Els Pardon

List of Publications by Year
in descending order

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120 papers	13,032 citations	53660 45 h-index	25716 108 g-index
140 all docs	140 docs citations	140 times ranked	14033 citing authors

#	Article	IF	Citations
1	Crystal structure of the Î²2 adrenergic receptorâ€“Gs protein complex. Nature, 2011, 477, 549-555.	13.7	2,712
2	Structure of a nanobody-stabilized active state of the Î²2 adrenoceptor. Nature, 2011, 469, 175-180.	13.7	1,523
3	Activation and allosteric modulation of a muscarinic acetylcholine receptor. Nature, 2013, 504, 101-106.	13.7	779
4	A general protocol for the generation of Nanobodies for structural biology. Nature Protocols, 2014, 9, 674-693.	5.5	571
5	GABAA receptor signalling mechanisms revealed by structural pharmacology. Nature, 2019, 565, 454-459.	13.7	386
6	Mutations in PMM2, a phosphomannomutase gene on chromosome 16p13 in carbohydrate-deficient glycoprotein type I syndrome (Jaeken syndrome). Nature Genetics, 1997, 16, 88-92.	9.4	333
7	Structure of the Nanobody-Stabilized Active State of the Kappa Opioid Receptor. Cell, 2018, 172, 55-67.e15.	13.5	299
8	Allosteric nanobodies reveal the dynamic range and diverse mechanisms of G-protein-coupled receptor activation. Nature, 2016, 535, 448-452.	13.7	290
9	Cryo-EM structure of the human Î±1Î²3Î³2 GABAA receptor in a lipid bilayer. Nature, 2019, 565, 516-520.	13.7	264
10	Allosteric coupling from G protein to the agonist-binding pocket in GPCRs. Nature, 2016, 535, 182-186.	13.7	235
11	Structures of P-glycoprotein reveal its conformational flexibility and an epitope on the nucleotide-binding domain. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13386-13391.	3.3	225
12	The Molecular Mechanism of Transport by the Mitochondrial ADP/ATP Carrier. Cell, 2019, 176, 435-447.e15.	13.5	221
13	Structure and flexibility of the endosomal Vps34 complex reveals the basis of its function on membranes. Science, 2015, 350, aac7365.	6.0	208
14	Structural flexibility of the GÎ±s Î±-helical domain in the Î² ₂ -adrenoceptor Gs complex. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16086-16091.	3.3	204
15	Identification of a Universal VHH Framework to Graft Non-canonical Antigen-binding Loops of Camel Single-domain Antibodies. Journal of Molecular Biology, 2005, 352, 597-607.	2.0	194
16	Crystal structure of a SLC11 (NRAMP) transporter reveals the basis for transition-metal ion transport. Nature Structural and Molecular Biology, 2014, 21, 990-996.	3.6	171
17	Crystal Structure of the N-Terminal Domain of the Secretin GspD from ETEC Determined with the Assistance of a Nanobody. Structure, 2009, 17, 255-265.	1.6	164
18	Structure and Properties of a Complex of Î±-Synuclein and a Single-Domain Camelid Antibody. Journal of Molecular Biology, 2010, 402, 326-343.	2.0	164

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19	Structures of Î²-klotho reveal a â€˜zip codeâ€™-like mechanism for endocrine FGF signalling. Nature, 2018, 553, 501-505.	13.7	160
20	Structure of a prokaryotic fumarate transporter reveals the architecture of the SLC26 family. Nature Structural and Molecular Biology, 2015, 22, 803-808.	3.6	159
21	Structural insights into binding specificity, efficacy and bias of a Î²2AR partial agonist. Nature Chemical Biology, 2018, 14, 1059-1066.	3.9	155
22	Structures of influenza A virus RNA polymerase offer insight into viral genome replication. Nature, 2019, 573, 287-290.	13.7	151
23	Structural basis for GABAA receptor potentiation by neurosteroids. Nature Structural and Molecular Biology, 2017, 24, 986-992.	3.6	145
24	SbsB structure and lattice reconstruction unveil Ca2+ triggered S-layer assembly. Nature, 2012, 487, 119-122.	13.7	125
25	Regulation ofÎ²₂-Adrenergic Receptor Function by Conformationally Selective Single-Domain Intrabodies. Molecular Pharmacology, 2014, 85, 472-481.	1.0	121
26	Crystal structure of the proteasomal deubiquitylation module Rpn8-Rpn11. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2984-2989.	3.3	120
27	Structure of PINK1 in complex with its substrate ubiquitin. Nature, 2017, 552, 51-56.	13.7	114
28	Atomic structure of a nanobody-trapped domain-swapped dimer of an amyloidogenic Î²2-microglobulin variant. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1314-1319.	3.3	108
29	Reduced Global Cooperativity is a Common Feature Underlying the Amyloidogenicity of Pathogenic Lysozyme Mutations. Journal of Molecular Biology, 2005, 346, 773-788.	2.0	100
30	Probing the N-Terminal Î²-Sheet Conversion in the Crystal Structure of the Human Prion Protein Bound to a Nanobody. Journal of the American Chemical Society, 2014, 136, 937-944.	6.6	97
31	Nanobody-enabled monitoring of kappa opioid receptor states. Nature Communications, 2020, 11, 1145.	5.8	93
32	Nanobodies Raised against Monomeric Î±-Synuclein Distinguish between Fibrils at Different Maturation Stages. Journal of Molecular Biology, 2013, 425, 2397-2411.	2.0	90
33	Structure of a bacterial type IV secretion core complex at subnanometre resolution. EMBO Journal, 2013, 32, 1195-1204.	3.5	85
34	Structural and Functional Studies on the Interaction of GspC and GspD in the Type II Secretion System. PLoS Pathogens, 2011, 7, e1002228.	2.1	83
35	Megabodies expand the nanobody toolkit for protein structure determination by single-particle cryo-EM. Nature Methods, 2021, 18, 60-68.	9.0	79
36	Crystal structure of the Bloom's syndrome helicase indicates a role for the HRDC domain in conformational changes. Nucleic Acids Research, 2015, 43, 5221-5235.	6.5	74

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37	Nanobody-aided structure determination of the EpsI:EpsJ pseudopilin heterodimer from Vibrio vulnificus. Journal of Structural Biology, 2009, 166, 8-15.	1.3	72
38	Engineering a Camelid Antibody Fragment That Binds to the Active Site of Human Lysozyme and Inhibits Its Conversion into Amyloid Fibrils. Biochemistry, 2008, 47, 11041-11054.	1.2	66
39	An improved yeast surface display platform for the screening of nanobody immune libraries. Scientific Reports, 2019, 9, 382.	1.6	66
40	Targeting G protein-coupled receptor signaling at the G protein level with a selective nanobody inhibitor. Nature Communications, 2018, 9, 1996.	5.8	65
41	Isolation of antigen-binding camelid heavy chain antibody fragments (nanobodies) from an immune library displayed on the surface of Pichia pastoris. Journal of Biotechnology, 2010, 145, 93-98.	1.9	64
42	An Intrabody Based on a Llama Single-domain Antibody Targeting the N-terminal Î±-Helical Multimerization Domain of HIV-1 Rev Prevents Viral Production. Journal of Biological Chemistry, 2010, 285, 21768-21780.	1.6	60
43	Nanobodies to study protein conformational states. Current Opinion in Structural Biology, 2020, 60, 117-123.	2.6	59
44	L amino acid transporter structure and molecular bases for the asymmetry of substrate interaction. Nature Communications, 2019, 10, 1807.	5.8	57
45	Structure, substrate recognition and initiation of hyaluronan synthase. Nature, 2022, 604, 195-201.	13.7	53
46	The morphogen Sonic hedgehog inhibits its receptor Patched by a pincer grasp mechanism. Nature Chemical Biology, 2019, 15, 975-982.	3.9	52
47	Structure of Prototypic Peptide Transporter DtpA from E. coli in Complex with Valganciclovir Provides Insights into Drug Binding of Human PepT1. Journal of the American Chemical Society, 2019, 141, 2404-2412.	6.6	51
48	A bacterial-two-hybrid selection system for one-step isolation of intracellularly functional Nanobodies. Archives of Biochemistry and Biophysics, 2012, 526, 114-123.	1.4	46
49	A lipid site shapes the agonist response of a pentameric ligand-gated ion channel. Nature Chemical Biology, 2019, 15, 1156-1164.	3.9	43
50	A Nanobody Binding to Non-Amyloidogenic Regions of the Protein Human Lysozyme Enhances Partial Unfolding but Inhibits Amyloid Fibril Formation. Journal of Physical Chemistry B, 2013, 117, 13245-13258.	1.2	42
51	Generation and Characterization of Anti-VGLUT Nanobodies Acting as Inhibitors of Transport. Biochemistry, 2017, 56, 3962-3971.	1.2	40
52	Development of a universal nanobody-binding Fab module for fiducial-assisted cryo-EM studies of membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	40
53	Binding-Site Compatible Fragment Growing Applied to the Design of Î²₂-Adrenergic Receptor Ligands. Journal of Medicinal Chemistry, 2018, 61, 1118-1129.	2.9	39
54	Crystal structure of a LacYâ€“nanobody complex in a periplasmic-open conformation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12420-12425.	3.3	38

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55	A Ca2+-binding Chimera of Human Lysozyme and Bovine Î±-Lactalbumin That Can Form a Molten Globule. Journal of Biological Chemistry, 1995, 270, 10514-10524.	1.6	36
56	Nanobodyâ€Enabled Reverse Pharmacology on Gâ€Proteinâ€Coupled Receptors. Angewandte Chemie - International Edition, 2018, 57, 5292-5295.	7.2	36
57	Crystal structure of a heterodimer of editosome interaction proteins in complex with two copies of a cross-reacting nanobody. Nucleic Acids Research, 2012, 40, 1828-1840.	6.5	35
58	Structural basis of sodium-dependent bile salt uptake into the liver. Nature, 2022, 606, 1015-1020.	13.7	35
59	Structure of autoinhibited Akt1 reveals mechanism of PIP₃-mediated activation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	33
60	Crystal Structure of a ligand-bound LacYâ€“Nanobody Complex. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8769-8774.	3.3	32
61	1H, 13C and 15N assignments of a camelid nanobody directed against human Î±-synuclein. Biomolecular NMR Assignments, 2009, 3, 231-233.	0.4	29
62	Modular transient nanoclustering of activated Î²2-adrenergic receptors revealed by single-molecule tracking of conformation-specific nanobodies. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30476-30487.	3.3	29
63	Snapshots of actin and tubulin folding inside the TRiC chaperonin. Nature Structural and Molecular Biology, 2022, 29, 420-429.	3.6	29
64	Structure, mechanism, and inhibition of Hedgehog acyltransferase. Molecular Cell, 2021, 81, 5025-5038.e10.	4.5	28
65	Structures of a key interaction protein from the Trypanosoma brucei editosome in complex with single domain antibodies. Journal of Structural Biology, 2011, 174, 124-136.	1.3	27
66	SAXS analysis of the tRNA-modifying enzyme complex MnmE/MnmG reveals a novel interaction mode and GTP-induced oligomerization. Nucleic Acids Research, 2014, 42, 5978-5992.	6.5	27
67	Structures of ligand-occupied Î²-Klotho complexes reveal a molecular mechanism underlying endocrine FGF specificity and activity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7819-7824.	3.3	27
68	The Molecular Mechanism of Shiga Toxin Stx2e Neutralization by a Single-domain Antibody Targeting the Cell Receptor-binding Domain. Journal of Biological Chemistry, 2014, 289, 25374-25381.	1.6	26
69	Structure of the phosphoinositide 3-kinase (PI3K) p110Î³-p101 complex reveals molecular mechanism of GPCR activation. Science Advances, 2021, 7, .	4.7	25
70	Domain-interface dynamics of CFTR revealed by stabilizing nanobodies. Nature Communications, 2019, 10, 2636.	5.8	24
71	Outward-facing conformers of LacY stabilized by nanobodies. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18548-18553.	3.3	23
72	Structural basis of inhibition of lipid-linked oligosaccharide flippase PglK by a conformational nanobody. Scientific Reports, 2017, 7, 46641.	1.6	23

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73	Structure of S-layer protein Sap reveals a mechanism for therapeutic intervention in anthrax. Nature Microbiology, 2019, 4, 1805-1814.	5.9	23
74	Nano-scale resolution of native retinal rod disk membranes reveals differences in lipid composition. Journal of Cell Biology, 2021, 220, .	2.3	23
75	Nanobody Mediated Inhibition of Attachment of F18 Fimbriae Expressing Escherichia coli. PLoS ONE, 2014, 9, e114691.	1.1	23
76	Transient conformers of LacY are trapped by nanobodies. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13839-13844.	3.3	22
77	Crystal structure of human Mediator subunit MED23. Nature Communications, 2018, 9, 3389.	5.8	22
78	Structural evidence for the critical role of the prion protein hydrophobic region in forming an infectious prion. PLoS Pathogens, 2019, 15, e1008139.	2.1	22
79	Nanobody Mediated Crystallization of an Archeal Mechanosensitive Channel. PLoS ONE, 2013, 8, e77984.	1.1	20
80	The structure of the C-terminal domain of the largest editosome interaction protein and its role in promoting RNA binding by RNA-editing ligase L2. Nucleic Acids Research, 2012, 40, 6966-6977.	6.5	19
81	A specific nanobody prevents amyloidogenesis of D76N Î²2-microglobulin in vitro and modifies its tissue distribution in vivo. Scientific Reports, 2017, 7, 46711.	1.6	18
82	Combining in-situ proteolysis and microseed matrix screening to promote crystallization of PrPc-nanobody complexes. Protein Engineering, Design and Selection, 2011, 24, 737-741.	1.0	17
83	Structural insight in the inhibition of adherence of F4 fimbriae producing enterotoxigenic Escherichia coli by llama single domain antibodies. Veterinary Research, 2015, 46, 14.	1.1	17
84	Interrogating dense ligand chemical space with a forward-synthetic library. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11496-11501.	3.3	16
85	Modulation of the Erwinia ligand-gated ion channel (ELIC) and the 5-HT3 receptor via a common vestibule site. ELife, 2020, 9, .	2.8	16
86	Llama immunization with full-length VAR2CSA generates cross-reactive and inhibitory single-domain antibodies against the DBL1X domain. Scientific Reports, 2014, 4, 7373.	1.6	15
87	The unexpected structure of the designed protein Octarellin V.1 forms a challenge for protein structure prediction tools. Journal of Structural Biology, 2016, 195, 19-30.	1.3	15
88	Binding Specificities of Nanobodyâ€¢Membrane Protein Complexes Obtained from Chemical Cross-Linking and High-Mass MALDI Mass Spectrometry. Analytical Chemistry, 2018, 90, 5306-5313.	3.2	15
89	Nanobodies as allosteric modulators of Parkinsonâ€™s diseaseâ€“associated LRRK2. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	15
90	Structure of an early nativeâ€like intermediate of Î²2â€microglobulin amyloidogenesis. Protein Science, 2013, 22, 1349-1357.	3.1	14

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91	Mapping inhibitory sites on the RNA polymerase of the 1918 pandemic influenza virus using nanobodies. Nature Communications, 2022, 13, 251.	5.8	14
92	The structure of the D3 domain of Plasmodium falciparum myosin tail interacting protein MTIP in complex with a nanobody. Molecular and Biochemical Parasitology, 2013, 190, 87-91.	0.5	13
93	Leishmania donovani tyrosyl-tRNA synthetase structure in complex with a tyrosyl adenylate analog and comparisons with human and protozoan counterparts. Biochimie, 2017, 138, 124-136.	1.3	13
94	Rational Design of Nanobody80 Loop Peptidomimetics: Towards Biased Î² 2 Adrenergic Receptor Ligands. Chemistry - A European Journal, 2017, 23, 9632-9640.	1.7	13
95	The G-Protein Rab5A Activates VPS34 Complex II, a Class III PI3K, by a Dual Regulatory Mechanism. Biophysical Journal, 2020, 119, 2205-2218.	0.2	13
96	A topological switch in CFTR modulates channel activity and sensitivity to unfolding. Nature Chemical Biology, 2021, 17, 989-997.	3.9	13
97	In vitro reconstitution of dynamically interacting integral membrane subunits of energy-coupling factor transporters. ELife, 2020, 9, .	2.8	13
98	Allosteric modulation of the GTPase activity of a bacterial LRRK2 homolog by conformation-specific Nanobodies. Biochemical Journal, 2020, 477, 1203-1218.	1.7	12
99	A structure of substrate-bound Synaptojanin1 provides new insights in its mechanism and the effect of disease mutations. ELife, 2020, 9, .	2.8	11
100	Measuring cooperative Rev protein-protein interactions on Rev responsive RNA by fluorescence resonance energy transfer. RNA Biology, 2011, 8, 316-324.	1.5	10
101	HDX-MS-optimized approach to characterize nanobodies as tools for biochemical and structural studies of class IB phosphoinositide 3-kinases. Structure, 2021, 29, 1371-1381.e6.	1.6	10
102	Crystallization and preliminary X-ray diffraction analysis of a specific VHH domain against mouse prion protein. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1644-1646.	0.7	8
103	Challenges in the Structuralâ€“Functional Characterization of Multidomain, Partially Disordered Proteins CBP and p300: Preparing Native Proteins and Developing Nanobody Tools. Methods in Enzymology, 2018, 611, 607-675.	0.4	7
104	Crystallographic and biochemical characterization of the dimeric architecture of site-2 protease. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 1859-1871.	1.4	6
105	Cryo-EM Structure of an Atypical Proton-Coupled Peptide Transporter: Di- and Tripeptide Permease C. Frontiers in Molecular Biosciences, 0, 9, .	1.6	6
106	Thermodynamics of Nanobody Binding to Lactose Permease. Biochemistry, 2016, 55, 5917-5926.	1.2	5
107	Functional and Biochemical Characterization of Alvinella pompejana Cys-Loop Receptor Homologues. PLoS ONE, 2016, 11, e0151183.	1.1	4
108	Nanobodyâ€Enabled Reverse Pharmacology on Gâ€Proteinâ€Coupled Receptors. Angewandte Chemie, 2018, 130, 5390-5393.	1.6	3

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109	Diversity in kinetics correlated with structure in nano body-stabilized LacY. PLoS ONE, 2020, 15, e0232846.	1.1	3
110	Production, crystallization and X-ray diffraction analysis of two nanobodies against the Duffy binding-like (DBL) domain DBL6âˆ’FCR3 of thePlasmodium falciparumVAR2CSA protein. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 270-274.	0.7	2
111	Nanobody-aided crystallization of the transcription regulator PaaR2 from Escherichia coli O157:H7. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 374-384.	0.4	2
112	Characterization and structure determination of a llama-derived nanobody targeting the J-base binding protein 1. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 690-695.	0.4	1
113	Production, crystallization and preliminary X-ray diffraction of the GÎ±s Î±-helical domain in complex with a nanobody. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1504-1507.	0.4	0
114	NANOBODIES FOR THE STRUCTURAL AND FUNCTIONAL INVESTIGATION OF GPCR TRANSMEMBRANE SIGNALING. , 2014, , .		0
115	Thermodynamic Insights into Conformational Dynamics of Sugar Transporters. Biophysical Journal, 2016, 110, 137a.	0.2	0
116	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
117	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
118	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
119	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
120	Stabilization of Metaâ€Ⅱ Rhodopsin Conformation by a Nanobody. FASEB Journal, 2022, 36, .	0.2	0