

# Silvia Spinelli

## List of Publications by Year in descending order

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94  
papers

6,813  
citations

50170

46  
h-index

62479

80  
g-index

94  
all docs

94  
docs citations

94  
times ranked

5795  
citing authors

#	ARTICLE	IF	CITATIONS
1	Conformations of immunoglobulin hypervariable regions. <i>Nature</i> , 1989, 342, 877-883.	13.7	1,199
2	Biogenesis and structure of a type VI secretion membrane core complex. <i>Nature</i> , 2015, 523, 555-560.	13.7	241
3	Mammalian odorant binding proteins. <i>BBA - Proteins and Proteomics</i> , 2000, 1482, 229-240.	2.1	234
4	Domain swapping creates a third putative combining site in bovine odorant binding protein dimer. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 863-867.	3.6	194
5	Directed in Vitro Evolution and Crystallographic Analysis of a Peptide-binding Single Chain Antibody Fragment (scFv) with Low Picomolar Affinity. <i>Journal of Biological Chemistry</i> , 2004, 279, 18870-18877.	1.6	160
6	A common protein fold and similar active site in two distinct families of Î²-glycanases. <i>Nature Structural Biology</i> , 1995, 2, 569-576.	9.7	149
7	Three Camelid VHH Domains in Complex with Porcine Pancreatic Î±-Amylase. <i>Journal of Biological Chemistry</i> , 2002, 277, 23645-23650.	1.6	145
8	Camelid Heavy-Chain Variable Domains Provide Efficient Combining Sites to Haptens. <i>Biochemistry</i> , 2000, 39, 1217-1222.	1.2	144
9	Complexes of porcine odorant binding protein with odorant molecules belonging to different chemical classes. <i>Journal of Molecular Biology</i> , 2000, 300, 127-139.	2.0	139
10	Crystal structure of <i>Apis mellifera</i> OBP14, a C-minus odorant-binding protein, and its complexes with odorant molecules. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 41-50.	1.2	135
11	The crystal structure of a llama heavy chain variable domain. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 752-757.	3.6	131
12	Priming and polymerization of a bacterial contractile tail structure. <i>Nature</i> , 2016, 531, 59-63.	13.7	127
13	The Structure of the Monomeric Porcine Odorant Binding Protein Sheds Light on the Domain Swapping Mechanism. <i>Biochemistry</i> , 1998, 37, 7913-7918.	1.2	126
14	Structure of the phage TP901-1 1.8ÅMDa baseplate suggests an alternative host adhesion mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8954-8958.	3.3	121
15	Lactococcal bacteriophage p2 receptor-binding protein structure suggests a common ancestor gene with bacterial and mammalian viruses. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 85-89.	3.6	117
16	Receptor-Binding Protein of <i>Lactococcus lactis</i> Phages: Identification and Characterization of the Saccharide Receptor-Binding Site. <i>Journal of Bacteriology</i> , 2006, 188, 2400-2410.	1.0	116
17	The Crystal Structure of a Cockroach Pheromone-binding Protein Suggests a New Ligand Binding and Release Mechanism. <i>Journal of Biological Chemistry</i> , 2003, 278, 30213-30218.	1.6	115
18	Isolation of Llama Antibody Fragments for Prevention of Dandruff by Phage Display in Shampoo. <i>Applied and Environmental Microbiology</i> , 2005, 71, 442-450.	1.4	113

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19	Crystal Structure of the Open Form of Dog Gastric Lipase in Complex with a Phosphonate Inhibitor. <i>Journal of Biological Chemistry</i> , 2002, 277, 2266-2274.	1.6	107
20	Modular Structure of the Receptor Binding Proteins of <i>Lactococcus lactis</i> Phages. <i>Journal of Biological Chemistry</i> , 2006, 281, 14256-14262.	1.6	102
21	Camelid nanobodies: killing two birds with one stone. <i>Current Opinion in Structural Biology</i> , 2015, 32, 1-8.	2.6	101
22	Crystal Structure of <i>E. coli</i> Alcohol Dehydrogenase YqhD: Evidence of a Covalently Modified NADP Coenzyme. <i>Journal of Molecular Biology</i> , 2004, 342, 489-502.	2.0	92
23	Structural Characterization and Oligomerization of the TssL Protein, a Component Shared by Bacterial Type VI and Type IVb Secretion Systems. <i>Journal of Biological Chemistry</i> , 2012, 287, 14157-14168.	1.6	91
24	Structural Basis of the Honey Bee PBP Pheromone and pH-induced Conformational Change. <i>Journal of Molecular Biology</i> , 2008, 380, 158-169.	2.0	87
25	Reverse chemical ecology: Olfactory proteins from the giant panda and their interactions with putative pheromones and bamboo volatiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9802-E9810.	3.3	86
26	Lateral recognition of a dye hapten by a llama VHH domain. <i>Journal of Molecular Biology</i> , 2001, 311, 123-129.	2.0	85
27	The Insect Attractant 1-Octen-3-ol Is the Natural Ligand of Bovine Odorant-binding Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 7150-7155.	1.6	80
28	Direct in Vivo Screening of Intrabody Libraries Constructed on a Highly Stable Single-chain Framework. <i>Journal of Biological Chemistry</i> , 2002, 277, 45075-45085.	1.6	80
29	The Crystal Structure of Odorant Binding Protein 7 from <i>Anopheles gambiae</i> Exhibits an Outstanding Adaptability of Its Binding Site. <i>Journal of Molecular Biology</i> , 2011, 414, 401-412.	2.0	76
30	Functional and structural dissection of the tape measure protein of lactococcal phage TP901-1. <i>Scientific Reports</i> , 2016, 6, 36667.	1.6	75
31	A medium-throughput crystallization approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2109-2115.	2.5	73
32	Structure of Human Pancreatic Lipase-Related Protein 2 with the Lid in an Open Conformation. <i>Biochemistry</i> , 2008, 47, 9553-9564.	1.2	68
33	Structures and host-adhesion mechanisms of lactococcal siphophages. <i>Frontiers in Microbiology</i> , 2014, 5, 3.	1.5	63
34	Crystal structure of a ternary complex between human chorionic gonadotropin (hCG) and two Fv fragments specific for the $\hat{1}\pm$ and $\hat{1}^2$ -subunits. Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1999, 289, 1375-1385.	2.0	62
35	Crystal Structure of the Receptor-Binding Protein Head Domain from <i>Lactococcus lactis</i> Phage bIL170. <i>Journal of Virology</i> , 2006, 80, 9331-9335.	1.5	62
36	Queen Bee Pheromone Binding Protein pH-Induced Domain Swapping Favors Pheromone Release. <i>Journal of Molecular Biology</i> , 2009, 390, 981-990.	2.0	62

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37	Crystal Structure of the VgrG1 Actin Cross-linking Domain of the <i>Vibrio cholerae</i> Type VI Secretion System. <i>Journal of Biological Chemistry</i> , 2012, 287, 38190-38199.	1.6	60
38	The Atomic Structure of the Phage Tuc2009 Baseplate Tripod Suggests that Host Recognition Involves Two Different Carbohydrate Binding Modules. <i>MBio</i> , 2016, 7, e01781-15.	1.8	58
39	Bivalent Llama Single-Domain Antibody Fragments against Tumor Necrosis Factor Have Picomolar Potencies due to Intramolecular Interactions. <i>Frontiers in Immunology</i> , 2017, 8, 867.	2.2	57
40	The Importance of Framework Residues H6, H7 and H10 in Antibody Heavy Chains: Experimental Evidence for a New Structural Subclassification of Antibody VH Domains. <i>Journal of Molecular Biology</i> , 2001, 309, 701-716.	2.0	55
41	Crystal Structure and Function of a DARPIn Neutralizing Inhibitor of Lactococcal Phage TP901-1. <i>Journal of Biological Chemistry</i> , 2009, 284, 30718-30726.	1.6	55
42	Structure and Molecular Assignment of Lactococcal Phage TP901-1 Baseplate. <i>Journal of Biological Chemistry</i> , 2010, 285, 39079-39086.	1.6	55
43	Molecular Insights on the Recognition of a <i>Lactococcus lactis</i> Cell Wall Pellicle by the Phage 1358 Receptor Binding Protein. <i>Journal of Virology</i> , 2014, 88, 7005-7015.	1.5	53
44	Boar salivary lipocalin. <i>FEBS Journal</i> , 2002, 269, 2449-2456.	0.2	52
45	Crystal structure of a novel type of odorant-binding protein from <i>Anopheles gambiae</i> , belonging to the C-plus class. <i>Biochemical Journal</i> , 2011, 437, 423-430.	1.7	52
46	Crystal structures of bovine odorant-binding protein in complex with odorant molecules. <i>FEBS Journal</i> , 2004, 271, 3832-3842.	0.2	51
47	Type VI secretion TssK baseplate protein exhibits structural similarity with phage receptor-binding proteins and evolved to bind the membrane complex. <i>Nature Microbiology</i> , 2017, 2, 17103.	5.9	48
48	Crystal structure of aphrodisin, a sex pheromone from female hamster. Edited by R Huber. <i>Journal of Molecular Biology</i> , 2001, 305, 459-469.	2.0	46
49	The <i>Escherichia coli</i> YadB Gene Product Reveals a Novel Aminoacyl-tRNA Synthetase Like Activity. <i>Journal of Molecular Biology</i> , 2004, 337, 273-283.	2.0	45
50	The crystal structure of the <i>Escherichia coli</i> lipocalin Blc suggests a possible role in phospholipid binding. <i>FEBS Letters</i> , 2004, 562, 183-188.	1.3	45
51	Viral infection modulation and neutralization by camelid nanobodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1371-9.	3.3	45
52	Cas9 Allosteric Inhibition by the Anti-CRISPR Protein AcrIIA6. <i>Molecular Cell</i> , 2019, 76, 922-937.e7.	4.5	44
53	Crystal Structure and Self-Interaction of the Type VI Secretion Tail-Tube Protein from Enteroggregative <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014, 9, e86918.	1.1	44
54	X-ray structure of a superinfection exclusion lipoprotein from phage TP34 and identification of the tape measure protein as its target. <i>Molecular Microbiology</i> , 2013, 89, 152-165.	1.2	43

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55	Structure of the host-recognition device of Staphylococcus aureus phage $\phi$ 11. Scientific Reports, 2016, 6, 27581.	1.6	42
56	Kinetics and interaction studies between cytochrome c3 and Fe-only hydrogenase from Desulfovibrio vulgaris hildenborough. Proteins: Structure, Function and Bioinformatics, 1998, 33, 590-600.	1.5	39
57	The targeted recognition of <i>actococcus lactis</i> phages to their polysaccharide receptors. Molecular Microbiology, 2015, 96, 875-886.	1.2	39
58	Selection, Characterization and X-ray Structure of Anti-ampicillin Single-chain Fv Fragments from Phage-displayed Murine Antibody Libraries. Journal of Molecular Biology, 2001, 309, 671-685.	2.0	36
59	Evolved distal tail carbohydrate binding modules of <i>actobacillus</i> phage $\phi$ 1: a novel type of anti-receptor widespread among lactic acid bacteria phages. Molecular Microbiology, 2017, 104, 608-620.	1.2	35
60	Neutralization of Human Interleukin 23 by Multivalent Nanobodies Explained by the Structure of Cytokine-Nanobody Complex. Frontiers in Immunology, 2017, 8, 884.	2.2	35
61	The structure of an entire noncovalent immunoglobulin kappa light-chain dimer (Bence-Jones protein) reveals a weak and unusual constant domains association. FEBS Journal, 1999, 260, 192-199.	0.2	34
62	Conserved and Diverse Traits of Adhesion Devices from Siphoviridae Recognizing Proteinaceous or Saccharidic Receptors. Viruses, 2020, 12, 512.	1.5	34
63	Domain swapping of a llama VHH domain builds a crystal-wide $\beta^2$ -sheet structure. FEBS Letters, 2004, 564, 35-40.	1.3	32
64	Structure and specificity of the Type VI secretion system ClpV-TssC interaction in enteroaggregative Escherichia coli. Scientific Reports, 2016, 6, 34405.	1.6	31
65	Cryo-Electron Microscopy Structure of Lactococcal Siphophage 1358 Virion. Journal of Virology, 2014, 88, 8900-8910.	1.5	30
66	Camelid nanobodies raised against an integral membrane enzyme, nitric oxide reductase. Protein Science, 2009, 18, 619-628.	3.1	28
67	Crystal Structure of ORF12 from <i>Lactococcus lactis</i> Phage p2 Identifies a Tape Measure Protein Chaperone. Journal of Bacteriology, 2009, 191, 728-734.	1.0	26
68	Structural Mimicry of Receptor Interaction by Antagonistic Interleukin-6 (IL-6) Antibodies. Journal of Biological Chemistry, 2016, 291, 13846-13854.	1.6	24
69	Crystal Structure of a Chimeric Receptor Binding Protein Constructed from Two Lactococcal Phages. Journal of Bacteriology, 2009, 191, 3220-3225.	1.0	22
70	Revisiting the host adhesion determinants of <i>Streptococcus thermophilus</i> siphophages. Microbial Biotechnology, 2020, 13, 1765-1779.	2.0	20
71	Optimization of crystals from nanodrops: crystallization and preliminary crystallographic study of a pheromone-binding protein from the honeybee <i>Apis mellifera</i> L.. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 919-921.	2.5	19
72	Structure and Assembly of TP901-1 Virion Unveiled by Mutagenesis. PLoS ONE, 2015, 10, e0131676.	1.1	19

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73	Occurrence, integrity and functionality of AcaML1-like viruses infecting extreme acidophiles of the Acidithiobacillus species complex. <i>Research in Microbiology</i> , 2018, 169, 628-637.	1.0	18
74	Inhibition of Type VI Secretion by an Anti-TssM Llama Nanobody. <i>PLoS ONE</i> , 2015, 10, e0122187.	1.1	16
75	Deswapping bovine odorant binding protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 651-657.	1.1	15
76	<i>Lactococcus lactis</i> phage TP901 as a model for Siphoviridae virion assembly. <i>Bacteriophage</i> , 2016, 6, e1123795.	1.9	15
77	The thermo- and acido-stable ORF99 from the archaeal virus AFV1. <i>Protein Science</i> , 2009, 18, 1316-1320.	3.1	13
78	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp22 shares fold similarity with a domain of lactococcal phage p2 RBP. <i>Protein Science</i> , 2010, 19, 1439-1443.	3.1	12
79	Biochemical and structural characterization of non-glycosylated <i>Yarrowia lipolytica</i> LIP2 lipase. <i>European Journal of Lipid Science and Technology</i> , 2013, 115, 429-441.	1.0	12
80	Crystallization and Preliminary Diffraction Analysis of the Catalytic Domain of Xylanase Z from <i>Clostridium thermocellum</i> . <i>Journal of Molecular Biology</i> , 1994, 235, 1348-1350.	2.0	11
81	The Baseplate of <i>Lactobacillus delbrueckii</i> Bacteriophage Ld17 Harbors a Glycerophosphodiesterase. <i>Journal of Biological Chemistry</i> , 2016, 291, 16816-16827.	1.6	11
82	Combining somatic mutations present in different <i>in vivo</i> affinity-matured antibodies isolated from immunized <i>Lama glama</i> yields ultra-potent antibody therapeutics. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 123-133.	1.0	10
83	Improved crystallization of the coxsackievirus B3 RNA-dependent RNA polymerase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 495-498.	0.7	8
84	Multiple crystal forms of endoglucanase CelD: Signal peptide residues modulate lattice formation. <i>Journal of Molecular Biology</i> , 1995, 248, 225-232.	2.0	7
85	Insight into odorant perception: the crystal structure and binding characteristics of antibody fragments directed against the musk odorant traseolide. <i>Journal of Molecular Biology</i> , 1999, 292, 855-869.	2.0	7
86	The crystal structure of ORF14 from <i>Sulfolobus islandicus</i> filamentous virus. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 1020-1022.	1.5	7
87	Structural Insights into Lactococcal Siphophage p2 Baseplate Activation Mechanism. <i>Viruses</i> , 2020, 12, 878.	1.5	7
88	Anchoring the T6SS to the cell wall: Crystal structure of the peptidoglycan binding domain of the TagL accessory protein. <i>PLoS ONE</i> , 2021, 16, e0254232.	1.1	7
89	Combining site-specific mutagenesis and seeding as a strategy to crystallize 'difficult' proteins: the case of <i>Staphylococcus aureus</i> thioredoxin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1255-1258.	0.7	6
90	Production, crystallization and X-ray diffraction analysis of a complex between a fragment of the TssM T6SS protein and a camelid nanobody. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 266-271.	0.4	6

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91	Structure-Function Analysis of the C-Terminal Domain of the Type VI Secretion TssB Tail Sheath Subunit. <i>Journal of Molecular Biology</i> , 2018, 430, 297-309.	2.0	6
92	Crystallization and preliminary X-ray diffraction analysis of protein 14 from <i>Sulfolobus islandicus</i> filamentous virus (SIFV). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 884-886.	0.7	4
93	Structure of odorant binding proteins and chemosensory proteins determined by X-ray crystallography. <i>Methods in Enzymology</i> , 2020, 642, 151-167.	0.4	2
94	Kinetics and interaction studies between cytochrome c3 and Fe-only hydrogenase from <i>Desulfovibrio vulgaris hildenborough</i> . , 1998, 33, 590.		2