

Gregers Rom Andersen

List of Publications by Year in descending order

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106
papers

6,049
citations

53751

45
h-index

76872

74
g-index

118
all docs

118
docs citations

118
times ranked

7159
citing authors

#	ARTICLE	IF	CITATIONS
1	Development, Characterization, and in vivo Validation of a Humanized C6 Monoclonal Antibody that Inhibits the Membrane Attack Complex. <i>Journal of Innate Immunity</i> , 2023, 15, 16-36.	1.8	2
2	Structure and function of a family of tick-derived complement inhibitors targeting properdin. <i>Nature Communications</i> , 2022, 13, 317.	5.8	8
3	Cryo-EM structures of human A2M1 elucidate the protease-inhibitory mechanism of the A2M family. <i>Nature Communications</i> , 2022, 13, .	5.8	4
4	Structural insights into the function-modulating effects of a nanobody binding to the integrin receptor $\alpha_5\beta_1$. <i>Journal of Biological Chemistry</i> , 2022, 298, 102168.	1.6	7
5	Properdin oligomers adopt rigid extended conformations supporting function. <i>ELife</i> , 2021, 10, .	2.8	10
6	ITIH4 acts as a protease inhibitor by a novel inhibitory mechanism. <i>Science Advances</i> , 2021, 7, .	4.7	22
7	Nanobodies Provide Insight into the Molecular Mechanisms of the Complement Cascade and Offer New Therapeutic Strategies. <i>Biomolecules</i> , 2021, 11, 298.	1.8	4
8	Complement Receptor 3 Forms a Compact High-Affinity Complex with iC3b. <i>Journal of Immunology</i> , 2021, 206, 3032-3042.	0.4	20
9	Mutation-induced dimerization of transforming growth factor- β -induced protein may drive protein aggregation in granular corneal dystrophy. <i>Journal of Biological Chemistry</i> , 2021, 297, 100858.	1.6	3
10	Purification of Human Complement Component C4 and Sample Preparation for Structural Biology Applications. <i>Methods in Molecular Biology</i> , 2021, 2227, 249-264.	0.4	3
11	Structural Investigations of Human A2M Identify a Hollow Native Conformation That Underlies Its Distinctive Protease-Trapping Mechanism. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100090.	2.5	21
12	A Complement C3-Specific Nanobody for Modulation of the Alternative Cascade Identifies the C-Terminal Domain of C3b as Functional in C5 Convertase Activity. <i>Journal of Immunology</i> , 2020, 205, 2287-2300.	0.4	9
13	Structure of intact IgE and the mechanism of ligelizumab revealed by electron microscopy. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 1956-1965.	2.7	22
14	An Ultrahigh-Affinity Complement C4b-Specific Nanobody Inhibits In Vivo Assembly of the Classical Pathway Proconvertase. <i>Journal of Immunology</i> , 2020, 205, 1678-1694.	0.4	12
15	Functional and Structural Characterization of a Potent C1q Inhibitor Targeting the Classical Pathway of the Complement System. <i>Frontiers in Immunology</i> , 2020, 11, 1504.	2.2	17
16	A C3-specific nanobody that blocks all three activation pathways in the human and murine complement system. <i>Journal of Biological Chemistry</i> , 2020, 295, 8746-8758.	1.6	18
17	Recruitment of properdin by bi-specific nanobodies activates the alternative pathway of complement. <i>Molecular Immunology</i> , 2020, 124, 200-210.	1.0	10
18	Complement activation by human IgG antibodies to galactose- α -1,3-galactose. <i>Immunology</i> , 2020, 161, 66-79.	2.0	13

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19	Size-Selective Phagocytic Clearance of Fibrillar $\hat{\alpha}$ -Synuclein through Conformational Activation of Complement Receptor 4. <i>Journal of Immunology</i> , 2020, 204, 1345-1361.	0.4	23
20	Substituting the Thiol Ester of Human A2M or C3 with a Disulfide Produces Native Proteins with Altered Proteolysis-Induced Conformational Changes. <i>Biochemistry</i> , 2020, 59, 4799-4809.	1.2	6
21	Soluble collectin-12 mediates C3-independent docking of properdin that activates the alternative pathway of complement. <i>ELife</i> , 2020, 9, .	2.8	15
22	Crystallization and X-ray analysis of monodisperse human properdin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 0.	0.4	15
23	Structural Basis for Properdin Oligomerization and Convertase Stimulation in the Human Complement System. <i>Frontiers in Immunology</i> , 2019, 10, 2007.	2.2	47
24	A potent complement factor C3 $\hat{\alpha}$ -specific nanobody inhibiting multiple functions in the alternative pathway of human and murine complement. <i>Journal of Biological Chemistry</i> , 2018, 293, 6269-6281.	1.6	47
25	Models of the complement C1 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3866-E3866.	3.3	3
26	Trapping IgE in a closed conformation by mimicking CD23 binding prevents and disrupts Fc $\hat{\mu}$ RI interaction. <i>Nature Communications</i> , 2018, 9, 7.	5.8	88
27	A Single-Domain Antibody Targeting Complement Component C5 Acts as a Selective Inhibitor of the Terminal Pathway of the Complement System and Thus Functionally Mimicks the C-Terminal Domain of the <i>Staphylococcus aureus</i> SSL7 Protein. <i>Frontiers in Immunology</i> , 2018, 9, 2822.	2.2	7
28	Maximizing Sequence Coverage in Top-Down Proteomics By Automated Multimodal Gas-Phase Protein Fragmentation. <i>Analytical Chemistry</i> , 2018, 90, 12519-12526.	3.2	25
29	Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation. <i>Journal of hand surgery Asian-Pacific volume, The</i> , 2018, , 361-372.	0.2	0
30	Structure and activation of C1, the complex initiating the classical pathway of the complement cascade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 986-991.	3.3	80
31	Functional and structural insight into properdin control of complement alternative pathway amplification. <i>EMBO Journal</i> , 2017, 36, 1084-1099.	3.5	69
32	Structure of the DEAH/RHA ATPase Prp43p bound to RNA implicates a pair of hairpins and motif Va in translocation along RNA. <i>Rna</i> , 2017, 23, 1110-1124.	1.6	39
33	Introducing site-specific cysteines into nanobodies for mercury labelling allows <i>de novo</i> phasing of their crystal structures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 804-813.	1.1	12
34	Protein glutamylation is a yeast-specific posttranslational modification of elongation factor 1A. <i>Journal of Biological Chemistry</i> , 2017, 292, 16014-16023.	1.6	13
35	Reply to Arlaud et al.: Structure of the C1 complex and the unbound C1r2s2 tetramer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5768-E5770.	3.3	1
36	Structural Basis for Simvastatin Competitive Antagonism of Complement Receptor 3. <i>Journal of Biological Chemistry</i> , 2016, 291, 16963-16976.	1.6	25

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37	Re-evaluation of low-resolution crystal structures <i>via</i> interactive molecular-dynamics flexible fitting (iMDFF): a case study in complement C4. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1006-1016.	1.1	43
38	Solution Structures of Complement C2 and Its C4 Complexes Propose Pathway-specific Mechanisms for Control and Activation of the Complement Proconvertases. <i>Journal of Biological Chemistry</i> , 2016, 291, 16494-16507.	1.6	24
39	Structural insight into proteolytic activation and regulation of the complement system. <i>Immunological Reviews</i> , 2016, 274, 59-73.	2.8	50
40	The Structure of the RAGE:S100A6 Complex Reveals a Unique Mode of Homodimerization for S100 Proteins. <i>Structure</i> , 2016, 24, 2043-2052.	1.6	39
41	Crystal structure of human S100A8 in complex with zinc and calcium. <i>BMC Structural Biology</i> , 2016, 16, 8.	2.3	22
42	Complement Regulators and Inhibitors in Health and Disease: A Structural Perspective. <i>Advances in Delivery Science and Technology</i> , 2016, , 13-42.	0.4	2
43	Structural Basis for Eculizumab-Mediated Inhibition of the Complement Terminal Pathway. <i>Journal of Immunology</i> , 2016, 197, 337-344.	0.4	76
44	The cationic peptide LL-37 binds Mac-1 (CD11b/CD18) with a low dissociation rate and promotes phagocytosis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 471-478.	1.1	36
45	Interacting with the Human Insulin Receptor. <i>Structure</i> , 2016, 24, 351-352.	1.6	1
46	Mutations in complement C3 from aHUS patients. <i>Blood</i> , 2015, 125, 2316-2318.	0.6	0
47	Complement activation, regulation, and molecular basis for complement-related diseases. <i>EMBO Journal</i> , 2015, 34, 2735-2757.	3.5	302
48	\hat{I}^2 -Macroglobulin Can Crosslink Multiple Plasmodium falciparum Erythrocyte Membrane Protein 1 (PfEMP1) Molecules and May Facilitate Adhesion of Parasitized Erythrocytes. <i>PLoS Pathogens</i> , 2015, 11, e1005022.	2.1	53
49	Structural basis for the targeting of complement anaphylatoxin C5a using a mixed L-RNA/L-DNA aptamer. <i>Nature Communications</i> , 2015, 6, 6481.	5.8	61
50	Structure of the omalizumab Fab. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 419-426.	0.4	16
51	Structural Insights into the Initiating Complex of the Lectin Pathway of Complement Activation. <i>Structure</i> , 2015, 23, 342-351.	1.6	48
52	Multiple low-affinity interactions support binding of human osteopontin to integrin \hat{I}^2 . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 930-938.	1.1	13
53	Structural Basis for the Function of Complement Component C4 within the Classical and Lectin Pathways of Complement. <i>Journal of Immunology</i> , 2015, 194, 5488-5496.	0.4	69
54	Complement activation by ligand-driven juxtaposition of discrete pattern recognition complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13445-13450.	3.3	63

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55	Structural and functional characterization of human and murine C5a anaphylatoxins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1704-1717.	2.5	35
56	The specificity of DNA recognition by the RAGE receptor. <i>Journal of Experimental Medicine</i> , 2014, 211, 749-750.	4.2	12
57	A Noncoding Expansion in EIF4A3 Causes Richieri-Costa-Pereira Syndrome, a Craniofacial Disorder Associated with Limb Defects. <i>American Journal of Human Genetics</i> , 2014, 94, 120-128.	2.6	99
58	Purification of Human Complement Protein C5. <i>Methods in Molecular Biology</i> , 2014, 1100, 93-102.	0.4	6
59	Toward a structure-based comprehension of the lectin pathway of complement. <i>Molecular Immunology</i> , 2013, 56, 413-422.	1.0	83
60	Toward a structure-based comprehension of the lectin pathway of complement. <i>Molecular Immunology</i> , 2013, 56, 222-231.	1.0	67
61	Structural insight on the recognition of surface-bound opsonins by the integrin I domain of complement receptor 3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16426-16431.	3.3	113
62	Human C3a and C3a desArg anaphylatoxins have conserved structures, in contrast to C5a and C5a desArg. <i>Protein Science</i> , 2013, 22, 204-212.	3.1	51
63	<i>Mimer</i> : an automated spreadsheet-based crystallization screening system. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 815-820.	0.7	13
64	Structural insights into the oligomerization mode of the human receptor for advanced glycation end-products. <i>FEBS Journal</i> , 2013, 280, 6556-6568.	2.2	63
65	Structural basis for activation of the complement system by component C4 cleavage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15425-15430.	3.3	115
66	Structural Analysis of RNA Helicases with Small-Angle X-ray Scattering. <i>Methods in Enzymology</i> , 2012, 511, 191-212.	0.4	5
67	Structure of the haptoglobin-haemoglobin complex. <i>Nature</i> , 2012, 489, 456-459.	13.7	180
68	The Crystal Structure of Human α_2 -Macroglobulin Reveals a Unique Molecular Cage. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 3340-3344.	7.2	103
69	Substrate recognition by complement convertases revealed in the C5-cobra venom factor complex. <i>EMBO Journal</i> , 2011, 30, 606-616.	3.5	87
70	Synergistic activation of eIF4A by eIF4B and eIF4G. <i>Nucleic Acids Research</i> , 2011, 39, 2678-2689.	6.5	67
71	The function and architecture of DEAH/RHA helicases. <i>Biomolecular Concepts</i> , 2011, 2, 315-326.	1.0	7
72	Structural basis for the function of DEAH helicases. <i>EMBO Reports</i> , 2010, 11, 180-186.	2.0	104

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73	Structural basis for receptor recognition of vitamin-B12â€™intrinsic factor complexes. <i>Nature</i> , 2010, 464, 445-448.	13.7	100
74	Structure of the QÎ² replicase, an RNA-dependent RNA polymerase consisting of viral and host proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10884-10889.	3.3	68
75	Structural basis for inhibition of complement C5 by the SSL7 protein from <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3681-3686.	3.3	89
76	The in Vivo Toxicity of Hydroxyurea Depends on Its Direct Target Catalase. <i>Journal of Biological Chemistry</i> , 2010, 285, 21411-21415.	1.6	49
77	Mechanism of ATP turnover inhibition in the EJC. <i>Rna</i> , 2009, 15, 67-75.	1.6	87
78	Structure of and influence of a tick complement inhibitor on human complement component 5. <i>Nature Immunology</i> , 2008, 9, 753-760.	7.0	121
79	Structural insights into the exon junction complex. <i>Current Opinion in Structural Biology</i> , 2008, 18, 112-119.	2.6	98
80	Sordarin Derivatives Induce a Novel Conformation of the Yeast Ribosome Translocation Factor eEF2. <i>Journal of Biological Chemistry</i> , 2007, 282, 657-666.	1.6	30
81	Structures of modified eEF2â€™80S ribosome complexes reveal the role of GTP hydrolysis in translocation. <i>EMBO Journal</i> , 2007, 26, 2421-2431.	3.5	171
82	Structure of the Exon Junction Core Complex with a Trapped DEAD-Box ATPase Bound to RNA. <i>Science</i> , 2006, 313, 1968-1972.	6.0	365
83	The Structure of Bovine Complement Component 3 Reveals the Basis for Thioester Function. <i>Journal of Molecular Biology</i> , 2006, 361, 115-127.	2.0	72
84	Mg2+ and a Key Lysine Modulate Exchange Activity of Eukaryotic Translation Elongation Factor 1BÎ±. <i>Journal of Biological Chemistry</i> , 2006, 281, 19457-19468.	1.6	34
85	Structure of eEF3 and the mechanism of transfer RNA release from the E-site. <i>Nature</i> , 2006, 443, 663-668.	13.7	147
86	Stealth and mimicry by deadly bacterial toxins. <i>Trends in Biochemical Sciences</i> , 2006, 31, 123-133.	3.7	104
87	Exotoxin Aâ€™eEF2 complex structure indicates ADP ribosylation by ribosome mimicry. <i>Nature</i> , 2005, 436, 979-984.	13.7	117
88	Structure of the Catalytic Fragment of Translation Initiation Factor 2B and Identification of a Critically Important Catalytic Residue. <i>Journal of Biological Chemistry</i> , 2004, 279, 10584-10592.	1.6	62
89	Crystal Structure of ADP-ribosylated Ribosomal Translocase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 45919-45925.	1.6	46
90	Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation. <i>EMBO Journal</i> , 2004, 23, 1008-1019.	3.5	373

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91	Purification and crystallization of the yeast translation elongation factor eEF3. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1304-1307.	2.5	13
92	¹ H, ¹⁵ N and ¹³ C resonance assignments of the highly conserved 19 kDa C-terminal domain from human elongation factor 1B γ . <i>Journal of Biomolecular NMR</i> , 2003, 26, 189-190.	1.6	5
93	Elongation factors in protein biosynthesis. <i>Trends in Biochemical Sciences</i> , 2003, 28, 434-441.	3.7	173
94	Two crystal structures demonstrate large conformational changes in the eukaryotic ribosomal translocase. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 379-385.	3.6	154
95	The Crystal Structure of the Glutathione S-Transferase-like Domain of Elongation Factor 1B β^3 from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 47190-47198.	1.6	53
96	Solution Structure of the 162 Residue C-terminal Domain of Human Elongation Factor 1B β^3 . <i>Journal of Biological Chemistry</i> , 2003, 278, 43443-43451.	1.6	14
97	Purification and crystallization of the yeast elongation factor eEF2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 712-715.	2.5	40
98	Bacterial Polypeptide Release Factor RF2 Is Structurally Distinct from Eukaryotic eRF1. <i>Molecular Cell</i> , 2001, 8, 1375-1382.	4.5	197
99	Crystallization of the yeast elongation factor complex eEF1A α -eEF1B β . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 159-161.	2.5	15
100	Crystal structures of nucleotide exchange intermediates in the eEF1A-eEF1B α complex. <i>Nature Structural Biology</i> , 2001, 8, 531-534.	9.7	105
101	High resolution crystal structure of bovine mitochondrial EF-tu in complex with GDP. <i>Journal of Molecular Biology</i> , 2000, 297, 421-436.	2.0	65
102	Structural Basis for Nucleotide Exchange and Competition with tRNA in the Yeast Elongation Factor Complex eEF1A:eEF1B β . <i>Molecular Cell</i> , 2000, 6, 1261-1266.	4.5	179
103	Crystallisation and preliminary X-ray analysis of the receptor-binding domain of human and bovine β_2 -macroglobulin. <i>FEBS Letters</i> , 1995, 372, 93-95.	1.3	5
104	Low Resolution X-ray Structure of Human Methylamine-treated β_2 -Macroglobulin. <i>Journal of Biological Chemistry</i> , 1995, 270, 25133-25141.	1.6	33
105	Crystallization of Proteins of the β_2 -Macroglobulin Superfamily. <i>Annals of the New York Academy of Sciences</i> , 1994, 737, 444-446.	1.8	5
106	Ternary Complex of EF-Tu and Its Action on the Ribosome. , 0, , 337-345.		0