

James J Chou

List of Publications by Year in descending order

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124
papers

10,424
citations

38660

50
h-index

32761

100
g-index

131
all docs

131
docs citations

131
times ranked

10396
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and mechanism of the M2 proton channel of influenza A virus. <i>Nature</i> , 2008, 451, 591-595.	13.7	951
2	Solution Structure of BID, an Intracellular Amplifier of Apoptotic Signaling. <i>Cell</i> , 1999, 96, 615-624.	13.5	461
3	DNA-nanotube-induced alignment of membrane proteins for NMR structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6644-6648.	3.3	447
4	Regulation of T Cell Receptor Activation by Dynamic Membrane Binding of the CD3 ϵ Cytoplasmic Tyrosine-Based Motif. <i>Cell</i> , 2008, 135, 702-713.	13.5	391
5	Mitochondrial uncoupling protein 2 structure determined by NMR molecular fragment searching. <i>Nature</i> , 2011, 476, 109-113.	13.7	350
6	Molecular Basis for Interaction of let-7 MicroRNAs with Lin28. <i>Cell</i> , 2011, 147, 1080-1091.	13.5	335
7	The structure of phospholamban pentamer reveals a channel-like architecture in membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10870-10875.	3.3	309
8	Solution structure of Ca(2+)-calmodulin reveals flexible hand-like properties of its domains. <i>Nature Structural Biology</i> , 2001, 8, 990-997.	9.7	305
9	Inhibition of Prolyl Hydroxylases Increases Erythropoietin Production in ESRD. <i>Journal of the American Society of Nephrology: JASN</i> , 2010, 21, 2151-2156.	3.0	304
10	Solution Structure of the RAIDD CARD and Model for CARD/CARD Interaction in Caspase-2 and Caspase-9 Recruitment. <i>Cell</i> , 1998, 94, 171-180.	13.5	301
11	Mechanism of drug inhibition and drug resistance of influenza A M2 channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7379-7384.	3.3	281
12	Architecture of the mitochondrial calcium uniporter. <i>Nature</i> , 2016, 533, 269-273.	13.7	256
13	Rapid Proton-Detected NMR Assignment for Proteins with Fast Magic Angle Spinning. <i>Journal of the American Chemical Society</i> , 2014, 136, 12489-12497.	6.6	254
14	Unusual architecture of the p7 channel from hepatitis C virus. <i>Nature</i> , 2013, 498, 521-525.	13.7	236
15	A simple apparatus for generating stretched polyacrylamide gels, yielding uniform alignment of proteins and detergent micelles. <i>Journal of Biomolecular NMR</i> , 2001, 21, 377-382.	1.6	223
16	The Structure of the α 1 β Transmembrane Dimer Reveals Features Essential for Its Assembly with the T Cell Receptor. <i>Cell</i> , 2006, 127, 355-368.	13.5	221
17	Micelle-Induced Curvature in a Water-Insoluble HIV-1 Env Peptide Revealed by NMR Dipolar Coupling Measurement in Stretched Polyacrylamide Gel. <i>Journal of the American Chemical Society</i> , 2002, 124, 2450-2451.	6.6	202
18	Kinetic studies with the non-nucleoside HIV-1 reverse transcriptase inhibitor U-88204E. <i>Biochemistry</i> , 1993, 32, 6548-6554.	1.2	178

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19	The structural basis for intramembrane assembly of an activating immunoreceptor complex. <i>Nature Immunology</i> , 2010, 11, 1023-1029.	7.0	176
20	Structural basis for membrane anchoring of HIV-1 envelope spike. <i>Science</i> , 2016, 353, 172-175.	6.0	169
21	Solution structure and functional analysis of the influenza B proton channel. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1267-1271.	3.6	156
22	Influenza M2 proton channels. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 522-529.	1.4	150
23	Solution structure of Apaf-1 CARD and its interaction with caspase-9 CARD: A structural basis for specific adaptor/caspase interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 11265-11270.	3.3	139
24	Structural Basis and Functional Role of Intramembrane Trimerization of the Fas/CD95 Death Receptor. <i>Molecular Cell</i> , 2016, 61, 602-613.	4.5	135
25	Insights into the Mobility of Methyl-Bearing Side Chains in Proteins from ^3JCC and ^3JCN Couplings. <i>Journal of the American Chemical Society</i> , 2003, 125, 8959-8966.	6.6	131
26	Characterization of Phospholipid Mixed Micelles by Translational Diffusion. <i>Journal of Biomolecular NMR</i> , 2004, 29, 299-308.	1.6	127
27	MemBrain: Improving the Accuracy of Predicting Transmembrane Helices. <i>PLoS ONE</i> , 2008, 3, e2399.	1.1	105
28	Higher-Order Clustering of the Transmembrane Anchor of DR5 Drives Signaling. <i>Cell</i> , 2019, 176, 1477-1489.e14.	13.5	104
29	Structure and Mechanism of the Influenza A M2 $^{\sim}60$ Dimer of Dimers. <i>Journal of the American Chemical Society</i> , 2015, 137, 14877-14886.	6.6	103
30	Solution NMR structure of the V27A drug resistant mutant of influenza A M2 channel. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 58-63.	1.0	97
31	Solution Structure of the CIDE-N Domain of CIDE-B and a Model for CIDE-N/CIDE-N Interactions in the DNA Fragmentation Pathway of Apoptosis. <i>Cell</i> , 1999, 99, 747-755.	13.5	94
32	Study of conformational rearrangement and refinement of structural homology models by the use of heteronuclear dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2000, 18, 217-227.	1.6	92
33	Capsid Protein VP4 of Human Rhinovirus Induces Membrane Permeability by the Formation of a Size-Selective Multimeric Pore. <i>PLoS Pathogens</i> , 2014, 10, e1004294.	2.1	88
34	Structure of a Central Component of the Yeast Kinetochores: The Spc24p/Spc25p Globular Domain. <i>Structure</i> , 2006, 14, 1003-1009.	1.6	86
35	Magic Angle Spinning NMR Investigation of Influenza A M2 $^{\sim}60$: Support for an Allosteric Mechanism of Inhibition. <i>Journal of the American Chemical Society</i> , 2010, 132, 10958-10960.	6.6	82
36	Flu channel drug resistance: a tale of two sites. <i>Protein and Cell</i> , 2010, 1, 246-258.	4.8	80

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37	Kinetic studies with the non-nucleoside human immunodeficiency virus type-1 reverse transcriptase inhibitor U-90152E. <i>Biochemical Pharmacology</i> , 1994, 47, 2017-2028.	2.0	75
38	Structural Investigation of Rimantadine Inhibition of the AM2-BM2 Chimera Channel of Influenza Viruses. <i>Structure</i> , 2011, 19, 1655-1663.	1.6	74
39	A Joint Prediction of the Folding Types of 1490 Human Proteins from their Genetic Codons. <i>Journal of Theoretical Biology</i> , 1993, 161, 251-262.	0.8	72
40	Structure of the membrane proximal external region of HIV-1 envelope glycoprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8892-E8899.	3.3	72
41	Amantadine partition and localization in phospholipid membrane: a solution NMR study. <i>Biochemical and Biophysical Research Communications</i> , 2004, 324, 212-217.	1.0	71
42	Fatty Acid Flippase Activity of UCP2 Is Essential for Its Proton Transport in Mitochondria. <i>Cell Metabolism</i> , 2014, 20, 541-552.	7.2	67
43	Dynamic Nuclear Polarization Study of Inhibitor Binding to the M2 ⁶⁰ Proton Transporter from Influenza A. <i>Biochemistry</i> , 2013, 52, 2774-2782.	1.2	66
44	Solution structure of an informationally complex high-affinity RNA aptamer to GTP. <i>Rna</i> , 2006, 12, 567-579.	1.6	64
45	Coordinating the impact of structural genomics on the human α -helical transmembrane proteome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 135-138.	3.6	64
46	Predicting cleavability of peptide sequences by HIV protease via correlation-angle approach. <i>The Protein Journal</i> , 1993, 12, 291-302.	1.1	62
47	DNA nanotubes for NMR structure determination of membrane proteins. <i>Nature Protocols</i> , 2013, 8, 755-770.	5.5	58
48	Steady-state kinetic studies with the polysulfonate U-9843, an HIV reverse transcriptase inhibitor. <i>Experientia</i> , 1994, 50, 23-28.	1.2	57
49	Probing the Interaction between the Coiled Coil Leucine Zipper of cGMP-dependent Protein Kinase α and the C Terminus of the Myosin Binding Subunit of the Myosin Light Chain Phosphatase. <i>Journal of Biological Chemistry</i> , 2008, 283, 32860-32869.	1.6	57
50	Measurement of one-bond ¹⁵ N- ¹³ C' dipolar couplings in medium sized proteins. <i>Journal of Biomolecular NMR</i> , 2000, 18, 101-105.	1.6	56
51	Magic-Angle-Spinning NMR of the Drug Resistant S31N M2 Proton Transporter from Influenza A. <i>Journal of the American Chemical Society</i> , 2012, 134, 7215-7218.	6.6	55
52	Ion and inhibitor binding of the double-ring ion selectivity filter of the mitochondrial calcium uniporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2846-E2851.	3.3	54
53	Substrate-modulated ADP/ATP-transporter dynamics revealed by NMR relaxation dispersion. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 636-641.	3.6	51
54	Structural basis of transmembrane coupling of the HIV-1 envelope glycoprotein. <i>Nature Communications</i> , 2020, 11, 2317.	5.8	49

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55	Proton Association Constants of His 37 in the Influenza-A M2 ₁₈ Dimer-of-Dimers. <i>Biochemistry</i> , 2014, 53, 5987-5994.	1.2	48
56	Kinetic Analysis of the M2 Proton Conduction of the Influenza Virus. <i>Journal of the American Chemical Society</i> , 2010, 132, 17695-17697.	6.6	45
57	Sortase A-Generated Highly Potent Anti-CD20-mMAE Conjugates for Efficient Elimination of B-Lineage Lymphomas. <i>Small</i> , 2017, 13, 1602267.	5.2	45
58	Optimal Bicelle Size $\langle i \rangle$ for Solution NMR Studies of the Protein Transmembrane Partition. <i>Chemistry - A European Journal</i> , 2017, 23, 1361-1367.	1.7	44
59	Rapid and accurate structure determination of coiled-coil domains using NMR dipolar couplings: Application to cGMP-dependent protein kinase II \pm . <i>Protein Science</i> , 2005, 14, 2421-2428.	3.1	43
60	Protein Side-Chain Rotamers from Dipolar Couplings in a Liquid Crystalline Phase. <i>Journal of the American Chemical Society</i> , 2001, 123, 3844-3845.	6.6	41
61	A formulation for correlating properties of peptides and its application to predicting human immunodeficiency virus protease-cleavable sites in proteins. <i>Biopolymers</i> , 1993, 33, 1405-1414.	1.2	40
62	The minimalist architectures of viroporins and their therapeutic implications. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 1058-1067.	1.4	39
63	Structure determination of symmetric homo-oligomers by a complete search of symmetry configuration space, using NMR restraints and van der Waals packing. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 203-219.	1.5	38
64	Evaluation of the Carcinogenic Potential of Roxadustat (FG-4592), a Small Molecule Inhibitor of Hypoxia-Inducible Factor Prolyl Hydroxylase in CD-1 Mice and Sprague Dawley Rats. <i>International Journal of Toxicology</i> , 2017, 36, 427-439.	0.6	35
65	Structure determination protocol for transmembrane domain oligomers. <i>Nature Protocols</i> , 2019, 14, 2483-2520.	5.5	35
66	Residual structure within the disordered C-terminal segment of p21 ^{Waf1/Cip1/Sdi1} and its implications for molecular recognition. <i>Protein Science</i> , 2009, 18, 337-347.	3.1	34
67	Response Multilayered Control of T Cell Receptor Phosphorylation. <i>Cell</i> , 2010, 142, 669-671.	13.5	32
68	Specific Interaction of the Human Mitochondrial Uncoupling Protein 1 with Free Long-Chain Fatty Acid. <i>Structure</i> , 2017, 25, 1371-1379.e3.	1.6	29
69	A Self-Sequestered Calmodulin-like Ca ²⁺ Sensor of Mitochondrial SCaMC Carrier and Its Implication to Ca ²⁺ -Dependent ATP-Mg/Pi Transport. <i>Structure</i> , 2014, 22, 209-217.	1.6	28
70	HIV-1 fusion inhibitors targeting the membrane-proximal external region of Env spikes. <i>Nature Chemical Biology</i> , 2020, 16, 529-537.	3.9	28
71	A View into the Blind Spot: Solution NMR Provides New Insights into Signal Transduction Across the Lipid Bilayer. <i>Structure</i> , 2010, 18, 1559-1569.	1.6	27
72	Structure and multistate function of the transmembrane electron transporter CcdA. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 809-814.	3.6	27

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73	Comparing the structure and dynamics of phospholamban pentamer in its unphosphorylated and pseudo-phosphorylated states. <i>Protein Science</i> , 2007, 16, 1977-1983.	3.1	25
74	Implementation of the prolyl hydroxylase inhibitor Roxadustat (FG4592) and its main metabolites into routine doping controls. <i>Drug Testing and Analysis</i> , 2017, 9, 1768-1778.	1.6	25
75	Stability and Water Accessibility of the Trimeric Membrane Anchors of the HIV-1 Envelope Spikes. <i>Journal of the American Chemical Society</i> , 2017, 139, 18432-18435.	6.6	25
76	A Trimeric Hydrophobic Zipper Mediates the Intramembrane Assembly of SARS-CoV-2 Spike. <i>Journal of the American Chemical Society</i> , 2021, 143, 8543-8546.	6.6	24
77	Genotype-specific differences in structural features of hepatitis C virus (HCV) p7 membrane protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 1383-1392.	1.4	23
78	An amphipathic Bax core dimer forms part of the apoptotic pore wall in the mitochondrial membrane. <i>EMBO Journal</i> , 2021, 40, e106438.	3.5	23
79	The present and future of solution NMR in investigating the structure and dynamics of channels and transporters. <i>Current Opinion in Structural Biology</i> , 2013, 23, 547-554.	2.6	20
80	Protein structure similarity from Principle Component Correlation analysis. <i>BMC Bioinformatics</i> , 2006, 7, 40.	1.2	19
81	Nonuniform sampling and maximum entropy reconstruction applied to the accurate measurement of residual dipolar couplings. <i>Journal of Magnetic Resonance</i> , 2007, 186, 201-211.	1.2	19
82	Molecular Basis of MgATP Selectivity of the Mitochondrial SCaMC Carrier. <i>Structure</i> , 2015, 23, 1394-1403.	1.6	19
83	Transverse relaxation dispersion of the p7 membrane channel from hepatitis C virus reveals conformational breathing. <i>Journal of Biomolecular NMR</i> , 2015, 61, 369-378.	1.6	19
84	The Diversity and Similarity of Transmembrane Trimerization of TNF Receptors. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 569684.	1.8	19
85	Structure and Evolutionary Analysis of a Non-biological ATP-binding Protein. <i>Journal of Molecular Biology</i> , 2007, 371, 501-513.	2.0	18
86	Structure of the transmembrane domain of HIV-1 envelope glycoprotein. <i>FEBS Journal</i> , 2017, 284, 1171-1177.	2.2	18
87	Oral Hypoxia-Inducible Factor Prolyl Hydroxylase Inhibitor Roxadustat (FG4592) for Treatment of Anemia in Chronic Kidney Disease: A Placebo-Controlled Study of Pharmacokinetic and Pharmacodynamic Profiles in Hemodialysis Patients. <i>Journal of Clinical Pharmacology</i> , 2020, 60, 1432-1440.	1.0	18
88	The Unusual Transmembrane Partition of the Hexameric Channel of the Hepatitis C Virus. <i>Structure</i> , 2018, 26, 627-634.e4.	1.6	17
89	Mapping Conformational Heterogeneity of Mitochondrial Nucleotide Transporter in Uninhibited States. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 2436-2441.	7.2	15
90	A functional NMR for membrane proteins: dynamics, ligand binding, and allosteric modulation. <i>Protein Science</i> , 2016, 25, 959-973.	3.1	14

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91	DNA-Mediated Assembly of Multispecific Antibodies for T Cell Engaging and Tumor Killing. <i>Advanced Science</i> , 2020, 7, 1900973.	5.6	14
92	The Three-Dimensional Structure of the cGMP-Dependent Protein Kinase I - Î± Leucine Zipper Domain and Its Interaction with the Myosin Binding Subunit.. <i>Blood</i> , 2004, 104, 3539-3539.	0.6	14
93	Identification of substrates of the small RNA methyltransferase Hen1 in mouse spermatogonial stem cells and analysis of its methyl-transfer domain. <i>Journal of Biological Chemistry</i> , 2018, 293, 9981-9994.	1.6	13
94	A Study on Local-Global Cooperativity in Protein Collapse. <i>Journal of Physical Chemistry B</i> , 1999, 103, 2535-2542.	1.2	10
95	Determination of the Packing Mode of the Coiled-Coil Domain of cGMP-Dependent Protein Kinase Î± in Solution Using Charge-Predicted Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2005, 127, 11918-11919.	6.6	9
96	Structural basis of interaction between the hepatitis C virus p7 channel and its blocker hexamethylene amiloride. <i>Protein and Cell</i> , 2016, 7, 300-304.	4.8	9
97	An Exhaustive Search Algorithm to Aid NMR-Based Structure Determination of Rotationally Symmetric Transmembrane Oligomers. <i>Scientific Reports</i> , 2017, 7, 17373.	1.6	9
98	Unidirectional Presentation of Membrane Proteins in Nanoparticle-Supported Liposomes. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 9866-9870.	7.2	9
99	Critical Effect of the Detergent:Protein Ratio on the Formation of the Hepatitis C Virus p7 Channel. <i>Biochemistry</i> , 2019, 58, 3834-3837.	1.2	8
100	Pharmacokinetics of Roxadustat: A Population Analysis of 2855 Dialysis- and Non-Dialysis-Dependent Patients with Chronic Kidney Disease. <i>Clinical Pharmacokinetics</i> , 2021, 60, 759-773.	1.6	8
101	NMR Model of the Entire Membrane-Interacting Region of the HIV-1 Fusion Protein and Its Perturbation of Membrane Morphology. <i>Journal of the American Chemical Society</i> , 2021, 143, 6609-6615.	6.6	8
102	Specific Lipid Binding of Membrane Proteins in Detergent Micelles Characterized by NMR and Molecular Dynamics. <i>Biochemistry</i> , 2016, 55, 5317-5320.	1.2	7
103	Reply to "Concerns with yeast mitochondrial ADP/ATP carrier's integrity in DPC" and "Dynamics and interactions of AAC3 in DPC are not functionally relevant". <i>Nature Structural and Molecular Biology</i> , 2018, 25, 749-750.	3.6	6
104	Structural Characterization of the N-Terminal Domain of the <i>Dictyostelium discoideum</i> Mitochondrial Calcium Uniporter. <i>ACS Omega</i> , 2020, 5, 6452-6460.	1.6	6
105	Developmental Compound E61 Overcomes Proteasome Inhibitor Resistance in Multiple Myeloma Cells By Targeting the Cellular Protein Folding Machinery. <i>Blood</i> , 2016, 128, 1139-1139.	0.6	6
106	Inhibitor Development against p7 Channel in Hepatitis C Virus. <i>Molecules</i> , 2021, 26, 1350.	1.7	5
107	Structural and Functional Properties of Viral Membrane Proteins. , 2018, , 147-181.		5
108	Chen et al. reply. <i>Nature</i> , 2018, 562, E19-E20.	13.7	5

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109	Structure of the Streptococcus pyogenes NAD ⁺ Glycohydrolase Translocation Domain and Its Essential Role in Toxin Binding to Oropharyngeal Keratinocytes. Journal of Bacteriology, 2022, 204, JB0036621.	1.0	4
110	Purification, crystallization and preliminary X-ray diffraction of the N-terminal calmodulin-like domain of the human mitochondrial ATP-Mg/Picarrier S _{Ca} MC1. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 68-71.	0.4	3
111	Solution Nuclear Magnetic Resonance Spectroscopy. Methods in Molecular Biology, 2013, 955, 495-517.	0.4	2
112	Mapping Conformational Heterogeneity of Mitochondrial Nucleotide Transporter in Uninhibited States. Angewandte Chemie, 2015, 127, 2466-2471.	1.6	2
113	Correction for Pielak et al., Mechanism of drug inhibition and drug resistance of influenza A M2 channel. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11425-11425.	3.3	0
114	Structure and Mechanism of Influenza Proton Channels. Biophysical Journal, 2010, 98, 198a-199a.	0.2	0
115	In Silico Assessment of Bundle Architectures of HCV P7 Protein. Biophysical Journal, 2014, 106, 54a.	0.2	0
116	Transmembrane signaling: A multiplex problem with converging solutions. Progress in Biophysics and Molecular Biology, 2015, 118, 87-88.	1.4	0
117	Pore Architecture and Ion Selectivity Filter of the Mitochondrial Calcium Uniporter. Biophysical Journal, 2017, 112, 3a-4a.	0.2	0
118	Unidirectional Presentation of Membrane Proteins in Nanoparticle-Supported Liposomes. Angewandte Chemie, 2019, 131, 9971-9975.	1.6	0
119	Unidirectional Presentation of Membrane Proteins in Nanoparticle-Supported Liposomes (Angew. Chem. 29/2019). Angewandte Chemie, 2019, 131, 10114-10114.	1.6	0
120	2590. Streptolysin O Enhances Binding of the Group A Streptococcal NAD ⁺ -Glycohydrolase Toxin to Oropharyngeal Keratinocytes. Open Forum Infectious Diseases, 2019, 6, S900-S900.	0.4	0
121	Higher-order Clustering of the Transmembrane Anchor of DR5 Drives Signaling. Biophysical Journal, 2020, 118, 354a.	0.2	0
122	Multispecific Antibodies: DNA-Mediated Assembly of Multispecific Antibodies for T Cell Engaging and Tumor Killing (Adv. Sci. 2/2020). Advanced Science, 2020, 7, 2070010.	5.6	0
123	Extended Abstract: Structure Determination of Symmetric Protein Complexes by a Complete Search of Symmetry Configuration Space Using NMR Distance Restraints. Springer Tracts in Advanced Robotics, 2008, , 335-340.	0.3	0
124	Higher-Order Clustering of the Transmembrane Anchor of DR5 Drives Signaling. FASEB Journal, 2019, 33, 792.3.	0.2	0