StevenÂ E Brenner

List of Publications by Year
in descending order

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159 papers	45,724 citations	17405 63 h-index	8599 146 g-index
181 all docs	181 docs citations	181 times ranked	51198 citing authors

#	Article	IF	Citations
1	WebLogo: A Sequence Logo Generator. Genome Research, 2004, 14, 1188-1190.	2.4	10,751
2	SCOP: a structural classification of proteins database for the investigation of sequences and structures. Journal of Molecular Biology, 1995, 247, 536-540.	2.0	5,400
3	SCOP: A structural classification of proteins database for the investigation of sequences and structures. Journal of Molecular Biology, 1995, 247, 536-540.	2.0	3,952
4	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	6.0	3,227
5	The Bioperl Toolkit: Perl Modules for the Life Sciences. Genome Research, 2002, 12, 1611-1618.	2.4	1,427
6	The developmental transcriptome of Drosophila melanogaster. Nature, 2011, 471, 473-479.	13.7	1,379
7	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
8	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	9.4	955
9	Evidence for the widespread coupling of alternative splicing and nonsense-mediated mRNA decay in humans. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 189-192.	3.3	920
10	Data growth and its impact on the SCOP database: new developments. Nucleic Acids Research, 2007, 36, D419-D425.	6.5	854
11	SCOP database in 2004: refinements integrate structure and sequence family data. Nucleic Acids Research, 2004, 32, 226D-229.	6.5	815
12	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
13	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	13.7	744
14	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. PLoS Biology, 2007, 5, e16.	2.6	736
15	SCOPe: Structural Classification of Proteinsâ€"extended, integrating SCOP and ASTRAL data and classification of new structures. Nucleic Acids Research, 2014, 42, D304-D309.	6.5	627
16	Unproductive splicing of SR genes associated with highly conserved and ultraconserved DNA elements. Nature, 2007, 446, 926-929.	13.7	593
17	Biases in Illumina transcriptome sequencing caused by random hexamer priming. Nucleic Acids Research, 2010, 38, e131-e131.	6.5	573
18	SCOP: a Structural Classification of Proteins database. Nucleic Acids Research, 2000, 28, 257-259.	6.5	533

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19	Assessing sequence comparison methods with reliable structurally identified distant evolutionary relationships. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 6073-6078.	3.3	493
20	The ASTRAL Compendium in 2004. Nucleic Acids Research, 2004, 32, 189D-192.	6.5	480
21	The ASTRAL compendium for protein structure and sequence analysis. Nucleic Acids Research, 2000, 28, 254-256.	6.5	432
22	SCOP database in 2002: refinements accommodate structural genomics. Nucleic Acids Research, 2002, 30, 264-267.	6.5	403
23	The Impact of Structural Genomics: Expectations and Outcomes. Science, 2006, 311, 347-351.	6.0	366
24	Errors in genome annotation. Trends in Genetics, 1999, 15, 132-133.	2.9	335
25	Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. ISME Journal, 2012, 6, 1440-1444.	4.4	326
26	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
27	The evolving roles of alternative splicing. Current Opinion in Structural Biology, 2004, 14, 273-282.	2.6	304
28	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	13.7	289
29	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	3.8	261
30	SCOP: a Structural Classification of Proteins database. Nucleic Acids Research, 1999, 27, 254-256.	6.5	208
31	Conservation of an RNA regulatory map between Drosophila and mammals. Genome Research, 2011, 21, 193-202.	2.4	208
32	The Coupling of Alternative Splicing and Nonsense-Mediated mRNA Decay. Advances in Experimental Medicine and Biology, 2007, 623, 190-211.	0.8	202
33	RNA structural motifs: building blocks of a modular biomolecule. Quarterly Reviews of Biophysics, 2005, 38, 221-243.	2.4	184
34	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	13.7	184
35	Newborn Sequencing in Genomic Medicine and Public Health. Pediatrics, 2017, 139, .	1.0	174
36	Population statistics of protein structures: lessons from structural classifications. Current Opinion in Structural Biology, 1997, 7, 369-376.	2.6	173

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37	Protein Molecular Function Prediction by Bayesian Phylogenomics. PLoS Computational Biology, 2005, 1, e45.	1.5	162
38	An unappreciated role for RNA surveillance. Genome Biology, 2004, 5, R8.	13.9	159
39	Widespread predicted nonsense-mediated mRNA decay of alternatively-spliced transcripts of human normal and disease genes. Bioinformatics, 2003, 19, i118-i121.	1.8	155
40	A tour of structural genomics. Nature Reviews Genetics, 2001, 2, 801-809.	7.7	152
41	Regulation of Splicing Factors by Alternative Splicing and NMD Is Conserved between Kingdoms Yet Evolutionarily Flexible. Molecular Biology and Evolution, 2015, 32, 1072-1079.	3.5	143
42	SCOPe: classification of large macromolecular structures in the structural classification of proteinsâ€"extended database. Nucleic Acids Research, 2019, 47, D475-D481.	6.5	122
43	ASTRAL compendium enhancements. Nucleic Acids Research, 2002, 30, 260-263.	6.5	117
44	The role of exome sequencing in newborn screening for inborn errors of metabolism. Nature Medicine, 2020, 26, 1392-1397.	15.2	112
45	Sulfotransferases and Sulfatases in Mycobacteria. Chemistry and Biology, 2002, 9, 767-776.	6.2	109
46	Target selection for structural genomics. , 2000, 7, 967-969.		108
47	Global analysis of positive and negative pre-mRNA splicing regulators in Drosophila. Genes and Development, 2005, 19, 1306-1314.	2.7	106
48	Multisystem Anomalies in Severe Combined Immunodeficiency with Mutant BCL11B. New England Journal of Medicine, 2016, 375, 2165-2176.	13.9	104
49	SCOR: a Structural Classification of RNA database. Nucleic Acids Research, 2002, 30, 392-394.	6.5	103
50	Expectations from structural genomics. Protein Science, 2000, 9, 197-200.	3.1	99
51	SCOR: Structural Classification of RNA, version 2.0. Nucleic Acids Research, 2004, 32, 182D-184.	6.5	98
52	Association of gut microbiota with post-operative clinical course in Crohnâ€™s disease. BMC Gastroenterology, 2013, 13, 131.	0.8	95
53	Combined Immunodeficiency Due to MALT1 Mutations, Treated by Hematopoietic Cell Transplantation. Journal of Clinical Immunology, 2015, 35, 135-146.	2.0	94
54	Newborn Screening for SCID Identifies Patients with Ataxia Telangiectasia. Journal of Clinical Immunology, 2013, 33, 540-549.	2.0	92

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55	Comparison of D. melanogaster and C. elegans developmental stages, tissues, and cells by modENCODE RNA-seq data. Genome Research, 2014, 24, 1086-1101.	2.4	88
56	Genome-Wide Identification of Alternative Splice Forms Down-Regulated by Nonsense-Mediated mRNA Decay in Drosophila. PLoS Genetics, 2009, 5, e1000525.	1.5	87
57	SCOPe: Manual Curation and Artifact Removal in the Structural Classification of Proteins â€“ extended Database. Journal of Molecular Biology, 2017, 429, 348-355.	2.0	85
58	A novel human autoimmune syndrome caused by combined hypomorphic and activating mutations in ZAP-70. Journal of Experimental Medicine, 2016, 213, 155-165.	4.2	83
59	Gene duplications in H. influenzae. Nature, 1995, 378, 140-140.	13.7	82
60	[37] Understanding protein structure: Using scop for fold interpretation. Methods in Enzymology, 1996, 266, 635-643.	0.4	80
61	Genome-wide Analysis of Alternative Pre-mRNA Splicing and RNA-Binding Specificities of the Drosophila hnRNP A/B Family Members. Molecular Cell, 2009, 33, 438-449.	4.5	79
62	DNA recognition code of transcription factors. Protein Engineering, Design and Selection, 1995, 8, 319-328.	1.0	78
63	Regulation of alternative splicing in Drosophila by 56 RNA binding proteins. Genome Research, 2015, 25, 1771-1780.	2.4	77
64	Protein secondary structure: entropy, correlations and prediction. Bioinformatics, 2004, 20, 1603-1611.	1.8	71
65	MeRNA: a database of metal ion binding sites in RNA structures. Nucleic Acids Research, 2006, 34, D131-D134.	6.5	67
66	Implications of structural genomics target selection strategies: Pfam5000, whole genome, and random approaches. Proteins: Structure, Function and Bioinformatics, 2004, 58, 166-179.	1.5	61
67	Three-dimensional motifs from the SCOR, structural classification of RNA database: extruded strands, base triples, tetraloops and U-turns. Nucleic Acids Research, 2004, 32, 2342-2352.	6.5	60
68	The RNA Ontology Consortium: An open invitation to the RNA community. Rna, 2006, 12, 533-541.	1.6	59
69	SCOPe: improvements to the structural classification of proteins â€“ extended database to facilitate variant interpretation and machine learning. Nucleic Acids Research, 2022, 50, D553-D559.	6.5	59
70	Genome-Wide Analysis Reveals an Unexpected Function for the Drosophila Splicing Factor U2AF50 in the Nuclear Export of Intronless mRNAs. Molecular Cell, 2004, 14, 775-786.	4.5	56
71	Genome-scale phylogenetic function annotation of large and diverse protein families. Genome Research, 2011, 21, 1969-1980.	2.4	54
72	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	2.6	54

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73	The evolution of function within the Nudix homology clan. Proteins: Structure, Function and Bioinformatics, 2017, 85, 775-811.	1.5	53
74	The PRESAGE database for structural genomics. Nucleic Acids Research, 1999, 27, 251-253.	6.5	48
75	A method for the alignment of heterogeneous macromolecules from electron microscopy. Journal of Structural Biology, 2009, 166, 67-78.	1.3	40
76	Opportunities and challenges for the computational interpretation of rare variation in clinically important genes. American Journal of Human Genetics, 2021, 108, 535-548.	2.6	40
77	Measurements of protein sequence-structure correlations. Proteins: Structure, Function and Bioinformatics, 2004, 57, 804-810.	1.5	39
78	SIFTER search: a web server for accurate phylogeny-based protein function prediction. Nucleic Acids Research, 2015, 43, W141-W147.	6.5	39
79	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	1.1	39
80	Reports from CAGI: The Critical Assessment of Genome Interpretation. Human Mutation, 2017, 38, 1039-1041.	1.1	38
81	The value of protein structure classification informationâ€"Surveying the scientific literature. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2025-2038.	1.5	37
82	Automated multi-model reconstruction from single-particle electron microscopy data. Journal of Structural Biology, 2010, 170, 98-108.	1.3	34
83	Nijmegen Breakage Syndrome Detected by Newborn Screening for T Cell Receptor Excision Circles (TRECs). Journal of Clinical Immunology, 2015, 35, 227-233.	2.0	34
84	Registered access: authorizing data access. European Journal of Human Genetics, 2018, 26, 1721-1731.	1.4	33
85	SCOP, Structural Classification of Proteins Database: Applications to Evaluation of the Effectiveness of Sequence Alignment Methods and Statistics of Protein Structural Data. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1147-1154.	2.5	31
86	Classification of multi-helical DNA-binding domains and application to predict the DBD structures of Ïf factor, LysR, OmpR/PhoB, CENP-B, Rap1, and XylS/Ada/AraC. FEBS Letters, 1995, 372, 215-221.	1.3	30
87	A generalized affine gap model significantly improves protein sequence alignment accuracy. Proteins: Structure, Function and Bioinformatics, 2004, 58, 329-338.	1.5	29
88	Structural Genomics of Minimal Organisms and Protein Fold Space. Journal of Structural and Functional Genomics, 2005, 6, 63-70.	1.2	29
89	Survey of large protein complexes in D. vulgaris reveals great structural diversity. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16580-16585.	3.3	29
90	StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants. American Journal of Human Genetics, 2022, 109, 195-209.	2.6	29

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91	Target selection and deselection at the Berkeley Structural Genomics Center. Proteins: Structure, Function and Bioinformatics, 2005, 62, 356-370.	1.5	27
92	Common sense for our genomes. Nature, 2007, 449, 783-784.	13.7	27
93	Structural Studies of the Nudix Hydrolase DR1025 From Deinococcus radiodurans and its Ligand Complexes. Journal of Molecular Biology, 2004, 339, 103-116.	2.0	25
94	Multiple breast cancer risk variants are associated with differential transcript isoform expression in tumors. Human Molecular Genetics, 2015, 24, 7421-7431.	1.4	24
95	VIPdb, a genetic Variant Impact Predictor Database. Human Mutation, 2019, 40, 1202-1214.	1.1	24
96	Be prepared for the big genome leak. Nature, 2013, 498, 139-139.	13.7	24
97	Statistical evaluation of pairwise protein sequence comparison with the Bayesian bootstrap. Bioinformatics, 2005, 21, 3824-3831.	1.8	22
98	High-throughput Isolation and Characterization of Untagged Membrane Protein Complexes: Outer Membrane Complexes of Desulfovibrio vulgaris. Journal of Proteome Research, 2012, 11, 5720-5735.	1.8	22
99	Application of full-genome analysis to diagnose rare monogenic disorders. Npj Genomic Medicine, 2021, 6, 77.	1.7	22
100	Putting benchmarks in their rightful place: The heart of computational biology. PLoS Computational Biology, 2018, 14, e1006494.	1.5	20
101	Using metabolic pathway databases for functional annotation. Trends in Genetics, 1998, 14, 332-333.	2.9	19
102	An alternative model of amino acid replacement. Bioinformatics, 2005, 21, 975-980.	1.8	19
103	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. Molecular and Cellular Proteomics, 2016, 15, 1539-1555.	2.5	16
104	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399.	1.1	16
105	Identification and experimental validation of splicing regulatory elements in Drosophila melanogaster reveals functionally conserved splicing enhancers in metazoans. Rna, 2011, 17, 1884-1894.	1.6	14
106	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	1.1	14
107	A novel plant enzyme with dual activity: an atypical Nudix hydrolase and a dipeptidyl peptidase III. Biological Chemistry, 2017, 398, 101-112.	1.2	14
108	Pairwise alignment incorporating dipeptide covariation. Bioinformatics, 2005, 21, 3704-3710.	1.8	13

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109	PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE. , 2014, , .		13
110	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	1.1	13
111	Blast, blitz, blocks and beauty; sequence comparison on the net. Trends in Genetics, 1995, 11, 330-331.	2.9	12
112	Phylogenetic molecular function annotation. Journal of Physics: Conference Series, 2009, 180, 012024.	0.3	12
113	Quantitative Tagless Copurification: A Method to Validate and Identify Protein-Protein Interactions. Molecular and Cellular Proteomics, 2016, 15, 2186-2202.	2.5	12
114	A quantitative methodology for the de novo design of proteins. Protein Science, 1994, 3, 1871-1882.	3.1	11
115	Alignment-free local structural search by writhe decomposition. Bioinformatics, 2010, 26, 1176-1184.	1.8	11
116	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGIâ€5 intellectual disability challenge. Human Mutation, 2019, 40, 1330-1345.	1.1	11
117	An SF1 affinity model to identify branch point sequences in human introns. Nucleic Acids Research, 2011, 39, 2344-2356.	6.5	10
118	Substrate specificity characterization for eight putative nudix hydrolases. Evaluation of criteria for substrate identification within the Nudix family. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1810-1822.	1.5	10
119	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. Human Mutation, 2019, 40, 1373-1391.	1.1	10
120	Assessment of predicted enzymatic activity of Î±â€•N â€acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	1.1	10
121	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	1.1	10
122	Newborn screening for neurodevelopmental diseases: Are we there yet?. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2022, 190, 222-230.	0.7	10
123	A novel PRRT2 pathogenic variant in a family with paroxysmal kinesigenic dyskinesia and benign familial infantile seizures. Journal of Physical Education and Sports Management, 2018, 4, a002287.	0.5	9
124	Genomic Analysis of Historical Cases with Positive Newborn Screens for Short-Chain Acyl-CoA Dehydrogenase Deficiency Shows That a Validated Second-Tier Biochemical Test Can Replace Future Sequencing. International Journal of Neonatal Screening, 2020, 6, 41.	1.2	9
125	Structural genomics and structural biology: compare and contrast. Genome Biology, 2004, 5, 343.	13.9	8
126	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGIâ€5. Human Mutation, 2019, 40, 1474-1485.	1.1	8

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127	Assessing the performance of in silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. Human Mutation, 2019, 40, 1612-1622.	1.1	8
128	Revealing molecular pathways for cancer cell fitness through a genetic screen of the cancer translatome. Cell Reports, 2021, 35, 109321.	2.9	8
129	A graphical model for predicting protein molecular function. , 2006, , .		7
130	PLoS Computational Biology: A New Community Journal. PLoS Computational Biology, 2005, 1, e4.	1.5	7
131	Molecular function prediction for a family exhibiting evolutionary tendencies toward substrate specificity swapping: Recurrence of tyrosine aminotransferase activity in the Î± subfamily. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1593-1609.	1.5	6
132	FDA oversight of NSIGHT genomic research: the need for an integrated systems approach to regulation. Npj Genomic Medicine, 2019, 4, 32.	1.7	6
133	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	1.1	5
134	A continuous fluorescence assay for the characterization of Nudix hydrolases. Analytical Biochemistry, 2013, 437, 178-184.	1.1	4
135	Automated particle correspondence and accurate tilt-axis detection in tilted-image pairs. Journal of Structural Biology, 2014, 187, 66-75.	1.3	4
136	PRECISION MEDICINE: DATA AND DISCOVERY FOR IMPROVED HEALTH AND THERAPY. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 243-8.	0.7	4
137	ANDY: a general, fault-tolerant tool for database searching on computer clusters. Bioinformatics, 2006, 22, 618-620.	1.8	3
138	PRECISION MEDICINE: FROM DIPLOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. , 2018, , .		3
139	When Biology Gets Personal: Hidden Challenges of Privacy and Ethics in Biological Big Data. , 2018, , .		3
140	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS THERAPY- SESSION INTRODUCTION. , 2013, 19, 224-8.		2
141	PRECISION MEDICINE: DATA AND DISCOVERY FOR IMPROVED HEALTH AND THERAPY. , 2016, , .		2
142	The evolving roles of alternative splicing. Current Opinion in Structural Biology, 2004, 14, 273-273.	2.6	1
143	Optimal and fast rotational alignment of volumes with missing data in Fourier space. Journal of Structural Biology, 2013, 184, 345-347.	1.3	1
144	Ten Years of PLoSâ€¡ Computational Biology: A Decade of Appreciation and Innovation. PLoS Computational Biology, 2015, 11, e1004317.	1.5	1

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145	Nijmegen Breakage Syndrome Detected By Newborn Screening for T Cell Receptor Excision Circles (TRECs). Journal of Allergy and Clinical Immunology, 2015, 135, AB14.	1.5	1
146	USE OF GENOME DATA IN NEWBORNS AS A STARTING POINT FOR LIFE-LONG PRECISION MEDICINE. , 2016, , .		1
147	Non-Coding Variation: The 2016 Annual Scientific Meeting of the Human Genome Variation Society. Human Mutation, 2017, 38, 460-463.	1.1	1
148	Abstract 3295: CAGI: The Critical Assessment of Genome Interpretation, a community experiment to evaluate phenotype prediction: implications for predicting impact of variants in cancer. Cancer Research, 2018, 78, 3295-3295.	0.4	1
149	Navigating ethical quandaries with the privacy dilemma of biomedical datasets. , 2019, , .		1
150	Characterization of Illumina Sequencing Errors: Implications for Investigations of the Gut Microbiota. Gastroenterology, 2011, 140, S-331.	0.6	0
151	THE FUTURE OF GENOME-BASED MEDICINE. , 2012, , .		0
152	Novel Presentation of Recurrent Infection in a Family with NOD2 Mutation. Journal of Allergy and Clinical Immunology, 2015, 135, AB383.	1.5	0
153	Back Cover, Volume 40, Issue 9. Human Mutation, 2019, 40, ii.	1.1	0
154	Computational Challenges and Artificial Intelligence in Precision Medicine. , 2020, , .		0
155	Developing Computational Biology. PLoS Computational Biology, 2007, 3, e157.	1.5	0
156	REGULATORY RNA. , 2016, , .		0
157	Precision Medicine: Improving health through high-resolution analysis of personal data. , 2018, , .		0
158	Precision Medicine: Addressing the Challenges of Sharing, Analysis, and Privacy at Scale. , 2019, , .		0
159	Precision Medicine: Using Artificial Intelligence to Improve Diagnostics and Healthcare. , 2021, , .		0