

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	Mapping inhibitory sites on the RNA polymerase of the 1918 pandemic influenza virus using nanobodies. <i>Nature Communications</i> , 2022, 13, 251.	5.8	14
2	Nanobodies as allosteric modulators of Parkinson's disease-associated LRRK2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	15
3	Structure, substrate recognition and initiation of hyaluronan synthase. <i>Nature</i> , 2022, 604, 195-201.	13.7	53
4	Snapshots of actin and tubulin folding inside the TRiC chaperonin. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 420-429.	3.6	29
5	Stabilization of Meta- Rhodopsin Conformation by a Nanobody. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
6	Structural basis of sodium-dependent bile salt uptake into the liver. <i>Nature</i> , 2022, 606, 1015-1020.	13.7	35
7	Nano-scale resolution of native retinal rod disk membranes reveals differences in lipid composition. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	23
8	Structure of the phosphoinositide 3-kinase (PI3K) p110 ^β -p101 complex reveals molecular mechanism of GPCR activation. <i>Science Advances</i> , 2021, 7, .	4.7	25
9	HDX-MS-optimized approach to characterize nanobodies as tools for biochemical and structural studies of class IB phosphoinositide 3-kinases. <i>Structure</i> , 2021, 29, 1371-1381.e6.	1.6	10
10	Structure of autoinhibited Akt1 reveals mechanism of PIP ₃ -mediated activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	33
11	A topological switch in CFTR modulates channel activity and sensitivity to unfolding. <i>Nature Chemical Biology</i> , 2021, 17, 989-997.	3.9	13
12	Nanobody-aided crystallization of the transcription regulator PaaR2 from <i>Escherichia coli</i> O157:H7. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 374-384.	0.4	2
13	Megabodies expand the nanobody toolkit for protein structure determination by single-particle cryo-EM. <i>Nature Methods</i> , 2021, 18, 60-68.	9.0	79
14	Development of a universal nanobody-binding Fab module for fiducial-assisted cryo-EM studies of membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	40
15	Structure, mechanism, and inhibition of Hedgehog acyltransferase. <i>Molecular Cell</i> , 2021, 81, 5025-5038.e10.	4.5	28
16	Modular transient nanoclustering of activated β 2-adrenergic receptors revealed by single-molecule tracking of conformation-specific nanobodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30476-30487.	3.3	29
17	The G-Protein Rab5A Activates VPS34 Complex II, a Class III PI3K, by a Dual Regulatory Mechanism. <i>Biophysical Journal</i> , 2020, 119, 2205-2218.	0.2	13
18	Diversity in kinetics correlated with structure in nano body-stabilized LacY. <i>PLoS ONE</i> , 2020, 15, e0232846.	1.1	3

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19	Nanobody-enabled monitoring of kappa opioid receptor states. <i>Nature Communications</i> , 2020, 11, 1145.	5.8	93
20	Nanobodies to study protein conformational states. <i>Current Opinion in Structural Biology</i> , 2020, 60, 117-123.	2.6	59
21	Allosteric modulation of the GTPase activity of a bacterial LRRK2 homolog by conformation-specific Nanobodies. <i>Biochemical Journal</i> , 2020, 477, 1203-1218.	1.7	12
22	Modulation of the <i>Erwinia</i> ligand-gated ion channel (ELIC) and the 5-HT ₃ receptor via a common vestibule site. <i>ELife</i> , 2020, 9, .	2.8	16
23	In vitro reconstitution of dynamically interacting integral membrane subunits of energy-coupling factor transporters. <i>ELife</i> , 2020, 9, .	2.8	13
24	A structure of substrate-bound Synaptojanin1 provides new insights in its mechanism and the effect of disease mutations. <i>ELife</i> , 2020, 9, .	2.8	11
25	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
26	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
27	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
28	Diversity in kinetics correlated with structure in nano body-stabilized LacY. , 2020, 15, e0232846.		0
29	Structure of S-layer protein Sap reveals a mechanism for therapeutic intervention in anthrax. <i>Nature Microbiology</i> , 2019, 4, 1805-1814.	5.9	23
30	Structures of influenza A virus RNA polymerase offer insight into viral genome replication. <i>Nature</i> , 2019, 573, 287-290.	13.7	151
31	A lipid site shapes the agonist response of a pentameric ligand-gated ion channel. <i>Nature Chemical Biology</i> , 2019, 15, 1156-1164.	3.9	43
32	The morphogen Sonic hedgehog inhibits its receptor Patched by a pincer grasp mechanism. <i>Nature Chemical Biology</i> , 2019, 15, 975-982.	3.9	52
33	An improved yeast surface display platform for the screening of nanobody immune libraries. <i>Scientific Reports</i> , 2019, 9, 382.	1.6	66
34	Domain-interface dynamics of CFTR revealed by stabilizing nanobodies. <i>Nature Communications</i> , 2019, 10, 2636.	5.8	24
35	Interrogating dense ligand chemical space with a forward-synthetic library. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11496-11501.	3.3	16
36	L amino acid transporter structure and molecular bases for the asymmetry of substrate interaction. <i>Nature Communications</i> , 2019, 10, 1807.	5.8	57

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37	Structures of ligand-occupied β -Klotho complexes reveal a molecular mechanism underlying endocrine FGF specificity and activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7819-7824.	3.3	27
38	Structural evidence for the critical role of the prion protein hydrophobic region in forming an infectious prion. <i>PLoS Pathogens</i> , 2019, 15, e1008139.	2.1	22
39	The Molecular Mechanism of Transport by the Mitochondrial ADP/ATP Carrier. <i>Cell</i> , 2019, 176, 435-447.e15.	13.5	221
40	GABAA receptor signalling mechanisms revealed by structural pharmacology. <i>Nature</i> , 2019, 565, 454-459.	13.7	386
41	Cryo-EM structure of the human β -GABAA receptor in a lipid bilayer. <i>Nature</i> , 2019, 565, 516-520.	13.7	264
42	Structure of Prototypic Peptide Transporter DtpA from <i>E. coli</i> in Complex with Valganciclovir Provides Insights into Drug Binding of Human PepT1. <i>Journal of the American Chemical Society</i> , 2019, 141, 2404-2412.	6.6	51
43	Nanobody-Enabled Reverse Pharmacology on G-Protein-Coupled Receptors. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 5292-5295.	7.2	36
44	Nanobody-Enabled Reverse Pharmacology on G-Protein-Coupled Receptors. <i>Angewandte Chemie</i> , 2018, 130, 5390-5393.	1.6	3
45	Structures of β -klotho reveal a "zip code"-like mechanism for endocrine FGF signalling. <i>Nature</i> , 2018, 553, 501-505.	13.7	160
46	Binding-Site Compatible Fragment Growing Applied to the Design of β -Adrenergic Receptor Ligands. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 1118-1129.	2.9	39
47	Structure of the Nanobody-Stabilized Active State of the Kappa Opioid Receptor. <i>Cell</i> , 2018, 172, 55-67.e15.	13.5	299
48	Binding Specificities of Nanobody-Membrane Protein Complexes Obtained from Chemical Cross-Linking and High-Mass MALDI Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 5306-5313.	3.2	15
49	Characterization and structure determination of a llama-derived nanobody targeting the J-base binding protein 1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 690-695.	0.4	1
50	Challenges in the Structural-Functional Characterization of Multidomain, Partially Disordered Proteins CBP and p300: Preparing Native Proteins and Developing Nanobody Tools. <i>Methods in Enzymology</i> , 2018, 611, 607-675.	0.4	7
51	Structural insights into binding specificity, efficacy and bias of a β 2AR partial agonist. <i>Nature Chemical Biology</i> , 2018, 14, 1059-1066.	3.9	155
52	Targeting G protein-coupled receptor signaling at the G protein level with a selective nanobody inhibitor. <i>Nature Communications</i> , 2018, 9, 1996.	5.8	65
53	Crystal structure of human Mediator subunit MED23. <i>Nature Communications</i> , 2018, 9, 3389.	5.8	22
54	Crystal Structure of a ligand-bound LacY-Nanobody Complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8769-8774.	3.3	32

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55	Structural basis of inhibition of lipid-linked oligosaccharide flippase PglK by a conformational nanobody. <i>Scientific Reports</i> , 2017, 7, 46641.	1.6	23
56	<i>Leishmania donovani</i> tyrosyl-tRNA synthetase structure in complex with a tyrosyl adenylate analog and comparisons with human and protozoan counterparts. <i>Biochimie</i> , 2017, 138, 124-136.	1.3	13
57	A specific nanobody prevents amyloidogenesis of D76N β 2-microglobulin in vitro and modifies its tissue distribution in vivo. <i>Scientific Reports</i> , 2017, 7, 46711.	1.6	18
58	Rational Design of Nanobody80 Loop Peptidomimetics: Towards Biased β 2 Adrenergic Receptor Ligands. <i>Chemistry - A European Journal</i> , 2017, 23, 9632-9640.	1.7	13
59	Crystallographic and biochemical characterization of the dimeric architecture of site-2 protease. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 1859-1871.	1.4	6
60	Structure of PINK1 in complex with its substrate ubiquitin. <i>Nature</i> , 2017, 552, 51-56.	13.7	114
61	Generation and Characterization of Anti-VGLUT Nanobodies Acting as Inhibitors of Transport. <i>Biochemistry</i> , 2017, 56, 3962-3971.	1.2	40
62	Structural basis for GABAA receptor potentiation by neurosteroids. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 986-992.	3.6	145
63	The unexpected structure of the designed protein Octarellin V.1 forms a challenge for protein structure prediction tools. <i>Journal of Structural Biology</i> , 2016, 195, 19-30.	1.3	15
64	Thermodynamics of Nanobody Binding to Lactose Permease. <i>Biochemistry</i> , 2016, 55, 5917-5926.	1.2	5
65	Allosteric nanobodies reveal the dynamic range and diverse mechanisms of G-protein-coupled receptor activation. <i>Nature</i> , 2016, 535, 448-452.	13.7	290
66	Crystal structure of a LacY ϵ nanobody complex in a periplasmic-open conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12420-12425.	3.3	38
67	Allosteric coupling from G protein to the agonist-binding pocket in GPCRs. <i>Nature</i> , 2016, 535, 182-186.	13.7	235
68	Thermodynamic Insights into Conformational Dynamics of Sugar Transporters. <i>Biophysical Journal</i> , 2016, 110, 137a.	0.2	0
69	Functional and Biochemical Characterization of <i>Alvinella pompejana</i> Cys-Loop Receptor Homologues. <i>PLoS ONE</i> , 2016, 11, e0151183.	1.1	4
70	Transient conformers of LacY are trapped by nanobodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13839-13844.	3.3	22
71	Crystal structure of the Bloom's syndrome helicase indicates a role for the HRDC domain in conformational changes. <i>Nucleic Acids Research</i> , 2015, 43, 5221-5235.	6.5	74
72	Structural insight in the inhibition of adherence of F4 fimbriae producing enterotoxigenic <i>Escherichia coli</i> by llama single domain antibodies. <i>Veterinary Research</i> , 2015, 46, 14.	1.1	17

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73	Structure and flexibility of the endosomal Vps34 complex reveals the basis of its function on membranes. <i>Science</i> , 2015, 350, aac7365.	6.0	208
74	Structure of a prokaryotic fumarate transporter reveals the architecture of the SLC26 family. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 803-808.	3.6	159
75	Production, crystallization and preliminary X-ray diffraction of the G \pm S $\hat{\pm}$ -helical domain in complex with a nanobody. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1504-1507.	0.4	0
76	Crystal structure of the proteasomal deubiquitylation module Rpn8-Rpn11. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2984-2989.	3.3	120
77	Outward-facing conformers of LacY stabilized by nanobodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18548-18553.	3.3	23
78	SAXS analysis of the tRNA-modifying enzyme complex MnmE/MnmG reveals a novel interaction mode and GTP-induced oligomerization. <i>Nucleic Acids Research</i> , 2014, 42, 5978-5992.	6.5	27
79	A general protocol for the generation of Nanobodies for structural biology. <i>Nature Protocols</i> , 2014, 9, 674-693.	5.5	571
80	Crystal structure of a SLC11 (NRAMP) transporter reveals the basis for transition-metal ion transport. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 990-996.	3.6	171
81	Probing the N-Terminal $\hat{\pm}$ -Sheet Conversion in the Crystal Structure of the Human Prion Protein Bound to a Nanobody. <i>Journal of the American Chemical Society</i> , 2014, 136, 937-944.	6.6	97
82	The Molecular Mechanism of Shiga Toxin Stx2e Neutralization by a Single-domain Antibody Targeting the Cell Receptor-binding Domain. <i>Journal of Biological Chemistry</i> , 2014, 289, 25374-25381.	1.6	26
83	Regulation of $\hat{\pm}$ -Adrenergic Receptor Function by Conformationally Selective Single-Domain Intrabodies. <i>Molecular Pharmacology</i> , 2014, 85, 472-481.	1.0	121
84	NANOBODIES FOR THE STRUCTURAL AND FUNCTIONAL INVESTIGATION OF GPCR TRANSMEMBRANE SIGNALING. , 2014, , .		0
85	Llama immunization with full-length VAR2CSA generates cross-reactive and inhibitory single-domain antibodies against the DBL1X domain. <i>Scientific Reports</i> , 2014, 4, 7373.	1.6	15
86	Nanobody Mediated Inhibition of Attachment of F18 Fimbriae Expressing Escherichia coli. <i>PLoS ONE</i> , 2014, 9, e114691.	1.1	23
87	The structure of the D3 domain of Plasmodium falciparum myosin tail interacting protein MTIP in complex with a nanobody. <i>Molecular and Biochemical Parasitology</i> , 2013, 190, 87-91.	0.5	13
88	Structure of a bacterial type IV secretion core complex at subnanometre resolution. <i>EMBO Journal</i> , 2013, 32, 1195-1204.	3.5	85
89	Activation and allosteric modulation of a muscarinic acetylcholine receptor. <i>Nature</i> , 2013, 504, 101-106.	13.7	779
90	Structures of P-glycoprotein reveal its conformational flexibility and an epitope on the nucleotide-binding domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13386-13391.	3.3	225

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91	Nanobodies Raised against Monomeric α -Synuclein Distinguish between Fibrils at Different Maturation Stages. <i>Journal of Molecular Biology</i> , 2013, 425, 2397-2411.	2.0	90
92	Production, crystallization and X-ray diffraction analysis of two nanobodies against the Duffy binding-like (DBL) domain DBL6 α -FCR3 of the <i>Plasmodium falciparum</i> VAR2CSA protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 270-274.	0.7	2
93	A Nanobody Binding to Non-Amyloidogenic Regions of the Protein Human Lysozyme Enhances Partial Unfolding but Inhibits Amyloid Fibril Formation. <i>Journal of Physical Chemistry B</i> , 2013, 117, 13245-13258.	1.2	42
94	Structure of an early native-like intermediate of β 2-microglobulin amyloidogenesis. <i>Protein Science</i> , 2013, 22, 1349-1357.	3.1	14
95	Nanobody Mediated Crystallization of an Archeal Mechanosensitive Channel. <i>PLoS ONE</i> , 2013, 8, e77984.	1.1	20
96	Crystal structure of a heterodimer of editosome interaction proteins in complex with two copies of a cross-reacting nanobody. <i>Nucleic Acids Research</i> , 2012, 40, 1828-1840.	6.5	35
97	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. <i>Nucleic Acids Research</i> , 2012, 40, 6966-6977.	6.5	19
98	A bacterial-two-hybrid selection system for one-step isolation of intracellularly functional Nanobodies. <i>Archives of Biochemistry and Biophysics</i> , 2012, 526, 114-123.	1.4	46
99	SbsB structure and lattice reconstruction unveil Ca ²⁺ triggered S-layer assembly. <i>Nature</i> , 2012, 487, 119-122.	13.7	125
100	Atomic structure of a nanobody-trapped domain-swapped dimer of an amyloidogenic β 2-microglobulin variant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1314-1319.	3.3	108
101	Crystal structure of the β 2 adrenergic receptor-Gs protein complex. <i>Nature</i> , 2011, 477, 549-555.	13.7	2,712
102	Structures of a key interaction protein from the <i>Trypanosoma brucei</i> editosome in complex with single domain antibodies. <i>Journal of Structural Biology</i> , 2011, 174, 124-136.	1.3	27
103	Structure of a nanobody-stabilized active state of the β 2 adrenoceptor. <i>Nature</i> , 2011, 469, 175-180.	13.7	1,523
104	Combining in-situ proteolysis and microseed matrix screening to promote crystallization of PrPc-nanobody complexes. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 737-741.	1.0	17
105	Structural flexibility of the G α s-helical domain in the β 2-adrenoceptor Gs complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16086-16091.	3.3	204
106	Measuring cooperative Rev protein-protein interactions on Rev responsive RNA by fluorescence resonance energy transfer. <i>RNA Biology</i> , 2011, 8, 316-324.	1.5	10
107	Structural and Functional Studies on the Interaction of GspC and GspD in the Type II Secretion System. <i>PLoS Pathogens</i> , 2011, 7, e1002228.	2.1	83
108	Isolation of antigen-binding camelid heavy chain antibody fragments (nanobodies) from an immune library displayed on the surface of <i>Pichia pastoris</i> . <i>Journal of Biotechnology</i> , 2010, 145, 93-98.	1.9	64

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109	Crystallization and preliminary X-ray diffraction analysis of a specific VHH domain against mouse prion protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1644-1646.	0.7	8
110	An Intrabody Based on a Llama Single-domain Antibody Targeting the N-terminal $\hat{\pm}$ -Helical Multimerization Domain of HIV-1 Rev Prevents Viral Production. <i>Journal of Biological Chemistry</i> , 2010, 285, 21768-21780.	1.6	60
111	Structure and Properties of a Complex of $\hat{\pm}$ -Synuclein and a Single-Domain Camelid Antibody. <i>Journal of Molecular Biology</i> , 2010, 402, 326-343.	2.0	164
112	Crystal Structure of the N-Terminal Domain of the Secretin GspD from ETEC Determined with the Assistance of a Nanobody. <i>Structure</i> , 2009, 17, 255-265.	1.6	164
113	^1H , ^{13}C and ^{15}N assignments of a camelid nanobody directed against human $\hat{\pm}$ -synuclein. <i>Biomolecular NMR Assignments</i> , 2009, 3, 231-233.	0.4	29
114	Nanobody-aided structure determination of the EpsI:EpsJ pseudopilin heterodimer from <i>Vibrio vulnificus</i> . <i>Journal of Structural Biology</i> , 2009, 166, 8-15.	1.3	72
115	Engineering a Camelid Antibody Fragment That Binds to the Active Site of Human Lysozyme and Inhibits Its Conversion into Amyloid Fibrils. <i>Biochemistry</i> , 2008, 47, 11041-11054.	1.2	66
116	Reduced Global Cooperativity is a Common Feature Underlying the Amyloidogenicity of Pathogenic Lysozyme Mutations. <i>Journal of Molecular Biology</i> , 2005, 346, 773-788.	2.0	100
117	Identification of a Universal VHH Framework to Graft Non-canonical Antigen-binding Loops of Camel Single-domain Antibodies. <i>Journal of Molecular Biology</i> , 2005, 352, 597-607.	2.0	194
118	Mutations in PMM2, a phosphomannomutase gene on chromosome 16p13 in carbohydrate-deficient glycoprotein type I syndrome (Jaeken syndrome). <i>Nature Genetics</i> , 1997, 16, 88-92.	9.4	333
119	A Ca^{2+} -binding Chimera of Human Lysozyme and Bovine $\hat{\pm}$ -Lactalbumin That Can Form a Molten Globule. <i>Journal of Biological Chemistry</i> , 1995, 270, 10514-10524.	1.6	36
120	Cryo-EM Structure of an Atypical Proton-Coupled Peptide Transporter: Di- and Tripeptide Permease C. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	6