journals:</u></p> <p>* Corresponding author \$ Equally contributing first author</p> <ol style="list-style-type: none"> 1. Junk P, Kiel C. Structure-based prediction of Ras-effector binding affinities and design of 'branchegetic' interface mutations. <i>Structure</i>, 31, 870-883 (2023).

2. Ternet C, Junk P, Sevrin T, Catozzi S, Wählén E, Heldin J, Oliviero G, Wynne K, Kiel C*. Analysis of context-specific KRAS-effector (sub)complexes in Caco-2 cells. *Life Sci Alliance* 6, e202201670 (2023).
3. Narayan B, Kiel C, Buchete NV. Classification of GTP-dependent K-Ras4B active and inactive conformational states. *J Chem Phys* 158, 091104 (2023).
4. Sevrin T, Strasser L, Ternet C, Junk P, Caffarini M, Prins S, D'Arcy C, Catozzi S, Oliviero G, Wynne K, Kiel C*, Luthert PJ. Whole-cell energy modeling reveals quantitative changes of predicted energy flows in RAS mutant cancer cell lines. *iScience* 26, 105931 (2023).
5. D'Arcy C, Bass O, Junk P, Sevrin T, Oliviero G, Wynne K, Halasz M, Kiel C*. Disease-Gene Networks of Skin Pigmentation Disorders and Reconstruction of Protein-Protein Interaction Networks. *Bioengineering (Basel)* 10, 13 (2022).
6. Catozzi S, Ternet C, Gourge A, Wynne K, Oliviero G, Kiel C*. Reconstruction and analysis of a large-scale binary Ras-effector signaling network. *Cell Commun Signal* 20, 24 (2022).
7. Junk P, Kiel C. HOMELETTE: a unified interface to homology modelling software. *Bioinformatics* 38, 1749-1751 (2022).
8. Nogales C, Mamdouh ZM, List M, Kiel C, Casas AI, Schmidt HHHW. Network pharmacology: curing causal mechanisms instead of treating symptoms. *Trends Pharmacol Sci* 43, 136-150 (2022).
9. D'Arcy C, Kiel C*. Cell Adhesion Molecules in Normal Skin and Melanoma. *Biomolecules* 11, 1213 (2021).
10. Ternet C, Kiel C*. Signaling pathways in intestinal homeostasis and colorectal cancer: KRAS at centre stage. *Cell Commun Signal* 19, 31 (2021).
11. Catozzi S, Halasz M, Kiel C*. Predicted 'wiring landscape' of Ras-effector interactions in 29 human tissues. *NPJ Syst Biol Appl* 7, 10 (2021).
12. Kiel C, Matallanas D, Kolch W. The Ins and Outs of RAS Effector Complexes. *Biomolecules* 11, 236 (2021).
13. Pickering KA, Gilroy K, Cassidy JW, Fey SK, Najumudeen AK, Zeiger LB, Vincent DF, Gay DM, Johansson J, Fordham RP, Miller B, Clark W, Hedley A, Unal EB, Kiel C, McGhee E, Machesky LM, Nixon C, Johnsson AE, Bain M, Strathdee D, van Hoof SR, Medema JP, Anderson KI, Brachmann SM, Stucke VM, Malliri A, Drysdale M, Turner M, Serrano L, Myant K, Campbell AD, Sansom OJ. RAC-GEF function as a critical factor in intestinal tumorigenesis. *Nat Commun* 12, 56 (2021).
14. Ibáñez Gaspar V, Catozzi S, Ternet C, Luthert PJ, Kiel C*. Analysis of Ras-effector interaction competition in large intestine and colorectal cancer context. *Small GTPases* 12, 209-225 (2021).
15. Shrager SH, Kiel C*. SnapShot: APC/ T-Cell Immune Checkpoints. *Cell* 183, 1142-1142 (2020).
16. Luthert PJ, Kiel C*. Combining gene-disease associations with single cell gene expression data provides anatomy-specific subnetworks in age-related macular degeneration. *Netw Syst Med* 3, 105-121 (2020).
17. Kennedy SA, Jarboui MA, Srihari S, Raso C, Bryan K, Dernayka L, Charitou T, Bernal-Llinares M, Herrera-Montavez C, Krstic A, Matallanas D, Kotlyar M, Jurisica I, Curak J, Wong V, Stagljar I, LeBihan T, Imrie L, Pillai P, Lynn MA, Fasterius E, Al-Khalili Szigyarto C, Breen J, Kiel C, Serrano L, Rauch N, Rukhlenko O, Kholodenko BN, Iglesias-Martinez LF, Ryan CJ, Pilkington R, Cammareri P, Sansom O, Shave S, Auer M, Horn N, Klose F, Ueffing M, Boldt K, Lynn DJ, Kolch W. Extensive rewiring of the EGFR network in colorectal cancer cells

- expressing transforming levels of KRASG13D. *Nat Commun* 11, 499 (2020).
18. Pool FM, Kiel C\$*, Serrano L, Luthert PJ. Repository of proposed pathways and protein-protein interaction networks in age-related macular degeneration. *NPJ Aging Mech Dis* 6, 2 (2020).
 19. Radusky L, Modenutti C, Delgado J, Bustamante JP, Vishnopolksa S, Kiel C, Serrano L, Marti M, Turjanski A. VarQ: A Tool for the Structural and Functional Analysis of Human Protein Variants. *Front Genet* 9, 620 (2018).
 20. Kolch W, Kiel C. From oncogenic mutation to dynamic code. *Science* 361, 844-845 (2018).
 21. Luthert PJ, Serrano L, Kiel C*. Opportunities and challenges of whole-cell and -tissue simulations of the outer retina in health and disease. *Annu Rev Biomed Data Sci* 1, 131-152 (2018).
 22. Besray Unal E, Kiel C\$*, Benisty H, Campbell A, Pickering K, Blüthgen N, Sansom OJ, Serrano L. Systems level expression correlation of Ras GTPase regulators. *Cell Commun Signal* 16, 46 (2018).
 23. Stojanovski K, Ferrar T, Benisty H, Uschner F, Delgado J, Jimenez J, Solé C, de Nadal E, Klipp E, Posas F, Serrano L, Kiel C*. Interaction Dynamics Determine Signaling and Output Pathway Responses. *Cell Rep* 19, 136-149 (2017).
 24. Crépieux P, Poupon A, Langonné-Gallay N, Reiter E, Delgado J, Schaefer MH, Bourquard T, Serrano L, Kiel C*. A Comprehensive View of the β-Arrestinome. *Front Endocrinol (Lausanne)* 8, 32 (2017).
 25. Kiel C*, Lastrucci C, Luthert PJ, Serrano L. Simple and complex retinal dystrophies are associated with profoundly different disease networks. *Sci Rep* 7, 41835 (2017).
 26. Kiel C*, Benisty H, Lloréns-Rico V, Serrano L. The yin-yang of kinase activation and unfolding explains the peculiarity of Val600 in the activation segment of BRAF. *Elife* 5, e12814 (2016).
 27. Beltran-Sastre V, Benisty H, Burnier J, Berger I, Serrano L, Kiel C*. Tuneable endogenous mammalian target complementation via multiplexed plasmid-based recombineering. *Sci Rep* 5, 17432 (2015).
 28. Toufighi K, Yang JS, Luis NM, Aznar Benitah S, Lehner B, Serrano L, Kiel C*. Dissecting the calcium-induced differentiation of human primary keratinocytes stem cells by integrative and structural network analyses. *PLoS Comput Biol* 11, e1004256 (2015).
 29. Yang JS, Sabidó E, Serrano L, Kiel C*. TAPAS: tools to assist the targeted protein quantification of human alternative splice variants. *Bioinformatics* 30, 2989-2990 (2014).
 30. Schaefer MH, Yang JS, Serrano L, Kiel C. Protein conservation and variation suggest mechanisms of cell type-specific modulation of signaling pathways. *PLoS Comput Biol* 10, e1003659 (2014).
 31. Kiel C*, Serrano L. Structure-energy-based predictions and network modelling of RASopathy and cancer missense mutations. *Mol Syst Biol* 10, 727 (2014).
 32. Piccoli G, Onofri F, Cirnaru MD, Kaiser CJ, Jagtap P, Kastenmüller A, Pischedda F, Marte A, von Zweydorf F, Vogt A, Giesert F, Pan L, Antonucci F, Kiel C, Zhang M, Weinkauf S, Sattler M, Sala C, Matteoli M, Ueffing M, Gloeckner CJ. Leucine-rich repeat kinase 2 binds to neuronal vesicles through protein interactions mediated by its C-terminal WD40 domain. *Mol Cell Biol* 34, 2147-2161 (2014).
 33. McKeone R, Wikstrom M, Kiel C, Rakoczy PE. Assessing the correlation between mutant rhodopsin stability and the severity of retinitis pigmentosa. *Mol Vis* 20, 183-199 (2014).

34. Kiel C*, Verschueren E, Yang JS, Serrano L. Integration of protein abundance and structure data reveals competition in the ErbB signaling network. *Sci Signal* 6, ra109 (2013).
35. Kiel C*, Ebhardt HA, Burnier J, Portugal C, Sabidó E, Zimmermann T, Aebersold R, Serrano L. Quantification of ErbB network proteins in three cell types using complementary approaches identifies cell-general and cell-type-specific signaling proteins. *J Proteome Res* 13, 300-313 (2014).
36. Kiel C*, Serrano L. Structural data in synthetic biology approaches for studying general design principles of cellular signaling networks. *Structure* 20, 1806-1813 (2012).
37. Yang JS, Campagna A, Delgado J, Vanhee P, Serrano L, Kiel C*. SAPIN: a framework for the structural analysis of protein interaction networks. *Bioinformatics* 28, 2998-2999 (2012).
38. Kiel C, Vogt A, Campagna A, Chatr-aryamontri A, Swiatek-de Lange M, Beer M, Bolz S, Mack AF, Kinkl N, Cesareni G, Serrano L, Ueffing M. Structural and functional protein network analyses predict novel signaling functions for rhodopsin. *Mol Syst Biol* 7, 551 (2011).
39. Kiel C*, Serrano L. Challenges ahead in signal transduction: MAPK as an example. *Curr Opin Biotechnol* 23, 305-14 (2012).
40. Rakoczy EP, Kiel C\$, McKeone R, Stricher F, Serrano L. Analysis of disease-linked rhodopsin mutations based on structure, function, and protein stability calculations. *J Mol Biol* 405, 584-606 (2011).
41. Kiel C, Yus E, Serrano L. Engineering signal transduction pathways. *Cell* 140, 33-47 (2010).
42. Kiel C, Filchtinski D, Spoerner M, Schreiber G, Kalbitzer HR, Herrmann C. Improved binding of raf to Ras.GDP is correlated with biological activity. *J Biol Chem* 284, 31893-31902 (2009).
43. Kiel C*, Serrano L. Cell type-specific importance of ras-c-raf complex association rate constants for MAPK signaling. *Sci Signal* 2, ra38 (2009).
44. Van der Sloot AM, Kiel C, Serrano L, Stricher F. Protein design in biological networks: from manipulating the input to modifying the output. *Protein Eng Des Sel* 22, 537-542 (2009).
45. Markson G, Kiel C, Hyde R, Brown S, Charalabous P, Bremm A, Semple J, Woodsmith J, Duley S, Salehi-Ashtiani K, Vidal M, Komander D, Serrano L, Lehner P, Sanderson CM. Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network. *Genome Res* 19, 1905-1911 (2009).
46. Kiel C*, Aydin D, Serrano L. Association rate constants of ras-effector interactions are evolutionarily conserved. *PLoS Comput Biol* 4, e1000245 (2008).
47. Kiel C*, Beltrao P, Serrano L. Analyzing protein interaction networks using structural information. *Annu Rev Biochem* 77, 415-441 (2008).
48. Campagna A, Serrano L, Kiel C*. Shaping dots and lines: adding modularity into protein interaction networks using structural information. *FEBS Lett* 582, 1231-1236 (2008).
49. Kiel C*, Serrano L. Prediction of Ras-effector interactions using position energy matrices. *Bioinformatics* 23, 2226-2230 (2007).
50. Kiel C*, Serrano L. Affinity can have many faces: Thermodynamic and kinetic properties of Ras effector complex formation. *Curr Chem Biol* 1, 215-225 (2007).
51. Beltrao P, Kiel C, Serrano L. Structures in systems biology. *Curr Opin Struct Biol* 17, 378-384 (2007).

52. Kiel C*, Foglierini M, Kuemmerer N, Beltrao P, Serrano L. A genome-wide Ras-effector interaction network. *J Mol Biol* 370, 1020-1032 (2007).
53. Kiel C*, Serrano L. The ubiquitin domain superfold: structure-based sequence alignments and characterization of binding epitopes. *J Mol Biol* 355(4):821-44 (2006).
54. Kiel C*, Wohlgemuth S, Rousseau F, Schymkowitz J, Ferkinghoff-Borg J, Wittinghofer F, Serrano L. Recognizing and defining true Ras binding domains II: in silico prediction based on homology modelling and energy calculations. *J Mol Biol* 348, 759-775 (2005).
55. Wohlgemuth S, Kiel C\$, Krämer A, Serrano L, Wittinghofer F, Herrmann C. Recognizing and defining true Ras binding domains I: biochemical analysis. *J Mol Biol* 348, 741-758 (2005).
56. Kiel C, Serrano L, Herrmann C. A detailed thermodynamic analysis of ras/effectors complex interfaces. *J Mol Biol* 340, 1039-1058 (2004).
57. Kiel C, Selzer T, Shaul Y, Schreiber G, Herrmann C. Electrostatically optimized Ras-binding Ral guanine dissociation stimulator mutants increase the rate of association by stabilizing the encounter complex. *Proc Natl Acad Sci U S A* 101, 9223-9228 (2004).
58. Gohlke H, Kiel C, Case DA. Insights into protein-protein binding by binding free energy calculation and free energy decomposition for the Ras-Raf and Ras-RalGDS complexes. *J Mol Biol* 330, 891-913 (2003).
59. Ahmadian MR, Kiel C, Stege P, Scheffzek K. Structural fingerprints of the Ras-GTPase activating proteins neurofibromin and p120GAP. *J Mol Biol* 329, 699-710 (2003).
60. Linnemann T, Kiel C, Herter P, Herrmann C. The activation of RalGDS can be achieved independently of its Ras binding domain. Implications of an activation mechanism in Ras effector specificity and signal distribution. *J Biol Chem* 277, 7831-7837 (2002).

Book chapters:

1. Junk P, Kiel C*. Engineering of Biological Pathways: Complex Formation and Signal Transduction. *Methods Mol Biol* 2315, 59-70 (2021).
2. Kiel C*, Serrano L. Complexities in quantitative systems analysis of signaling networks. "Computational Systems Biology" edited by Eils R and Kriete A, Elsevier (2014).
3. Kiel C*, Serrano L. The impact of structural proteomics on the prediction of protein-protein interactions. Published in "Structural proteomics and its impact on the life sciences", edited by Sussman JL and Silman I, World Scientific (2008).
4. Kiel C, Herrmann C. Double mutant cycle analysis of Ras proteins and their effectors: Quantification of binding specificity. Published in "Protein Modules in Cellular Signaling", edited by Heilmeyer L and Friedrich P, IOS Press (2001).