## Francesca M Marassi

List of Publications by Year in descending order

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FRANCESCA M MARASSI

#	Article	IF	CITATIONS
1	Structure of the chemokine receptor CXCR1 in phospholipid bilayers. Nature, 2012, 491, 779-783.	27.8	407
2	Structure Determination of Membrane Proteins by NMR Spectroscopy. Chemical Reviews, 2004, 104, 3587-3606.	47.7	396
3	A Solid-State NMR Index of Helical Membrane Protein Structure and Topology. Journal of Magnetic Resonance, 2000, 144, 150-155.	2.1	345
4	Simultaneous assignment and structure determination of a membrane protein from NMR orientational restraints. Protein Science, 2003, 12, 403-411.	7.6	183
5	Dipolar Waves as NMR Maps of Protein Structure. Journal of the American Chemical Society, 2002, 124, 4206-4207.	13.7	109
6	Expression, purification, and activities of full-length and truncated versions of the integral membrane protein Vpu from HIV-1. Protein Science, 2009, 11, 546-557.	7.6	108
7	Dipolar Waves Map the Structure and Topology of Helices in Membrane Proteins. Journal of the American Chemical Society, 2003, 125, 8928-8935.	13.7	99
8	Bicelles: A natural â€~molecular goniometer' for structural, dynamical and topological studies of molecules in membranes. Biochimie, 2009, 91, 744-751.	2.6	97
9	Structure Determination of a Membrane Protein in Proteoliposomes. Journal of the American Chemical Society, 2012, 134, 2047-2056.	13.7	89
10	Orientation of Cecropin A Helices in Phospholipid Bilayers Determined by Solid-State NMR Spectroscopy. Biophysical Journal, 1999, 77, 3152-3155.	0.5	88
11	A Simple Approach to Membrane Protein Secondary Structure and Topology based on NMR Spectroscopy. Biophysical Journal, 2001, 80, 994-1003.	0.5	81
12	Structure of the Na,K-ATPase Regulatory Protein FXYD1 in Micellesâ€. Biochemistry, 2007, 46, 6774-6783.	2.5	81
13	FXYD Proteins Reverse Inhibition of the Na+-K+ Pump Mediated by Glutathionylation of Its β1 Subunit. Journal of Biological Chemistry, 2011, 286, 18562-18572.	3.4	79
14	Nuclear Magnetic Resonance of Membrane-Associated Peptides and Proteins. Methods in Enzymology, 2001, 339, 285-313.	1.0	72
15	Structure and Dynamics of the Membrane-Bound Form of Pf1 Coat Protein: Implications of Structural Rearrangement for Virus Assembly. Biophysical Journal, 2010, 99, 1465-1474.	0.5	70
16	Applications of NMR to membrane proteins. Archives of Biochemistry and Biophysics, 2017, 628, 92-101.	3.0	65
17	Orientation of the <i>Escherichia coli</i> Outer Membrane Protein OmpX in Phospholipid Bilayer Membranes Determined by Solid-State NMR. Biochemistry, 2008, 47, 6531-6538.	2.5	59
18	Conformation of BCL-XL upon Membrane Integration. Journal of Molecular Biology, 2015, 427, 2262-2270.	4.2	54

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19	Conformation of Membrane-associated Proapoptotic tBid. Journal of Biological Chemistry, 2004, 279, 28954-28960.	3.4	52
20	Structural Similarity of a Membrane Protein in Micelles and Membranes. Journal of the American Chemical Society, 2007, 129, 8078-8079.	13.7	50
21	A practical implicit solvent potential for NMR structure calculation. Journal of Magnetic Resonance, 2014, 243, 54-64.	2.1	45
22	Surface acoustic wave sensor response and molecular modeling: selective binding of nitrobenzene derivatives to (aminopropyl)triethoxysilane. Analytical Chemistry, 1990, 62, 32-37.	6.5	43
23	Regulation of apoptosis by an intrinsically disordered region of Bcl-xL. Nature Chemical Biology, 2018, 14, 458-465.	8.0	42
24	Structural studies of apoptosis and ion transport regulatory proteins in membranes. Magnetic Resonance in Chemistry, 2004, 42, 172-179.	1.9	40
25	Serine 68 Phospholemman Phosphorylation during Forskolin-Induced Swine Carotid Artery Relaxation. Journal of Vascular Research, 2005, 42, 483-491.	1.4	35
26	Influence of the lipid membrane environment on structure and activity of the outer membrane protein Ail from Yersinia pestis. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 712-720.	2.6	32
27	Structure of monomeric Interleukin-8 and its interactions with the N-terminal Binding Site-I of CXCR1 by solution NMR spectroscopy. Journal of Biomolecular NMR, 2017, 69, 111-121.	2.8	31
28	High quality NMR structures: a new force field with implicit water and membrane solvation for Xplor-NIH. Journal of Biomolecular NMR, 2017, 67, 35-49.	2.8	30
29	NMR structural studies of the bacterial outer membrane protein OmpX in oriented lipid bilayer membranes. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 3216-3224.	2.6	29
30	Mapping the Interaction of Pro-Apoptotic tBID with Pro-Survival BCL-XL. Biochemistry, 2009, 48, 8704-8711.	2.5	28
31	Structure determination of membrane proteins in five easy pieces. Methods, 2011, 55, 363-369.	3.8	28
32	Structural Insights into the <i>Yersinia pestis</i> Outer Membrane Protein Ail in Lipid Bilayers. Journal of Physical Chemistry B, 2017, 121, 7561-7570.	2.6	28
33	Using pisa pies to resolve ambiguities in angular constraints from PISEMA spectra of aligned proteins. Journal of Biomolecular NMR, 2002, 23, 239-242.	2.8	27
34	Bcl-XL as a fusion protein for the high-level expression of membrane-associated proteins. Protein Science, 2005, 14, 948-955.	7.6	27
35	The Structure of the Mercury Transporter MerF in Phospholipid Bilayers: A Large Conformational Rearrangement Results from N-Terminal Truncation. Journal of the American Chemical Society, 2013, 135, 9299-9302.	13.7	27
36	Membrane Protein Structure Determination <i>in Membrana</i> . Accounts of Chemical Research, 2013, 46, 2182-2190.	15.6	27

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37	Structures of the FXYD regulatory proteins in lipid micelles and membranes. Journal of Bioenergetics and Biomembranes, 2007, 39, 379-383.	2.3	25

## 38 Yersinia pestis uses the Ail outer membrane protein to recruit vitronectin. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7

39	A Practical Implicit Membrane Potential for NMR Structure Calculations of Membrane Proteins. Biophysical Journal, 2015, 109, 574-585.	0.5	24
40	Solid-state NMR of the Yersinia pestis outer membrane protein Ail in lipid bilayer nanodiscs sedimented by ultracentrifugation. Journal of Biomolecular NMR, 2015, 61, 275-286.	2.8	24
41	Backbone structure of Yersinia pestis Ail determined in micelles by NMR-restrained simulated annealing with implicit membrane solvation. Journal of Biomolecular NMR, 2015, 63, 59-65.	2.8	24
42	Characterization of the membrane-inserted C-terminus of cytoprotective BCL-XL. Protein Expression and Purification, 2016, 122, 56-63.	1.3	22
43	Competitive Interactions of Collagen and a Jararhagin-derived Disintegrin Peptide with the Integrin α2-I Domain. Journal of Biological Chemistry, 2008, 283, 16665-16672.	3.4	21
44	Expression, refolding, and initial structural characterization of the Y. pestis Ail outer membrane protein in lipids. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 482-489.	2.6	21
45	The Anti-angiogenic Peptide Anginex Disrupts the Cell Membrane. Journal of Molecular Biology, 2006, 356, 876-885.	4.2	20
46	Structure of human Vitronectin C-terminal domain and interaction with <i>Yersinia pestis</i> outer membrane protein Ail. Science Advances, 2019, 5, eaax5068.	10.3	19
47	Mutually constructive roles of Ail and LPS in <i>Yersinia pestis</i> serum survival. Molecular Microbiology, 2020, 114, 510-520.	2.5	19
47 48	Mutually constructive roles of Ail and LPS in <i>Yersinia pestis</i> serum survival. Molecular Microbiology, 2020, 114, 510-520. AssignFit: A program for simultaneous assignment and structure refinement from solid-state NMR spectra. Journal of Magnetic Resonance, 2012, 214, 42-50.	2.5 2.1	19 18
47 48 49	Mutually constructive roles of Ail and LPS in <i>Yersinia pestis</i> serum survival. Molecular         Microbiology, 2020, 114, 510-520.         AssignFit: A program for simultaneous assignment and structure refinement from solid-state NMR         spectra. Journal of Magnetic Resonance, 2012, 214, 42-50.         NMR-Based Simulation Studies of Pf1 Coat Protein in Explicit Membranes. Biophysical Journal, 2013, 105, 691-698.	2.5 2.1 0.5	19 18 18
47 48 49 50	Mutually constructive roles of Ail and LPS in <i>Yersinia pestis</i> serum survival. Molecular         Microbiology, 2020, 114, 510-520.         AssignFit: A program for simultaneous assignment and structure refinement from solid-state NMR         spectra. Journal of Magnetic Resonance, 2012, 214, 42-50.         NMR-Based Simulation Studies of Pf1 Coat Protein in Explicit Membranes. Biophysical Journal, 2013, 105, 691-698.         Structural basis for the association of PLEKHA7 with membrane-embedded phosphatidylinositol lipids.         Structure, 2021, 29, 1029-1039.e3.	2.5 2.1 0.5 3.3	19 18 18 18
47 48 49 50 51	<ul> <li>Mutually constructive roles of Ail and LPS in <i>Yersinia pestis</i> serum survival. Molecular</li> <li>Microbiology, 2020, 114, 510-520.</li> <li>AssignFit: A program for simultaneous assignment and structure refinement from solid-state NMR spectra. Journal of Magnetic Resonance, 2012, 214, 42-50.</li> <li>NMR-Based Simulation Studies of Pf1 Coat Protein in Explicit Membranes. Biophysical Journal, 2013, 105, 691-698.</li> <li>Structural basis for the association of PLEKHA7 with membrane-embedded phosphatidylinositol lipids. Structure, 2021, 29, 1029-1039.e3.</li> <li>Mapping the Specific Cytoprotective Interaction of Humanin with the Pro-apoptotic Protein Bid. Chemical Biology and Drug Design, 2007, 70, 383-392.</li> </ul>	2.5 2.1 0.5 3.3 3.2	19 18 18 18 18
47 48 49 50 51 52	Mutually constructive roles of Ail and LPS in <i>Yersinia pestis</i> serum survival. Molecular         Microbiology, 2020, 114, 510-520.         AssignFit: A program for simultaneous assignment and structure refinement from solid-state NMR         spectra. Journal of Magnetic Resonance, 2012, 214, 42-50.         NMR-Based Simulation Studies of Pf1 Coat Protein in Explicit Membranes. Biophysical Journal, 2013, 105, 691-698.         Structural basis for the association of PLEKHA7 with membrane-embedded phosphatidylinositol lipids.         Structure, 2021, 29, 1029-1039.e3.         Mapping the Specific Cytoprotective Interaction of Humanin with the Pro-apoptotic Protein Bid.         Chemical Biology and Drug Design, 2007, 70, 383-392.         Molecular Structure and Peptidoglycan Recognition of Mycobacterium tuberculosis ArfA (Rv0899).         Journal of Molecular Biology, 2012, 416, 208-220.	2.5 2.1 0.5 3.3 3.2 4.2	19       18       18       18       17
47 48 49 50 51 52 53	Mutually constructive roles of Ail and LPS in <i>Yersinia pestis</i> serum survival. Molecular         Microbiology, 2020, 114, 510-520.         AssignFit: A program for simultaneous assignment and structure refinement from solid-state NMR         spectra. Journal of Magnetic Resonance, 2012, 214, 42-50.         NMR-Based Simulation Studies of Pf1 Coat Protein in Explicit Membranes. Biophysical Journal, 2013, 105, 691-698.         Structural basis for the association of PLEKHA7 with membrane-embedded phosphatidylinositol lipids.         Structure, 2021, 29, 1029-1039.e3.         Mapping the Specific Cytoprotective Interaction of Humanin with the Pro-apoptotic Protein Bid.         Chemical Biology and Drug Design, 2007, 70, 383-392.         Molecular Structure and Peptidoglycan Recognition of Mycobacterium tuberculosis ArfA (Rv0899).         Journal of Molecular Biology, 2012, 416, 208-220.         Orphan Nuclear Receptor NR4A1 Binds a Novel Protein Interaction Site on Anti-apoptotic B Cell         Lymphoma Gene 2 Family Proteins. Journal of Biological Chemistry, 2016, 291, 14072-14084.	2.5 2.1 0.5 3.3 3.2 4.2 3.4	19       18       18       18       17       17       17

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55	Structure of the membrane protein MerF, a bacterial mercury transporter, improved by the inclusion of chemical shift anisotropy constraints. Journal of Biomolecular NMR, 2014, 60, 67-71.	2.8	16
56	Structure and Activity of CPNGRC: A Modified CD13/APN Peptidic Homing Motif. Chemical Biology and Drug Design, 2010, 75, 551-562.	3.2	14
57	Membrane proteins in magnetically aligned phospholipid polymer discs for solid-state NMR spectroscopy. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183333.	2.6	14
58	Solid-State NMR-Restrained Ensemble Dynamics of a Membrane Protein in Explicit Membranes. Biophysical Journal, 2015, 108, 1954-1962.	0.5	11
59	High resolution solid-state NMR spectroscopy of the Yersinia pestis outer membrane protein Ail in lipid membranes. Journal of Biomolecular NMR, 2017, 67, 179-190.	2.8	11
60	Calcium and hydroxyapatite binding site of human vitronectin provides insights to abnormal deposit formation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18504-18510.	7.1	11
61	Conformational States of the Cytoprotective Protein Bcl-xL. Biophysical Journal, 2020, 119, 1324-1334.	0.5	10
62	Structure of the Na,K-ATPase regulatory protein FXYD2b in micelles: Implications for membrane–water interfacial arginines. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 299-306.	2.6	9
63	Membrane Protein Structure Determination: Back to the Membrane. Methods in Molecular Biology, 2013, 1063, 145-158.	0.9	8
64	Reconstitution and Characterization of BCL-2 Family Proteins in Lipid Bilayer Nanodiscs. Methods in Molecular Biology, 2019, 1877, 233-246.	0.9	8
65	A periplasmic cinched protein is required for siderophore secretion and virulence of Mycobacterium tuberculosis. Nature Communications, 2022, 13, 2255.	12.8	8
66	Correlating the Structure and Activity of Y.Âpestis Ail in a Bacterial Cell Envelope. Biophysical Journal, 2021, 120, 453-462.	0.5	7
67	Improved chemical shift prediction by Rosetta conformational sampling. Journal of Biomolecular NMR, 2012, 54, 237-243.	2.8	6
68	BAX and BAK Caught in the Act. Molecular Cell, 2009, 36, 353-354.	9.7	4
69	<i>Mycobacterium tuberculosis</i> Rv0899 defines a family of membrane proteins widespread in nitrogenâ€fixing bacteria. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2946-2955.	2.6	4
70	PLEKHA7 signaling is necessary for the growth of mutant KRAS driven colorectal cancer. Experimental Cell Research, 2021, 409, 112930.	2.6	4
71	NMR Structure Determination of Proteins in Bilayer Lipid Membranes: The FXYD Family Proteins. Behavior Research Methods, 2005, 2, 77-93.	4.0	2
72	The Discreet Charm of the Curve. Biophysical Journal, 2013, 104, 1215-1216.	0.5	2

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73	Lipoprotein Particle Formation by Proapoptotic tBid. Biophysical Journal, 2018, 115, 533-542.	0.5	2
74	Structure of the Mycobacterium Tuberculosis Virulence Factor Rv0899 (ompATb). Biophysical Journal, 2010, 98, 624a-625a.	0.5	0
75	Structural and Functional Studies of the Outer Membrane Protein Ail from Yersinia Pestis. Biophysical Journal, 2014, 106, 47a.	0.5	0
76	NMR Structural Studies of the Yersinia Pestis Outer Membrane Protein AIL in Lipid Bilayers. Biophysical Journal, 2018, 114, 237a.	0.5	0
77	Determining Vitronectin's Role in Forming the Hallmark of Age-Related Macular Degeneration. Biophysical Journal, 2021, 120, 202a.	0.5	0