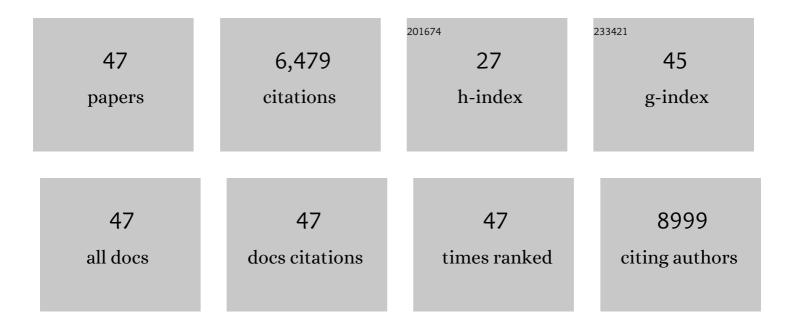
Geoffrey S Waldo

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Solution structure of the type I polyketide synthase Pks13 from Mycobacterium tuberculosis. BMC Biology, 2022, 20, .	3.8	5
2	Construction, characterization and crystal structure of a fluorescent single-chain Fv chimera. Protein Engineering, Design and Selection, 2021, 34, .	2.1	4
3	Engineering an efficient and bright split Corynactis californica green fluorescent protein. Scientific Reports, 2021, 11, 18440.	3.3	2
4	Selection and verification of antibodies against the cytoplasmic domain of M2 of influenza, a transmembrane protein. MAbs, 2020, 12, 1843754.	5.2	7
5	High-Throughput Isolation of Soluble Protein Domains Using a Bipartite Split-GFP Complementation System. Methods in Molecular Biology, 2019, 2025, 321-333.	0.9	1
6	High-Throughput Protein–Protein Interaction Assays Using Tripartite Split-GFP Complementation. Methods in Molecular Biology, 2019, 2025, 423-437.	0.9	6
7	A Suite of Engineered GFP Molecules for Oligomeric Scaffolding. Structure, 2015, 23, 1754-1768.	3.3	30
8	In-Depth High-Throughput Screening of Protein Engineering Libraries by Split-GFP Direct Crude Cell Extract Data Normalization. Chemistry and Biology, 2015, 22, 1406-1414.	6.0	37
9	Subfamily-Specific Adaptations in the Structures of Two Penicillin-Binding Proteins from Mycobacterium tuberculosis. PLoS ONE, 2014, 9, e116249.	2.5	6
10	Library methods for structural biology of challenging proteins and their complexes. Current Opinion in Structural Biology, 2013, 23, 403-408.	5.7	19
11	Split green fluorescent protein as a modular binding partner for protein crystallization. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2513-2523.	2.5	29
12	A New Protein-Protein Interaction Sensor Based on Tripartite Split-GFP Association. Scientific Reports, 2013, 3, 2854.	3.3	190
13	The Brucella TIR-like protein TcpB interacts with the death domain of MyD88. Biochemical and Biophysical Research Communications, 2012, 417, 299-304.	2.1	49
14	Disulfide Bonds within the C2 Domain of RAGE Play Key Roles in Its Dimerization and Biogenesis. PLoS ONE, 2012, 7, e50736.	2.5	32
15	Experimental mapping of soluble protein domains using a hierarchical approach. Nucleic Acids Research, 2011, 39, e125-e125.	14.5	29
16	A photophysical study of two fluorogen-activating proteins bound to their cognate fluorogens. Proceedings of SPIE, 2011, , .	0.8	0
17	A high-throughput immobilized bead screen for stable proteins and multi-protein complexes. Protein Engineering, Design and Selection, 2011, 24, 565-578.	2.1	12
18	Fluorescent Labeling of Antibody Fragments Using Split GFP. PLoS ONE, 2011, 6, e25727.	2.5	16

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19	The optimization of in vitro high-throughput chemical lysis of Escherichia coli. Application to ACP domain of the polyketide synthase ppsC from Mycobacterium tuberculosis. Journal of Structural and Functional Genomics, 2010, 11, 41-49.	1.2	19
20	One-step split GFP staining for sensitive protein detection and localization in mammalian cells. BioTechniques, 2010, 49, 727-736.	1.8	53
21	Split GFP Complementation Assay for Quantitative Measurement of Tau Aggregation In Situ. Methods in Molecular Biology, 2010, 670, 109-123.	0.9	22
22	Directed evolution of an extremely stable fluorescent protein. Protein Engineering, Design and Selection, 2009, 22, 313-323.	2.1	58
23	Automated, high-throughput platform for protein solubility screening using a split-GFP system. Journal of Structural and Functional Genomics, 2009, 10, 47-55.	1.2	32
24	Protein production and purification. Nature Methods, 2008, 5, 135-146.	19.0	763
25	Expression and use of superfolder green fluorescent protein at high temperatures <i>in vivo</i> : a tool to study extreme thermophile biology. Environmental Microbiology, 2008, 10, 605-613.	3.8	51
26	From No Expression to High-Level Soluble Expression in Escherichia coli by Screening a Library of the Target Proteins with Randomized N-Termini. Methods in Molecular Biology, 2008, 426, 187-195.	0.9	3
27	New Molecular Reporters for Rapid Protein Folding Assays. PLoS ONE, 2008, 3, e2387.	2.5	40
28	Domain Orientation in the Inactive Response RegulatorMycobacterium tuberculosisMtrA Provides a Barrier to Activationâ€,‡. Biochemistry, 2007, 46, 6733-6743.	2.5	76
29	Split GFP complementation assay: a novel approach to quantitatively measure aggregation of tau <i>in situ</i> : effects of GSK3β activation and caspase 3 cleavage. Journal of Neurochemistry, 2007, 103, 2529-2539.	3.9	69
30	Engineering and characterization of a superfolder green fluorescent protein. Nature Biotechnology, 2006, 24, 79-88.	17.5	1,949
31	In vivo and in vitro protein solubility assays using split GFP. Nature Methods, 2006, 3, 845-854.	19.0	239
32	A Comparison of the Fluorescence Dynamics of Single Molecules of a Green Fluorescent Protein: One- versus Two-Photon Excitation. ChemPhysChem, 2006, 7, 250-260.	2.1	42
33	A Toolbox of GFP Technologies. Imaging & Microscopy, 2006, 8, 60-61.	0.1	0
34	Antibody binding loop insertions as diversity elements. Nucleic Acids Research, 2006, 34, e132-e132.	14.5	37
35	Structural and functional features of an NDP kinase from the hyperthermophile crenarchaeonPyrobaculum aerophilum. Protein Science, 2005, 14, 2562-2573.	7.6	12
36	Protein tagging and detection with engineered self-assembling fragments of green fluorescent protein. Nature Biotechnology, 2005, 23, 102-107.	17.5	781

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37	Recent Advances in GFP Folding Reporter and Split-GFP Solubility Reporter Technologies. Application to Improving the Folding and Solubility of Recalcitrant Proteins from Mycobacterium tuberculosis. Journal of Structural and Functional Genomics, 2005, 6, 113-119.	1.2	65
38	Genetic screens and directed evolution for protein solubility. Current Opinion in Chemical Biology, 2003, 7, 33-38.	6.1	137
39	Fluorobodies combine GFP fluorescence with the binding characteristics of antibodies. Nature Biotechnology, 2003, 21, 1473-1479.	17.5	31
40	Directed evolution approach to a structural genomics project: Rv2002 from Mycobacterium tuberculosis. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 455-460.	7.1	55
41	The TB Structural Genomics Consortium: Providing a Structural Foundation for Drug Discovery. Current Drug Targets Infectious Disorders, 2002, 2, 121-141.	2.1	66
42	Crystallization and preliminary X-ray crystallographic analysis of the Rv2002 gene product fromMycobacterium tuberculosis, a β-ketoacyl carrier protein reductase homologue. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 303-305.	2.5	14
43	Engineering soluble proteins for structural genomics. Nature Biotechnology, 2002, 20, 927-932.	17.5	174
44	Solution structure of <i>Pyrobaculum aerophilum</i> DsrC, an archaeal homologue of the gamma subunit of dissimilatory sulfite reductase. FEBS Journal, 2001, 268, 5842-5850.	0.2	37
45	Rapid protein-folding assay using green fluorescent protein. Nature Biotechnology, 1999, 17, 691-695.	17.5	840
46	Determination of the chemical environment of sulphur in petroleum asphaltenes by X-ray absorption spectroscopy. Fuel, 1992, 71, 53-57.	6.4	133
47	Sulfur speciation in heavy petroleums: Information from X-ray absorption near-edge structure. Geochimica Et Cosmochimica Acta, 1991, 55, 801-814.	3.9	207