Florian Richter

List of Publications by Year in Descending Order

18 papers	3,480 citations	15 h-index	18 g-index
18 ext. papers	4,198 ext. citations	9.7 avg, IF	4.38 L-index

#	Paper	IF	Citations
18	A Light-Oxygen-Voltage Receptor Integrates Light and Temperature. *Journal of Molecular Biology*, **2021**, 433, 167107	6.5	5
17	Computational Aminoacyl-tRNA Synthetase Library Design for Photocaged Tyrosine. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	16
16	Optogenetic Control by Pulsed Illumination. *ChemBioChem*, **2018**, 19, 1296-1304	3.8	15
15	Switchable Cas9. *Current Opinion in Biotechnology*, **2017**, 48, 119-126	11.4	32
14	Photoactivatable Mussel-Based Underwater Adhesive Proteins by an Expanded Genetic Code. *ChemBioChem*, **2017**, 18, 1819-1823	3.8	39
13	Engineering of temperature- and light-switchable Cas9 variants. *Nucleic Acids Research*, **2016**, 44, 10003-10014	10.1	70
12	Library-Aided Probing of Linker Determinants in Hybrid Photoreceptors. *ACS Synthetic Biology*, **2016**, 5, 1117-1126	5.7	32
11	Upgrading a microplate reader for photobiology and all-optical experiments. *Photochemical and Photobiological Sciences*, **2015**, 14, 270-9	4.2	27
10	Light-Induced Rearrangement of the β5 Strand in the BLUF Photoreceptor SyPixD (Slr1694). *Journal of Physical Chemistry Letters*, **2015**, 6, 4749-53	6.4	11
9	Computational design of a red fluorophore ligase for site-specific protein labeling in living cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E4551-9	11.5	57
8	Design of activated serine-containing catalytic triads with atomic-level accuracy. *Nature Chemical Biology*, **2014**, 10, 386-91	11.7	52
7	Computational Protein Design for Synthetic Biology **2013**, 101-122		3
6	Computational design of catalytic dyads and oxyanion holes for ester hydrolysis. *Journal of the American Chemical Society*, **2012**, 134, 16197-206	16.4	114
5	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. *Methods in Enzymology*, **2011**, 487, 545-74	1.7	1216
4	De novo enzyme design using Rosetta3. *PLoS ONE*, **2011**, 6, e19230	3.7	224
3	RosettaScripts: a scripting language interface to the Rosetta macromolecular modeling suite. *PLoS ONE*, **2011**, 6, e20161	3.7	311
2	RosettaRemodel: a generalized framework for flexible backbone protein design. *PLoS ONE*, **2011**, 6, e24109	3.7	200

1	Quantitative reactivity profiling predicts functional cysteines in proteomes. *Nature*, **2010**, 468, 790-5	50.4	1056