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**MotionCor2: anisotropic correction of beam-induced motion for improved cryo-electron microscopy**

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1846	Second Messenger cA Formation within the Composite Csm1 Palm Pocket of Type III-A CRISPR-Cas Csm Complex and Its Release Path. <b>2019</b> , 75, 933-943.e6	23
1845	Conformation space of a heterodimeric ABC exporter under turnover conditions. <b>2019</b> , 571, 580-583	94
1844	Structural visualization of key steps in nucleosome reorganization by human FACT. <b>2019</b> , 9, 10183	24
1843	Molecular basis of tRNA recognition by the Elongator complex. <b>2019</b> , 5, eaaw2326	21
1842	Content-aware image restoration for electron microscopy. <b>2019</b> , 152, 277-289	21



1841	Unique Structural Features of the Mitochondrial AAA+ Protease AFG3L2 Reveal the Molecular Basis for Activity in Health and Disease. <b>2019</b> , 75, 1073-1085.e6	36
1840	Structural and Functional Insights into GluK3-kainate Receptor Desensitization and Recovery. <b>2019</b> , 9, 10254	13
1839	Structural basis for the adsorption of a single-stranded RNA bacteriophage. <b>2019</b> , 10, 3130	23
1838	Bypassing pan-enterovirus host factor PLA2G16. <b>2019</b> , 10, 3171	16
1837	Structure of S-layer protein Sap reveals a mechanism for therapeutic intervention in anthrax. <b>2019</b> , 4, 1805-1814	12
1836	Cryo-EM Studies of TMEM16F Calcium-Activated Ion Channel Suggest Features Important for Lipid Scrambling. <b>2019</b> , 28, 567-579.e4	35
1835	The Molecular Architecture of Native BBSome Obtained by an Integrated Structural Approach. <b>2019</b> , 27, 1384-1394.e4	33
1834	Structural basis for transcription antitermination at bacterial intrinsic terminator. <b>2019</b> , 10, 3048	9
1833	Target preference of Type III-A CRISPR-Cas complexes at the transcription bubble. <b>2019</b> , 10, 3001	22
1832	Cryo EM structure of the rabies virus ribonucleoprotein complex. <b>2019</b> , 9, 9639	13
1831	Cryo-EM structures reveal coordinated domain motions that govern DNA cleavage by Cas9. <b>2019</b> , 26, 679-685	45
1830	Structure of the eukaryotic protein O-mannosyltransferase Pmt1-Pmt2 complex. <b>2019</b> , 26, 704-711	20
1829	Differences in the Binding Affinity of an HIV-1 V2 Apex-Specific Antibody for the SIV Envelope Glycoprotein Uncouple Antibody-Dependent Cellular Cytotoxicity from Neutralization. <b>2019</b> , 10,	9
1828	Structures of the Rhodopsin-Transducin Complex: Insights into G-Protein Activation. <b>2019</b> , 75, 781-790.e3	41
1827	A polymorphic helix of a Salmonella needle protein relays signals defining distinct steps in type III secretion. <b>2019</b> , 17, e3000351	14
1826	The cryo-electron microscopy supramolecular structure of the bacterial stressosome unveils its mechanism of activation. <b>2019</b> , 10, 3005	14
1825	Structure and assembly of the mitochondrial membrane remodelling GTPase Mgm1. <b>2019</b> , 571, 429-433	50
1824	Structure of the Mechanosensitive Channel MscS Embedded in the Membrane Bilayer. <b>2019</b> , 431, 3081-3090	27

1823	Molecular mechanism of setron-mediated inhibition of full-length 5-HT receptor. <b>2019</b> , 10, 3225	27
1822	Evolutionary compaction and adaptation visualized by the structure of the dormant microsporidian ribosome. <b>2019</b> , 4, 1798-1804	24
1821	Radiation Brightening from Virus-like Particles. <b>2019</b> , 13, 11401-11408	3
1820	Structural basis for the multitasking nature of the potato virus Y coat protein. <b>2019</b> , 5, eaaw3808	27
1819	Cryo-electron microscopy structures of ArnA, a key enzyme for polymyxin resistance, revealed unexpected oligomerizations and domain movements. <b>2019</b> , 208, 43-50	4
1818	Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. <b>2019</b> , 178, 567-584.e19	64
1817	Resting-State Structure and Gating Mechanism of a Voltage-Gated Sodium Channel. <b>2019</b> , 178, 993-1003.e12	75
1816	Structure of the Human Core Centromeric Nucleosome Complex. <b>2019</b> , 29, 2625-2639.e5	35
1815	Cryo-EM Structures of a Group II Intron Reverse Splicing into DNA. <b>2019</b> , 178, 612-623.e12	20
1814	Structure-based mechanism for activation of the AAA+ GTPase McrB by the endonuclease McrC. <b>2019</b> , 10, 3058	7
1813	Bile Salts Alter the Mouse Norovirus Capsid Conformation: Possible Implications for Cell Attachment and Immune Evasion. <b>2019</b> , 93,	27
1812	Cryo-EM and directed evolution reveal how nitrilase specificity is influenced by its quaternary structure. <b>2019</b> , 2, 260	8
1811	Cryo-EM structure of TRPC5 at 2.8-Å resolution reveals unique and conserved structural elements essential for channel function. <b>2019</b> , 5, eaaw7935	42
1810	Structure of the Cag type IV secretion system. <b>2019</b> , 8,	38
1809	Early Scanning of Nascent Polypeptides inside the Ribosomal Tunnel by NAC. <b>2019</b> , 75, 996-1006.e8	25
1808	A one-gate elevator mechanism for the human neutral amino acid transporter ASCT2. <b>2019</b> , 10, 3427	51
1807	Structure and mechanism of the cation-chloride cotransporter NKCC1. <b>2019</b> , 572, 488-492	49
1806	Microfluidic protein isolation and sample preparation for high-resolution cryo-EM. <b>2019</b> , 116, 15007-15012	28

1805	Structure of the Cdc48 segregase in the act of unfolding an authentic substrate. <b>2019</b> , 365, 502-505	74
1804	Substrate processing by the Cdc48 ATPase complex is initiated by ubiquitin unfolding. <b>2019</b> , 365,	110
1803	Structural and functional analysis of the role of the chaperonin CCT in mTOR complex assembly. <b>2019</b> , 10, 2865	22
1802	Structure of the substrate-engaged SecA-SecY protein translocation machine. <b>2019</b> , 10, 2872	26
1801	VIPP1 rods engulf membranes containing phosphatidylinositol phosphates. <b>2019</b> , 9, 8725	19
1800	Structural basis of Q-dependent transcription antitermination. <b>2019</b> , 10, 2925	20
1799	Role of Era in assembly and homeostasis of the ribosomal small subunit. <b>2019</b> , 47, 8301-8317	20
1798	Structure and assembly of pilotin-dependent and -independent secretins of the type II secretion system. <b>2019</b> , 15, e1007731	14
1797	Toxic Activation of an AAA+ Protease by the Antibacterial Drug Cyclomarin A. <b>2019</b> , 26, 1169-1179.e4	14
1796	Modulation of cardiac ryanodine receptor 2 by calmodulin. <b>2019</b> , 572, 347-351	60
1795	Contamination and health risk assessment of heavy metals in soil surrounding an electroplating factory in Jiaxing, China. <b>2019</b> , 310, 052026	2
1794	Cromwell's House of Lords: Politics, Parliaments and Constitutional Revolution, 1642-1660, by Jonathan Fitzgibbons. <b>2019</b> ,	
1793	Structure of a CSMN-type PSII-LHCII supercomplex from the green alga. <b>2019</b> , 116, 21246-21255	50
1792	Multisystem Proteinopathy Mutations in VCP/p97 Increase NPLOC4-UFD1L Binding and Substrate Processing. <b>2019</b> , 27, 1820-1829.e4	20
1791	Cryo-EM Structure of Actin Filaments from Pollen. <b>2019</b> , 31, 2855-2867	12
1790	Structure and genome ejection mechanism of phage P68. <b>2019</b> , 5, eaaw7414	26
1789	Mechanism of Filamentation-Induced Allosteric Activation of the SgrAI Endonuclease. <b>2019</b> , 27, 1497-1507.e3	4
1788	Common architecture of Tc toxins from human and insect pathogenic bacteria. <b>2019</b> , 5, eaax6497	10

1787	Structural and functional insights into the tetrameric photosystem I from heterocyst-forming cyanobacteria. <b>2019</b> , 5, 1087-1097	31
1786	Structural basis of the activation of type 1 insulin-like growth factor receptor. <b>2019</b> , 10, 4567	56
1785	On the Mechanism of Bilayer Separation by Extrusion, or Why Your LUVs Are Not Really Unilamellar. <b>2019</b> , 117, 1381-1386	37
1784	Functionally critical residues in the aminoglycoside resistance-associated methyltransferase RmtC play distinct roles in 30S substrate recognition. <b>2019</b> , 294, 17642-17653	22
1783	Cas9 Allosteric Inhibition by the Anti-CRISPR Protein AcrIIA6. <b>2019</b> , 76, 922-937.e7	24
1782	Alpha-synuclein stepwise aggregation reveals features of an early onset mutation in Parkinson's disease. <b>2019</b> , 2, 374	41
1781	Architecture of human Rag GTPase heterodimers and their complex with mTORC1. <b>2019</b> , 366, 203-210	46
1780	Structural basis for the docking of mTORC1 on the lysosomal surface. <b>2019</b> , 366, 468-475	70
1779	Combining Transient Expression and Cryo-EM to Obtain High-Resolution Structures of Luteovirid Particles. <b>2019</b> , 27, 1761-1770.e3	15
1778	Defects in the Assembly of Ribosomes Selected for $\beta$ Amino Acid Incorporation. <b>2019</b> , 58, 4494-4504	7
1777	Cryo-EM structure of the bacterial Ton motor subcomplex ExbB-ExbD provides information on structure and stoichiometry. <b>2019</b> , 2, 358	36
1776	Stanford-SLAC Cryo-EM Center (S2C2). <b>2019</b> , 25, 2658-2659	
1775	Structure of the Decorated Ciliary Doublet Microtubule. <b>2019</b> , 179, 909-922.e12	80
1774	Structural consequences of the interaction of RbgA with a 50S ribosomal subunit assembly intermediate. <b>2019</b> , 47, 10414-10425	20
1773	Structural mechanism of the active bicarbonate transporter from cyanobacteria. <b>2019</b> , 5, 1184-1193	30
1772	Atomic Structure of the Francisella T6SS Central Spike Reveals a Unique $\beta$ Helical Lid and a Putative Cargo. <b>2019</b> , 27, 1811-1819.e6	2
1771	Conservative transcription in three steps visualized in a double-stranded RNA virus. <b>2019</b> , 26, 1023-1034	16
1770	Cryo-EM structure of the complete E. coli DNA gyrase nucleoprotein complex. <b>2019</b> , 10, 4935	40

1769	Cryo-EM structure of a transthyretin-derived amyloid fibril from a patient with hereditary ATTR amyloidosis. <b>2019</b> , 10, 5008	71
1768	Structural mechanism of a Rag GTPase activation checkpoint by the lysosomal folliculin complex. <b>2019</b> , 366, 971-977	53
1767	A generalized HIV vaccine design strategy for priming of broadly neutralizing antibody responses. <b>2019</b> , 366,	89
1766	Structure of the RSC complex bound to the nucleosome. <b>2019</b> , 366, 838-843	49
1765	Cryo-EM Structure of the Human FLCN-FNIP2-Rag-Ragulator Complex. <b>2019</b> , 179, 1319-1329.e8	51
1764	Structure of a Tc holotoxin pore provides insights into the translocation mechanism. <b>2019</b> , 116, 23083-23090	16
1763	LDAF1 and Seipin Form a Lipid Droplet Assembly Complex. <b>2019</b> , 51, 551-563.e7	79
1762	Structural Basis of H2B Ubiquitination-Dependent H3K4 Methylation by COMPASS. <b>2019</b> , 76, 712-723.e4	40
1761	Homologous bd oxidases share the same architecture but differ in mechanism. <b>2019</b> , 10, 5138	36
1760	Structures of a RAG-like transposase during cut-and-paste transposition. <b>2019</b> , 575, 540-544	13
1759	Development of "Plug and Play" Fiducial Marks for Structural Studies of GPCR Signaling Complexes by Single-Particle Cryo-EM. <b>2019</b> , 27, 1862-1874.e7	12
1758	Partially inserted nascent chain unzips the lateral gate of the Sec translocon. <b>2019</b> , 20, e48191	22
1757	Cryo-EM structure and polymorphism of A $\beta$ amyloid fibrils purified from Alzheimer's brain tissue. <b>2019</b> , 10, 4760	217
1756	Structure of a cyanobacterial photosystem I tetramer revealed by cryo-electron microscopy. <b>2019</b> , 10, 4929	29
1755	HOTSPUR: A Real-time Interactive Preprocessing System for Cryo-EM Data. <b>2019</b> , 25, 1212-1213	4
1754	Development of an Intact Mammalian System for High-resolution Imaging by Cryo-Electron Tomography. <b>2019</b> , 25, 1306-1307	
1753	Structural Organization of the Guinea Pig A-Crystallin and A66B0 Peptide Complex. <b>2019</b> , 25, 1318-1319	
1752	Strategies for Data Flow and Storage for High Throughput, High Resolution Cryo-EM Data Collection. <b>2019</b> , 25, 1394-1395	

1751	Structure of a P element transposase-DNA complex reveals unusual DNA structures and GTP-DNA contacts. <b>2019</b> , 26, 1013-1022	13
1750	Cryo-EM structures of the human cation-chloride cotransporter KCC1. <b>2019</b> , 366, 505-508	41
1749	Cyclin A2 degradation during the spindle assembly checkpoint requires multiple binding modes to the APC/C. <b>2019</b> , 10, 3863	18
1748	Structure and mechanism of mitochondrial proton-translocating transhydrogenase. <b>2019</b> , 573, 291-295	32
1747	Atomic structure of the Epstein-Barr virus portal. <b>2019</b> , 10, 3891	20
1746	Visualizing structural transitions of ligand-dependent gating of the TRPM2 channel. <b>2019</b> , 10, 3740	17
1745	Structure of the dynein-2 complex and its assembly with intraflagellar transport trains. <b>2019</b> , 26, 823-829	47
1744	Force-induced conformational changes in PIEZO1. <b>2019</b> , 573, 230-234	106
1743	Structure and mechanogating of the mammalian tactile channel PIEZO2. <b>2019</b> , 573, 225-229	115
1742	The structural basis of lipid scrambling and inactivation in the endoplasmic reticulum scramblase TMEM16K. <b>2019</b> , 10, 3956	55
1741	A unified mechanism for intron and exon definition and back-splicing. <b>2019</b> , 573, 375-380	57
1740	Structural basis of nucleosome recognition and modification by MLL methyltransferases. <b>2019</b> , 573, 445-449	68
1739	Structures of influenza A virus RNA polymerase offer insight into viral genome replication. <b>2019</b> , 573, 287-290	73
1738	Molecular Basis for ATP-Hydrolysis-Driven DNA Translocation by the CMG Helicase of the Eukaryotic Replisome. <b>2019</b> , 28, 2673-2688.e8	32
1737	Cryo-EM reveals active site coordination within a multienzyme pre-rRNA processing complex. <b>2019</b> , 26, 830-839	8
1736	Structural insights into TRPM8 inhibition and desensitization. <b>2019</b> , 365, 1434-1440	66
1735	Agonist Selectivity and Ion Permeation in the $\alpha 5$ Ganglionic Nicotinic Receptor. <b>2019</b> , 104, 501-511.e6	63
1734	Structural Dynamics of Nonenveloped Virus Disassembly Intermediates. <b>2019</b> , 93,	6

1733	Structure of the Centromere Binding Factor 3 Complex from <i>Kluyveromyces lactis</i> . <b>2019</b> , 431, 4444-4454	1
1732	CryoEM structures of Arabidopsis DDR complexes involved in RNA-directed DNA methylation. <b>2019</b> , 10, 3916	12
1731	Unravelling Atomic Structure and Degradation Mechanisms of Organic-Inorganic Halide Perovskites by Cryo-EM. <b>2019</b> , 3, 2854-2866	69
1730	Structures of Respiratory Supercomplex I+III Reveal Functional and Conformational Crosstalk. <b>2019</b> , 75, 1131-1146.e6	89
1729	Mechanism of DNA End Sensing and Processing by the Mre11-Rad50 Complex. <b>2019</b> , 76, 382-394.e6	51
1728	The structure of bactofilin filaments reveals their mode of membrane binding and lack of polarity. <b>2019</b> , 4, 2357-2368	11
1727	Molecular basis for metabolite channeling in a ring opening enzyme of the phenylacetate degradation pathway. <b>2019</b> , 10, 4127	9
1726	Structural basis of assembly of the human T cell receptor-CD3 complex. <b>2019</b> , 573, 546-552	108
1725	Mitoribosomal small subunit biogenesis in trypanosomes involves an extensive assembly machinery. <b>2019</b> , 365, 1144-1149	33
1724	Heparin-induced tau filaments are polymorphic and differ from those in Alzheimer's and Pick's diseases. <b>2019</b> , 8,	173
1723	The cryo-EM structure of the acid activatable pore-forming immune effector Macrophage-expressed gene 1. <b>2019</b> , 10, 4288	32
1722	Structural Insight into Eukaryotic Sterol Transport through Niemann-Pick Type C Proteins. <b>2019</b> , 179, 485-497.e18	61
1721	Filling Adeno-Associated Virus Capsids: Estimating Success by Cryo-Electron Microscopy. <b>2019</b> , 30, 1449-1460	9
1720	Cryo-EM structure of a dimeric B-Raf:14-3-3 complex reveals asymmetry in the active sites of B-Raf kinases. <b>2019</b> , 366, 109-115	63
1719	The Architecture of Talin1 Reveals an Autoinhibition Mechanism. <b>2019</b> , 179, 120-131.e13	51
1718	Autoinhibition and activation mechanisms of the eukaryotic lipid flippase Drs2p-Cdc50p. <b>2019</b> , 10, 4142	28
1717	Cryo-EM structures of lipopolysaccharide transporter LptBFGC in lipopolysaccharide or AMP-PNP-bound states reveal its transport mechanism. <b>2019</b> , 10, 4175	26
1716	eIF5B gates the transition from translation initiation to elongation. <b>2019</b> , 573, 605-608	25

1715	Tubulin lattice in cilia is in a stressed form regulated by microtubule inner proteins. <b>2019</b> , 116, 19930-19938	29
1714	The molecular mechanism of cotranslational membrane protein recognition and targeting by SecA. <b>2019</b> , 26, 919-929	14
1713	Mind the gap: Micro-expansion joints drastically decrease the bending of FIB-milled cryo-lamellae. <b>2019</b> , 208, 107389	31
1712	Structural insights into the mechanism of human soluble guanylate cyclase. <b>2019</b> , 574, 206-210	54
1711	Structure of the inner kinetochore CCAN complex assembled onto a centromeric nucleosome. <b>2019</b> , 574, 278-282	63
1710	Cryo-EM structure and dynamics of eukaryotic DNA polymerase $\beta$ holoenzyme. <b>2019</b> , 26, 955-962	28
1709	Purified F-ATP synthase forms a Ca-dependent high-conductance channel matching the mitochondrial permeability transition pore. <b>2019</b> , 10, 4341	85
1708	Structural Definition of a Neutralization-Sensitive Epitope on the MERS-CoV S1-NTD. <b>2019</b> , 28, 3395-3405.e6	53
1707	High-quality, high-throughput cryo-electron microscopy data collection via beam tilt and astigmatism-free beam-image shift. <b>2019</b> , 208, 107396	32
1706	A robust approach to ab initio cryo-electron microscopy initial volume determination. <b>2019</b> , 208, 107397	6
1705	Structural characterization of the PCV2d virus-like particle at 3.3 Å resolution reveals differences to PCV2a and PCV2b capsids, a tetranucleotide, and an N-terminus near the icosahedral 3-fold axes. <b>2019</b> , 537, 186-197	8
1704	Full-Length P2X Structures Reveal How Palmitoylation Prevents Channel Desensitization. <b>2019</b> , 179, 659-670.e13	69
1703	Aldehyde-alcohol dehydrogenase forms a high-order spiroosome architecture critical for its activity. <b>2019</b> , 10, 4527	17
1702	Structural pathway for allosteric activation of the autophagic PI 3-kinase complex I. <b>2019</b> , 116, 21508-21513	20
1701	Enhancing and shaping the immunogenicity of native-like HIV-1 envelope trimers with a two-component protein nanoparticle. <b>2019</b> , 10, 4272	80
1700	The elusive actin cytoskeleton of a green alga expressing both conventional and divergent actins. <b>2019</b> , 30, 2827-2837	9
1699	Structure of Flagellar Hook Reveals Intermolecular Domain Interactions for the Universal Joint Function. <b>2019</b> , 9,	8
1698	Structural basis of sterol recognition by human hedgehog receptor PTCH1. <b>2019</b> , 5, eaaw6490	35



1697	An Assembly Intermediate Structure of Rice Dwarf Virus Reveals a Hierarchical Outer Capsid Shell Assembly Mechanism. <b>2019</b> , 27, 439-448.e3	2
1696	In Situ Imaging and Structure Determination of Bacterial Toxin Delivery Systems Using Electron Cryotomography. <b>2019</b> , 1921, 249-265	2
1695	Consideration of sample motion in cryo-tomography based on alignment residual interpolation. <b>2019</b> , 205, 1-6	17
1694	Capabilities of the Falcon III detector for single-particle structure determination. <b>2019</b> , 203, 145-154	15
1693	Structure of the post-translational protein translocation machinery of the ER membrane. <b>2019</b> , 566, 136-139	67
1692	Unexpected Receptor Functional Mimicry Elucidates Activation of Coronavirus Fusion. <b>2019</b> , 176, 1026-1039.e14	6
1691	A human postcatalytic spliceosome structure reveals essential roles of metazoan factors for exon ligation. <b>2019</b> , 363, 710-714	53
1690	Rubisco condensate formation by CcmM in <i>E</i> carboxysome biogenesis. <b>2019</b> , 566, 131-135	102
1689	Structural insights into the activation of metabotropic glutamate receptors. <b>2019</b> , 566, 79-84	148
1688	Structures and operating principles of the replisome. <b>2019</b> , 363,	73
1687	Nanoscale mosaicity revealed in peptide microcrystals by scanning electron nanodiffraction. <b>2019</b> , 2, 26	32
1686	Cryo-EM structure of the essential ribosome assembly AAA-ATPase Rix7. <b>2019</b> , 10, 513	16
1685	Functional role of PGAM5 multimeric assemblies and their polymerization into filaments. <b>2019</b> , 10, 531	16
1684	Potent anti-influenza H7 human monoclonal antibody induces separation of hemagglutinin receptor-binding head domains. <b>2019</b> , 17, e3000139	26
1683	Atomic resolution cryo-EM structure of a native-like CENP-A nucleosome aided by an antibody fragment. <b>2019</b> , 10, 2301	36
1682	A Tunable Microfluidic Device Enables Cargo Encapsulation by Cell- or Organelle-Sized Lipid Vesicles Comprising Asymmetric Lipid Bilayers. <b>2019</b> , 3, 1900010	9
1681	The structure of the stress-induced photosystem I-lsiA antenna supercomplex. <b>2019</b> , 26, 443-449	32
1680	Structural basis for the inhibition of translation through eIF2 $\alpha$ phosphorylation. <b>2019</b> , 10, 2640	28

1679	The structural basis for release-factor activation during translation termination revealed by time-resolved cryogenic electron microscopy. <b>2019</b> , 10, 2579	25
1678	Convergent allostery in ribonucleotide reductase. <b>2019</b> , 10, 2653	20
1677	Structural insight into RNA synthesis by influenza D polymerase. <b>2019</b> , 4, 1750-1759	35
1676	A small-molecule inhibitor of C5 complement protein. <b>2019</b> , 15, 666-668	12
1675	Two-Step Activation Mechanism of the ClpB Disaggregase for Sequential Substrate Threading by the Main ATPase Motor. <b>2019</b> , 27, 3433-3446.e4	34
1674	Structural and biochemical analyses of the nuclear pore complex component ELYS identify residues responsible for nucleosome binding. <b>2019</b> , 2, 163	6
1673	Structural identification of a hotspot on CFTR for potentiation. <b>2019</b> , 364, 1184-1188	96
1672	Rotary substates of mitochondrial ATP synthase reveal the basis of flexible F-F coupling. <b>2019</b> , 364,	87
1671	Native top-down mass spectrometry provides insights into the copper centers of membrane-bound methane monooxygenase. <b>2019</b> , 10, 2675	45
1670	Plant-Made Nervous Necrosis Virus-Like Particles Protect Fish Against Disease. <b>2019</b> , 10, 880	19
1669	In situ Structure of Rotavirus VP1 RNA-Dependent RNA Polymerase. <b>2019</b> , 431, 3124-3138	28
1668	Conformational proofreading of distant 40S ribosomal subunit maturation events by a long-range communication mechanism. <b>2019</b> , 10, 2754	20
1667	Conformational transitions of a neurotensin receptor '1-G' complex. <b>2019</b> , 572, 80-85	110
1666	Structure and autoregulation of a P4-ATPase lipid flippase. <b>2019</b> , 571, 366-370	69
1665	The Structure of an Injectisome Export Gate Demonstrates Conservation of Architecture in the Core Export Gate between Flagellar and Virulence Type III Secretion Systems. <b>2019</b> , 10,	30
1664	Late steps in bacterial translation initiation visualized using time-resolved cryo-EM. <b>2019</b> , 570, 400-404	48
1663	Structure of the green algal photosystem I supercomplex with a decameric light-harvesting complex I. <b>2019</b> , 5, 626-636	80
1662	Inhibition of tetrameric Patched1 by Sonic Hedgehog through an asymmetric paradigm. <b>2019</b> , 10, 2320	49

1661	Metabolic control of BRISC-SHMT2 assembly regulates immune signalling. <b>2019</b> , 570, 194-199	33
1660	Immunization expands B cells specific to HIV-1 V3 glycan in mice and macaques. <b>2019</b> , 570, 468-473	95
1659	DNA damage detection in nucleosomes involves DNA register shifting. <b>2019</b> , 571, 79-84	41
1658	Molecular Basis for Ligand Modulation of a Mammalian Voltage-Gated Ca Channel. <b>2019</b> , 177, 1495-1506.e12	84
1657	Alanine Tails Signal Proteolysis in Bacterial Ribosome-Associated Quality Control. <b>2019</b> , 178, 76-90.e22	39
1656	Structural Basis for the Inhibition of CRISPR-Cas12a by Anti-CRISPR Proteins. <b>2019</b> , 25, 815-826.e4	35
1655	Structure of the SARS-CoV nsp12 polymerase bound to nsp7 and nsp8 co-factors. <b>2019</b> , 10, 2342	466
1654	Effect of processing and end groups on the crystal structure of polypeptoids studied by cryogenic electron microscopy at atomic length scales. <b>2019</b> , 15, 4723-4736	10
1653	Single particle cryo-EM reconstruction of 52 kDa streptavidin at 3.2 Angstrom resolution. <b>2019</b> , 10, 2386	71
1652	Structural snapshots of actively transcribing influenza polymerase. <b>2019</b> , 26, 460-470	41
1651	Structures of the otopetrin proton channels Otop1 and Otop3. <b>2019</b> , 26, 518-525	28
1650	Cryo-EM structure of the human L-type amino acid transporter 1 in complex with glycoprotein CD98hc. <b>2019</b> , 26, 510-517	67
1649	Coupling of ATPase activity, microtubule binding, and mechanics in the dynein motor domain. <b>2019</b> , 38, e101414	8
1648	Hands on Methods for High Resolution Cryo-Electron Microscopy Structures of Heterogeneous Macromolecular Complexes. <b>2019</b> , 6, 33	15
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1646	Structural basis for substrate gripping and translocation by the ClpB AAA+ disaggregase. <b>2019</b> , 10, 2393	50
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1644	A novel druggable interprotomer pocket in the capsid of rhino- and enteroviruses. <b>2019</b> , 17, e3000281	25

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1642	Structural mechanism for NEK7-licensed activation of NLRP3 inflammasome. <b>2019</b> , 570, 338-343	238
1641	Structure and function of Vms1 and Arb1 in RQC and mitochondrial proteome homeostasis. <b>2019</b> , 570, 538-542	35
1640	Cryo-EM structure of the mammalian ATP synthase tetramer bound with inhibitory protein IF1. <b>2019</b> , 364, 1068-1075	81
1639	3.1 $\beta$ Structure of yeast RNA polymerase II elongation complex stalled at a cyclobutane pyrimidine dimer lesion solved using streptavidin affinity grids. <b>2019</b> , 207, 270-278	12
1638	Cryo-electron microscopy structure of an archaeal ribonuclease P holoenzyme. <b>2019</b> , 10, 2617	19
1637	The pore structure of Clostridium perfringens epsilon toxin. <b>2019</b> , 10, 2641	25
1636	Extracellular Albumin and Endosomal Ions Prime Enterovirus Particles for Uncoating That Can Be Prevented by Fatty Acid Saturation. <b>2019</b> , 93,	16
1635	Reducing cryoEM file storage using lossy image formats. <b>2019</b> , 207, 49-55	2
1634	Coiled-Coil-Mediated Assembly of an Icosahedral Protein Cage with Extremely High Thermal and Chemical Stability. <b>2019</b> , 141, 9207-9216	34
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1626	Structures of the M1 and M2 muscarinic acetylcholine receptor/G-protein complexes. <b>2019</b> , 364, 552-557	130

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1624	Fusion of DARPin to Aldolase Enables Visualization of Small Protein by Cryo-EM. <b>2019</b> , 27, 1148-1155.e3	17
1623	The Chimpanzee SIV Envelope Trimer: Structure and Deployment as an HIV Vaccine Template. <b>2019</b> , 27, 2426-2441.e6	20
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1614	Kappa chain maturation helps drive rapid development of an infant HIV-1 broadly neutralizing antibody lineage. <b>2019</b> , 10, 2190	19
1613	Retrieving high-resolution information from disordered 2D crystals by single-particle cryo-EM. <b>2019</b> , 10, 1722	14
1612	A 3.8 Å resolution cryo-EM structure of a small protein bound to an imaging scaffold. <b>2019</b> , 10, 1864	39
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1598	Cryo-EM structures of vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution. <b>2019</b> , 116, 6800-6805	20
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1593	A folded conformation of MukBEF and cohesin. <b>2019</b> , 26, 227-236	75
1592	High-resolution structure determination of sub-100 kDa complexes using conventional cryo-EM. <b>2019</b> , 10, 1032	109
1591	Cryo-EM structures of STING reveal its mechanism of activation by cyclic GMP-AMP. <b>2019</b> , 567, 389-393	192
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1580	Structure of a green algal photosystem I in complex with a large number of light-harvesting complex I subunits. <b>2019</b> , 5, 263-272	61
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1578	Volta Phase Plate Cryo-EM Structure of the Human Heterodimeric Amino Acid Transporter 4F2hc-LAT2. <b>2019</b> , 20,	8
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1461	Cryo-EM structures and dynamics of substrate-engaged human 26S proteasome. <b>2019</b> , 565, 49-55	155
1460	A 2.8-Angstrom-Resolution Cryo-Electron Microscopy Structure of Human Parechovirus 3 in Complex with Fab from a Neutralizing Antibody. <b>2019</b> , 93,	11
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1251	The In Situ Structure of Parkinson's Disease-Linked LRRK2. <b>2020</b> , 182, 1508-1518.e16	57
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1244	Coupling of 5S RNP rotation with maturation of functional centers during large ribosomal subunit assembly. <b>2020</b> , 11, 3751	5
1243	Structures of capsid and capsid-associated tegument complex inside the Epstein-Barr virus. <b>2020</b> , 5, 1285-12986	
1242	Crystallographic and cryogenic electron microscopic structures and enzymatic characterization of sulfur oxygenase reductase from. <b>2020</b> , 4, 100030	2
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1237	A thermostable, closed SARS-CoV-2 spike protein trimer. <b>2020</b> , 27, 934-941	128
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1229	Direct label-free imaging of nanodomains in biomimetic and biological membranes by cryogenic electron microscopy. <b>2020</b> , 117, 19943-19952	35
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1226	High-Throughput Cryo-EM Enabled by User-Free Preprocessing Routines. <b>2020</b> , 28, 858-869.e3	16
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1221	Cryo-EM Reveals Unanchored M1-Ubiquitin Chain Binding at hRpn11 of the 26S Proteasome. <b>2020</b> , 28, 1206-1217.e4	9
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1214	Structure, lipid scrambling activity and role in autophagosome formation of ATG9A. <b>2020</b> , 27, 1194-1201	73
1213	Cryo-EM analysis of the SctV cytosolic domain from the enteropathogenic E. coli T3SS injectisome. <b>2020</b> , 212, 107660	8
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1211	CryoEM structure of the type IVa pilus secretin required for natural competence in <i>Vibrio cholerae</i> . <b>2020</b> , 11, 5080	8
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1208	Cryo-electron tomography of cardiac myofibrils reveals a 3D lattice spring within the Z-discs. <b>2020</b> , 3, 585	9
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1206	MZT Proteins Form Multi-Faceted Structural Modules in the $\beta$ Tubulin Ring Complex. <b>2020</b> , 31, 107791	18
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1204	Cryo-electron microscopy structure of the 70S ribosome from <i>Enterococcus faecalis</i> . <b>2020</b> , 10, 16301	5
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1202	Single particle cryo-EM of the complex between interphotoreceptor retinoid-binding protein and a monoclonal antibody. <b>2020</b> , 34, 13918-13934	3
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1197	Structure of the Capsid Size-Determining Scaffold of "Satellite" Bacteriophage P4. <b>2020</b> , 12,	6
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1195	Apple latent spherical virus structure with stable capsid frame supports quasi-stable protrusions expediting genome release. <b>2020</b> , 3, 488	5
1194	Structure of nucleosome-bound DNA methyltransferases DNMT3A and DNMT3B. <b>2020</b> , 586, 151-155	26

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1192	Cryo-EM structure of the varicella-zoster virus A-capsid. <b>2020</b> , 11, 4795	5
1191	Structural characterization of a neutralizing mAb H16.001, a potent candidate for a common potency assay for various HPV16 VLPs. <b>2020</b> , 5, 89	1
1190	The coupling mechanism of mammalian respiratory complex I. <b>2020</b> , 370,	58
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1188	Dual Functions of a Rubisco Activase in Metabolic Repair and Recruitment to Carboxysomes. <b>2020</b> , 183, 457-473.e20	9
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1185	Lipid Nanodiscs via Ordered Copolymers. <b>2020</b> , 6, 2782-2795	15
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1179	Free fatty acid binding pocket in the locked structure of SARS-CoV-2 spike protein. <b>2020</b> , 370, 725-730	182
1178	Structural mechanism of two gain-of-function cardiac and skeletal RyR mutations at an equivalent site by cryo-EM. <b>2020</b> , 6, eabb2964	16
1177	Cryo-EM structure of the ribosome functional complex of the human pathogen Staphylococcus aureus at 3.2 Å resolution. <b>2020</b> , 594, 3551-3567	5
1176	PSGL-1 inhibits HIV-1 infection by restricting actin dynamics and sequestering HIV envelope proteins. <b>2020</b> , 6, 53	7

1175	Cryo-EM structure of trimeric Mycobacterium smegmatis succinate dehydrogenase with a membrane-anchor SdhF. <b>2020</b> , 11, 4245	6
1174	Structure of the C9orf72 ARF GAP complex that is haploinsufficient in ALS and FTD. <b>2020</b> , 585, 251-255	21
1173	Cryo-EM structure of the fully-loaded asymmetric anthrax lethal toxin in its heptameric pre-pore state. <b>2020</b> , 16, e1008530	5
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1168	Structures of mouse DUOX1-DUOX1 provide mechanistic insights into enzyme activation and regulation. <b>2020</b> , 27, 1086-1093	6
1167	Cryo-EM structure of the entire mammalian F-type ATP synthase. <b>2020</b> , 27, 1077-1085	60
1166	Cryo-EM structure of coronavirus-HKU1 haemagglutinin esterase reveals architectural changes arising from prolonged circulation in humans. <b>2020</b> , 11, 4646	16
1165	Bridging of DNA breaks activates PARP2-HPF1 to modify chromatin. <b>2020</b> , 585, 609-613	43
1164	Cryo-EM structure of 90 small ribosomal subunit precursors in transition states. <b>2020</b> , 369, 1477-1481	17
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1162	Near-atomic cryo-electron microscopy structures of varicella-zoster virus capsids. <b>2020</b> , 5, 1542-1552	4
1161	Molecular mechanism for rotational switching of the bacterial flagellar motor. <b>2020</b> , 27, 1041-1047	34
1160	Mechanisms for target recognition and cleavage by the Cas12i RNA-guided endonuclease. <b>2020</b> , 27, 1069-10768	
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1157	SARS-CoV-2 spike produced in insect cells elicits high neutralization titres in non-human primates. <b>2020</b> , 9, 2076-2090	33
1156	Cryo-EM structure of human Cx31.3/GJC3 connexin hemichannel. <b>2020</b> , 6, eaba4996	19
1155	Structural basis for the inhibition of cGAS by nucleosomes. <b>2020</b> , 370, 455-458	80
1154	Cryo-EM structure of an activated VIP1 receptor-G protein complex revealed by a NanoBiT tethering strategy. <b>2020</b> , 11, 4121	48
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1151	Mechanism of ribosome rescue by alternative ribosome-rescue factor B. <b>2020</b> , 11, 4106	14
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1148	Interaction of the pioneer transcription factor GATA3 with nucleosomes. <b>2020</b> , 11, 4136	16
1147	Structural basis for dimerization quality control. <b>2020</b> , 586, 452-456	17
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1144	Cryo-electron Microscopy Structure of the Swine Acute Diarrhea Syndrome Coronavirus Spike Glycoprotein Provides Insights into Evolution of Unique Coronavirus Spike Proteins. <b>2020</b> , 94,	7
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1141	Targeting HIV Env immunogens to B cell follicles in nonhuman primates through immune complex or protein nanoparticle formulations. <b>2020</b> , 5, 72	20
1140	Structural Basis of Zika Virus Specific Neutralization in Subsequent Flavivirus Infections. <b>2020</b> , 12,	3

1139	Structure of eukaryotic DNA polymerase bound to the PCNA clamp while encircling DNA. <b>2020</b> , 117, 30344-30353	13
1138	Assembly of the asymmetric human tubulin ring complex by RUVBL1-RUVBL2 AAA ATPase. <b>2020</b> , 6,	12
1137	A 3.4-Å cryo-electron microscopy structure of the human coronavirus spike trimer computationally derived from vitrified NL63 virus particles. <b>2020</b> , 1, e11	2
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1133	Structure of the respiratory MBS complex reveals iron-sulfur cluster catalyzed sulfane sulfur reduction in ancient life. <b>2020</b> , 11, 5953	10
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1129	Human TRPC5 structures reveal interaction of a xanthine-based TRPC1/4/5 inhibitor with a conserved lipid binding site. <b>2020</b> , 3, 704	12
1128	Gating by ionic strength and safety check by cyclic-di-AMP in the ABC transporter OpuA. <b>2020</b> , 6,	13
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1125	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. <b>2020</b> , 3, 766	13
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1121	SIMPLE 3.0. Stream single-particle cryo-EM analysis in real time. <b>2020</b> , 4, 100040	9
1120	Disulfide stabilization of human norovirus GI.1 virus-like particles focuses immune response toward blockade epitopes. <b>2020</b> , 5, 110	1
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1116	Human Antibodies Protect against Aerosolized Eastern Equine Encephalitis Virus Infection. <b>2020</b> , 183, 1884-1900.e23	8
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1110	Lipoprotein Particles Interact with Membranes and Transfer Their Cargo without Receptors. <b>2020</b> , 59, 4421-4428	6
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1105	Structural basis for sequestration and autoinhibition of cGAS by chromatin. <b>2020</b> , 587, 678-682	74
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1097	Structure of the AAVhu.37 capsid by cryoelectron microscopy. <b>2020</b> , 76, 58-64	7
1096	Structure of the Polar Flagellum Reveals a Distinct Outer Membrane Complex and Its Specific Interaction with the Stator. <b>2020</b> , 202,	14
1095	Molecular architecture of the luminal ring of the <i>Xenopus laevis</i> nuclear pore complex. <b>2020</b> , 30, 532-540	31
1094	Potent Neutralizing Antibodies against SARS-CoV-2 Identified by High-Throughput Single-Cell Sequencing of Convalescent Patients' B Cells. <b>2020</b> , 182, 73-84.e16	806
1093	Cryo-EM structure of the volume-regulated anion channel LRRC8D isoform identifies features important for substrate permeation. <b>2020</b> , 3, 240	13
1092	Cryo-electron microscopy structure and potential enzymatic function of human six-transmembrane epithelial antigen of the prostate 1 (STEAP1). <b>2020</b> , 295, 9502-9512	11
1091	Structural insights into the inhibition mechanism of human sterol O-acyltransferase 1 by a competitive inhibitor. <b>2020</b> , 11, 2478	20
1090	A distinct inhibitory mechanism of the V-ATPase by <i>Vibrio</i> VopQ revealed by cryo-EM. <b>2020</b> , 27, 589-597	5
1089	Structural basis for assembly and function of a diatom photosystem I-light-harvesting supercomplex. <b>2020</b> , 11, 2481	24
1088	Structure and mechanism of the mitochondrial Ca uniporter holocomplex. <b>2020</b> , 582, 129-133	75
1087	Cryo-electron microscopy structure of the glucagon receptor with a dual-agonist peptide. <b>2020</b> , 295, 9313-9325	15
1086	Thermoresponsive Molecular Brushes with Propylene Oxide/Ethylene Oxide Copolymer Side Chains in Aqueous Solution. <b>2020</b> , 53, 4068-4081	6

1085	A unique binding mode of Nek2A to the APC/C allows its ubiquitination during prometaphase. <b>2020</b> , 21, e49831	10
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1083	The oligomeric structures of plant cryptochromes. <b>2020</b> , 27, 480-488	25
1082	Structure of the cytoplasmic ring of the <i>Xenopus laevis</i> nuclear pore complex by cryo-electron microscopy single particle analysis. <b>2020</b> , 30, 520-531	29
1081	Structural insights into secretory immunoglobulin A and its interaction with a pneumococcal adhesin. <b>2020</b> , 30, 602-609	11
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1079	Structure and catalytic mechanism of a human triacylglycerol-synthesis enzyme. <b>2020</b> , 581, 323-328	32
1078	Structure of nevanimibe-bound tetrameric human ACAT1. <b>2020</b> , 581, 339-343	24
1077	Structure of a cyanobacterial photosystem I surrounded by octadecameric IsiA antenna proteins. <b>2020</b> , 3, 232	10
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1075	Glycan-dependent cell adhesion mechanism of Tc toxins. <b>2020</b> , 11, 2694	6
1074	Structural insights into assembly, operation and inhibition of a type I restriction-modification system. <b>2020</b> , 5, 1107-1118	7
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1072	Interactions of a Bacterial RND Transporter with a Transmembrane Small Protein in a Lipid Environment. <b>2020</b> , 28, 625-634.e6	26
1071	AcrIF9 tethers non-sequence specific dsDNA to the CRISPR RNA-guided surveillance complex. <b>2020</b> , 11, 2730	12
1070	Microtubule Nucleation Properties of Single Human $\beta$ uRCs Explained by Their Cryo-EM Structure. <b>2020</b> , 53, 603-617.e8	49
1069	Cryo-EM structures of inactive and active GABA receptor. <b>2020</b> , 30, 564-573	40
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1067	Structures of human pannexin 1 reveal ion pathways and mechanism of gating. <b>2020</b> , 584, 646-651	51
1066	Structure of the ER membrane complex, a transmembrane-domain insertase. <b>2020</b> , 584, 475-478	42
1065	Structural Insights into a Plant Mechanosensitive Ion Channel MSL1. <b>2020</b> , 30, 4518-4527.e3	16
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1063	Molecular dysregulation of ciliary polycystin-2 channels caused by variants in the TOP domain. <b>2020</b> , 117, 10329-10338	8
1062	Cryo-EM structure of the human cohesin-NIPBL-DNA complex. <b>2020</b> , 368, 1454-1459	71
1061	Cooperative transport mechanism of human monocarboxylate transporter 2. <b>2020</b> , 11, 2429	18
1060	Structural and Proteomic Characterization of the Initiation of Giant Virus Infection. <b>2020</b> , 181, 1046-1061.e6	8
1059	HIV-1 Envelope and MPER Antibody Structures in Lipid Assemblies. <b>2020</b> , 31, 107583	29
1058	Cryo-EM Structures and Regulation of Arabinofuranosyltransferase AftD from Mycobacteria. <b>2020</b> , 78, 683-699.e11	11
1057	Structural and Biochemical Characterization of the nsp12-nsp7-nsp8 Core Polymerase Complex from SARS-CoV-2. <b>2020</b> , 31, 107774	130
1056	Parkinson's disease associated mutation E46K of $\alpha$ -synuclein triggers the formation of a distinct fibril structure. <b>2020</b> , 11, 2643	31
1055	Structural transitions in influenza haemagglutinin at membrane fusion pH. <b>2020</b> , 583, 150-153	32
1054	Electromechanical coupling in the hyperpolarization-activated K channel KAT1. <b>2020</b> , 583, 145-149	20
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851	Structural morphing in a symmetry-mismatched viral vertex. <b>2020</b> , 11, 1713	13
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846	Cryo-EM structure of a human prion fibril with a hydrophobic, protease-resistant core. <b>2020</b> , 27, 417-423	37
845	Membrane constriction and thinning by sequential ESCRT-III polymerization. <b>2020</b> , 27, 392-399	33
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842	Cryo-EM structure of the PlexinC1/A39R complex reveals inter-domain interactions critical for ligand-induced activation. <b>2020</b> , 11, 1953	8
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839	Structure of severe fever with thrombocytopenia syndrome virus L protein elucidates the mechanisms of viral transcription initiation. <b>2020</b> , 5, 864-871	16
838	Conformational plasticity of the ClpAP AAA+ protease couples protein unfolding and proteolysis. <b>2020</b> , 27, 406-416	27
837	Structure of Super-Potent Antibody CAP256-VRC26.25 in Complex with HIV-1 Envelope Reveals a Combined Mode of Trimer-Apex Recognition. <b>2020</b> , 31, 107488	22
836	Structural Insights into the Mammalian Late-Stage Initiation Complexes. <b>2020</b> , 31, 107497	15
835	Structural basis of ER-associated protein degradation mediated by the Hrd1 ubiquitin ligase complex. <b>2020</b> , 368,	60
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832	VSV-Displayed HIV-1 Envelope Identifies Broadly Neutralizing Antibodies Class-Switched to IgG and IgA. <b>2020</b> , 27, 963-975.e5	16
831	Cryo-EM structures reveal intricate Fe-S cluster arrangement and charging in <i>Rhodobacter capsulatus</i> formate dehydrogenase. <b>2020</b> , 11, 1912	18
830	Inhibition mechanisms of AcrF9, AcrF8, and AcrF6 against type I-F CRISPR-Cas complex revealed by cryo-EM. <b>2020</b> , 117, 7176-7182	17
829	Phase-plate cryo-EM structure of the Widom 601 CENP-A nucleosome core particle reveals differential flexibility of the DNA ends. <b>2020</b> , 48, 5735-5748	13
828	Structural and functional characterization of the severe fever with thrombocytopenia syndrome virus L protein. <b>2020</b> , 48, 5749-5765	15
827	Cryo-EM structure of the human heteromeric amino acid transporter bAT-rBAT. <b>2020</b> , 6, eaay6379	13
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824	Ribosome Dimerization Protects the Small Subunit. <b>2020</b> , 202,	14
823	Capsid Structure of a Marine Algal Virus of the Order. <b>2020</b> , 94,	5
822	Dynamics in the murine norovirus capsid revealed by high-resolution cryo-EM. <b>2020</b> , 18, e3000649	11
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820	Structure of the protective nematode protease complex H-gal-GP and its conservation across roundworm parasites. <b>2020</b> , 16, e1008465	5
819	Visualization of Ligand-Bound Ectodomain Assembly in the Full-Length Human IGF-1 Receptor by Cryo-EM Single-Particle Analysis. <b>2020</b> , 28, 555-561.e4	14
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816	Mechanism of auto-inhibition and activation of Mec1 checkpoint kinase. <b>2021</b> , 28, 50-61	9

815	High-resolution structure and biophysical characterization of the nucleocapsid phosphoprotein dimerization domain from the Covid-19 severe acute respiratory syndrome coronavirus 2. <b>2021</b> , 538, 54-62	37
814	CueR activates transcription through a DNA distortion mechanism. <b>2021</b> , 17, 57-64	16
813	A mammalian system for high-resolution imaging of intact cells by cryo-electron tomography. <b>2021</b> , 160, 87-96	0
812	Molecular goniometers for single-particle cryo-electron microscopy of DNA-binding proteins. <b>2021</b> , 39, 378-386	9
811	Cryo-EM Structure of an Extended SARS-CoV-2 Replication and Transcription Complex Reveals an Intermediate State in Cap Synthesis. <b>2021</b> , 184, 184-193.e10	82
810	The cytoplasmic domain of the AAA+ protease FtsH is tilted with respect to the membrane to facilitate substrate entry. <b>2021</b> , 296, 100029	5
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808	Structural Basis for Bacterial Ribosome-Associated Quality Control by RqcH and RqcP. <b>2021</b> , 81, 115-126.e7	17
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806	Cryo-EM Structures Reveal Transcription Initiation Steps by Yeast Mitochondrial RNA Polymerase. <b>2021</b> , 81, 268-280.e5	5
805	Structural insights into outer membrane asymmetry maintenance in Gram-negative bacteria by MlaFEDB. <b>2021</b> , 28, 81-91	17
804	Recapitulation of HIV-1 Env-antibody coevolution in macaques leading to neutralization breadth. <b>2021</b> , 371,	22
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802	ISRIB Blunts the Integrated Stress Response by Allosterically Antagonising the Inhibitory Effect of Phosphorylated eIF2 on eIF2B. <b>2021</b> , 81, 88-103.e6	25
801	Distinct Structures and Dynamics of Chromatosomes with Different Human Linker Histone Isoforms. <b>2021</b> , 81, 166-182.e6	27
800	Structural Basis for High-Affinity Trapping of the Na1.7 Channel in Its Resting State by Tarantula Toxin. <b>2021</b> , 81, 38-48.e4	17
799	Structural Basis for the Modulation of Human KCNQ4 by Small-Molecule Drugs. <b>2021</b> , 81, 25-37.e4	17
798	Steps toward translocation-independent RNA polymerase inactivation by terminator ATPase □ <b>2021</b> , 371,	32

797	Mechanism of spliceosome remodeling by the ATPase/helicase Prp2 and its coactivator Spp2. <b>2021</b> , 371,	8
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795	Pre-termination Transcription Complex: Structure and Function. <b>2021</b> , 81, 281-292.e8	18
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789	Structural basis of human monocarboxylate transporter 1 inhibition by anti-cancer drug candidates. <b>2021</b> , 184, 370-383.e13	37
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787	Conformational dynamics of SARS-CoV-2 trimeric spike glycoprotein in complex with receptor ACE2 revealed by cryo-EM. <b>2021</b> , 7,	132
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779	Structural basis of nucleosome dynamics modulation by histone variants H2A.B and H2A.Z.2.2. <b>2021</b> , 40, e105907	10
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758	Robust and ultrafast fiducial marker correspondence in electron tomography by a two-stage algorithm considering local constraints. <b>2021</b> ,	1
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753	Cryo-electron tomography related radiation-damage parameters for individual-molecule 3D structure determination. 10,	0
752	Structural basis for intrinsic transcription termination.	0
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749	Cryo-EM structure of the human IgM B cell receptor. <b>2022</b> , 377, 875-880	1
748	Structural basis for antagonism of the ubiquitin ligase BIRC6 by SMAC.	0
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746	Structural basis for activation of Arf1 at the Golgi complex. <b>2022</b> , 40, 111282	0
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744	Structural basis for directional chitin biosynthesis.	4

743	Structures and membrane interactions of native serotonin transporter in complexes with psychostimulants.	0
742	Molecular basis for the selective G protein signaling of somatostatin receptors.	1
741	Structural characterization of human tryptophan hydroxylase 2 reveals L-Phe as the superior regulatory domain ligand relevant for serotonin biosynthesis.	0
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739	Structure of cyanobacterial photosystem I complexed with ferredoxin at 1.97 Å resolution. 2022, 5,	0
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736	Cryo-electron tomography with mixed-scale dense neural networks reveals key steps in deployment of Toxoplasma invasion machinery.	0
735	The structure, catalytic mechanism, and inhibitor identification of phosphatidylinositol remodeling MBOAT7.	1
734	Molecular insights into peptide agonist engagement with the PTH1 receptor.	0
733	Triglyceride lipolysis triggers liquid crystalline phases in lipid droplets and alters the LD proteome. 2022, 221,	1
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728	Plant receptor-like protein activation by a microbial glycoside hydrolase.	2
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724	Cryo-electron microscopy unveils unique structural features of the human Kir2.1 channel. <b>2022</b> , 8,	2
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635	Cryo-EM structure-based selection of computed ligand poses enables design of MTA-synergic PRMT5 inhibitors of better potency. <b>2022</b> , 5,	0
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633	DELE1 oligomerization promotes integrated stress response activation.	0
632	SEC62 and TMX4 control asymmetric autophagy of the nuclear envelope upon LINC complex disassembly.	0
631	Structures of +1 nucleosome-bound PIC-Mediator complex. <b>2022</b> , 378, 62-68	2
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629	Structure of the NuA4 acetyltransferase complex bound to the nucleosome.	1
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626	Structure of V-ATPase from citrus fruit. <b>2022</b> , 30, 1403-1410.e4	2
625	Prion-like low complexity regions enable avid virus-host interactions during HIV-1 infection. <b>2022</b> , 13,	0
624	SPACA9 is a luminal protein of human ciliary singlet and doublet microtubules. <b>2022</b> , 119,	2
623	Native doublet microtubules from <i>Tetrahymena thermophila</i> reveal the importance of outer junction proteins.	1
622	Structure of mycobacterial respiratory Complex I.	0
621	Structural insights for neutralization of Omicron variants BA.1, BA.2, BA.4, and BA.5 by a broadly neutralizing SARS-CoV-2 antibody. <b>2022</b> , 8,	3
620	Developmental Transitions Coordinate Assembly of the <i>Coxiella burnetii</i> Dot/Icm Type IV Secretion System.	0
619	Analysis and comparison of electron radiation damage assessments in Cryo-EM by single particle analysis and micro-crystal electron diffraction. 9,	0
618	Molecular basis of the TRAP complex function in ER protein biogenesis.	1

617	A step-by-step protocol for capturing conformational snapshots of ligand gated ion channels by single-particle cryo-EM. <b>2022</b> , 3, 101732	0
616	Structural basis of CHMP2A-CHMP3 ESCRT-III polymer assembly and membrane cleavage.	0
615	Production and Characterisation of Stabilised PV-3 Virus-like Particles Using <i>Pichia pastoris</i> . <b>2022</b> , 14, 2159	0
614	Tau amyloid polymorphism is shaped by local structural propensities of its protein sequence.	0
613	Molecular insights into the distinct signaling duration for the peptide-induced PTH1R activation. <b>2022</b> , 13,	0
612	Structural and functional basis of the universal transcription factor NusG pro-pausing activity in <i>Mycobacterium tuberculosis</i> .	0
611	Molecular structures reveal synergistic rescue of B08 CFTR by Trikafta modulators. <b>2022</b> , 378, 284-290	2
610	Computationally restoring the potency of a clinical antibody against SARS-CoV-2 Omicron subvariants.	0
609	Structural basis of three different transcription activation strategies adopted by a single regulator SoxS.	0
608	Transient Prenyltransferase-Cyclase Association in Fusicoccadiene Synthase, an Assembly-Line Terpene Synthase. <b>2022</b> , 61, 2417-2430	0
607	Cryo-EM structures of LolCDE reveal the molecular mechanism of bacterial lipoprotein sorting in <i>Escherichia coli</i> . <b>2022</b> , 20, e3001823	1
606	Structural insights into RNA-mediated transcription regulation in bacteria. <b>2022</b> , 82, 3885-3900.e10	0
605	The entry of unclosed autophagosomes into vacuoles and its physiological relevance. <b>2022</b> , 18, e1010431	0
604	Structure of the human heterodimeric transporter 4F2hc-LAT2 in complex with Anticalin, an alternative binding protein for applications in single-particle cryo-EM. <b>2022</b> , 12,	1
603	Structures of the CcmABCD heme release complex at multiple states. <b>2022</b> , 13,	0
602	Bending forces and nucleotide state jointly regulate F-actin structure.	2
601	Time-resolved cryo-EM using a combination of droplet microfluidics with on-demand jetting.	1
600	The role of bivalent ions in the regulation of D-loop extension mediated by DMC1 during meiotic recombination. <b>2022</b> , 105439	0

599	SARS-CoV-2 nsp3-4 suffice to form a pore shaping replication organelles.	0
598	Structure of a G protein-coupled receptor with GRK2 and a biased ligand.	0
597	Structure of human TRPM8 channel.	0
596	Chemical inhibition of PIN auxin transporters by the anti-inflammatory drug Naproxen.	0
595	Structure of the OMEGA nickase IsrB in complex with RNA and target DNA. <b>2022</b> , 610, 575-581	0
594	Structural insight into Tn3 family transposition mechanism. <b>2022</b> , 13,	0
593	Structural journey of an insecticidal pore-forming protein targeting western corn rootworm.	0
592	Structural basis of actin filament assembly and aging.	1
591	Dynamic HIV-1 spike motion creates vulnerability for its membrane-bound tripod to antibody attack. <b>2022</b> , 13,	0
590	Structural Genomics of the Human Dopamine Receptor System.	0
589	Inhibited KdpFABC transitions into an E1 off-cycle state. 11,	0
588	HIV-1 CD4-binding site germline antibodyEnv structures inform vaccine design. <b>2022</b> , 13,	0
587	Helical ultrastructure of the metalloprotease meprin Bn complex with a small molecule inhibitor. <b>2022</b> , 13,	2
586	Algal photosystem I dimer and high-resolution model of PSI-plastocyanin complex. <b>2022</b> , 8, 1191-1201	2
585	Method for 3D atomic structure determination of multi-element nanoparticles with graphene liquid-cell TEM.	0
584	Structural analysis shows that the BIR2 domain of E3 ligase XIAP binds across the RIP2 kinase dimer interface.	0
583	Target RNA activates the protease activity of Craspase to confer antiviral defense. <b>2022</b> ,	0
582	Helicobacter pyloriFlgV forms a flagellar motor ring structure required for optimal motility.	0

581	Bestrophin-2 and glutamine synthetase form a complex for glutamate release. <b>2022</b> , 611, 180-187	0
580	Structural and Functional insights into the action mode of a Mitochondrial AAA+ Disaggregase CLPB.	0
579	Structural and functional analyses of a GPCR-inhibited ion channel TRPM3. <b>2022</b> ,	2
578	A distinct mammalian disome collision interface harbors K63-linked polyubiquitination of uS10 to trigger hRQT-mediated subunit dissociation. <b>2022</b> , 13,	3
577	YcaO-mediated ATP-dependent peptidase activity in ribosomal peptide biosynthesis.	0
576	Molecular basis for isoform-selective inhibition of presenilin-1 by MRK-560. <b>2022</b> , 13,	0
575	Phase Separation of Rubisco by the Folded SSUL Domains of CcmM in Beta-Carboxysome Biogenesis. <b>2023</b> , 269-296	0
574	Structure and flexibility of the yeast NuA4 histone acetyltransferase complex. 11,	0
573	A dynamic rRNA ribomethylome drives stemness in acute myeloid leukemia.	0
572	Activation mechanism of the mouse cold-sensing TRPM8 channel by cooling agonist and PIP 2. <b>2022</b> , 378,	0
571	Disulfide stabilization reveals conserved dynamic features between SARS-CoV-1 and SARS-CoV-2 spikes.	0
570	Structures of the holo CRISPR RNA-guided transposon integration complex.	0
569	Structural basis of colibactin activation by the ClbP peptidase.	0
568	The Ycf48 accessory factor occupies the site of the oxygen-evolving manganese cluster during photosystem II biogenesis.	0
567	Structural insights into adhesion GPCR ADGRL3 activation and Gq, Gs, Gi, and G12 coupling. <b>2022</b> ,	0
566	Isotropic reconstruction for electron tomography with deep learning. <b>2022</b> , 13,	1
565	Structure of a mitochondrial ribosome with fragmented rRNA in complex with membrane-targeting elements. <b>2022</b> , 13,	1
564	Structural basis for HflXr-mediated antibiotic resistance in <i>Listeria monocytogenes</i> .	1

563	Structural basis of TRPV3 inhibition by an antagonist.	0
562	Lineage-mosaic and mutation-patched spike proteins for broad-spectrum COVID-19 vaccine. <b>2022,</b>	0
561	Structural Consequences of Deproteinizing the 50S Ribosome. <b>2022, 12, 1605</b>	0
560	Unravelling the regulation pathway of photosynthetic AB-GAPDH. <b>2022, 78, 1399-1411</b>	0
559	Structural basis for ion selectivity in potassium-selective channelrhodopsins.	0
558	The ABC transporter MsbA adopts the wide inward-open conformation in E. coli cells. <b>2022, 8,</b>	1
557	Cryo-EM structure of the octameric pore of Clostridium perfringens $\beta$ toxin.	0
556	Structural insights into PA3488-mediated inactivation of Pseudomonas aeruginosa PldA. <b>2022, 13,</b>	0
555	Structural principles of B-cell antigen receptor assembly.	1
554	Atomic model of vesicular stomatitis virus and mechanism of assembly. <b>2022, 13,</b>	1
553	In vitro structural maturation of an early stage pre-40S particle coupled with U3 snoRNA release and central pseudoknot formation.	0
552	Capsid Structure of Aleutian Mink Disease Virus and Human Parvovirus 4: New Faces in the Parvovirus Family Portrait. <b>2022, 14, 2219</b>	0
551	Ion transfer mechanisms in Mrp-type antiporters from high resolution cryoEM and molecular dynamics simulations. <b>2022, 13,</b>	1
550	Cryo-EM Structure of Gokushovirus $\beta$ C6098 Reveals a Novel Capsid Architecture for a Single-Scaffolding Protein, Microvirus Assembly System.	0
549	Structure and functionality of a multimeric human COQ7:COQ9 complex. <b>2022,</b>	0
548	Gossypol Broadly Inhibits Coronaviruses by Targeting RNA-Dependent RNA Polymerases. 2203499	0
547	CryoEM structural exploration of catalytically active enzyme pyruvate carboxylase. <b>2022, 13,</b>	0
546	Cryomicroscopy reveals the structural basis for a flexible hinge motion in the immunoglobulin M pentamer. <b>2022, 13,</b>	1



545	Structural mechanism of SGLT1 inhibitors. <b>2022</b> , 13,	0
544	Structure and mechanism of the type I-G CRISPR effector.	0
543	Structural and molecular biology of <i>Acheta domesticus</i> segmented densovirus, the first parvovirus to harbor a bipartite genome.	0
542	Coinfection by influenza A virus and respiratory syncytial virus produces hybrid virus particles. <b>2022</b> , 7, 1879-1890	2
541	Cryo-EM structures of perforin-2 in isolation and assembled on a membrane suggest a mechanism for pore formation.	0
540	Near-atomic, non-icosahedrally averaged structure of giant virus <i>Paramecium bursaria chlorella virus 1</i> . <b>2022</b> , 13,	0
539	Structure-Based Discovery of a Novel Class of Small-Molecule Pure Antagonists of Integrin $\alpha 5 \beta 1$ .	0
538	Near-Atomic Resolution Cryo-EM Image Reconstruction of RNA. <b>2023</b> , 179-192	0
537	Mechanism of 4-aminopyridine inhibition of the lysosomal channel TMEM175. <b>2022</b> , 119,	2
536	Purification and structural characterization of the Na <sup>+</sup> -translocating ferredoxin: NAD <sup>+</sup> reductase (Rnf) complex of <i>Clostridium tetanomorphum</i> . <b>2022</b> , 13,	2
535	Architecture of the chikungunya virus replication organelle. 11,	0
534	Cryo-EM structures of the translocational binary toxin complex CDTa-bound CDTb-pore from <i>Clostridioides difficile</i> . <b>2022</b> , 13,	0
533	Recognition of cyclic dinucleotides and folates by human SLC19A1.	0
532	Membrane-assisted assembly and selective secretory autophagy of enteroviruses. <b>2022</b> , 13,	1
531	Polyelectrolyte coating of cryo-EM grids improves lateral distribution and prevents aggregation of macromolecules. <b>2022</b> , 78, 1337-1346	0
530	Spatial definition of the human progesterone receptor-B transcriptional complex. <b>2022</b> , 25, 105321	2
529	Structure of the human UBR5 E3 ubiquitin ligase.	0
528	AAA+ protease-adaptor structures reveal altered conformations and ring specialization.	1

527	Characterization of heterogeneity in nanodisc samples using Feret signatures. <b>2022</b> , 107916	0
526	Molecular Mechanism for Bacterial Degradation of Plant Hormone Auxin.	0
525	Cryo-EM structures of mitochondrial respiratory complex I from <i>Drosophila melanogaster</i> .	0
524	Virion structure of Leishmania RNA virus 1. <b>2022</b> ,	0
523	The RIG-I receptor adopts two different conformations for distinguishing host from viral RNA ligands. <b>2022</b> , 82, 4131-4144.e6	1
522	Resting mitochondrial complex I from <i>Drosophila melanogaster</i> adopts a helix-locked state.	1
521	The nucleoplasmic phase of pre-40S formation prior to nuclear export.	1
520	Mechanistic insight into allosteric activation of human pyruvate carboxylase by acetyl-CoA. <b>2022</b> , 82, 4116-4130.e6	0
519	Structural and functional basis of mammalian microRNA biogenesis by Dicer. <b>2022</b> , 82, 4064-4079.e13	2
518	Broad-Spectrum Virus Trapping with Heparan Sulfate-Modified DNA Origami Shells.	3
517	Assembly and purification of AvrSr35-induced Sr35 resistosome and determination of its structure by cryo-EM. <b>2022</b> , 3, 101796	0
516	Structural insights into blue-green light utilization by marine green algal light harvesting complex II at 2.78 Å. <b>2022</b> , 2, 100064	0
515	Distinct structure and gating mechanism in diverse NMDA receptors with GluN2C and GluN2D subunits.	0
514	Functionalized graphene grids with various charges for single-particle cryo-EM. <b>2022</b> , 13,	1
513	An essential periplasmic protein coordinates lipid trafficking and is required for asymmetric polar growth in mycobacteria. 11,	0
512	Insights into complex I assembly: Function of NDUFAF1 and a link with cardiolipin remodeling. <b>2022</b> , 8,	0
511	High-resolution structural analysis of enterovirus-reactive polyclonal antibodies in complex with whole virions.	0
510	Structural and functional insights of the human peroxisomal ABC transporter ALDP. 11,	0

509	CryoEM reveals unprecedented binding site for NaV1.7 inhibitors enabling rational design of potent hybrid inhibitors.	0
508	Time-resolved cryo-EM reveals early ribosome assembly in action.	0
507	Near-Physiological in vitro Assembly of 50S Ribosomes Involves Parallel Pathways.	0
506	An LH1RC photocomplex from an extremophilic phototroph provides insight into origins of two photosynthesis proteins. <b>2022</b> , 5,	2
505	Antigenic mapping reveals sites of vulnerability on HCoV spike protein. <b>2022</b> , 5,	0
504	Structure insights into selective coupling of G protein subtypes by a class B G protein-coupled receptor. <b>2022</b> , 13,	1
503	Cryo-EM structure of the agonist-bound Hsp90-XAP2-AHR cytosolic complex. <b>2022</b> , 13,	1
502	The SspB adaptor drives structural changes in the AAA+ClpXP protease during ssrA-tagged substrate delivery.	0
501	Cryo-EM reveals the architecture of the PELP1-WDR18 molecular scaffold. <b>2022</b> , 13,	1
500	The photosystem I supercomplex from a primordial green alga <i>Ostreococcus tauri</i> harbors three light-harvesting complex trimers.	0
499	Structural dynamics of AAA + ATPase Drg1 and mechanism of benzo-diazaborine inhibition. <b>2022</b> , 13,	0
498	Molecular recognition of morphine and fentanyl by the human $\mu$ opioid receptor. <b>2022</b> , 185, 4361-4375.e19	3
497	Structure of the GOLD-domain seven-transmembrane helix protein family member TMEM87A. 11,	0
496	Cryo-EM structures of prefusion SIV envelope trimer. <b>2022</b> , 29, 1080-1091	0
495	Anionic lipids unlock the gates of select ion channels in the pacemaker family. <b>2022</b> , 29, 1092-1100	1
494	The Nse5/6-like SIMC1-SLF2 complex localizes SMC5/6 to viral replication centers. 11,	0
493	Co-immunization with hemagglutinin stem immunogens elicits cross-group neutralizing antibodies and broad protection against influenza A viruses. <b>2022</b> ,	1
492	Structural insights into broadly neutralizing antibodies against SARS-CoV-2 elicited by hybrid immunity. 1-52	0

491	Cryo-EM Structures of Amyloid- $\beta$ Filaments With the Arctic Mutation (E22G) From Human and Mouse Brains.	0
490	CryoEM structures of the multimeric secreted NS1, a major factor for dengue hemorrhagic fever. <b>2022</b> , 13,	0
489	Structural basis of human SNAPc recognizing proximal sequence element of snRNA promoter. <b>2022</b> , 13,	0
488	Structure of the RhlR-PqsE complex from <i>Pseudomonas aeruginosa</i> reveals mechanistic insights into quorum-sensing gene regulation. <b>2022</b> ,	0
487	Calaxin stabilizes the docking of outer arm dyneins onto ciliary doublet microtubule in vertebrates.	0
486	Unsupervised Voxel-based Segmentation reveals a Landscape of Bacterial Ribosome Large Subunit Early Assembly.	0
485	Open-channel structure of a pentameric ligand-gated ion channel reveals a mechanism of leaflet-specific phospholipid modulation. <b>2022</b> , 13,	2
484	Structural basis of sRNA RsmZ regulation of <i>Pseudomonas aeruginosa</i> virulence.	0
483	Understanding VPAC receptor family peptide binding and selectivity. <b>2022</b> , 13,	0
482	ATG9A and ATG2A form a heteromeric complex essential for autophagosome formation. <b>2022</b> ,	0
481	Structure of <i>Escherichia coli</i> heat shock protein Hsp15 in complex with the ribosomal 50S subunit bearing peptidyl-tRNA.	0
480	Concurrent remodelling of nucleolar 60S subunit precursors by the Rea1 ATPase and Spb4 RNA helicase.	0
479	Multishot Tomography for High-Resolution In Situ Subtomogram Averaging. <b>2022</b> , 107911	0
478	Potent SARS-CoV-2 neutralizing antibodies with therapeutic effects in two animal models.. <b>2022</b> , 105596	0
477	Structure of the reduced microsporidian proteasome bound by PI31-like peptides in dormant spores. <b>2022</b> , 13,	0
476	Conformational motions and ligand-binding underlying gating and regulation in IP3R channel. <b>2022</b> , 13,	1
475	LIPID MEMBRANE MIMETICS AND OLIGOMERIZATION TUNE FUNCTIONAL PROPERTIES OF PROTEORHODOPSIN. <b>2022</b> ,	0
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- 469 Donor-strand exchange drives assembly of the TasA scaffold in *Bacillus subtilis* biofilms. **2022**, 13, ○
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- 449 Structures and comparison of endogenous 2-oxoglutarate and pyruvate dehydrogenase complexes from bovine kidney. **2022**, 8, 1
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- 442 Ultrastructural characterization of a viral RNA and G-protein containing, membranous organelle formed in respiratory syncytial virus infected cells. ○
- 441 Structures of the holo CRISPR RNA-guided transposon integration complex. ○
- 440 A conserved glutathione binding site in poliovirus is a target for antivirals and vaccine stabilisation. **2022**, 5, ○
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- 438 Divisome core complex in bacterial cell division revealed by cryo-EM. ○

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436	Structural basis of tankyrase activation by polymerization. <b>2022</b> , 612, 162-169	0
435	NewSNCA mutation and structures of $\beta$ -synuclein filaments from juvenile-onset synucleinopathy.	0
434	Human antibody recognition and neutralization mode on the NTD and RBD domains of SARS-CoV-2 spike protein. <b>2022</b> , 12,	1
433	Doublet microtubule inner junction protein FAP20 recruits tubulin to the microtubule lattice.	0
432	Amyloid fibril structure from the vascular variant of systemic AA amyloidosis. <b>2022</b> , 13,	0
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430	Structures of the R-type human Cav2.3 channel reveal conformational crosstalk of the intracellular segments. <b>2022</b> , 13,	0
429	The free fatty acid binding pocket is a conserved hallmark in pathogenic $\beta$ -coronavirus spike proteins from SARS-CoV to Omicron. <b>2022</b> , 8,	0
428	High-resolution reconstruction of a Jumbo-bacteriophage infecting capsulated bacteria using hyperbranched tail fibers. <b>2022</b> , 13,	0
427	Conformational changes in mitochondrial complex I of the thermophilic eukaryote Chaetomium thermophilum. <b>2022</b> , 8,	2
426	Direct Cryo-ET observation of platelet deformation induced by SARS-CoV-2 Spike protein.	0
425	Structures of RecBCD in complex with phage-encoded inhibitor proteins reveal distinctive strategies for evasion of a bacterial immunity hub. 11,	0
424	The compact Cas1 (Cas12I) bracelet provides a unique structural platform for DNA manipulation.	0
423	HSP90-CDC37-PP5 forms a structural platform for kinase dephosphorylation. <b>2022</b> , 13,	1
422	Structure of the Acidobacteria homodimeric reaction center bound with cytochrome c. <b>2022</b> , 13,	0
421	Structure of monkeypox virus DNA polymerase holoenzyme.	3
420	Uniform thin ice on ultraflat graphene for high-resolution cryo-EM.	1

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- 409 Subtle change of fibrillation condition leads to substantial alteration of recombinant Tau fibril structure. **2022**, 25, 105645 0
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400	Structural basis for the non-self RNA-activated protease activity of the type III-E CRISPR nuclease-protease Craspase. <b>2022</b> , 13,	0
399	Autoinhibition and activation mechanisms revealed by the triangular-shaped structure of myosin Va. <b>2022</b> , 8,	0
398	Mechanism of receptor assembly via the pleiotropic adipokine Leptin.	0
397	Sequence-specific remodeling of a topologically complex RNP substrate by Spb4. <b>2022</b> , 29, 1228-1238	0
396	Bacterial crystalline cellulose secretion via a supramolecular BcsHD scaffold. <b>2022</b> , 8,	0
395	Structural basis for BIRC6 to balance apoptosis and autophagy.	0
394	Structural basis for Parkinson's disease-linked LRRK2's binding to microtubules. <b>2022</b> , 29, 1196-1207	2
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392	Structural visualization of the tubulin folding pathway directed by human chaperonin TRiC/CCT. <b>2022</b> , 185, 4770-4787.e20	0
391	Improved interface packing and design opportunities revealed by CryoEM analysis of a designed protein nanocage. <b>2022</b> , 8, e12280	0
390	Structural insights into p300 regulation and acetylation-dependent genome organisation. <b>2022</b> , 13,	0
389	High-resolution cryo-EM structure of the Shigella virus Sf6 genome delivery tail machine. <b>2022</b> , 8,	0
388	The structure of the human LACTB filament reveals the mechanisms of assembly and membrane binding. <b>2022</b> , 20, e3001899	0
387	Structure of a dimeric photosystem II complex from a cyanobacterium acclimated to far-red light. <b>2022</b> , 102815	0
386	Structure of a volume-regulated heteromeric LRRC8A/C channel.	1
385	Structural basis of odorant recognition by a human odorant receptor.	1
384	G $\alpha$ Activates PIP <sub>2</sub> Hydrolysis by Recruiting and Orienting PLC $\beta$ on the Membrane Surface.	0

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