Jean-Christophe Nebel

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Prediction of Honeybee Swarms Using Audio Signals and Convolutional Neural Networks. Ambient Intelligence and Smart Environments, 2022, , .	0.2	2
2	Game theory to enhance stock management of Personal Protective Equipment (PPE) during the COVID-19 outbreak. PLoS ONE, 2021, 16, e0246110.	1.1	10
3	<i>In silico</i> design of bioisosteric modifications of drugs for the treatment of diabetes. Future Medicinal Chemistry, 2021, 13, 691-700.	1.1	4
4	Adjusting Local Conformational Sampling For Fragment Assembly Protein Structure Prediction Based On Secondary Structure Complexity. , 2021, , .		0
5	Security attacks on smart grid scheduling and their defences: a game-theoretic approach. International Journal of Information Security, 2020, 19, 427-443.	2.3	18
6	Scalable System for Smart Urban Transport Management. Journal of Advanced Transportation, 2020, 2020, 1-13.	0.9	4
7	Enhancing fragment-based protein structure prediction by customising fragment cardinality according to local secondary structure. BMC Bioinformatics, 2020, 21, 170.	1.2	7
8	Deep phosphoproteome analysis of Schistosoma mansoni leads development of a kinomic array that highlights sex-biased differences in adult worm protein phosphorylation. PLoS Neglected Tropical Diseases, 2020, 14, e0008115.	1.3	11
9	Rosetta and the Journey to Predict Proteins' Structures, 20 Years on. Current Bioinformatics, 2020, 15, 611-628.	0.7	9
10	Enhanced Rosetta-based Protein Structure Prediction For non-Beta Sheet Dominated Targets. , 2020, , .		0
11	Dynamic Spatio-Temporal Bag of Expressions (D-STBoE) Model for Human Action Recognition. Sensors, 2019, 19, 2790.	2.1	9
12	Chapter 11 Online Resources for Biologists. , 2019, , 161-174.		0
13	SCOP-Aided Fragment Assembly Protein Structure Prediction. , 2019, , .		0
14	A Bag of Expression framework for improved human action recognition. Pattern Recognition Letters, 2018, 103, 39-45.	2.6	46
15	How genomes could transform surveillance and facial recognition. Biometric Technology Today, 2018, 2018, 5-7.	0.7	0
16	Vide-omics: A genomics-inspired paradigm for video analysis. Computer Vision and Image Understanding, 2018, 166, 28-40.	3.0	5
17	Profile Hidden Markov Models for Foreground Object Modelling. , 2018, , .		1
18	Automated Detection of Hands and Objects in Egocentric Videos, for Ambient Assisted Living		3

Applications. , 2018, , .

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19	A Practical Approach to Energy Scheduling: A Game Worth Playing?. , 2018, , .		6
20	Coil conversion to βâ€strand induced by dimerization. Proteins: Structure, Function and Bioinformatics, 2018, 86, 1221-1230.	1.5	0
21	Identifying human diamine sensors for death related putrescine and cadaverine molecules. PLoS Computational Biology, 2018, 14, e1005945.	1.5	29
22	Recognition of Activities of Daily Living from Egocentric Videos Using Hands Detected by a Deep Convolutional Network. Lecture Notes in Computer Science, 2018, , 390-398.	1.0	2
23	Data Mining the Protein Data Bank to Identify and Characterise Chameleon Coil Sequences that Form Symmetric Homodimer Î ² -Sheet Interfaces. Lecture Notes in Computer Science, 2017, , 118-126.	1.0	0
24	Inversion of Correia repeat enclosed elements in Neisseria gonorrhoeae. Microbiology (United) Tj ETQq0 0 0 rgB	[Qverlock	۹ 10 Tf 50 54
25	Reduced Fragment Diversity for Alpha and Alpha-Beta Protein Structure Prediction using Rosetta. Protein and Peptide Letters, 2017, 24, 215-222.	0.4	7
26	Recognition of Activities of Daily Living with Egocentric Vision: A Review. Sensors, 2016, 16, 72.	2.1	87
27	Correia Repeat Enclosed Elements and Non-Coding RNAs in the Neisseria Species. Microorganisms, 2016, 4, 31.	1.6	9
28	An optimized stereo vision implementation for embedded systems: application to RGB and infra-red images. Journal of Real-Time Image Processing, 2016, 12, 725-746.	2.2	8
29	Progress and challenges in predicting protein interfaces. Briefings in Bioinformatics, 2016, 17, 117-131.	3.2	115
30	Nutrigenomics 2.0: The Need for Ongoing and <i>Independent</i> Evaluation and Synthesis of Commercial Nutrigenomics Tests' Scientific Knowledge Base for Responsible Innovation. OMICS A Journal of Integrative Biology, 2016, 20, 65-68.	1.0	26
31	Kinect and Episodic Reasoning for Human Action Recognition. Advances in Intelligent Systems and Computing, 2016, , 147-154.	0.5	2
32	Database of Peptides Susceptible to Aggregation as a Tool for Studying Mechanisms of Diseases of Civilization. Lecture Notes in Computer Science, 2016, , 310-319.	1.0	0
33	Customised fragments libraries for protein structure prediction based on structural class annotations. BMC Bioinformatics, 2015, 16, 136.	1.2	20
34	Efficient tracking of human poses using a manifold hierarchy. Computer Vision and Image Understanding, 2015, 132, 75-86.	3.0	6
35	Meta-Analysis of Genes in Commercially Available Nutrigenomic Tests Denotes Lack of Association with Dietary Intake and Nutrient-Related Pathologies. OMICS A Journal of Integrative Biology, 2015, 19, 512-520.	1.0	35
36	Identification of NAD(P)H Quinone Oxidoreductase Activity in Azoreductases from P. aeruginosa: Azoreductases and NAD(P)H Quinone Oxidoreductases Belong to the Same FMN-Dependent Superfamily of Enzymes. PLoS ONE, 2014, 9, e98551.	1.1	55

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37	Episodic Reasoning for Vision-Based Human Action Recognition. Scientific World Journal, The, 2014, 2014, 1-18.	0.8	11
38	Generalized Laplacian Eigenmaps for Modeling and Tracking Human Motions. IEEE Transactions on Cybernetics, 2014, 44, 1646-1660.	6.2	18
39	Structural Laplacian Eigenmaps for Modeling Sets of Multivariate Sequences. IEEE Transactions on Cybernetics, 2014, 44, 936-949.	6.2	27
40	Scoring docking conformations using predicted protein interfaces. BMC Bioinformatics, 2014, 15, 171.	1.2	14
41	Primary sequence contribution to the optical function of the eye lens. Scientific Reports, 2014, 4, 5195.	1.6	28
42	Comparative study and meta-analysis of meta-analysis studies for the correlation of genomic markers with early cancer detection. Human Genomics, 2013, 7, 14.	1.4	15
43	Common-sense reasoning for human action recognition. Pattern Recognition Letters, 2013, 34, 1849-1860.	2.6	19
44	Probabilistic grammatical model for helixâ€helix contact site classification. Algorithms for Molecular Biology, 2013, 8, 31.	0.3	6
45	Bioinformatics-Motivated Approach to Stereo Matching. Communications in Computer and Information Science, 2013, , 172-186.	0.4	Ο
46	Quality assessment of protein model-structures based on structural and functional similarities. BMC Bioinformatics, 2012, 13, 242.	1.2	11
47	Structure Prediction of LDLR-HNP1 Complex Based on Docking Enhanced by LDLR Binding 3D Motif. Protein and Peptide Letters, 2012, 19, 458-467.	0.4	3
48	Proteomics and Bioinformatics Soon to Resolve the Human Structural Interactome. Journal of Proteomics and Bioinformatics, 2012, 05, .	0.4	1
49	Common-Sense Knowledge for a Computer Vision System for Human Action Recognition. Lecture Notes in Computer Science, 2012, , 159-166.	1.0	2
50	Comparative Analysis of Genomic Signal Processing for Microarray Data Clustering. IEEE Transactions on Nanobioscience, 2011, 10, 225-238.	2.2	11
51	Tracking Human Position and Lower Body Parts Using Kalman and Particle Filters Constrained by Human Biomechanics. IEEE Transactions on Systems, Man, and Cybernetics, 2011, 41, 26-37.	5.5	51
52	Integration of bottom-up/top-down approaches for 2D pose estimation using probabilistic Gaussian modelling. Computer Vision and Image Understanding, 2011, 115, 242-255.	3.0	12
53	Human pose tracking in low dimensional space enhanced by limb correction. , 2011, , .		4
54	Probabilistic Feature Extraction from Multivariate Time Series Using Spatio-Temporal Constraints. Lecture Notes in Computer Science, 2011, , 173-184.	1.0	1

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55	Are Current Monocular Computer Vision Systems for Human Action Recognition Suitable for Visual Surveillance Applications?. Lecture Notes in Computer Science, 2011, , 290-299.	1.0	9
56	2D and 3D Pose Recovery from a Single Uncalibrated Video. Studies in Computational Intelligence, 2011, , 391-411.	0.7	0
57	Graph-based Particle Filter for Human Tracking with Stylistic Variations. , 2011, , .		0
58	Why Inverse Proteins Are Relatively Abundant. Protein and Peptide Letters, 2010, 17, 854-860.	0.4	2
59	Automatic configuration of spectral dimensionality reduction methods. Pattern Recognition Letters, 2010, 31, 1720-1727.	2.6	7
60	Temporal Extension of Laplacian Eigenmaps for Unsupervised Dimensionality Reduction of Time Series. , 2010, , .		34
61	View and Style-Independent Action Manifolds for Human Activity Recognition. Lecture Notes in Computer Science, 2010, , 547-560.	1.0	20
62	Towards 3D Modeling of Interacting TM Helix Pairs Based on Classification of Helix Pair Sequence. Lecture Notes in Computer Science, 2010, , 62-73.	1.0	1
63	Automatic configuration of spectral dimensionality reduction methods for 3D human pose estimation. , 2009, , .		3
64	A stochastic context free grammar based framework for analysis of protein sequences. BMC Bioinformatics, 2009, 10, 323.	1.2	25
65	Automation of the CCTV-mediated detection of individuals illegally carrying firearms: combining psychological and technological approaches. Proceedings of SPIE, 2009, , .	0.8	6
66	Accuracy in Predicting Secondary Structure of Ionic Channels. Studies in Computational Intelligence, 2009, , 315-326.	0.7	3
67	Fractal dimension and wavelet decomposition for robust microarray data clustering. , 2008, 2008, 4106-9.		1
68	Integration of Local Image Cues for Probabilistic 2D Pose Recovery. Lecture Notes in Computer Science, 2008, , 214-223.	1.0	5
69	Tracking Human Body Parts Using Particle Filters Constrained by Human Biomechanics. , 2008, , .		8
70	Linear Predictive Coding and Wavelet Decomposition for Robust Microarray Data Clustering. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 4629-32.	0.5	3
71	Linear Predictive Coding for Enhanced Microarray Data Clustering. , 2007, , .		2

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73	A probabilistic context-free grammar for the detection of binding sites from a protein sequence. BMC Systems Biology, 2007, 1, .	3.0	3
74	Automatic generation of 3D motifs for classification of protein binding sites. BMC Bioinformatics, 2007, 8, 321.	1.2	21
75	Generation of 3D templates of active sites of proteins with rigid prosthetic groups. Bioinformatics, 2006, 22, 1183-1189.	1.8	17
76	Pre-commercial 3-D digital TV studio. IET Computer Vision, 2005, 152, 665.	1.3	0
77	Nestor3D: multiple alignment of protein structures based on ligand or prosthetic group position. BMC Bioinformatics, 2005, 6, S10.	1.2	0
78	3D thermography imaging standardization technique for inflammation diagnosis. , 2005, , .		28
79	Experimental 3-D digital TV studio. IET Computer Vision, 2003, 150, 28.	1.3	7
80	A New Automated Workflow for 3D Character Creation Based on 3D Scanned Data. Lecture Notes in Computer Science, 2003, , 155-158.	1.0	1
81	Generation of True 3D Films. Lecture Notes in Computer Science, 2001, , 10-19.	1.0	1
82	Soft Tissue Modelling from 3D Scanned Data. , 2001, , 85-97.		8
83	Realistic Collision Avoidance of Upper Limbs Based on Neuroscience Models. Computer Graphics Forum, 2000, 19, 219-228.	1.8	4
84	Keyframe interpolation with self-collision avoidance. Eurographics, 1999, , 77-86.	0.4	7
85	Computational Intelligence in Bioinformatics. Journal of Proteomics and Bioinformatics, 0, s9, .	0.4	0

86 Stroboscopic stereo rangefinder. , 0, , .

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