# CURRICULUM VITAE ET STUDIORUM

# Dr. Armida Di Fenza

## EDUCATION

**PhD in Pharmaceutical Sciences:** University of Salerno, Italy. Mar 2002.
*Design and synthesis of peptides for the study of protein-protein and peptide-protein interactions*

**Laurea in Biological Sciences (110/110 cum laude):** University of Pisa, Italy. Nov 1997.
*Design and synthesis of pseudo peptide analogues of bradykinin hormone*

## WORK EXPERIENCES

**Jul 2015 – Present Maternity break**

During this time I worked as full time mother and I started to turn my ceramic hobby into a business.

- Ceramic studio set up
- Study of the chemistry of ceramic glazes and their development
- Development of firing programs at low, medium and high temperature
- Online shop set up
- Web page and marketing
- Communication, project management and multitasking

**Jan 2012 – Jul 2015 Data wrangler** – Mammalian Genetic Unit (MGU), MRC Harwell, Didcot, UK.

I had a key role as part of the Data Coordination Centre (DCC) for the NHI-funded IMPC project (International Mouse Phenotyping Consortium), focusing on the capture, quality control and integration of multi-dimensional data from over 10 international centres. The IMPC is an international effort to identify the function of every protein-coding gene in the mouse genome and to illuminate the function of the large proportion of the mammalian genome that remains undefined. The intensive relational working net with collegues and other collaborators of the DCC have helped me developing also excellent team working skills.

- Statistical analyses of large amount of data by using commercial software and/or implementing scripting programs.
- Definition of Standard Operational Protocols (SOPs) and pipelines for the measurements of experimental mouse mutagenesis data aggregated from multiple geographical locations and studies.
- Data management: quality control (QC), collection and storing of valid experimental data to enable reproducible and robust data analysis across several international laboratories.
- Development of statistical multivariate models for the analysis of factors influencing experimental measurements in mouse facilities.
- User support and coordination in a multidisciplinary research environment

**Apr 2007 – Jun 2010 Post-doctoral researcher** – National Enterprise for nanoScience and nanoTechnology (NEST), Scuola Normale Superiore, Pisa, Italy.

I worked in a biophysical theoretical group and I extensively applied computational tools for the study of biological systems contributing to the projects: NGLAB-National Nanotechnology Laboratory for Genomics and Post-Genomics (FIRB) and UdR IIT Scuola Normale Superiore - WP1 "Advanced tools for characterisation and imaging".

- Implementation of a protein-protein docking software specific for antibody-antigen complexes using genetic algorithms.
- Development of algorithms to automate coarse-grained protein force-field parameterization using heuristic optimization and searching algorithms.
- Development of structural and dynamic models of the viral protein HIV-1 Integrase complexed to the host enzymes acetyltransferases G5N5 and p300.
- Experience in structural biology and in various molecular modeling techniques of biological systems (homology modeling, protein-protein docking, all-atom and coarse-grained molecular dynamic simulations, essential dynamics analysis).
- Creation of a database of experimental antibody binding affinity values from the scientific literature.

**Feb 2005 – Mar 2007 Post-doctoral researcher** – Institute for the Chemical and Physical Processes (IPCF), National Research Council, Pisa, Italy.

I developed computational models based on machine learning algorithms, for the prediction of physico-chemical properties of pharmacological molecules (like intestinal absorption and oral bio-availability) from their molecular structure.

- Development of the software Ganesh (Genetic Algorithm Neural nEtwork SearcH) for the prediction of physico-chemical properties (intestinal absorption and oral bio-availability) of pharmacological molecules from their molecular structure.
- Experience of machine learning and their applications (neural networks).
- Ab-initio quantum chemistry methods to calculate solute-solvent partition molecular descriptors.

**Oct 2002 – Dec 2004 Marie-Curie post-doc fellow** – Institute for Pharmaceutical Chemistry, Philipps-Universität, Marburg, Germany.

I worked in an experimental drug design group investigating the molecular features which characterize binding selectivity.

- Protein engineering to obtain Trypsin mutants with hybrid binding sites between Trypsin and Factor Xa.
- Crystal structure of protein-ligand complexes (coordinates are deposited in the Protein Data Bank as 1Y59, 1Y5A, 1Y5B and 1Y5U).
- Structure-activity relationship analysis on enzyme selectivity modulation.
- Use of different experimental techniques (protein expression, purification and refolding, inhibition activity measurement).

**Mar 2002 – Jul 2002 Contract for Professional Consulting Performance** – Department of Pharmaceutical Science, University of Salerno, Italy.

This contract followed my Laurea degree and PhD studies during which I set-up and directed a peptide synthesis laboratory for a period of 4 years acquiring excellent management skills and experience of different chemical methodologies (reverse phase and affinity HPLC, mass spectrometry ESI, organic chemistry).

- Design and production of linear and cyclic peptides and pseudpeptides by manual and automatic Fmoc solid phase peptide synthesis to study peptide-protein and protein-protein interactions, and for the design of anti-HIV drugs.
- Optimization of peptide synthesis strategies to obtain higher qualitative and quantitative yield of synthetic products.
- Development of synthesis protocols for the production of diketopiperazine heterocyclic structures and the racemization side-reaction reduction of new Cl-HOBt coupling reagents.

## PROFESSIONAL SKILLS

- **Informatics**
  C/C++, Fortran, Matlab, R. SQL and database management. Technical writing in LaTeX.
- **Software**
  Data analysis and visualization with Tableau. Molecular modeling (DL-Poly, Amber, Haddock, Rosetta). Molecular graphic: (Sybyl, InsightII, Pymol, VMD). Protein crystallography: (HLK2000, CNS, AMoRe, SHELXL-97).
- **Theoretical methodologies**
  Molecular dynamics simulations of coarse-grained proteins. Protein-protein docking. Homology modeling. Structure-based drug design, QSPR (quantitative structure-property relationship). Data mining: clustering, PCA (principal component analysis). Machine learning: neural networks. Genetic algorithms.
- **Experimental methodologies**
  Reverse phase and affinity HPLC. Protein crystallization. Mass spectrometry ESI. Manual and automatic Fmoc solid phase continuous flow peptide synthesis. E. Coli protein expression, purification and refolding. SDS Electrophoresis. Enzyme kinetic assays. Isothermal titration microcalorimetry.

## PERSONAL SKILLS

- **Languages.** Italian: native speaker. English spoken, written and comprehension: fluent.
- **Social ans organisational skills and competences.**
  - Enthusiastic and self-motivated individual.
  - Developed management skills and competencies through my research career, including: project and time management, multi-tasking, giving presentations, teamwork.
  - Great experience in working in multidisciplinary research teams
  - Experienced in running progress reports on research projects and publishing papers in scientific journals.
  - Capable of learning new concepts and technology independently.
  - Possess an independent mindset, enabling self-sufficiency and creativity.

## RESEARCH FUNDING AND AWARDS

- Two-years post-doc fellowship funded by the Fifth Framework Programme (FP5) European Commission (2002-2004), category Marie Curie Individual Fellowship.
- PhD research project “Design and synthesis of kinin B1 receptor pseudopeptidic agonists” funded by Ministero Università e Ricerca Scientifica Tecnologica, MURST, part of Progetto Speciale Giovani Ricercatori 2001.

- Travel grant from the 2th International Peptide Symposium/17th American Peptide Symposium Organizing Committee (San Diego, California, June, 2001).
- Travel grant from the 26th European Peptide Symposium Organizing Committee (Montpellier, France, September, 2000).

## INVITED TALKS

- Seminar for the course "Training of highly qualified researchers in developing innovative processes and products in the field of anti-infective drugs", Sanofi-Aventis S.p.A., Brindisi, Italy, February 23, 2010.

## TRAINING COURSES

- "Communication skills" at MRC Harwell, UK, May 2013.
- "Assertiveness" at MRC Harwell, UK, June 2012.
- "From Structural Genomics to Drug Discovery: Modeling the flexibility" University of Parma, Italy, September 2007.
- "From Structural Genomics to Drug Discovery", University of Parma, Italy, September 2004.
- Hands-on Workshop "Structural biology elements and protein crystallography" (PR15249), Prof. Dr. Lars-Oliver Essen, Chemistry Department, Philipps-Universität Marburg, Germany, February 2004.
- 9° Thermo Week, Chromatography-Mass Spectrometry Course, Acitrezza, Catania, Italy, March 2001.
- Training on automatic peptide synthesizer, Bioorganische Chemie, Max Planck Institut für Biochemie, Martinsried, München, Germany, Jun 2000 – Jul 2000.
- Training on molecular modeling of proteins, Institute of Quantistic Chemistry and Molecular Energetic, National Research Council, Pisa, Italy, Mar 1998 – Jun 1998.

## PUBLICATIONS IN INTERNATIONAL JOURNALS

1. Ring N., Meehan T. F., Blake A., Brown J., Chen C-K., Conte N., Di Fenza A., Fiegel T., Horner N., Jacobsen J. O. B., Karp N., Lawson T., Mason J. C., Matthews P., Morgan H., Relac M., Santos L., Smedley D., Sneddon D., Tobin A., Tudose I., Warren J. W. G., Westerberg H., Yaikhom G., Parkinson H., Mallon A-M."A Mouse Informatics Platform for Phenotypic and Translational Discovery." *Mammalian Genome*, 2015; 26, pages 413-421.
2. de Angelis MH, Nicholson G, Selloum M, White JK, Morgan H, Ramirez-Solis R, Sorg T, Wells S, Fuchs H, Fray M, Adams DJ, Adams NC, Adler T, Aguilar-Pimentel A, Ali-Hadji D, Amann G, Andr P, Atkins S, Auburtin A, Ayadi A, Becker J, Becker L, Bedu E, Bekeredjian R, Birling MC, Blake A, Bottomley J, Bowl MR, Brault V, Busch DH, Bussell JN, Calzada-Wack J, Cater H, Champy MF, Charles P, Chevalier C, Chiani F, Codner GF, Combe R, Cox R, Dalloneau E, Dierich A, Di Fenza A, Doe B, Duchon A, Eickelberg O, Esapa CT, Fertak LE, Feigel T, Emelyanova I, Estabel J, Favor J, Flenniken A, Gambadoro A, Garrett L, Gates H, Gerdin AK, Gkoutos G, Greenaway S, Glasl L, Goetz P, Da Cruz IG, Gtz A, Graw J, Guimond A, Hans W, Hicks G, Hlter SM, Hfler H, Hancock JM, Hoehndorf R, Hough T, Houghton R, Hurt A, Ivandic B, Jacobs H, Jacquot S, Jones N, Karp NA, Katus HA, Kitchen S, Klein-Rodewald T, Klingenspor M, Klopstock T, Lalanne V, Leblanc S, Lengger C, le Marchand E, Ludwig T, Lux A, McKerlie C, Maier H, Mandel JL, Marschall S, Mark M, Melvin DG, Meziane H, Micklich K, Mittelhauser C, Monassier L, Moulaert D, Muller S, Naton B, Neff F, Nolan PM, Nutter LM, Ollert M, Pavlovic G, Pellegata NS, Peter E, Petit-Demoulire B, Pickard A, Podrini C,

Potter P, Pouilly L, Puk O, Richardson D, Rousseau S, Quintanilla-Fend L, Quwailid MM, Racz I, Rathkolb B, Riet F, Rossant J, Roux M, Rozman J, Ryder E, Salisbury J, Santos L, Schble KH, Schiller E, Schrewe A, Schulz H, Steinkamp R, Simon M, Stewart M, Stger C, Stger T, Sun M, Sunter D, Teboul L, Tilly I, Tocchini-Valentini GP, Tost M, Treise I, Vasseur L, Velot E, Vogt-Weisenhorn D, Wagner C, Walling A, Wattenhofer-Donze M, Weber B, Wendling O, Westerberg H, Willershuser M, Wolf E, Wolter A, Wood J, Wurst W, Yildirim A, Zeh R, Zimmer A, Zimprich A, EUMODIC Consortium, Holmes C, Steel KP, Herault Y, Gailus-Durner V, Mallon AM, Brown SD. "Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics." *Nat Genet*, 2015 July; doi:10.1038/ng.3360.

3. Gagarine Y., Morgan H.,Sneddon D., Retha A., Atienza-Herrero J., Blake A., Brown J., Di Fenza A., Fiegel T., Horner N., Ring N., Santos L., Westerberg H., Brown S. D., Mallon A-M. "Comparative visualization of genotype-phenotype relationships." *Nat Meth*, 2015 Aug; doi:10.1038/nmeth.3477.

4. Koscielny G., Yaikhom G., Iyer V., Meehan T.F., Morgan H., Atienza-Herrero J., Blake A., Chen C.K, Easty R., Di Fenza A., Fiegel T., Grifiths M., Horne A., Karp N.A., Kurbatova N., Mason J.C., Matthews P., Oakley D.J., Qazi A., Regnart J., Retha A., Santos L.A., Sneddon D.J., Warren J., Westerberg H., Wilson R.J., Melvin D.G, Smedley D., Brown S.D., Flicek P., Skarnes W. C., Mallon A.M., Parkinson H. "The International Mouse Phenotyping Consortium Web Portal, a unified point of access for knockout mice and related phenotyping data." *Nucleic Acids Research*, 2013 November; 42: D802-D809.

5. Trovato F., Nifosì R., Di Fenza A., Tozzini V. "A minimalist model of protein diffusion and interactions: the green fluorescent protein within the cytoplasm." *Macromolecules*, 2013 October; 46:8311.

6. Simon M.M., Greenaway S., White J.K., Fuchs H., Gailus-Durner V., Wells S., Sorg T., Wong K., Bedu E., Cartwright E.J., Dacquin R., Djebali S., Estabel J., Graw J., Ingham N.J., Jackson I.J., Lengeling A., Mandillo S., Marvel J., Meziane H., Preitner F., Puk O., Roux M., Adams D.J., Atkins S., Ayadi A., Becker L., Blake A., Brooker D., Cater H., Champy M.F., Combe R., Danecek P., Di Fenza A., Gates H., Gerdin A.K., Golini E., Hancock J.M., Hans W., Hlter S.M., Hough T., Jurdic P., Keane T.M., Morgan H., Mller W., Neff F., Nicholson G., Pasche B., Roberson L.A., Rozman J., Sanderson M., Santos L., Selloum M., Shannon C., Southwell A., Tocchini-Valentini G.P., Vancollie V.E., Westerberg H., Wurst W., Zi M., Yalcin B., Ramirez-Solis R., Steel K.P., Mallon A.M., De Angelis M.H., Herault Y., Brown S.D. "A comparative phenotypic and genomic analysis of C57BL/6J and C57BL/6N mouse strains." *Genome Biology*, 2013 July; 14(7):R82.

7. Terreni M., Liverani V., Gutierrez M.I., Di Primio C., Di Fenza A., Tozzini V., Albanese A., Arosio D., Giacca M. and Cereseto A. "GCN5-dependent acetylation of HIV-1 integrase enhances viral integration." *Retrovirology*, 2010; 7:18.

8. Di Fenza A., Rocchia W. and Tozzini V. "Complexes of HIV-1 Integrase with HAT proteins: multiscale models, dynamics and hypotheses on allosteric sites of inhibition." *Proteins*, 2009 July; 76(4):946-958.

9. Di Fenza A., Alagona G., Ghio C., Leonardi R., Giolitti A. and Madami A. "Caco-2 cell permeability modeling: a neural network coupled genetic algorithm approach." *J Comput Aid Mol Des* , 2007 Apr; 21(4):207-221.

10. Di Fenza A., Heine A., Koert, U. and Klebe G. "Understanding binding selectivity towards trypsin and factor Xa: the role of aromatic interactions." *Chem Med Chem* , 2007 Mar; 2(3):297-308.

11. D'Ursi A.M., Giannecchini S., Di Fenza A., Esposito C., Armenante M. R., Carotenuto A., Bendinelli M. and Rovero P. "Retroinverso analogue of the antiviral octapeptide C8 inhibits feline immunodeficiency virus in serum." *J Med Chem* , 2003 May 8; 46(10):1807-1810.
12. Giannecchini S., Di Fenza A., D'Ursi A.M., Matteucci D., Rovero P. and Bendinelli M. "Antiviral activity and conformational features of an octapeptide derived from the membrane-proximal ectodomain of the feline immunodeficiency virus transmembrane glycoprotein." *J Virol* , 2003 Mar; 77(6):3724-3733.
13. Di Fenza A. and Rovero P. "Assessment of new 6-Cl-HOBt based coupling reagents for peptide synthesis. Part 2: racemization studies." *Lett Pept Sci* , 2003 Jan; 9(2):125-129.
14. D'Ursi A.M., Albrizio S., Di Fenza A., Crescenzi O., Carotenuto A., Picone D., Novellino E. and Rovero P. "Structural studies on Hgr3 orphan receptor ligand prolactin-releasing peptide." *J Med Chem.*, 2002 Dec 5; 45(25):5483-5491.
15. Rovero P., Pellegrini M., Di Fenza A., Meini S., Quartara L., Maggi C. A., Formaggio F., Toniolo C. and Mierke D. F. "Agonist activity at the kinin B1 receptor: structural requirements of the central tetrapeptide." *J Med Chem*, 2001 Jan 18; 44(2):274-278.
16. Galoppini C., Meini S., Tancredi M., Di Fenza A., Triolo A., Maggi C.A., Formaggio F., Toniolo C. and Rovero P. "A new class of pseudopetide antagonists of the kinin B1 receptor containing alkyl spacers." *J Med Chem*, 1999 Feb 11; 42(3):409-414.
17. Di Fenza A., Tancredi M., Galoppini C. and Rovero P. "Racemization studies of Fmoc-Ser(tBu)-OH stepwise continuous-flow solid-phase synthesis." *Tetrahedron Lett* , 1998 Nov 12; 39(46):8529-8532.

## PUBLICATIONS IN INTERNATIONAL CONFERENCES ACTS

18. Terreni M., Liverani V., Gutierrez M.I., Di Primio C., Di Fenza A., Tozzini V., Albanese A., Arosio D., Giacca M., Cereseto A. "GCN5-dependent acetylation of HIV-1 integrase enhances viral integration." Retrovirology 6 Suppl 2 P20 (2009).
19. Tozzini V., Di Fenza A., Trovato F. Nifosi R., Amat P., Voltz K., Trylska J. "Bridging atomistic and meso- scale with minimalist models for bio-molecules." Eur Biophys J 38, Supplement 1 S59 (2009).
20. Di Fenza A. and Rovero P. "Racemization studies on novel Cl-HOBT-based coupling reagents." Proceedings of the 27th European Peptide Symposium at Sorrento, Italy, September 2002, 84-85.
21. D'Ursi A. M., Armenante M. R., Di Fenza A. and Rovero P. "Conformational analysis of peptides derived from feline immunodeficiency virus TM-glycoprotein." Proceedings of the 27th European Peptide Symposium at Sorrento, Italy, September 2002, 722-723.
22. Alcaro M. C., Sabatino G., Ginanneschi M., Chelli M., Di Fenza A., Rovero, P. and Papini A. M. "A synthetic strategy toward constrained head-to-tail cyclopeptides." Proceedings of the 27th European Peptide Symposium at Sorrento, Italy, September 2002, 16-17.
23. Di Fenza A., Albrizio S., D'Ursi A., Picone D. and Rovero, P. "Conformational studies on a synthetic peptide with Prolactin-releasing activity in a membrane mimetic environment." Proceedings of the 2nd International and the 17th American Peptide Symposium at S. Diego, California, U.S.A., June 2001, 314-315.
24. Carotenuto A., Di Fenza A., Nardi E., Papini Anna M. and Rovero P. "Conformational studies on a glycopeptide recognized with high affinity by autoantibodies in multiple sclerosis." Proceedings of the 2nd International and the 17th American Peptide Symposium at S. Diego, California, U.S.A., June 2001, 340-341.

25. Uziel J., Alcaro M. C., Sabatino G., Di Fenza A., Ginanneschi M., Chelli M., Rovero P. and Papini A. M. “Constrained head-to-tail cyclopeptides by amino-acid side-chain anchoring to trityl resins.” Proceedings of the 26th European Peptide Symposium at Montpellier, France, September 2000, 285-286.

## PARTICIPATIONS AT CONFERENCES

26. Di Fenza A. et al. “IMPC project: a source of data for epigenetics studies.” 3rd Oxford Symposium on Epigenetics Mechanisms in Health and Disease - Neuropsichiatry and inflammation: Epigenetic target discovery beyond oncology, Oxford, UK, March 14-15, 2013.
27. Di Fenza A., Rocchia W., Tozzini V. and Trovato F. “Development of a coarse-grained force-field for the study of antibody-antigen interactions.” Winter Modeling 2010, Pisa, Italy, February 26, 2010.
28. Trovato F., Di Fenza A. and Tozzini F. “Green Fluorescent Protein aggregations dynamics explored with a minimalist Coarse Grained model.” Biophysical Society 54th Annual Meeting, San Francisco, California, February 20-24, 2010.
29. Di Fenza A., Rocchia W. and Tozzini V. “Complexes of HIV-1 Integrase with HAT proteins: multiscale models, dynamics and hypotheses on allosteric sites of inhibition.” Winter Modeling 2008, Pisa, Italy, December 19, 2008.
30. Di Fenza A., Alagona G., Ghio C., Leonardi R., Giolitti A., and Madami A. “Human oral absorption models using a neural network couplet genetic algorithm.” 1° Congresso Nazionale della “Italian Proteomic Association - ItPA”, Pisa, Italy, July, 2006.
31. Di Fenza A., Heine A., Stürzebecher J., Stubbs M. T., Koert U. and Klebe G. “Crystal structures of Factor Xa-Trypsin mutants in complex with dianhydrosugar-based benzamidine inhibitors.” XVII Congresso Nazionale della Società di Biofisica Pura e Applicata, Pisa, Italy, September, 2004.
32. Di Fenza A., Heine A., Stubbs M. T., Koert U. and Klebe G. “Structural studies of Factor Xa-Trypsin mutants complexed by dianhydrosugar-based benzamidine inhibitors.” 22nd European Crystallographic Meeting, Budapest, Hungary, August, 2004.
33. Giannecchini S., Di Fenza A., D’Ursi A.M., Matteucci D., Rovero P., Bendinelli M. “Minimal size for the antiviral activity of a synthetic peptide derived from the TM gp of FIV.” 6th International Feline Retrovirus Research Symposium, Amelia Island, Florida, USA, 2002.
34. D’Ursi A. M., Armenante M. R., Di Fenza A. and Rovero P. “Conformational analysis of peptides derived from feline immunodeficiency virus TM-glycoprotein.” 27th European Peptide Symposium, Sorrento, Italy, September, 2002.
35. Alcaro M. C., Sabatino G., Ginanneschi M., Chelli M., Di Fenza A., Rovero P. and Papini A. M. “A synthetic strategy toward constrained head-to-tail cyclopeptides.” 27th European Peptide Symposium, Sorrento, Italy, September, 2002.
36. Di Fenza A. and Rovero P. “Racemization studies on novel Cl-HOBT-based coupling reagents.” 27th European Peptide Symposium, Sorrento, Italy, September, 2002.
37. Di Fenza A., Carotenuto A., Nardi E., Papini A. M. and Rovero P. “Conformational studies on a glycopeptide recognized with high affinity by autoantibodies in multiple sclerosis.” 17th American Peptide Symposium, San Diego, CA, U.S.A., June, 2001.
38. Di Fenza A., Albrizio S., D’Ursi A. M., Picone D. and Rovero P. “Conformational studies on a synthetic peptide with a prolactin-releasing activity in a membrane mimetic environment.” 17th American Peptide Symposium, San Diego, CA, U.S.A., June, 2001.

39. Di Fenza A., Giannecchini S., D'Ursi A. M., Matteucci D., Bendinelli M. and Rovero P. "The antiviral activity of a synthetic peptide from the membrane-proximal domain of feline immunodeficiency virus TM glicoprotein maps in correspondence of a conseved tryptophan-rich region." 17th American Peptide Symposium, San Diego, CA, U.S.A, June, 2001.
40. Uziel J., Alcaro M. C., Sabatino G., Di Fenza A., Ginanneschi M., Chelli M., Rovero, P. and Papini A.M. "Constrained head-to-tail cyclopeptides by amino-acid side-chain anchoring to trityl resins." 26th European Peptide Symposium, Montpellier, France, September, 2000.
41. Di Fenza A., Meini S., Quartara L., Maggi C. A., Formaggio F., Toniolo C. and Rovero P. "Agonist activity at the kinin B1 receptor: structural requirements of the central tetrapeptide." 26th European Peptide Symposium, Montpellier, France, September, 2000.
42. Sabatino G., Di Fenza A., Chelli M., Ginanneschi M., Rovero P. and Papini A. M. "Allyl esters of amminoacids linked to trytil-resin by their side-chain as useful starting supports to obtain diketopiperazine based combinatorial libraries." 16th American Peptide Symposium, Minneapolis, Minnesota, June, 1999.

## REFEREES

- Dr. Ann-Marie Mallon – The Alan Turing Institute, London, UK. Email: a.mallon@har.mrc.ac.uk
- Dr. Valentina Tozzini – CNR NANO, Pisa, Italy. Email: valentina.tozzini@nano.cnr.it
- Dr. Caterina Ghio – Institute for the Physico-Chemical Processes (IPCF), Pisa, Italy. Email: C.Ghio@ipcf.cnr.it
- Prof. Dr. Gerhard Klebe – Institut für Pharmazeutische Chemie, Philipps-Universität, Marburg, Germany. Email: klebe@mailer.uni-marburg.de

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