

David Ian Stuart

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

399 papers	29,843 citations	94 h-index	159 g-index
419 ext. papers	35,465 ext. citations	13.3 avg, IF	6.67 L-index

#	Paper	IF	Citations
399	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses.. <i>Cell</i> , 2022 ,	56.2	154
398	Structures and therapeutic potential of anti-RBD human monoclonal antibodies against SARS-CoV-2.. <i>Theranostics</i> , 2022 , 12, 1-17	12.1	1
397	Antibody responses and correlates of protection in the general population after two doses of the ChAdOx1 or BNT162b2 vaccines.. <i>Nature Medicine</i> , 2022 ,	50.5	11
396	Purification of African Swine Fever Virus.. <i>Methods in Molecular Biology</i> , 2022 , 2503, 179-186	1.4	
395	Potential long-term effects of SARS-CoV-2 infection on the pulmonary vasculature: a global perspective. <i>Nature Reviews Cardiology</i> , 2021 ,	14.8	5
394	Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. 2021 ,		25
393	Bacteriophage PRD1 as a nanoscaffold for drug loading. <i>Nanoscale</i> , 2021 ,	7.7	1
392	The antibody response to SARS-CoV-2 Beta underscores the antigenic distance to other variants.. <i>Cell Host and Microbe</i> , 2021 ,	23.4	14
391	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. <i>Nature Communications</i> , 2021 , 12, 6250	17.4	13
390	Site-specific steric control of SARS-CoV-2 spike glycosylation 2021 ,		3
389	The antigenic anatomy of SARS-CoV-2 receptor binding domain. <i>Cell</i> , 2021 , 184, 2183-2200.e22	56.2	145
388	Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. <i>Cell</i> , 2021 , 184, 2348-2361.e6	56.2	549
387	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. <i>Cell</i> , 2021 , 184, 2201-2211.e7	56.2	269
386	Antibody evasion by the P.1 strain of SARS-CoV-2. <i>Cell</i> , 2021 , 184, 2939-2954.e9	56.2	281
385	Quantitative SARS-CoV-2 anti-spike responses to Pfizer-BioNTech and Oxford-AstraZeneca vaccines by previous infection status. <i>Clinical Microbiology and Infection</i> , 2021 , 27, 1516.e7-1516.e14	9.5	43
384	Bispecific repurposed medicines targeting the viral and immunological arms of COVID-19. <i>Scientific Reports</i> , 2021 , 11, 13208	4.9	9
383	Site-Specific Steric Control of SARS-CoV-2 Spike Glycosylation. <i>Biochemistry</i> , 2021 , 60, 2153-2169	3.2	20

382	Ptychographic Single Particle Analysis for Biological Science. <i>Microscopy and Microanalysis</i> , 2021 , 27, 190-192	0.5	
381	Diamond Light Source: contributions to SARS-CoV-2 biology and therapeutics. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 538, 40-46	3.4	4
380	Antibody Status and Incidence of SARS-CoV-2 Infection in Health Care Workers. <i>New England Journal of Medicine</i> , 2021 , 384, 533-540	59.2	482
379	A COVID-19 vaccine candidate using SpyCatcher multimerization of the SARS-CoV-2 spike protein receptor-binding domain induces potent neutralising antibody responses. <i>Nature Communications</i> , 2021 , 12, 542	17.4	86
378	Stringent thresholds in SARS-CoV-2 IgG assays lead to under-detection of mild infections. <i>BMC Infectious Diseases</i> , 2021 , 21, 187	4	12
377	An observational cohort study on the incidence of SARS-CoV-2 infection and B.1.1.7 variant infection in healthcare workers by antibody and vaccination status. <i>Clinical Infectious Diseases</i> , 2021 , ,	11.6	31
376	Antibody responses to SARS-CoV-2 vaccines in 45,965 adults from the general population of the United Kingdom. <i>Nature Microbiology</i> , 2021 , 6, 1140-1149	26.6	74
375	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. <i>Cell</i> , 2021 , 184, 4220-4236.e13	42.36	136
374	Mammalian expression of virus-like particles as a proof of principle for next generation polio vaccines. <i>Npj Vaccines</i> , 2021 , 6, 5	9.5	2
373	The Duration, Dynamics, and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antibody Responses in Individual Healthcare Workers. <i>Clinical Infectious Diseases</i> , 2021 , 73, e699-e709	11.6	120
372	Low-dose phase retrieval of biological specimens using cryo-electron ptychography. <i>Nature Communications</i> , 2020 , 11, 2773	17.4	25
371	Neutralization of SARS-CoV-2 by Destruction of the Prefusion Spike. <i>Cell Host and Microbe</i> , 2020 , 28, 445-454.e6	23.4	187
370	3D Correlative Cryo-Structured Illumination Fluorescence and Soft X-ray Microscopy Elucidates Reovirus Intracellular Release Pathway. <i>Cell</i> , 2020 , 182, 515-530.e17	56.2	29
369	Scanning electron microscopy as a method for sample visualization in protein X-ray crystallography. <i>IUCrJ</i> , 2020 , 7, 500-508	4.7	4
368	Antibody testing for COVID-19: A report from the National COVID Scientific Advisory Panel. <i>Wellcome Open Research</i> , 2020 , 5, 139	4.8	120
367	SARS-CoV-2 antibody prevalence, titres and neutralising activity in an antenatal cohort, United Kingdom, 14 April to 15 June 2020. <i>Eurosurveillance</i> , 2020 , 25,	19.8	9
366	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020 , 9,	8.9	122
365	Author response: Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study 2020 ,		4

364	Broad and strong memory CD4 and CD8 T cells induced by SARS-CoV-2 in UK convalescent COVID-19 patients 2020 ,		47
363	Glutathione facilitates enterovirus assembly by binding at a druggable pocket. <i>Communications Biology</i> , 2020 , 3, 9	6.7	6
362	Hand-foot-and-mouth disease virus receptor KREMEN1 binds the canyon of Coxsackie Virus A10. <i>Nature Communications</i> , 2020 , 11, 38	17.4	12
361	Symmetrical arrangement of positively charged residues around the 5-fold axes of SAT type foot-and-mouth disease virus enhances cell culture of field viruses. <i>PLoS Pathogens</i> , 2020 , 16, e1008828	7.6	2
360	Neutralizing nanobodies bind SARS-CoV-2 spike RBD and block interaction with ACE2. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 846-854	17.6	275
359	Structural basis for the neutralization of SARS-CoV-2 by an antibody from a convalescent patient. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 950-958	17.6	175
358	Structural and functional analysis of protective antibodies targeting the threefold plateau of enterovirus 71. <i>Nature Communications</i> , 2020 , 11, 5253	17.4	6
357	CryoSIM: super-resolution 3D structured illumination cryogenic fluorescence microscopy for correlated ultrastructural imaging. <i>Optica</i> , 2020 , 7, 802-812	8.6	23
356	Broad and strong memory CD4 and CD8 T cells induced by SARS-CoV-2 in UK convalescent individuals following COVID-19. <i>Nature Immunology</i> , 2020 , 21, 1336-1345	19.1	615
355	Performance characteristics of five immunoassays for SARS-CoV-2: a head-to-head benchmark comparison. <i>Lancet Infectious Diseases</i> , 2020 , 20, 1390-1400	25.5	212
354	Assembly intermediates of orthoreovirus captured in the cell. <i>Nature Communications</i> , 2020 , 11, 4445	17.4	13
353	Symmetrical arrangement of positively charged residues around the 5-fold axes of SAT type foot-and-mouth disease virus enhances cell culture of field viruses 2020 , 16, e1008828		
352	Symmetrical arrangement of positively charged residues around the 5-fold axes of SAT type foot-and-mouth disease virus enhances cell culture of field viruses 2020 , 16, e1008828		
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348	Symmetrical arrangement of positively charged residues around the 5-fold axes of SAT type foot-and-mouth disease virus enhances cell culture of field viruses 2020 , 16, e1008828		
347	Atomic structure of the Epstein-Barr virus portal. <i>Nature Communications</i> , 2019 , 10, 3891	17.4	20

346	Multiple liquid crystalline geometries of highly compacted nucleic acid in a dsRNA virus. <i>Nature</i> , 2019 , 570, 252-256	50.4	30
345	The role of the light chain in the structure and binding activity of two cattle antibodies that neutralize bovine respiratory syncytial virus. <i>Molecular Immunology</i> , 2019 , 112, 123-130	4.3	4
344	Assembly of complex viruses exemplified by a halophilic euryarchaeal virus. <i>Nature Communications</i> , 2019 , 10, 1456	17.4	12
343	Hepatitis A Virus Capsid Structure. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019 , 9,	5.4	7
342	Structure-Based in Silico Screening Identifies a Potent Ebolavirus Inhibitor from a Traditional Chinese Medicine Library. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 2928-2937	8.3	18
341	The structure of a prokaryotic viral envelope protein expands the landscape of membrane fusion proteins. <i>Nature Communications</i> , 2019 , 10, 846	17.4	17
340	Unexpected mode of engagement between enterovirus 71 and its receptor SCARB2. <i>Nature Microbiology</i> , 2019 , 4, 414-419	26.6	45
339	Towards in cellulo virus crystallography. <i>Scientific Reports</i> , 2018 , 8, 3771	4.9	8
338	Target Identification and Mode of Action of Four Chemically Divergent Drugs against Ebolavirus Infection. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 724-733	8.3	49
337	Building the atomic model of a boreal lake virus of unknown fold in a 3.9 Å cryo-EM map. <i>Journal of Structural Biology</i> , 2018 , 202, 94-99	3.4	2
336	Neutralization Mechanisms of Two Highly Potent Antibodies against Human Enterovirus 71. <i>MBio</i> , 2018 , 9,	7.8	19
335	Structures of Ebola Virus Glycoprotein Complexes with Tricyclic Antidepressant and Antipsychotic Drugs. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 4938-4945	8.3	20
334	Generation and characterisation of recombinant FMDV antibodies: Applications for advancing diagnostic and laboratory assays. <i>PLoS ONE</i> , 2018 , 13, e0201853	3.7	3
333	Where is crystallography going?. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 152-166	5.5	43
332	Lentiviral transduction of mammalian cells for fast, scalable and high-level production of soluble and membrane proteins. <i>Nature Protocols</i> , 2018 , 13, 2991-3017	18.8	57
331	Seneca Valley virus attachment and uncoating mediated by its receptor anthrax toxin receptor 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 13087-13092	11.5	16
330	Machining protein microcrystals for structure determination by electron diffraction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 9569-9573	11.5	48
329	Redundant Late Domain Functions of Tandem VP2 YPXL Motifs in Nonlytic Cellular Egress of Quasi-enveloped Hepatitis A Virus. <i>Journal of Virology</i> , 2018 , 92,	6.6	19

328	Chimeric O1K foot-and-mouth disease virus with SAT2 outer capsid as an FMD vaccine candidate. <i>Scientific Reports</i> , 2018 , 8, 13654	4.9	7
327	Potent neutralization of hepatitis A virus reveals a receptor mimic mechanism and the receptor recognition site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 770-775	11.5	35
326	The B Cell Response to Foot-and-Mouth Disease Virus in Cattle following Sequential Vaccination with Multiple Serotypes. <i>Journal of Virology</i> , 2017 , 91,	6.6	3
325	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. <i>Nature Communications</i> , 2017 , 8, 14	17.4	72
324	High-speed fixed-target serial virus crystallography. <i>Nature Methods</i> , 2017 , 14, 805-810	21.6	79
323	Rules of engagement between $\alpha 5$ integrin and foot-and-mouth disease virus. <i>Nature Communications</i> , 2017 , 8, 15408	17.4	54
322	Double-stranded RNA virus outer shell assembly by bona fide domain-swapping. <i>Nature Communications</i> , 2017 , 8, 14814	17.4	28
321	SAT2 Foot-and-Mouth Disease Virus Structurally Modified for Increased Thermostability. <i>Journal of Virology</i> , 2017 , 91,	6.6	20
320	Incorporation of tetanus-epitope into virus-like particles achieves vaccine responses even in older recipients in models of psoriasis, Alzheimer's and cat allergy. <i>Npj Vaccines</i> , 2017 , 2, 30	9.5	47
319	Plant-made polio type 3 stabilized VLPs-a candidate synthetic polio vaccine. <i>Nature Communications</i> , 2017 , 8, 245	17.4	56
318	Structures of foot and mouth disease virus pentamers: Insight into capsid dissociation and unexpected pentamer reassociation. <i>PLoS Pathogens</i> , 2017 , 13, e1006607	7.6	16
317	Virus found in a boreal lake links ssDNA and dsDNA viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 8378-8383	11.5	30
316	The slip-and-slide algorithm: a refinement protocol for detector geometry. <i>Journal of Synchrotron Radiation</i> , 2017 , 24, 1152-1162	2.4	4
315	Electron Bio-Imaging Centre (eBIC): the UK national research facility for biological electron microscopy. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 488-495	5.5	17
314	Fixed target combined with spectral mapping: approaching 100% hit rates for serial crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 944-55	5.5	54
313	Structure of human Aichi virus and implications for receptor binding. <i>Nature Microbiology</i> , 2016 , 1, 16150	6.6	24
312	Recovery of data from perfectly twinned virus crystals revisited. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 817-22	5.5	6
311	The Structure of HIV-1 Rev Filaments Suggests a Bilateral Model for Rev-RRE Assembly. <i>Structure</i> , 2016 , 24, 1068-80	5.2	14

310	Toremifene interacts with and destabilizes the Ebola virus glycoprotein. <i>Nature</i> , 2016 , 535, 169-172	50.4	168
309	Crystal structures of penicillin-binding protein 3 in complexes with azlocillin and cefoperazone in both acylated and deacylated forms. <i>FEBS Letters</i> , 2016 , 590, 288-97	3.8	15
308	On the release of for processing X-ray free-electron laser images. <i>Journal of Applied Crystallography</i> , 2016 , 49, 1065-1072	3.8	28
307	Imperfection and radiation damage in protein crystals studied with coherent radiation. <i>Journal of Synchrotron Radiation</i> , 2016 , 23, 228-37	2.4	4
306	TakeTwo: an indexing algorithm suited to still images with known crystal parameters. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 956-65	5.5	28
305	Structure of glycosylated NPC1 luminal domain C reveals insights into NPC2 and Ebola virus interactions. <i>FEBS Letters</i> , 2016 , 590, 605-12	3.8	30
304	The democratization of cryo-EM. <i>Nature Methods</i> , 2016 , 13, 607-8	21.6	25
303	A revised partiality model and post-refinement algorithm for X-ray free-electron laser data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 1400-10		52
302	A national facility for biological cryo-electron microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 127-35		20
301	Structure-based energetics of protein interfaces guides foot-and-mouth disease virus vaccine design. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 788-94	17.6	64
300	Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. <i>Nature</i> , 2015 , 527, 114-7	30.4	116
299	Polyhedra structures and the evolution of the insect viruses. <i>Journal of Structural Biology</i> , 2015 , 192, 88-99	3.4	16
298	Structures of Coxsackievirus A16 Capsids with Native Antigenicity: Implications for Particle Expansion, Receptor Binding, and Immunogenicity. <i>Journal of Virology</i> , 2015 , 89, 10500-11	6.6	40
297	Hepatitis A virus and the origins of picornaviruses. <i>Nature</i> , 2015 , 517, 85-88	50.4	115
296	A RANKL mutant used as an inter-species vaccine for efficient immunotherapy of osteoporosis. <i>Scientific Reports</i> , 2015 , 5, 14150	4.9	12
295	Localized reconstruction of subunits from electron cryomicroscopy images of macromolecular complexes. <i>Nature Communications</i> , 2015 , 6, 8843	17.4	149
294	Diamond Light Source: status and perspectives. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2015 , 373,	3	10
293	Potent antiviral agents fail to elicit genetically-stable resistance mutations in either enterovirus 71 or Coxsackievirus A16. <i>Antiviral Research</i> , 2015 , 124, 77-82	10.8	15

292	The human otubain2-ubiquitin structure provides insights into the cleavage specificity of poly-ubiquitin-linkages. <i>PLoS ONE</i> , 2015 , 10, e0115344	3.7	19
291	Tandem fusion of hepatitis B core antigen allows assembly of virus-like particles in bacteria and plants with enhanced capacity to accommodate foreign proteins. <i>PLoS ONE</i> , 2015 , 10, e0120751	3.7	73
290	Structure of CPV17 polyhedrin determined by the improved analysis of serial femtosecond crystallographic data. <i>Nature Communications</i> , 2015 , 6, 6435	17.4	51
289	Structure of Ljungan virus provides insight into genome packaging of this picornavirus. <i>Nature Communications</i> , 2015 , 6, 8316	17.4	36
288	Structure Elucidation of Coxsackievirus A16 in Complex with GPP3 Informs a Systematic Review of Highly Potent Capsid Binders to Enteroviruses. <i>PLoS Pathogens</i> , 2015 , 11, e1005165	7.6	13
287	Application of in situ diffraction in high-throughput structure determination platforms. <i>Methods in Molecular Biology</i> , 2015 , 1261, 233-53	1.4	16
286	Automated structural comparisons clarify the phylogeny of the right-hand-shaped polymerases. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2741-52	8.3	34
285	Unexpected structure for the N-terminal domain of hepatitis C virus envelope glycoprotein E1. <i>Nature Communications</i> , 2014 , 5, 4874	17.4	56
284	Exploiting fast detectors to enter a new dimension in room-temperature crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1248-56		64
283	More-powerful virus inhibitors from structure-based analysis of HEV71 capsid-binding molecules. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 282-288	17.6	75
282	In cellulo structure determination of a novel cypovirus polyhedrin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1435-41		33
281	Lysosome sorting of β -glucocerebrosidase by LIMP-2 is targeted by the mannose 6-phosphate receptor. <i>Nature Communications</i> , 2014 , 5, 4321	17.4	58
280	Pushing the limits of sulfur SAD phasing: de novo structure solution of the N-terminal domain of the ectodomain of HCV E1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 2197-203		25
279	New methods for indexing multi-lattice diffraction data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 2652-66		51
278	: an iOS app for ISPyB. <i>Journal of Applied Crystallography</i> , 2014 , 47, 1781-1783	3.8	5
277	Crystal structure of signal regulatory protein gamma (SIRP γ) in complex with an antibody Fab fragment. <i>BMC Structural Biology</i> , 2013 , 13, 13	2.7	8
276	Structure of a pestivirus envelope glycoprotein E2 clarifies its role in cell entry. <i>Cell Reports</i> , 2013 , 3, 30-5	10.6	99
275	Efficient production of foot-and-mouth disease virus empty capsids in insect cells following down regulation of 3C protease activity. <i>Journal of Virological Methods</i> , 2013 , 187, 406-12	2.6	46

274	Structure of a VP1-VP3 complex suggests how birnaviruses package the VP1 polymerase. <i>Journal of Virology</i> , 2013 , 87, 3229-36	6.6	13
273	Plate tectonics of virus shell assembly and reorganization in phage B , a distant relative of mammalian reoviruses. <i>Structure</i> , 2013 , 21, 1384-95	5.2	36
272	Automatic comparison and classification of protein structures. <i>Journal of Structural Biology</i> , 2013 , 183, 47-56	3.4	33
271	Expression, purification and crystallization of the ectodomain of the envelope glycoprotein E2 from Bovine viral diarrhoea virus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 35-8		8
270	Antigenic switching of hepatitis B virus by alternative dimerization of the capsid protein. <i>Structure</i> , 2013 , 21, 133-142	5.2	47
269	Bacteriophage P23-77 capsid protein structures reveal the archetype of an ancient branch from a major virus lineage. <i>Structure</i> , 2013 , 21, 718-26	5.2	34
268	Binding of (5S)-penicilloic acid to penicillin binding protein 3. <i>ACS Chemical Biology</i> , 2013 , 8, 2112-6	4.9	18
267	Picornavirus uncoating intermediate captured in atomic detail. <i>Nature Communications</i> , 2013 , 4, 1929	17.4	124
266	Rational engineering of recombinant picornavirus capsids to produce safe, protective vaccine antigen. <i>PLoS Pathogens</i> , 2013 , 9, e1003255	7.6	106
265	Structure determination from a single high-pressure-frozen virus crystal. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 308-12		8
264	From lows to highs: using low-resolution models to phase X-ray data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 2257-65		9
263	Tracking in atomic detail the functional specializations in viral RecA helicases that occur during evolution. <i>Nucleic Acids Research</i> , 2013 , 41, 9396-410	20.1	17
262	Evaluation and use of in-silico structure-based epitope prediction with foot-and-mouth disease virus. <i>PLoS ONE</i> , 2013 , 8, e61122	3.7	30
261	Combined approaches to study virus structures. <i>Sub-Cellular Biochemistry</i> , 2013 , 68, 203-46	5.5	2
260	In situ macromolecular crystallography using microbeams. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 592-600		109
259	Outrunning free radicals in room-temperature macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 810-8		70
258	Crystallization and preliminary crystallographic analysis of the major capsid proteins VP16 and VP17 of bacteriophage P23-77. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 580-3		7
257	Structure of the regulatory domain of the LysR family regulator NMB2055 (MetR-like protein) from <i>Neisseria meningitidis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 730-7		1

256	Chemical and structural analysis of an antibody folding intermediate trapped during glycan biosynthesis. <i>Journal of the American Chemical Society</i> , 2012 , 134, 17554-63	16.4	62
255	Characterization of epitope-tagged foot-and-mouth disease virus. <i>Journal of General Virology</i> , 2012 , 93, 2371-2381	4.9	27
254	The C-terminal priming domain is strongly associated with the main body of bacteriophage ϕ 6 RNA-dependent RNA polymerase. <i>Virology</i> , 2012 , 432, 184-93	3.6	8
253	A plate-based high-throughput assay for virus stability and vaccine formulation. <i>Journal of Virological Methods</i> , 2012 , 185, 166-70	2.6	73
252	A sensor-adaptor mechanism for enterovirus uncoating from structures of EV71. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 424-9	17.6	284
251	Structure unifies the viral universe. <i>Annual Review of Biochemistry</i> , 2012 , 81, 795-822	29.1	215
250	Louise N. Johnson 1940-2012. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1216-7	17.6	1
249	Noncatalytic ions direct the RNA-dependent RNA polymerase of bacterial double-stranded RNA virus ϕ 6 from de novo initiation to elongation. <i>Journal of Virology</i> , 2012 , 86, 2837-49	6.6	28
248	How vaccinia virus has evolved to subvert the host immune response. <i>Journal of Structural Biology</i> , 2011 , 175, 127-34	3.4	52
247	Cells under siege: viral glycoprotein interactions at the cell surface. <i>Journal of Structural Biology</i> , 2011 , 175, 120-6	3.4	27
246	Automation of large scale transient protein expression in mammalian cells. <i>Journal of Structural Biology</i> , 2011 , 175, 209-15	3.4	50
245	xtalPiMS: a PiMS-based web application for the management and monitoring of crystallization trials. <i>Journal of Structural Biology</i> , 2011 , 175, 230-5	3.4	8
244	Recording information on protein complexes in an information management system. <i>Journal of Structural Biology</i> , 2011 , 175, 224-9	3.4	3
243	Crystal structures of penicillin-binding protein 3 from <i>Pseudomonas aeruginosa</i> : comparison of native and antibiotic-bound forms. <i>Journal of Molecular Biology</i> , 2011 , 405, 173-84	6.5	63
242	Insights into the evolution of a complex virus from the crystal structure of vaccinia virus D13. <i>Structure</i> , 2011 , 19, 1011-20	5.2	59
241	The use of low-resolution phasing followed by phase extension from 7.6 to 2.5 Å resolution with noncrystallographic symmetry to solve the structure of a bacteriophage capsid protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 228-32		6
240	The Protein Information Management System (PiMS): a generic tool for any structural biology research laboratory. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 249-60		17
239	Use of the β -mannosidase I inhibitor kifunensine allows the crystallization of apo CTLA-4 homodimer produced in long-term cultures of Chinese hamster ovary cells. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 785-9		14

238	"4D Biology for health and disease" workshop report. <i>New Biotechnology</i> , 2011 , 28, 291-3	6.4	2
237	Rigid-body ligand recognition drives cytotoxic T-lymphocyte antigen 4 (CTLA-4) receptor triggering. <i>Journal of Biological Chemistry</i> , 2011 , 286, 6685-96	5.4	29
236	Mapping the I κ B kinase beta (IKK β)-binding interface of the B14 protein, a vaccinia virus inhibitor of IKK β -mediated activation of nuclear factor kappaB. <i>Journal of Biological Chemistry</i> , 2011 , 286, 20727-35	5.4	43
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13	Correlative cryo-structured illumination fluorescence microscopy and soft X-ray tomography elucidates reovirus intracellular release pathway		2
12	CryoSIM: super resolution 3D structured illumination cryogenic fluorescence microscopy for correlated ultra-structural imaging		1
11	Neutralization of SARS-CoV-2 by destruction of the prefusion Spike		4
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