

# Patrick Penner

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## EDUCATION

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|---|-----------------------|
| <b>Novartis</b><br>Innovation Postdoc GDC/CADD, Advisor: Dr. Anna Vulpetti  | Basel<br>2022–Current |
| <b>University of Hamburg</b><br>Doctorate in Computer Science, Advisor: Prof. Dr. Matthias Rarey<br>– Thesis: “Interactive Pocket Exploration and Fragment Growing”               | Hamburg<br>2018–2023  |
| <b>University of Vienna</b><br>Mag. Pharm. in Pharmaceutical Science, Advisor: Univ.-Prof. Mag. Dr. Thierry Langer<br>– Thesis: “Bulk Processing of Patent Molecule Associations” | Vienna<br>2012–2018   |

## PROFESSIONAL EXPERIENCE

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| <b>Inte:Ligand</b><br>Project Work<br>– Pharmacophore Features for Halogen Bonding | Vienna<br>Winter Semester 2017/18 |
| <b>Boehringer Ingelheim</b><br>Internship in the CompChem Department               | Vienna<br>Summer 2017             |

## PROJECTS

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- **FastGrow** (2022)  
Integrated in BioSolveIT SeeSAR
- **Halogen Bonding in Pharmacophores** (2018)  
Integrated in Inte:Ligand LigandScout
- **Torsion Library** (2022)  
Used in RDKit, Roche, OE etc.
- **Patent Molecule Associations** (2017)  
Integrated in Inte:Ligand KNIME nodes

## DOMAIN KNOWLEDGE

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- **Structure-based Design** Advanced knowledge in development and application of structure-based methods
- **Statistical Modelling** Advanced knowledge in classical statistics/models and initial experience with emerging methods
- **Cheminformatics** In-depth knowledge of concepts, algorithms and design of systems
- **Pharmacophore Modelling** Advanced knowledge in development and application of pharmacophore methods, with or without receptor structure contributions
- **Chemical Patent Information** Experience with concepts specific to chemical and pharmaceutical patents
- **Quantum Chemistry** Experience in concepts and application
- **Drug Discovery** Initial experience in collaborative drug discovery projects

## PROGRAMMING

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- C++ (>100.000 Lines, >5 Years)
- Javascript (>10.000 Lines, >3 Years)
- Python (>10.000 Lines, >6 Years)
- Java (>10.000 Lines, >2 Years)
- Linux Environments and Configuration
- Data Science Packages
- Database Optimization
- Containerization
- Development Operations
- COBOL

## PUBLICATIONS

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- [1] **P. Penner** and A. Vulpetti, “QM assisted ML for 19f NMR chemical shift prediction”, Oct. 2023. DOI: 10.26434/chemrxiv-2023-sd3vq-v2.
- [2] **P. Penner**, W. Guba, R. Schmidt, A. Meyder, M. Stahl, and M. Rarey, “The torsion library: Semiautomated improvement of torsion rules with smartcompare”, *Journal of Chemical Information and Modeling*, Mar. 2022. DOI: 10.1021/acs.jcim.2c00043.
- [3] **P. Penner**, V. Martiny, L. Bellmann, F. Flachsenberg, M. Gastreich, I. Theret, C. Meyer, and M. Rarey, “Fastgrow: On-the-fly growing and its application to dyrk1a”, *Journal of Computer-Aided Molecular Design*, vol. 36, no. 9, pp. 639–651, Aug. 2022. DOI: 10.1007/s10822-022-00469-y.
- [4] K. Schöning-Stierand, K. Diedrich, C. Ehrt, F. Flachsenberg, J. Graef, J. Sieg, **P. Penner**, M. Poppinga, A. Ungethüm, and M. Rarey, “ProteinsPlus: a comprehensive collection of web-based molecular modeling tools”, *Nucleic Acids Research*, Apr. 2022. DOI: 10.1093/nar/gkac305.
- [5] L. Bellmann, **P. Penner**, and M. Rarey, “Topological similarity search in large combinatorial fragment spaces”, *Journal of Chemical Information and Modeling*, vol. 61, pp. 238–251, 1 Oct. 2021. DOI: 10.1021/acs.jcim.0c00850.
- [6] F. Flachsenberg, A. Meyder, K. Sommer, **P. Penner**, and M. Rarey, “A consistent scheme for gradient-based optimization of protein–ligand poses”, *J. Chem. Inf. Model.*, vol. 60, pp. 6502–6522, 12 Dec. 2020. DOI: 10.1021/acs.jcim.0c01095.
- [7] **P. Penner**, V. Martiny, A. Gohier, M. Gastreich, P. Ducrot, D. Brown, and M. Rarey, “Shape-based descriptors for efficient structure-based fragment growing”, *J. Chem. Inf. Model.*, vol. 60, pp. 6269–6281, 12 Nov. 2020. DOI: 10.1021/acs.jcim.0c00920.

## CONFERENCE PARTICIPATION/CONTRIBUTIONS

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|---|------------------------------|
| <b>12th International Conference on Chemical Structures (ICCS)</b>            | Noordwijkerhout, Netherlands |
| Improving Torsion Library Patterns with SMARTScompare                         | 2022                         |
| <b>16th German Conference on Cheminformatics and SAMPL Satellite Workshop</b> | Online                       |
| Research Talk: Fragment Growing Validation Dataset                            | 2020                         |
| <b>2019 GRS/GRC Computer Aided Drug Design</b>                                | West Dover VT, USA           |
| GRC Poster: Next Generation Methods for Structure-Based Fragment Growing      | 2019                         |
| GRS Talk: Next Generation Methods for Structure-Based Fragment Growing        |                              |
| <b>6th Strasbourg Summer School in Chemoinformatics</b>                       | Strasbourg, France           |
| Participant   | 2018                         |