

Juan Antonio Vizcaño

List of Publications by Year in descending order

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Version: 2024-02-01

137
papers

27,664
citations

38660

50
h-index

9311

143
g-index

164
all docs

164
docs citations

164
times ranked

45397
citing authors

#	ARTICLE	IF	CITATIONS
1	The PRIDE database resources in 2022: a hub for mass spectrometry-based proteomics evidences. <i>Nucleic Acids Research</i> , 2022, 50, D543-D552.	6.5	2,766
2	Expression Atlas update: gene and protein expression in multiple species. <i>Nucleic Acids Research</i> , 2022, 50, D129-D140.	6.5	78
3	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. <i>Journal of Proteome Research</i> , 2022, 21, 1189-1195.	1.8	14
4	Proteomic tools for the quantitative analysis of artificial peptide libraries: detection and characterization of target-amplified PD-1 inhibitors. <i>ChemBioChem</i> , 2022, , .	1.3	2
5	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1603-1615.	1.8	14
6	Integrated view and comparative analysis of baseline protein expression in mouse and rat tissues. <i>PLoS Computational Biology</i> , 2022, 18, e1010174.	1.5	11
7	Implementing the reuse of public DIA proteomics datasets: from the PRIDE database to Expression Atlas. <i>Scientific Data</i> , 2022, 9, .	2.4	13
8	Data Management of Sensitive Human Proteomics Data: Current Practices, Recommendations, and Perspectives for the Future. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100071.	2.5	25
9	BioContainers Registry: Searching Bioinformatics and Proteomics Tools, Packages, and Containers. <i>Journal of Proteome Research</i> , 2021, 20, 2056-2061.	1.8	19
10	An integrated landscape of protein expression in human cancer. <i>Scientific Data</i> , 2021, 8, 115.	2.4	38
11	Protamine Characterization by Top-Down Proteomics: Boosting Proteoform Identification with DBSCAN. <i>Proteomes</i> , 2021, 9, 21.	1.7	7
12	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021, 18, 768-770.	9.0	47
13	The growing need for controlled data access models in clinical proteomics and metabolomics. <i>Nature Communications</i> , 2021, 12, 5787.	5.8	17
14	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	5.8	45
15	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020, 48, D77-D83.	6.5	363
16	The ProteomeXchange consortium in 2020: enabling "big data" approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	6.5	491
17	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	9.4	273
18	The Human Immunopeptidome Project: A Roadmap to Predict and Treat Immune Diseases. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 31-49.	2.5	65

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19	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	5.8	152
20	Using Deep Learning to Extrapolate Protein Expression Measurements. <i>Proteomics</i> , 2020, 20, e2000009.	1.3	9
21	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020, 36, 2636-2642.	1.8	47
22	Review of Issues and Solutions to Data Analysis Reproducibility and Data Quality in Clinical Proteomics. <i>Methods in Molecular Biology</i> , 2020, 2051, 345-371.	0.4	3
23	Quantifying the impact of public omics data. <i>Nature Communications</i> , 2019, 10, 3512.	5.8	79
24	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019, 16, 939-940.	9.0	55
25	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. <i>Analytical Chemistry</i> , 2019, 91, 3302-3310.	3.2	43
26	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	1.8	22
27	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
28	Spectral Clustering Improves Label-Free Quantification of Low-Abundant Proteins. <i>Journal of Proteome Research</i> , 2019, 18, 1477-1485.	1.8	13
29	Quantitative Proteomics Data in the Public Domain: Challenges and Opportunities. <i>Methods in Molecular Biology</i> , 2019, 1977, 217-235.	0.4	5
30	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , 2019, 47, D442-D450.	6.5	6,449
31	Response to "Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra". <i>Journal of Proteome Research</i> , 2018, 17, 1993-1996.	1.8	9
32	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018, 17, 1321-1325.	1.8	35
33	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018, 46, D246-D251.	6.5	365
34	Direct Evidence of the Presence of Cross-Linked A β 2 Dimers in the Brains of Alzheimer's Disease Patients. <i>Analytical Chemistry</i> , 2018, 90, 4552-4560.	3.2	37
35	The SystemMHC Atlas project. <i>Nucleic Acids Research</i> , 2018, 46, D1237-D1247.	6.5	119
36	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	1.8	47

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37	Minimal Information About an Immuno- Peptidomics Experiment (MIAIPE) . <i>Proteomics</i> , 2018, 18, e1800110.	1.3	23
38	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. <i>Genome Biology</i> , 2018, 19, 12.	3.8	21
39	Future Prospects of Spectral Clustering Approaches in Proteomics. <i>Proteomics</i> , 2018, 18, e1700454.	1.3	15
40	A Golden Age for Working with Public Proteomics Data. <i>Trends in Biochemical Sciences</i> , 2017, 42, 333-341.	3.7	92
41	Synthetic human proteomes for accelerating protein research. <i>Nature Methods</i> , 2017, 14, 240-242.	9.0	6
42	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409.	9.4	159
43	Enhanced Missing Proteins Detection in NCI60 Cell Lines Using an Integrative Search Engine Approach. <i>Journal of Proteome Research</i> , 2017, 16, 4374-4390.	1.8	13
44	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	1.8	87
45	Using the PRIDE Database and ProteomeXchange for Submitting and Accessing Public Proteomics Datasets. <i>Current Protocols in Bioinformatics</i> , 2017, 59, 13.31.1-13.31.12.	25.8	48
46	OLS Client and OLS Dialog: Open Source Tools to Annotate Public Omics Datasets. <i>Proteomics</i> , 2017, 17, 1700244.	1.3	17
47	Lack of Glycogenin Causes Glycogen Accumulation and Muscle Function Impairment. <i>Cell Metabolism</i> , 2017, 26, 256-266.e4.	7.2	59
48	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1275-1285.	2.5	55
49	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017, 45, D1100-D1106.	6.5	860
50	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	0.8	13
51	Accurate and fast feature selection workflow for high-dimensional omics data. <i>PLoS ONE</i> , 2017, 12, e0189875.	1.1	60
52	Detection of Missing Proteins Using the PRIDE Database as a Source of Mass Spectrometry Evidence. <i>Journal of Proteome Research</i> , 2016, 15, 4101-4115.	1.8	15
53	2016 update of the PRIDE database and its related tools. <i>Nucleic Acids Research</i> , 2016, 44, D447-D456.	6.5	3,451
54	Making sense of big data in health research: Towards an EU action plan. <i>Genome Medicine</i> , 2016, 8, 71.	3.6	190

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55	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016, 13, 651-656.	9.0	147
56	Exploring the potential of public proteomics data. <i>Proteomics</i> , 2016, 16, 214-225.	1.3	72
57	PRIDE Inspector Toolsuite: Moving Toward a Universal Visualization Tool for Proteomics Data Standard Formats and Quality Assessment of ProteomeXchange Datasets. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 305-317.	2.5	140
58	Ten Simple Rules for Taking Advantage of Git and GitHub. <i>PLoS Computational Biology</i> , 2016, 12, e1004947.	1.5	96
59	Introducing the PRIDE Archive RESTful web services. <i>Nucleic Acids Research</i> , 2015, 43, W599-W604.	6.5	18
60	A public repository for mass spectrometry imaging data. <i>Analytical and Bioanalytical Chemistry</i> , 2015, 407, 2027-2033.	1.9	31
61	Delicate Metabolic Control and Coordinated Stress Response Critically Determine Antifungal Tolerance of <i>Candida albicans</i> Biofilm Persisters. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6101-6112.	1.4	67
62	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. <i>Bioinformatics</i> , 2015, 31, 2903-2905.	1.8	30
63	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3415-3431.	1.8	53
64	Proteomics Data Visualisation. <i>Proteomics</i> , 2015, 15, 1339-1340.	1.3	3
65	Development of data representation standards by the human proteome organization proteomics standards initiative. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 495-506.	2.2	54
66	Embedding standards in metabolomics: the Metabolomics Society data standards task group. <i>Metabolomics</i> , 2015, 11, 782-783.	1.4	13
67	Open source libraries and frameworks for biological data visualisation: A guide for developers. <i>Proteomics</i> , 2015, 15, 1356-1374.	1.3	43
68	Analysis of the tryptic search space in UniProt databases. <i>Proteomics</i> , 2015, 15, 48-57.	1.3	13
69	Identifying novel biomarkers through data mining—A realistic scenario?. <i>Proteomics - Clinical Applications</i> , 2015, 9, 437-443.	0.8	20
70	Making proteomics data accessible and reusable: Current state of proteomics databases and repositories. <i>Proteomics</i> , 2015, 15, 930-950.	1.3	181
71	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014, 14, 2389-2399.	1.3	23
72	Analysis of the Protein Domain and Domain Architecture Content in Fungi and Its Application in the Search of New Antifungal Targets. <i>PLoS Computational Biology</i> , 2014, 10, e1003733.	1.5	25

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73	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	2.5	42
74	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2765-2775.	2.5	130
75	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	9.4	2,505
76	How to submit MS proteomics data to ProteomeXchange via the PRIDE database. <i>Proteomics</i> , 2014, 14, 2233-2241.	1.3	54
77	jmzTab: A Java interface to the mzTab data standard. <i>Proteomics</i> , 2014, 14, 1328-1332.	1.3	16
78	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 98-107.	1.1	36
79	Open source libraries and frameworks for mass spectrometry based proteomics: A developer's perspective. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 63-76.	1.1	67
80	A Survey of Molecular Descriptors Used in Mass Spectrometry Based Proteomics. <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 388-397.	1.0	5
81	PRIDE Cluster: building a consensus of proteomics data. <i>Nature Methods</i> , 2013, 10, 95-96.	9.0	62
82	Pride-asap: Automatic fragment ion annotation of identified PRIDE spectra. <i>Journal of Proteomics</i> , 2013, 95, 89-92.	1.2	17
83	HI-Bone: A Scoring System for Identifying Phenylisothiocyanate-Derivatized Peptides Based on Precursor Mass and High Intensity Fragment Ions. <i>Analytical Chemistry</i> , 2013, 85, 3515-3520.	3.2	7
84	The mzQuantML Data Standard for Mass Spectrometry-based Quantitative Studies in Proteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2332-2340.	2.5	66
85	Tools (Viewer, Library and Validator) that Facilitate Use of the Peptide and Protein Identification Standard Format, Termed mzIdentML. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3026-3035.	2.5	32
86	Shorthand notation for lipid structures derived from mass spectrometry. <i>Journal of Lipid Research</i> , 2013, 54, 1523-1530.	2.0	689
87	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the <i>Journal of Biological Databases and Curation</i> , 2013, 2013, bat009-bat009.	1.4	76
88	From Peptidome to PRIDE : Public proteomics data migration at a large scale. <i>Proteomics</i> , 2013, 13, 1692-1695.	1.3	12
89	LipidHome: A Database of Theoretical Lipids Optimized for High Throughput Mass Spectrometry Lipidomics. <i>PLoS ONE</i> , 2013, 8, e61951.	1.1	69
90	Proteomics Data Exchange and Storage: The Need for Common Standards and Public Repositories. <i>Methods in Molecular Biology</i> , 2013, 1007, 317-333.	0.4	11

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91	Ontology Lookup Service for Controlled Vocabularies and Data Annotation. , 2013, , 1562-1565.		0
92	The PRoteomics IDentification (PRIDE) Converter 2 Framework: An Improved Suite of Tools to Facilitate Data Submission to the PRIDE Database and the ProteomeXchange Consortium. Molecular and Cellular Proteomics, 2012, 11, 1682-1689.	2.5	105
93	Improvements in the protein identifier cross-reference service. Nucleic Acids Research, 2012, 40, W276-W280.	6.5	27
94	PRIDE: Quality control in a proteomics data repository. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas004-bas004.	1.4	35
95	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. Molecular and Cellular Proteomics, 2012, 11, M111.014381-1-M111.014381-10.	2.5	175
96	The Proteomics Identifications (PRIDE) database and associated tools: status in 2013. Nucleic Acids Research, 2012, 41, D1063-D1069.	6.5	1,858
97	Isoelectric point optimization using peptide descriptors and support vector machines. Journal of Proteomics, 2012, 75, 2269-2274.	1.2	36
98	Ten Years of Standardizing Proteomic Data: A Report on the HUPOâ€PSI Spring Workshop. Proteomics, 2012, 12, 2767-2772.	1.3	16
99	jmz<sc>l</sc>dent<sc>ML API</sc>: A <sc>J</sc>ava interface to the mz<sc>l</sc>dent<sc>ML</sc> standard for peptide and protein identification data. Proteomics, 2012, 12, 790-794.	1.3	29
100	jmzReader: A Java parser library to process and visualize multiple text and XMLâ€based mass spectrometry data formats. Proteomics, 2012, 12, 795-798.	1.3	30
101	PRIDE Inspector: a tool to visualize and validate MS proteomics data. Nature Biotechnology, 2012, 30, 135-137.	9.4	109
102	Consequences of the discontinuation of the International Protein Index (IPI) database and its substitution by the UniProtKB â€complete proteomeâ€sets. Proteomics, 2011, 11, 4434-4438.	1.3	25
103	Quality Control in Proteomics. Proteomics, 2011, 11, 1015-1016.	1.3	11
104	Proteomic Temporal Profile of Human Brain Endothelium After Oxidative Stress. Stroke, 2011, 42, 37-43.	1.0	51
105	Published and Perished? The Influence of the Searched Protein Database on the Long-Term Storage of Proteomics Data. Molecular and Cellular Proteomics, 2011, 10, M111.008490.	2.5	20
106	Critical amino acid residues in proteins: a BioMart integration of Reactome protein annotations with PRIDE mass spectrometry data and COSMIC somatic mutations. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar047.	1.4	8
107	Submitting Proteomics Data to PRIDE Using PRIDE Converter. Methods in Molecular Biology, 2011, 694, 237-253.	0.4	2
108	PRIDE and â€Database on Demandâ€as Valuable Tools for Computational Proteomics. Methods in Molecular Biology, 2011, 696, 93-105.	0.4	13

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109	EST Analysis Pipeline: Use of Distributed Computing Resources. <i>Methods in Molecular Biology</i> , 2011, 722, 103-120.	0.4	0
110	Proteomics data repositories: Providing a safe haven for your data and acting as a springboard for further research. <i>Journal of Proteomics</i> , 2010, 73, 2136-2146.	1.2	61
111	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	1.3	54
112	The Ontology Lookup Service: bigger and better. <i>Nucleic Acids Research</i> , 2010, 38, W155-W160.	6.5	108
113	The Proteomics Identifications database: 2010 update. <i>Nucleic Acids Research</i> , 2010, 38, D736-D742.	6.5	220
114	PRIDE: Data Submission and Analysis. <i>Current Protocols in Protein Science</i> , 2010, 60, Unit 25.4.	2.8	13
115	A guide to the Proteomics Identifications Database proteomics data repository. <i>Proteomics</i> , 2009, 9, 4276-4283.	1.3	220
116	Charting online OMICS resources: A navigational chart for clinical researchers. <i>Proteomics - Clinical Applications</i> , 2009, 3, 18-29.	0.8	12
117	PRIDE Converter: making proteomics data-sharing easy. <i>Nature Biotechnology</i> , 2009, 27, 598-599.	9.4	159
118	A HUPO test sample study reveals common problems in mass spectrometry-based proteomics. <i>Nature Methods</i> , 2009, 6, 423-430.	9.0	316
119	Gene expression analysis of the biocontrol fungus <i>Trichoderma harzianum</i> in the presence of tomato plants, chitin, or glucose using a high-density oligonucleotide microarray. <i>BMC Microbiology</i> , 2009, 9, 217.	1.3	58
120	Analysis of the experimental detection of central nervous system-related genes in human brain and cerebrospinal fluid datasets. <i>Proteomics</i> , 2008, 8, 1138-1148.	1.3	18
121	Analyzing Large-Scale Proteomics Projects with Latent Semantic Indexing. <i>Journal of Proteome Research</i> , 2008, 7, 182-191.	1.8	41
122	Partial silencing of a hydroxy-methylglutaryl-CoA reductase-encoding gene in <i>Trichoderma harzianum</i> CECT 2413 results in a lower level of resistance to lovastatin and lower antifungal activity. <i>Fungal Genetics and Biology</i> , 2007, 44, 269-283.	0.9	60
123	The PSI formal document process and its implementation on the PSI website. <i>Proteomics</i> , 2007, 7, 2355-2357.	1.3	45
124	Generation, annotation, and analysis of ESTs from four different <i>Trichoderma</i> strains grown under conditions related to biocontrol. <i>Applied Microbiology and Biotechnology</i> , 2007, 75, 853-862.	1.7	39
125	Characterization of genes encoding novel peptidases in the biocontrol fungus <i>Trichoderma harzianum</i> CECT 2413 using the TrichoEST functional genomics approach. <i>Current Genetics</i> , 2007, 51, 331-342.	0.8	71
126	Cloning and characterization of the <i>erg1</i> gene of <i>Trichoderma harzianum</i> : Effect of the <i>erg1</i> silencing on ergosterol biosynthesis and resistance to terbinafine. <i>Fungal Genetics and Biology</i> , 2006, 43, 164-178.	0.9	77

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127	ThPTR2, a di/tri-peptide transporter gene from <i>Trichoderma harzianum</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 234-246.	0.9	41
128	Detection of peptaibols and partial cloning of a putative peptaibol synthetase gene from <i>T. harzianum</i> CECT 2413. <i>Folia Microbiologica</i> , 2006, 51, 114-120.	1.1	18
129	Generation, annotation and analysis of ESTs from <i>Trichoderma harzianum</i> CECT 2413. <i>BMC Genomics</i> , 2006, 7, 193.	1.2	60
130	A comparison of the phenotypic and genetic stability of recombinant <i>Trichoderma</i> spp. generated by protoplast- and <i>Agrobacterium</i> -mediated transformation. <i>Journal of Microbiology</i> , 2006, 44, 383-95.	1.3	43
131	Detection of putative peptide synthetase genes in <i>Trichoderma</i> species: Application of this method to the cloning of a gene from <i>T. harzianum</i> CECT 2413. <i>FEMS Microbiology Letters</i> , 2005, 244, 139-148.	0.7	41
132	Screening of antimicrobial activities in <i>Trichoderma</i> isolates representing three <i>Trichoderma</i> sections. <i>Mycological Research</i> , 2005, 109, 1397-1406.	2.5	47
133	Genetic diversity shown in <i>Trichoderma</i> biocontrol isolates. <i>Mycological Research</i> , 2004, 108, 897-906.	2.5	74
134	Cell wall-degrading isoenzyme profiles of <i>Trichoderma</i> biocontrol strains show correlation with rDNA taxonomic species. <i>Current Genetics</i> , 2004, 46, 277-286.	0.8	49
135	Colour pigments of <i>Trichoderma harzianum</i> . <i>Journal of Chromatography A</i> , 2000, 896, 61-68.	1.8	15
136	Microbial Contamination of Carcasses and Equipment from an Iberian Pig Slaughterhouse. <i>Journal of Food Protection</i> , 2000, 63, 1670-1675.	0.8	34
137	Separation and Identification of Volatile Components in the Fermentation Broth of <i>Trichoderma atroviride</i> by Solid-Phase Extraction and Gas Chromatography–Mass Spectrometry. <i>Journal of Chromatographic Science</i> , 2000, 38, 421-424.	0.7	66