

David Ian Stuart

List of Publications by Citations

Source: <https://exaly.com/author-pdf/4036243/david-ian-stuart-publications-by-citations.pdf>
Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
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	The three-dimensional structure of foot-and-mouth disease virus at 2.9 Å resolution. <i>Nature</i> , 1989 , 337, 709-16	50.4	765
398	Protein production and purification. <i>Nature Methods</i> , 2008 , 5, 135-46	21.6	655
397	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
396	Structural basis for the recognition of hydroxyproline in HIF-1 α by pVHL. <i>Nature</i> , 2002 , 417, 975-8	50.4	550
395	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
394	The atomic structure of the bluetongue virus core. <i>Nature</i> , 1998 , 395, 470-8	50.4	488
393	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
392	The interaction properties of costimulatory molecules revisited. <i>Immunity</i> , 2002 , 17, 201-10	32.3	477
391	High resolution structures of HIV-1 RT from four RT-inhibitor complexes. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 293-302	17.6	477
390	A functional and structural basis for TCR cross-reactivity in multiple sclerosis. <i>Nature Immunology</i> , 2002 , 3, 940-3	19.1	432
389	A mechanism for initiating RNA-dependent RNA polymerization. <i>Nature</i> , 2001 , 410, 235-40	50.4	432
388	Crystal structure of cat muscle pyruvate kinase at a resolution of 2.6 Å. <i>Journal of Molecular Biology</i> , 1979 , 134, 109-42	6.5	419
387	Lysine methylation as a routine rescue strategy for protein crystallization. <i>Structure</i> , 2006 , 14, 1617-22	5.2	407
386	Crystal structure of the complex between human CD8 α (α) and HLA-A2. <i>Nature</i> , 1997 , 387, 630-4	50.4	388
385	Fitness cost of escape mutations in p24 Gag in association with control of human immunodeficiency virus type 1. <i>Journal of Virology</i> , 2006 , 80, 3617-23	6.6	388
384	A versatile ligation-independent cloning method suitable for high-throughput expression screening applications. <i>Nucleic Acids Research</i> , 2007 , 35, e45	20.1	385
383	Mechanism of inhibition of HIV-1 reverse transcriptase by non-nucleoside inhibitors. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 303-8	17.6	381

382	Complexes of HIV-1 reverse transcriptase with inhibitors of the HEPT series reveal conformational changes relevant to the design of potent non-nucleoside inhibitors. <i>Journal of Medicinal Chemistry</i> , 1996 , 39, 1589-600	8.3	326
381	What does structure tell us about virus evolution?. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 655-683	3.1	314
380	Structure of a major immunogenic site on foot-and-mouth disease virus. <i>Nature</i> , 1993 , 362, 566-8	50.4	313
379	Crystal structure at 2.8 Å resolution of a soluble form of the cell adhesion molecule CD2. <i>Nature</i> , 1992 , 360, 232-9	50.4	300
378	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. <i>Cell</i> , 2021 , 184, 4220-4236.e13	42.6	286
377	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
376	Antibody evasion by the P.1 strain of SARS-CoV-2. <i>Cell</i> , 2021 , 184, 2939-2954.e9	56.2	281
375	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
374	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
373	A structural basis for immunodominant human T cell receptor recognition. <i>Nature Immunology</i> , 2003 , 4, 657-63	19.1	258
372	The crystal structure of plasma gelsolin: implications for actin severing, capping, and nucleation. <i>Cell</i> , 1997 , 90, 661-70	56.2	246
371	Glycoprotein structural genomics: solving the glycosylation problem. <i>Structure</i> , 2007 , 15, 267-73	5.2	234
370	A mechanical explanation of RNA pseudoknot function in programmed ribosomal frameshifting. <i>Nature</i> , 2006 , 441, 244-7	50.4	232
369	Structural basis for the resilience of efavirenz (DMP-266) to drug resistance mutations in HIV-1 reverse transcriptase. <i>Structure</i> , 2000 , 8, 1089-94	5.2	231
368	Structure and functionality in flavivirus NS-proteins: perspectives for drug design. <i>Antiviral Research</i> , 2010 , 87, 125-48	10.8	227
367	Insights into assembly from structural analysis of bacteriophage PRD1. <i>Nature</i> , 2004 , 432, 68-74	50.4	223
366	A procedure for setting up high-throughput nanolitre crystallization experiments. Crystallization workflow for initial screening, automated storage, imaging and optimization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 651-7		217
365	Structure unifies the viral universe. <i>Annual Review of Biochemistry</i> , 2012 , 81, 795-822	29.1	215

364	Structure of the TRAIL-DR5 complex reveals mechanisms conferring specificity in apoptotic initiation. <i>Nature Structural Biology</i> , 1999 , 6, 1048-53		214
363	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
362	Crystal structure of human alpha-lactalbumin at 1.7 Å resolution. <i>Journal of Molecular Biology</i> , 1991 , 221, 571-81	6.5	205
361	Structure and dimerization of a soluble form of B7-1. <i>Immunity</i> , 2000 , 12, 51-60	32.3	197
360	Towards rationalization of crystallization screening for small- to medium-sized academic laboratories: the PACT/JCSG+ strategy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 1426-31		191
359	The structure of HIV-1 reverse transcriptase complexed with 9-chloro-TIBO: lessons for inhibitor design. <i>Structure</i> , 1995 , 3, 915-26	5.2	189
358	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
357	Structural and serological evidence for a novel mechanism of antigenic variation in foot-and-mouth disease virus. <i>Nature</i> , 1990 , 347, 569-72	50.4	182
356	The nsp9 replicase protein of SARS-coronavirus, structure and functional insights. <i>Structure</i> , 2004 , 12, 341-53	5.2	175
355	Crystal structure of SIV matrix antigen and implications for virus assembly. <i>Nature</i> , 1995 , 378, 743-7	50.4	175
354	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
353	The postfusion structure of baculovirus gp64 supports a unified view of viral fusion machines. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 1024-30	17.6	172
352	Toremifene interacts with and destabilizes the Ebola virus glycoprotein. <i>Nature</i> , 2016 , 535, 169-172	50.4	168
351	Structural features impose tight peptide binding specificity in the nonclassical MHC molecule HLA-E. <i>Molecular Cell</i> , 1998 , 1, 531-41	17.6	165
350	The highly ordered double-stranded RNA genome of bluetongue virus revealed by crystallography. <i>Cell</i> , 1999 , 97, 481-90	56.2	162
349	Structural basis of superantigen action inferred from crystal structure of toxic-shock syndrome toxin-1. <i>Nature</i> , 1994 , 367, 94-7	50.4	161
348	An altered position of the alpha 2 helix of MHC class I is revealed by the crystal structure of HLA-B*3501. <i>Immunity</i> , 1996 , 4, 203-13	32.3	154
347	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses.. <i>Cell</i> , 2022 ,	56.2	154

346	Structural basis of Nipah and Hendra virus attachment to their cell-surface receptor ephrin-B2. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 567-72	17.6	150
345	Localized reconstruction of subunits from electron cryomicroscopy images of macromolecular complexes. <i>Nature Communications</i> , 2015 , 6, 8843	17.4	149
344	Atomic snapshots of an RNA packaging motor reveal conformational changes linking ATP hydrolysis to RNA translocation. <i>Cell</i> , 2004 , 118, 743-55	56.2	145
343	The antigenic anatomy of SARS-CoV-2 receptor binding domain. <i>Cell</i> , 2021 , 184, 2183-2200.e22	56.2	145
342	Crystal structure of the extracellular region of the human cell adhesion molecule CD2 at 2.5 Å resolution. <i>Structure</i> , 1994 , 2, 755-66	5.2	143
341	The crystal structure of bluetongue virus VP7. <i>Nature</i> , 1995 , 373, 167-70	50.4	142
340	Bound water structure and polymorphic amino acids act together to allow the binding of different peptides to MHC class I HLA-B53. <i>Immunity</i> , 1996 , 4, 215-28	32.3	142
339	The crystal structure of the catalytic domain of human urokinase-type plasminogen activator. <i>Structure</i> , 1995 , 3, 681-91	5.2	142
338	Functional and structural studies of the vaccinia virus virulence factor N1 reveal a Bcl-2-like anti-apoptotic protein. <i>Journal of General Virology</i> , 2007 , 88, 1656-1666	4.9	138
337	Evolution of viral structure. <i>Theoretical Population Biology</i> , 2002 , 61, 461-70	1.2	135
336	Crystal structure of a soluble CD28-Fab complex. <i>Nature Immunology</i> , 2005 , 6, 271-9	19.1	129
335	Picornavirus uncoating intermediate captured in atomic detail. <i>Nature Communications</i> , 2013 , 4, 1929	17.4	124
334	Membrane structure and interactions with protein and DNA in bacteriophage PRD1. <i>Nature</i> , 2004 , 432, 122-5	50.4	124
333	Design of MKC-442 (emivirine) analogues with improved activity against drug-resistant HIV mutants. <i>Journal of Medicinal Chemistry</i> , 1999 , 42, 4500-5	8.3	124
332	Antagonist HIV-1 Gag peptides induce structural changes in HLA B8. <i>Journal of Experimental Medicine</i> , 1996 , 184, 2279-86	16.6	123
331	Paired receptor specificity explained by structures of signal regulatory proteins alone and complexed with CD47. <i>Molecular Cell</i> , 2008 , 31, 266-77	17.6	122
330	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020 , 9,	8.9	122
329	Vaccinia virus proteins A52 and B14 Share a Bcl-2-like fold but have evolved to inhibit NF-kappaB rather than apoptosis. <i>PLoS Pathogens</i> , 2008 , 4, e1000128	7.6	121

328	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
327	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
326	The ligand-binding face of the semaphorins revealed by the high-resolution crystal structure of SEMA4D. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 843-8	17.6	119
325	Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. <i>Nature</i> , 2015 , 527, 114-7	30.4	116
324	The structure of a cypovirus and the functional organization of dsRNA viruses. <i>Nature Structural Biology</i> , 1999 , 6, 565-8		116
323	Hepatitis A virus and the origins of picornaviruses. <i>Nature</i> , 2015 , 517, 85-88	50.4	115
322	The human low affinity Fcγ receptors IIa, IIb, and III bind IgG with fast kinetics and distinct thermodynamic properties. <i>Journal of Biological Chemistry</i> , 2001 , 276, 44898-904	5.4	113
321	Classical and nonclassical class I major histocompatibility complex molecules exhibit subtle conformational differences that affect binding to CD8αα. <i>Journal of Biological Chemistry</i> , 2000 , 275, 15232-8	5.4	111
320	In situ macromolecular crystallography using microbeams. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 592-600		109
319	Rational engineering of recombinant picornavirus capsids to produce safe, protective vaccine antigen. <i>PLoS Pathogens</i> , 2013 , 9, e1003255	7.6	106
318	Implications of the HIV-1 Rev dimer structure at 3.2 Å resolution for multimeric binding to the Rev response element. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 5810-4	11.5	106
317	Signaling lymphocytic activation molecule (CDw150) is homophilic but self-associates with very low affinity. <i>Journal of Biological Chemistry</i> , 2000 , 275, 28100-9	5.4	106
316	An atomic model of the outer layer of the bluetongue virus core derived from X-ray crystallography and electron cryomicroscopy. <i>Structure</i> , 1997 , 5, 885-93	5.2	105
315	Structure of the brain-derived neurotrophic factor/neurotrophin 3 heterodimer. <i>Biochemistry</i> , 1995 , 34, 4139-46	3.2	105
314	Structure of the integrin binding fragment from fibrillin-1 gives new insights into microfibril organization. <i>Structure</i> , 2004 , 12, 717-29	5.2	101
313	Structure of a pestivirus envelope glycoprotein E2 clarifies its role in cell entry. <i>Cell Reports</i> , 2013 , 3, 30-5	10.6	99
312	Lessons from structural genomics. <i>Annual Review of Biophysics</i> , 2009 , 38, 371-83	21.1	99
311	Crystal structure of a novel conformational state of the flavivirus NS3 protein: implications for polyprotein processing and viral replication. <i>Journal of Virology</i> , 2009 , 83, 12895-906	6.6	97

310	Evolution of complex RNA polymerases: the complete archaeal RNA polymerase structure. <i>PLoS Biology</i> , 2009 , 7, e1000102	9.7	97
309	Insights into virus evolution and membrane biogenesis from the structure of the marine lipid-containing bacteriophage PM2. <i>Molecular Cell</i> , 2008 , 31, 749-61	17.6	97
308	Killer cell immunoglobulin receptors and T cell receptors bind peptide-major histocompatibility complex class I with distinct thermodynamic and kinetic properties. <i>Journal of Biological Chemistry</i> , 1999 , 274, 28329-34	5.4	97
307	Three-dimensional structures of translating ribosomes by Cryo-EM. <i>Molecular Cell</i> , 2004 , 14, 57-66	17.6	95
306	Binding of the second generation non-nucleoside inhibitor S-1153 to HIV-1 reverse transcriptase involves extensive main chain hydrogen bonding. <i>Journal of Biological Chemistry</i> , 2000 , 275, 14316-20	5.4	95
305	Specificity of the VP1 GH loop of Foot-and-Mouth Disease virus for alphav integrins. <i>Journal of Virology</i> , 2006 , 80, 9798-810	6.6	94
304	Evidence for the role of His-142 of protein 1C in the acid-induced disassembly of foot-and-mouth disease virus capsids. <i>Journal of General Virology</i> , 1999 , 80 (Pt 8), 1911-1918	4.9	94
303	Crystal structures of HIV-1 reverse transcriptase in complex with carboxanilide derivatives. <i>Biochemistry</i> , 1998 , 37, 14394-403	3.2	93
302	Perturbations in the surface structure of A22 Iraq foot-and-mouth disease virus accompanying coupled changes in host cell specificity and antigenicity. <i>Structure</i> , 1996 , 4, 135-45	5.2	91
301	Structural and functional insights of RANKL-RANK interaction and signaling. <i>Journal of Immunology</i> , 2010 , 184, 6910-9	5.3	90
300	Phenylethylthiazolylthiourea (PETT) non-nucleoside inhibitors of HIV-1 and HIV-2 reverse transcriptases. Structural and biochemical analyses. <i>Journal of Biological Chemistry</i> , 2000 , 275, 5633-9	5.4	90
299	Crystal structure and carbohydrate analysis of Nipah virus attachment glycoprotein: a template for antiviral and vaccine design. <i>Journal of Virology</i> , 2008 , 82, 11628-36	6.6	89
298	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
297	How baculovirus polyhedra fit square pegs into round holes to robustly package viruses. <i>EMBO Journal</i> , 2010 , 29, 505-14	13	82
296	Structure and binding kinetics of three different human CD1d-alpha-galactosylceramide-specific T cell receptors. <i>Journal of Experimental Medicine</i> , 2006 , 203, 699-710	16.6	82
295	High-speed fixed-target serial virus crystallography. <i>Nature Methods</i> , 2017 , 14, 805-810	21.6	79
294	Structure of Foot-and-mouth disease virus serotype A10 61 alone and complexed with oligosaccharide receptor: receptor conservation in the face of antigenic variation. <i>Journal of General Virology</i> , 2005 , 86, 1909-1920	4.9	79
293	Design of non-nucleoside inhibitors of HIV-1 reverse transcriptase with improved drug resistance properties. 1. <i>Journal of Medicinal Chemistry</i> , 2004 , 47, 5912-22	8.3	79

292	Hepatitis B small surface antigen particles are octahedral. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 14783-8	11.5	79
291	The crystal structure of coxsackievirus A9: new insights into the uncoating mechanisms of enteroviruses. <i>Structure</i> , 1999 , 7, 1527-38	5.2	78
290	Crystal structure of the human p58 killer cell inhibitory receptor (KIR2DL3) specific for HLA-Cw3-related MHC class I. <i>Structure</i> , 1999 , 7, 391-8	5.2	77
289	The crystal structure of ORF-9b, a lipid binding protein from the SARS coronavirus. <i>Structure</i> , 2006 , 14, 1157-65	5.2	76
288	The N-glycosidase mechanism of ribosome-inactivating proteins implied by crystal structures of alpha-momorcharin. <i>Structure</i> , 1994 , 2, 7-16	5.2	76
287	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
286	Dimeric architecture of the Hendra virus attachment glycoprotein: evidence for a conserved mode of assembly. <i>Journal of Virology</i> , 2010 , 84, 6208-17	6.6	75
285	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
284	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
283	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
282	Structural plasticity of eph receptor A4 facilitates cross-class ephrin signaling. <i>Structure</i> , 2009 , 17, 1386-92	3.7	73
281	Bluetongue virus VP4 is an RNA-capping assembly line. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 449-51	17.6	73
280	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. <i>Nature Communications</i> , 2017 , 8, 14	17.4	72
279	Structure of pyruvate kinase and similarities with other enzymes: possible implications for protein taxonomy and evolution. <i>Nature</i> , 1978 , 271, 626-30	50.4	72
278	Outrunning free radicals in room-temperature macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 810-8		70
277	The structure of an RNAi polymerase links RNA silencing and transcription. <i>PLoS Biology</i> , 2006 , 4, e434	9.7	70
276	2-Amino-6-arylsulfonylbenzonitriles as non-nucleoside reverse transcriptase inhibitors of HIV-1. <i>Journal of Medicinal Chemistry</i> , 2001 , 44, 1866-82	8.3	69
275	Structural comparison of two strains of foot-and-mouth disease virus subtype O1 and a laboratory antigenic variant, G67. <i>Structure</i> , 1995 , 3, 571-80	5.2	68

274	3NAzido-3'-deoxythymidine drug resistance mutations in HIV-1 reverse transcriptase can induce long range conformational changes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 9518-23	11.5	67
273	High-resolution structure of the catalytic region of MICAL (molecule interacting with CasL), a multidomain flavoenzyme-signaling molecule. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 16836-41	11.5	66
272	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
271	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
270	Determination of the affinity and kinetic constants for the interaction between the human virus echovirus 11 and its cellular receptor, CD55. <i>Journal of Biological Chemistry</i> , 1998 , 273, 30443-7	5.4	64
269	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
268	Unusual molecular architecture of the machupo virus attachment glycoprotein. <i>Journal of Virology</i> , 2009 , 83, 8259-65	6.6	63
267	Carbohydrate and domain architecture of an immature antibody glycoform exhibiting enhanced effector functions. <i>Journal of Molecular Biology</i> , 2009 , 387, 1061-6	6.5	63
266	A similar pattern of interaction for different antibodies with a major antigenic site of foot-and-mouth disease virus: implications for intratypic antigenic variation. <i>Journal of Virology</i> , 1998 , 72, 739-48	6.6	63
265	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
264	The structures of the neurotrophin 4 homodimer and the brain-derived neurotrophic factor/neurotrophin 4 heterodimer reveal a common Trk-binding site. <i>Protein Science</i> , 1999 , 8, 2589-97	6.3	61
263	Nonstandard peptide binding revealed by crystal structures of HLA-B*5101 complexed with HIV immunodominant epitopes. <i>Journal of Immunology</i> , 2000 , 165, 3260-7	5.3	61
262	Implications for viral uncoating from the structure of bovine enterovirus. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 224-31	17.6	61
261	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
260	alphaVbeta6 is a novel receptor for human fibrillin-1. Comparative studies of molecular determinants underlying integrin-rgd affinity and specificity. <i>Journal of Biological Chemistry</i> , 2007 , 282, 6743-51	5.4	59
259	Lysosome sorting of Eglucocerebrosidase by LIMP-2 is targeted by the mannose 6-phosphate receptor. <i>Nature Communications</i> , 2014 , 5, 4321	17.4	58
258	Design of non-nucleoside inhibitors of HIV-1 reverse transcriptase with improved drug resistance properties. 2. <i>Journal of Medicinal Chemistry</i> , 2004 , 47, 5923-36	8.3	58
257	Inhibition of apoptosis and NF- κ B activation by vaccinia protein N1 occur via distinct binding surfaces and make different contributions to virulence. <i>PLoS Pathogens</i> , 2011 , 7, e1002430	7.6	57

256	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
255	Plant-made polio type 3 stabilized VLPs-a candidate synthetic polio vaccine. <i>Nature Communications</i> , 2017 , 8, 245	17.4	56
254	Unexpected structure for the N-terminal domain of hepatitis C virus envelope glycoprotein E1. <i>Nature Communications</i> , 2014 , 5, 4874	17.4	56
253	Equine rhinitis A virus and its low pH empty particle: clues towards an aphthovirus entry mechanism?. <i>PLoS Pathogens</i> , 2009 , 5, e1000620	7.6	55
252	Rules of engagement between $\alpha 5$ integrin and foot-and-mouth disease virus. <i>Nature Communications</i> , 2017 , 8, 15408	17.4	54
251	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
250	Using structural information to change the phosphotransfer specificity of a two-component chemotaxis signalling complex. <i>PLoS Biology</i> , 2010 , 8, e1000306	9.7	53
249	Ligand binding by the immunoglobulin superfamily recognition molecule CD2 is glycosylation-independent. <i>Journal of Biological Chemistry</i> , 1995 , 270, 369-75	5.4	53
248	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
247	How vaccinia virus has evolved to subvert the host immune response. <i>Journal of Structural Biology</i> , 2011 , 175, 127-34	3.4	52
246	Structure of CPV17 polyhedrin determined by the improved analysis of serial femtosecond crystallographic data. <i>Nature Communications</i> , 2015 , 6, 6435	17.4	51
245	New methods for indexing multi-lattice diffraction data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 2652-66		51
244	The structure of CrgA from <i>Neisseria meningitidis</i> reveals a new octameric assembly state for LysR transcriptional regulators. <i>Nucleic Acids Research</i> , 2009 , 37, 4545-58	20.1	51
243	The structure of the macrophage signal regulatory protein alpha (SIRPalpha) inhibitory receptor reveals a binding face reminiscent of that used by T cell receptors. <i>Journal of Biological Chemistry</i> , 2007 , 282, 14567-75	5.4	51
242	Automation of large scale transient protein expression in mammalian cells. <i>Journal of Structural Biology</i> , 2011 , 175, 209-15	3.4	50
241	Atomic resolution structure of Moloney murine leukemia virus matrix protein and its relationship to other retroviral matrix proteins. <i>Structure</i> , 2002 , 10, 1627-36	5.2	50
240	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
239	Structure and function of A41, a vaccinia virus chemokine binding protein. <i>PLoS Pathogens</i> , 2008 , 4, e5	7.6	49

238	A tick protein with a modified Kunitz fold inhibits human trypsin. <i>Journal of Molecular Biology</i> , 2007 , 368, 1172-86	6.5	49
237	Flexibility of the major antigenic loop of foot-and-mouth disease virus bound to a Fab fragment of a neutralising antibody: structure and neutralisation. <i>Virology</i> , 1999 , 255, 260-8	3.6	49
236	Expression of soluble recombinant glycoproteins with predefined glycosylation: application to the crystallization of the T-cell glycoprotein CD2. <i>Protein Engineering, Design and Selection</i> , 1993 , 6, 229-32	1.9	49
235	Rhabdovirus matrix protein structures reveal a novel mode of self-association. <i>PLoS Pathogens</i> , 2008 , 4, e1000251	7.6	48
234	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
233	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
232	Antigenic switching of hepatitis B virus by alternative dimerization of the capsid protein. <i>Structure</i> , 2013 , 21, 133-142	5.2	47
231	Broad and strong memory CD4 and CD8 T cells induced by SARS-CoV-2 in UK convalescent COVID-19 patients 2020 ,		47
230	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
229	Crystal structure of the Murray Valley encephalitis virus NS5 methyltransferase domain in complex with cap analogues. <i>Journal of General Virology</i> , 2007 , 88, 2228-2236	4.9	46
228	Unexpected mode of engagement between enterovirus 71 and its receptor SCARB2. <i>Nature Microbiology</i> , 2019 , 4, 414-419	26.6	45
227	Determination of the structure of a decay accelerating factor-binding clinical isolate of echovirus 11 allows mapping of mutants with altered receptor requirements for infection. <i>Journal of Virology</i> , 2002 , 76, 7694-704	6.6	44
226	Mapping the IkappaB kinase beta (IKKbeta)-binding interface of the B14 protein, a vaccinia virus inhibitor of IKKbeta-mediated activation of nuclear factor kappaB. <i>Journal of Biological Chemistry</i> , 2011 , 286, 20727-35	5.4	43
225	Where is crystallography going?. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 152-166	5.5	43
224	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
223	Building meaningful models of glycoproteins. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 354; discussion 354-5	17.6	41
222	A critical evaluation of the predicted and X-ray structures of alpha-lactalbumin. <i>The Protein Journal</i> , 1990 , 9, 549-63		41
221	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

220	Benefits of automated crystallization plate tracking, imaging, and analysis. <i>Structure</i> , 2005 , 13, 175-82	5.2	39
219	Structural explanation for the role of Mn ²⁺ in the activity of phi6 RNA-dependent RNA polymerase. <i>Nucleic Acids Research</i> , 2008 , 36, 6633-44	20.1	38
218	Structure of CrmE, a virus-encoded tumour necrosis factor receptor. <i>Journal of Molecular Biology</i> , 2007 , 372, 660-71	6.5	38
217	Crystallographic analysis of the binding modes of thiazoloisoindolinone non-nucleoside inhibitors to HIV-1 reverse transcriptase and comparison with modeling studies. <i>Journal of Medicinal Chemistry</i> , 1999 , 42, 3845-51	8.3	38
216	Structure of equine infectious anemia virus matrix protein. <i>Journal of Virology</i> , 2002 , 76, 1876-83	6.6	37
215	Plate tectonics of virus shell assembly and reorganization in phage Φ , a distant relative of mammalian reoviruses. <i>Structure</i> , 2013 , 21, 1384-95	5.2	36
214	Structure of Ljungan virus provides insight into genome packaging of this picornavirus. <i>Nature Communications</i> , 2015 , 6, 8316	17.4	36
213	An ion-channel modulator from the saliva of the brown ear tick has a highly modified Kunitz/BPTI structure. <i>Journal of Molecular Biology</i> , 2009 , 389, 734-47	6.5	36
212	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
211	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
210	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
209	Diffraction quality crystals of PRD1, a 66-MDa dsDNA virus with an internal membrane. <i>Journal of Structural Biology</i> , 2002 , 139, 103-12	3.4	34
208	In cellulo structure determination of a novel cypovirus polyhedrin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1435-41		33
207	Automatic comparison and classification of protein structures. <i>Journal of Structural Biology</i> , 2013 , 183, 47-56	3.4	33
206	A human embryonic kidney 293T cell line mutated at the Golgi alpha-mannosidase II locus. <i>Journal of Biological Chemistry</i> , 2009 , 284, 21684-95	5.4	33
205	Models which explain the inhibition of reverse transcriptase by HIV-1-specific (thio)carboxanilide derivatives. <i>Biochemical and Biophysical Research Communications</i> , 1997 , 234, 458-64	3.4	33
204	Effects of N-butyldeoxynojirimycin and the Lec3.2.8.1 mutant phenotype on N-glycan processing in Chinese hamster ovary cells: application to glycoprotein crystallization. <i>Protein Science</i> , 1999 , 8, 1696-701	6.3	33
203	Crystal structure and binding properties of the CD2 and CD244 (2B4)-binding protein, CD48. <i>Journal of Biological Chemistry</i> , 2006 , 281, 29309-20	5.4	32

202	The structural basis for RNA specificity and Ca ²⁺ inhibition of an RNA-dependent RNA polymerase. <i>Structure</i> , 2004 , 12, 307-16	5.2	32
201	Lipofectin increases the specific activity of cypovirus particles for cultured insect cells. <i>Journal of Virological Methods</i> , 1999 , 78, 177-89	2.6	31
200	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
199	Multiple liquid crystalline geometries of highly compacted nucleic acid in a dsRNA virus. <i>Nature</i> , 2019 , 570, 252-256	50.4	30
198	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
197	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
196	Structures of orbivirus VP7: implications for the role of this protein in the viral life cycle. <i>Structure</i> , 1997 , 5, 871-83	5.2	30
195	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
194	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
193	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
192	Production, crystallization, and preliminary X-ray analysis of the human MHC class Ib molecule HLA-E. <i>Protein Science</i> , 1998 , 7, 1264-6	6.3	29
191	Crystallization and preliminary X-ray diffraction analysis of foot-and-mouth disease virus. <i>Journal of Molecular Biology</i> , 1987 , 196, 591-7	6.5	29
190	Double-stranded RNA virus outer shell assembly by bona fide domain-swapping. <i>Nature Communications</i> , 2017 , 8, 14814	17.4	28
189	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
188	Shared paramyxoviral glycoprotein architecture is adapted for diverse attachment strategies. <i>Biochemical Society Transactions</i> , 2010 , 38, 1349-55	5.1	28
187	Structure of the Murray Valley encephalitis virus RNA helicase at 1.9 Angstrom resolution. <i>Protein Science</i> , 2007 , 16, 2294-300	6.3	28
186	Production and crystallization of MHC class I B allele single peptide complexes. <i>FEBS Letters</i> , 1996 , 383, 119-23	3.8	28
185	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

184	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
183	Characterization of epitope-tagged foot-and-mouth disease virus. <i>Journal of General Virology</i> , 2012 , 93, 2371-2381	4.9	27
182	Cells under siege: viral glycoprotein interactions at the cell surface. <i>Journal of Structural Biology</i> , 2011 , 175, 120-6	3.4	27
181	Structural basis of mechanochemical coupling in a hexameric molecular motor. <i>Journal of Biological Chemistry</i> , 2008 , 283, 3607-3617	5.4	27
180	The structure and function of the outer coat protein VP9 of Banna virus. <i>Structure</i> , 2005 , 13, 17-28	5.2	27
179	The N-terminus of the RNA polymerase from infectious pancreatic necrosis virus is the determinant of genome attachment. <i>PLoS Pathogens</i> , 2011 , 7, e1002085	7.6	26
178	Semi-automated microseeding of nanolitre crystallization experiments. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 14-8		26
177	Low-dose phase retrieval of biological specimens using cryo-electron ptychography. <i>Nature Communications</i> , 2020 , 11, 2773	17.4	25
176	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
175	Crystal structure of Swine vesicular disease virus and implications for host adaptation. <i>Journal of Virology</i> , 2003 , 77, 5475-86	6.6	25
174	Utility of recombinant integrin alpha v beta6 as a capture reagent in immunoassays for the diagnosis of foot-and-mouth disease. <i>Journal of Virological Methods</i> , 2005 , 127, 69-79	2.6	25
173	Back-priming mode of phi6 RNA-dependent RNA polymerase. <i>Journal of General Virology</i> , 2005 , 86, 521-526	4.26	25
172	Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. 2021 ,		25
171	The democratization of cryo-EM. <i>Nature Methods</i> , 2016 , 13, 607-8	21.6	25
170	Structure of human Aichi virus and implications for receptor binding. <i>Nature Microbiology</i> , 2016 , 1, 16150	6.6	24
169	Generation and characterization of a chimeric rabbit/human Fab for co-crystallization of HIV-1 Rev. <i>Journal of Molecular Biology</i> , 2010 , 397, 697-708	6.5	24
168	Structure of signal-regulatory protein alpha: a link to antigen receptor evolution. <i>Journal of Biological Chemistry</i> , 2009 , 284, 26613-9	5.4	24
167	Models of the three-dimensional structures of echidna, horse, and pigeon lysozymes: calcium-binding lysozymes and their relationship with alpha-lactalbumins. <i>The Protein Journal</i> , 1994 , 13, 569-84		24

166	Crystal lattice as biological phenotype for insect viruses. <i>Protein Science</i> , 2005 , 14, 2741-3	6.3	23
165	Expression cloning of an equine T-lymphocyte glycoprotein CD2 cDNA. Structure-based analysis of conserved sequence elements. <i>FEBS Journal</i> , 1994 , 219, 969-76		23
164	Antibodies to SARS-CoV-2 are associated with protection against reinfection		23
163	CryoSIM: super-resolution 3D structured illumination cryogenic fluorescence microscopy for correlated ultrastructural imaging. <i>Optica</i> , 2020 , 7, 802-812	8.6	23
162	Gene silencing pathway RNA-dependent RNA polymerase of <i>Neurospora crassa</i> : yeast expression and crystallization of selenomethionated QDE-1 protein. <i>Journal of Structural Biology</i> , 2005 , 149, 111-5	3.4	22
161	Design of a data model for developing laboratory information management and analysis systems for protein production. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 278-84	4.2	21
160	Virus crystallography. <i>Molecular Biotechnology</i> , 1999 , 12, 13-23	3	21
159	SAT2 Foot-and-Mouth Disease Virus Structurally Modified for Increased Thermostability. <i>Journal of Virology</i> , 2017 , 91,	6.6	20
158	Atomic structure of the Epstein-Barr virus portal. <i>Nature Communications</i> , 2019 , 10, 3891	17.4	20
157	A national facility for biological cryo-electron microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 127-35		20
156	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
155	Insights into the pre-initiation events of bacteriophage phi 6 RNA-dependent RNA polymerase: towards the assembly of a productive binary complex. <i>Nucleic Acids Research</i> , 2009 , 37, 1182-92	20.1	20
154	Recognition surfaces of MHC class I. <i>Immunological Reviews</i> , 1998 , 163, 121-8	11.3	20
153	Reconfiguration of yeast 40S ribosomal subunit domains by the translation initiation multifactor complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 5788-93	11.5	20
152	Macromolecular assemblies: greater than their parts. <i>Current Opinion in Structural Biology</i> , 2001 , 11, 1078-13	11.3	20
151	Early peak and rapid decline of SARS-CoV-2 seroprevalence in a Swiss metropolitan region		20
150	Site-Specific Steric Control of SARS-CoV-2 Spike Glycosylation. <i>Biochemistry</i> , 2021 , 60, 2153-2169	3.2	20
149	Neutralization Mechanisms of Two Highly Potent Antibodies against Human Enterovirus 71. <i>MBio</i> , 2018 , 9,	7.8	19

148	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
147	The structure of a reduced form of OxyR from <i>Neisseria meningitidis</i> . <i>BMC Structural Biology</i> , 2010 , 10, 10	2.7	19
146	Characterizing sequence variation in the VP1 capsid proteins of foot and mouth disease virus (serotype 0) with respect to virion structure. <i>Journal of Molecular Evolution</i> , 1998 , 46, 465-75	3.1	19
145	Crystal structure of a 3-oxoacyl-(acylcarrier protein) reductase (BA3989) from <i>Bacillus anthracis</i> at 2.4-A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 562-7	4.2	19
144	Time-resolved structural studies on catalysis in the crystal with glycogen phosphorylase b. <i>Biochemical Society Transactions</i> , 1986 , 14, 538-41	5.1	19
143	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
142	Binding of (5S)-penicilloic acid to penicillin binding protein 3. <i>ACS Chemical Biology</i> , 2013 , 8, 2112-6	4.9	18
141	Domain metastability: a molecular basis for immunoglobulin deposition?. <i>Journal of Molecular Biology</i> , 2010 , 399, 207-13	6.5	18
140	Functional characteristics of HIV-1 subtype C compatible with increased heterosexual transmissibility. <i>Aids</i> , 2009 , 23, 1047-57	3.5	18
139	Crystallization and preliminary X-ray crystallographic studies on the bacteriophage phi6 RNA-dependent RNA polymerase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 1473-5		18
138	Crystallization and preliminary X-ray analysis of three serotypes of foot-and-mouth disease virus. <i>Journal of Molecular Biology</i> , 1992 , 228, 1263-8	6.5	18
137	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
136	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
135	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
134	The mechanics of translocation: a molecular "spring-and-ratchet" system. <i>Structure</i> , 2008 , 16, 664-72	5.2	17
133	Disruption of alpha-mannosidase processing induces non-canonical hybrid-type glycosylation. <i>FEBS Letters</i> , 2007 , 581, 1963-8	3.8	17
132	The structure of foot-and-mouth disease virus: implications for its physical and biological properties. <i>Veterinary Microbiology</i> , 1990 , 23, 21-34	3.3	17
131	Uridine(5')diphospho(1)-alpha-D-glucose. A binding study to glycogen phosphorylase b in the crystal. <i>FEBS Journal</i> , 1988 , 173, 569-78		17

130	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
129	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
128	Polyhedra structures and the evolution of the insect viruses. <i>Journal of Structural Biology</i> , 2015 , 192, 88-99	3.4	16
127	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
126	Specific interactions between human integrin alpha v beta 3 and chimeric hepatitis B virus core particles bearing the receptor-binding epitope of foot-and-mouth disease virus. <i>Virology</i> , 1997 , 239, 150-7	3.6	16
125	What Does it Take to Make a Virus: The Concept of the Viral Self. <i>PLoS Pathogens</i> , 2010 , 35-58		16
124	Application of in situ diffraction in high-throughput structure determination platforms. <i>Methods in Molecular Biology</i> , 2015 , 1261, 233-53	1.4	16
123	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		16
122	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
121	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
120	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
119	Expression, purification and crystallization of a lyssavirus matrix (M) protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 258-62		15
118	Structures of an alanine racemase from <i>Bacillus anthracis</i> (BA0252) in the presence and absence of (R)-1-aminoethylphosphonic acid (L-Ala-P). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 327-33		15
117	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
116	Use of the α -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
115	Crystallization and functional analysis of a soluble deglycosylated form of the human costimulatory molecule B7-1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 605-8		14
114	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
113	Antibody evasion by the Brazilian P.1 strain of SARS-CoV-2		14

112	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
111	Crystal structure of equine rhinitis A virus in complex with its sialic acid receptor. <i>Journal of General Virology</i> , 2010 , 91, 1971-1977	4.9	13
110	Recognition at the cell surface: recent structural insights. <i>Current Opinion in Structural Biology</i> , 1995 , 5, 735-43	8.1	13
109	Weissenberg data collection for macromolecular crystallography. <i>Current Opinion in Structural Biology</i> , 1993 , 3, 737-740	8.1	13
108	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
107	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. <i>Nature Communications</i> , 2021 , 12, 6250	17.4	13
106	Assembly intermediates of orthoreovirus captured in the cell. <i>Nature Communications</i> , 2020 , 11, 4445	17.4	13
105	Assembly of complex viruses exemplified by a halophilic euryarchaeal virus. <i>Nature Communications</i> , 2019 , 10, 1456	17.4	12
104	A RANKL mutant used as an inter-species vaccine for efficient immunotherapy of osteoporosis. <i>Scientific Reports</i> , 2015 , 5, 14150	4.9	12
103	In vitro activities of the multifunctional RNA silencing polymerase QDE-1 of <i>Neurospora crassa</i> . <i>Journal of Biological Chemistry</i> , 2010 , 285, 29367-74	5.4	12
102	The crystal structure of UMP kinase from <i>Bacillus anthracis</i> (BA1797) reveals an allosteric nucleotide-binding site. <i>Journal of Molecular Biology</i> , 2008 , 381, 1098-105	6.5	12
101	Production, crystallization and preliminary X-ray crystallographic studies of the bacteriophage phi 12 packaging motor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 588-90		12
100	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
99	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
98	Crystallization and preliminary X-ray analysis of CrgA, a LysR-type transcriptional regulator from pathogenic <i>Neisseria meningitidis</i> MC58. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 797-801		11
97	Model of the equine rhinitis A virus capsid: identification of a major neutralizing immunogenic site. <i>Journal of General Virology</i> , 2003 , 84, 2365-2373	4.9	11
96	Complementing crystallography: the role of cryo-electron microscopy in structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1742-9		11
95	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

94	Diamond Light Source: status and perspectives. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2015 , 373,	3	10
93	Preliminary crystallographic analysis of bovine enterovirus. <i>Journal of Molecular Biology</i> , 1993 , 231, 930-5	3.5	10
92	The duration, dynamics and determinants of SARS-CoV-2 antibody responses in individual healthcare workers		10
91	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
90	The tandem zinc-finger region of human ZHX adopts a novel C2H2 zinc finger structure with a C-terminal extension. <i>Biochemistry</i> , 2009 , 48, 4431-9	3.2	9
89	Structure of 5-formyltetrahydrofolate cyclo-ligase from <i>Bacillus anthracis</i> (BA4489). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 168-72		9
88	Cloning, expression, purification, and crystallisation of HIV-2 reverse transcriptase. <i>Protein Expression and Purification</i> , 2003 , 27, 12-8	2	9
87	Preliminary crystallographic analysis of the major capsid protein P2 of the lipid-containing bacteriophage PM2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005 , 61, 762-5		9
86	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
85	Bispecific repurposed medicines targeting the viral and immunological arms of COVID-19. <i>Scientific Reports</i> , 2021 , 11, 13208	4.9	9
84	Towards in cellulo virus crystallography. <i>Scientific Reports</i> , 2018 , 8, 3771	4.9	8
83	Crystal structure of signal regulatory protein gamma (SIRP) in complex with an antibody Fab fragment. <i>BMC Structural Biology</i> , 2013 , 13, 13	2.7	8
82	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
81	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
80	Structure determination from a single high-pressure-frozen virus crystal. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 308-12		8
79	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
78	Some lessons from the systematic production and structural analysis of soluble (alpha)(beta) T-cell receptors. <i>Journal of Immunological Methods</i> , 2009 , 350, 14-21	2.5	8
77	Selenomethionine labeling of large biological macromolecular complexes: probing the structure of marine bacterial virus PM2. <i>Journal of Structural Biology</i> , 2008 , 161, 204-10	3.4	8

76	Hepatitis A Virus Capsid Structure. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019 , 9,	5.4	7
75	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
74	Crystallization and X-ray diffraction study of recombinant platelet-derived endothelial cell growth factor. <i>Journal of Molecular Biology</i> , 1993 , 234, 879-80	6.5	7
73	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
72	Recovery of data from perfectly twinned virus crystals revisited. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 817-22	5.5	6
71	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
70	Humidity control as a strategy for lattice optimization applied to crystals of HLA-A*1101 complexed with variant peptides from dengue virus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 386-92		6
69	SPINE: Structural Proteomics IN Europe – the best of both worlds. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, ii-i		6
68	Hybrid vigor: hybrid methods in viral structure determination. <i>Advances in Protein Chemistry</i> , 2003 , 64, 37-91		6
67	Differential occupational risks to healthcare workers from SARS-CoV-2: A prospective observational study		6
66	Glutathione facilitates enterovirus assembly by binding at a druggable pocket. <i>Communications Biology</i> , 2020 , 3, 9	6.7	6
65	Structural and functional analysis of protective antibodies targeting the threefold plateau of enterovirus 71. <i>Nature Communications</i> , 2020 , 11, 5253	17.4	6
64	Structure determination of human semaphorin 4D as an example of the use of MAD in non-optimal cases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 108-15		5
63	Going soft and SAD with manganese. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 108-11		5
62	Preliminary crystallographic analysis of coxsackievirus A9. <i>Journal of Molecular Biology</i> , 1993 , 230, 667-96.5		5
61	Crystallization and preliminary X-ray investigation of recombinant simian immunodeficiency virus matrix protein. <i>Journal of Molecular Biology</i> , 1994 , 241, 744-6	6.5	5
60	Crystallization of human tumour necrosis factor. <i>Journal of Crystal Growth</i> , 1990 , 100, 168-170	1.6	5
59	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

58	: an iOS app for ISPyB. <i>Journal of Applied Crystallography</i> , 2014 , 47, 1781-1783	3.8	5
57	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
56	Large unit cells and cellular mechanics. <i>Nature Structural Biology</i> , 1998 , 5 Suppl, 630-4		4
55	Overcoming the false-minima problem in direct methods: structure determination of the packaging enzyme P4 from bacteriophage phi13. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 1238-44		4
54	HEPT: From an investigation of lithiation of nucleosides towards a rational design of non-nucleoside reverse transcriptase inhibitors of HIV-1. <i>Advances in Antiviral Drug Design</i> , 1999 , 93-144		4
53	Crystallization and preliminary X-ray analysis of human rhinovirus serotype 2 (HRV2). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1459-61		4
52	Viral envelope glycoproteins swing into action. <i>Structure</i> , 1995 , 3, 645-8	5.2	4
51	Some problems in relation to the structures of insulin derivatives. <i>Biochemical Society Transactions</i> , 1983 , 11, 419-425	5.1	4
50	Structure of cat muscle pyruvate kinase at 0.26 nm resolution. <i>Biochemical Society Transactions</i> , 1977 , 5, 654-7	5.1	4
49	Imperfection and radiation damage in protein crystals studied with coherent radiation. <i>Journal of Synchrotron Radiation</i> , 2016 , 23, 228-37	2.4	4
48	The slip-and-slide algorithm: a refinement protocol for detector geometry. <i>Journal of Synchrotron Radiation</i> , 2017 , 24, 1152-1162	2.4	4
47	Scanning electron microscopy as a method for sample visualization in protein X-ray crystallography. <i>IUCrJ</i> , 2020 , 7, 500-508	4.7	4
46	Author response: Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study 2020 ,		4
45	Neutralization of SARS-CoV-2 by destruction of the prefusion Spike		4
44	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
43	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
42	Generation and characterisation of recombinant FMDV antibodies: Applications for advancing diagnostic and laboratory assays. <i>PLoS ONE</i> , 2018 , 13, e0201853	3.7	3
41	Recording information on protein complexes in an information management system. <i>Journal of Structural Biology</i> , 2011 , 175, 224-9	3.4	3

40	An idea whose time has come. <i>Genome Biology</i> , 2007 , 8, 408	18.3	3
39	The SARS-CoV-2 Spike harbours a lipid binding pocket which modulates stability of the prefusion trimer		3
38	Site-specific steric control of SARS-CoV-2 spike glycosylation 2021 ,		3
37	Further antibody escape by Omicron BA.4 and BA.5 from vaccine and BA.1 serum		3
36	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
35	Crystallization and preliminary X-ray analysis of mouse RANK and its complex with RANKL. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 597-600		2
34	"4D Biology for health and disease" workshop report. <i>New Biotechnology</i> , 2011 , 28, 291-3	6.4	2
33	Order and disorder in crystals of hexameric NTPases from dsRNA bacteriophages. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 2337-41		2
32	Virus crystallography. <i>Methods in Molecular Biology</i> , 1996 , 56, 319-63	1.4	2
31	Structure of Foot-and-Mouth Disease Virus 1990 , 161-171		2
30	Phosphate-recognition sites in catalysis and control of glycogen phosphorylase b. <i>Biochemical Society Transactions</i> , 1987 , 15, 1001-5	5.1	2
29	European Structural Proteomics: A Perspective 2008 , 463-504		2
28	Structural basis for the neutralization of SARS-CoV-2 by an antibody from a convalescent patient		2
27	Correlative cryo-structured illumination fluorescence microscopy and soft X-ray tomography elucidates reovirus intracellular release pathway		2
26	Combined approaches to study virus structures. <i>Sub-Cellular Biochemistry</i> , 2013 , 68, 203-46	5.5	2
25	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
24	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
23	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

22	Louise N. Johnson 1940-2012. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1216-7	17.6	1
21	Crystallization and preliminary diffraction studies of the extracellular region of human p58 killer cell inhibitory receptor (KIR2). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 433-5		1
20	Crystals of the neurotrophins. <i>Protein Science</i> , 1996 , 5, 973-7	6.3	1
19	Universal detection of foot and mouth disease virus based on the conserved VP0 protein. <i>Wellcome Open Research</i> , 3, 88	4.8	1
18	Bacteriophage PRD1 as a nanoscaffold for drug loading. <i>Nanoscale</i> , 2021 ,	7.7	1
17	Structures and therapeutic potential of anti-RBD human monoclonal antibodies against SARS-CoV-2.. <i>Theranostics</i> , 2022 , 12, 1-17	12.1	1
16	CryoSIM: super resolution 3D structured illumination cryogenic fluorescence microscopy for correlated ultra-structural imaging		1
15	Assembly intermediates of orthoreovirus captured in the cell		1
14	The crystal structure and dimerization of a co-stimulator B7-1. <i>Seibutsu Butsuri</i> , 2000 , 40, S30	0	
13	Bluetongue virus: the role of synchrotron radiation. <i>Journal of Synchrotron Radiation</i> , 1999 , 6, 865-874	2.4	
12	Looking-glass land. <i>Nature</i> , 1989 , 338, 196-196	50.4	
11	Structural studies on the leukocyte co-stimulatory molecule, B7-1 2001 , 63-72		
10	Molecular recognition by Ig-like receptors, KIRs and FcRs 2001 , 45-54		
9	Virion Structure 57-71		
8	Ptychographic Single Particle Analysis for Biological Science. <i>Microscopy and Microanalysis</i> , 2021 , 27, 190-192	0.5	
7	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		
6	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		
5	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		

- 4 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
- 3 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
- 2 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
- 1 Purification of African Swine Fever Virus.. *Methods in Molecular Biology*, **2022**, 2503, 179-186 1.4