Haim J Wolfson

List of Publications by Year
in descending order

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158 papers	17,811 citations	20759 60 h-index	14702 127 g-index
165 all docs	165 docs citations	165 times ranked	15705 citing authors

#	Article	IF	Citations
1	Pepâ€“Whisperer: Inhibitory peptide design. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1886-1895.	1.5	3
2	ScanNet: an interpretable geometric deep learning model for structure-based protein binding site prediction. Nature Methods, 2022, 19, 730-739.	9.0	68
3	Memdock: An Î±-Helical Membrane Protein Docking Algorithm. Methods in Molecular Biology, 2021, 2315, 111-117.	0.4	4
4	Design of Disruptors of the Hsp90â€“Cdc37 Interface. Molecules, 2020, 25, 360.	1.7	14
5	Modeling of Multimolecular Complexes. Methods in Molecular Biology, 2020, 2112, 163-174.	0.4	12
6	AAnchor: CNN guided detection of anchor amino acids in high resolution cryo-EM density maps. , 2018, , .		6
7	Protein-Peptide Interaction Design: PepCrawler and PinaColada. Methods in Molecular Biology, 2017, 1561, 279-290.	0.4	2
8	SnapDockâ€”template-based docking by Geometric Hashing. Bioinformatics, 2017, 33, i30-i36.	1.8	11
9	Accelerating protein-protein complex validation by GPU based funnel generation. , 2016, , .		0
10	Memdock: an Î±-helical membrane protein docking algorithm. Bioinformatics, 2016, 32, 2444-2450.	1.8	42
11	PinaColada: peptideâ€“inhibitor ant colony ad-hoc design algorithm. Bioinformatics, 2016, 32, 2289-2296.	1.8	24
12	DockStar: a novel ILP-based integrative method for structural modeling of multimolecular protein complexes. Bioinformatics, 2015, 31, 2801-2807.	1.8	12
13	Diameter-selective dispersion of carbon nanotubes by Î²-lactoglobulin whey protein. Colloids and Surfaces B: Biointerfaces, 2013, 112, 16-22.	2.5	13
14	Proteinâ€Protein Interaction Modeling and Inhibition: The TAU Bioinfo3D Perspective. Israel Journal of Chemistry, 2013, 53, 180-184.	1.0	0
15	Structure-based in silico identification of ubiquitin-binding domains provides insights into the ALIX-V:ubiquitin complex and retrovirus budding. EMBO Journal, 2013, 32, 538-551.	3.5	59
16	Conformational transitions in human translin enable nucleic acid binding. Nucleic Acids Research, 2013, 41, 9956-9966.	6.5	11
17	Symmetry-Based Self-Assembled Nanotubes Constructed Using Native Protein Structures: The Key Role of Flexible Linkers. Protein and Peptide Letters, 2011, 18, 362-372.	0.4	1
18	Protein structure prediction using a dockingâ€based hierarchical folding scheme. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1759-1773.	1.5	3

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19	SymmRef: A flexible refinement method for symmetric multimers. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2607-2623.	1.5	16
20	MultiFit: a web server for fitting multiple protein structures into their electron microscopy density map. Nucleic Acids Research, 2011, 39, W167-W170.	6.5	27
21	PepCrawler: a fast RRT-based algorithm for high-resolution refinement and binding affinity estimation of peptide inhibitors. Bioinformatics, 2011, 27, 2836-2842.	1.8	78
22	FiberDock: Flexible inducedâ€fit backbone refinement in molecular docking. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1503-1519.	1.5	162
23	An integrated suite of fast docking algorithms. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3197-3204.	1.5	117
24	Determining macromolecular assembly structures by molecular docking and fitting into an electron density map. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3205-3211.	1.5	63
25	FiberDock: a web server for flexible induced-fit backbone refinement in molecular docking. Nucleic Acids Research, 2010, 38, W457-W461.	6.5	88
26	How Does the Reductase Help To Regulate the Catalytic Cycle of Cytochrome P450 3A4 Using the Conserved Water Channel?. Journal of Physical Chemistry B, 2010, 114, 5964-5970.	1.2	54
27	Allosteric Regulation of Glycogen Synthase Kinase 3Î²: A Theoretical Study. Biochemistry, 2010, 49, 10890-10901.	1.2	30
28	RsiteDB: a database of protein binding pockets that interact with RNA nucleotide bases. Nucleic Acids Research, 2009, 37, D369-D373.	6.5	27
29	Multiple structural alignment by secondary structures: Algorithm and applications. Protein Science, 2009, 12, 2492-2507.	3.1	58
30	Multiple diverse ligands binding at a single protein site: A matter of pre-existing populations. Protein Science, 2009, 11, 184-197.	3.1	364
31	Inferential Optimization for Simultaneous Fitting of Multiple Components into a CryoEM Map of Their Assembly. Journal of Molecular Biology, 2009, 388, 180-194.	2.0	117
32	Theoretical Characterization of Substrate Access/Exit Channels in the Human Cytochrome P450 3A4 Enzyme: Involvement of Phenylalanine Residues in the Gating Mechanism. Journal of Physical Chemistry B, 2009, 113, 13018-13025.	1.2	105
33	Novel Approach for Efficient Pharmacophore-Based Virtual Screening: Method and Applications. Journal of Chemical Information and Modeling, 2009, 49, 2333-2343.	2.5	111
34	Computational Validation of Protein Nanotubes. Nano Letters, 2009, 9, 1096-1102.	4.5	6
35	HingeProt: Automated prediction of hinges in protein structures. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1219-1227.	1.5	195
36	MolAxis: Efficient and accurate identification of channels in macromolecules. Proteins: Structure, Function and Bioinformatics, 2008, 73, 72-86.	1.5	101

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37	Constructing templates for protein structure prediction by simulation of protein folding pathways. Proteins: Structure, Function and Bioinformatics, 2008, 73, 380-394.	1.5	9
38	Principles of flexible proteinâ€“protein docking. Proteins: Structure, Function and Bioinformatics, 2008, 73, 271-289.	1.5	186
39	Metabolic stereoselectivity of cytochrome P450 3A4 towards deoxypodophyllotoxin: In silico predictions and experimental validation. European Journal of Medicinal Chemistry, 2008, 43, 1171-1179.	2.6	21
40	Algorithms for Multiple Protein Structure Alignment and Structure-Derived Multiple Sequence Alignment. , 2008, 413, 125-146.		3
41	Structural similarity of genetically interacting proteins. BMC Systems Biology, 2008, 2, 69.	3.0	5
42	Protein Structure Fitting and Refinement Guided by Cryo-EM Density. Structure, 2008, 16, 295-307.	1.6	334
43	Deterministic Pharmacophore Detection via Multiple Flexible Alignment of Drug-Like Molecules. Journal of Computational Biology, 2008, 15, 737-754.	0.8	67
44	Prediction of Interacting Single-Stranded RNA Bases by Protein-Binding Patterns. Journal of Molecular Biology, 2008, 379, 299-316.	2.0	35
45	MultiBind and MAPPIS: webservers for multiple alignment of protein 3D-binding sites and their interactions. Nucleic Acids Research, 2008, 36, W260-W264.	6.5	86
46	FireDock: a web server for fast interaction refinement in molecular docking. Nucleic Acids Research, 2008, 36, W229-W232.	6.5	657
47	MolAxis: a server for identification of channels in macromolecules. Nucleic Acids Research, 2008, 36, W210-W215.	6.5	62
48	PharmaGist: a webserver for ligand-based pharmacophore detection. Nucleic Acids Research, 2008, 36, W223-W228.	6.5	231
49	Analysis and classification of RNA tertiary structures. Rna, 2008, 14, 2274-2289.	1.6	42
50	Self-Assembly of Fused Homo-Oligomers to Create Nanotubes. Methods in Molecular Biology, 2008, 474, 117-131.	0.4	0
51	A Hierarchical Protein Folding Scheme Based on the Building Block Folding Model. , 2007, 350, 189-204.		2
52	QM/MM Study of the Active Species of the Human Cytochrome P450 3A4, and the Influence Thereof of the Multiple Substrate Binding. Journal of Physical Chemistry B, 2007, 111, 13822-13832.	1.2	36
53	EMatch: Discovery of High Resolution Structural Homologues of Protein Domains in Intermediate Resolution Cryo-EM Maps. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 28-39.	1.9	37
54	Changing the Charge Distribution of Î²-Helical-Based Nanostructures Can Provide the Conditions for Charge Transfer. Biophysical Journal, 2007, 93, 245-253.	0.2	18

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55	Structural Dynamics of the Cooperative Binding of Organic Molecules in the Human Cytochrome P450 3A4. Journal of the American Chemical Society, 2007, 129, 1602-1611.	6.6	48
56	EMatch: an efficient method for aligning atomic resolution subunits into intermediate-resolution cryo-EM maps of large macromolecular assemblies. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 42-49.	2.5	20
57	Spatial chemical conservation of hot spot interactions in protein-protein complexes. BMC Biology, 2007, 5, 43.	1.7	65
58	Principles of nanostructure design with protein building blocks. Proteins: Structure, Function and Bioinformatics, 2007, 68, 1-12.	1.5	51
59	FireDock: Fast interaction refinement in molecular docking. Proteins: Structure, Function and Bioinformatics, 2007, 69, 139-159.	1.5	607
60	Automatic prediction of protein interactions with large scale motion. Proteins: Structure, Function and Bioinformatics, 2007, 69, 764-773.	1.5	47
61	Mechanism of Two Classes of Cancer Mutations in the Phosphoinositide 3-Kinase Catalytic Subunit. Science, 2007, 317, 239-242.	6.0	364
62	Deterministic Pharmacophore Detection Via Multiple Flexible Alignment of Drug-Like Molecules. Lecture Notes in Computer Science, 2007, , 412-429.	1.0	17
63	Correlated mutations: Advances and limitations. A study on fusion proteins and on the Cohesin-Dockerin families. Proteins: Structure, Function and Bioinformatics, 2006, 63, 832-845.	1.5	95
64	Interaction of C60-Fullerene and Carboxyfullerene with Proteins:Â Docking and Binding Site Alignment. Bioconjugate Chemistry, 2006, 17, 378-386.	1.8	111
65	De Novo Tubular Nanostructure Design Based on Self-Assembly of Î²-Helical Protein Motifs. Structure, 2006, 14, 1137-1148.	1.6	41
66	The ARTS web server for aligning RNA tertiary structures. Nucleic Acids Research, 2006, 34, W412-W415.	6.5	40
67	A permissive secondary structure-guided superposition tool for clustering of protein fragments toward protein structure prediction via fragment assembly. Bioinformatics, 2006, 22, 1343-1352.	1.8	4
68	Concepts and schemes for the re-engineering of physical protein modules: generating nanodevices via targeted replacements with constrained amino acids. Physical Biology, 2006, 3, S54-S62.	0.8	20
69	The Multiple Common Point Set Problem and Its Application to Molecule Binding Pattern Detection. Journal of Computational Biology, 2006, 13, 407-428.	0.8	67
70	SiteEngines: recognition and comparison of binding sites and protein-protein interfaces. Nucleic Acids Research, 2005, 33, W337-W341.	6.5	99
71	Recognition of Binding Patterns Common to a Set of Protein Structures. Lecture Notes in Computer Science, 2005, , 440-455.	1.0	23
72	Fibril modelling by sequence and structure conservation analysis combined with protein docking techniques: Î²2-microglobulin amyloidosis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1753, 121-130.	1.1	6

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73	Approaching the CAPRI challenge with an efficient geometry-based docking. Proteins: Structure, Function and Bioinformatics, 2005, 60, 217-223.	1.5	20
74	Geometry-based flexible and symmetric protein docking. Proteins: Structure, Function and Bioinformatics, 2005, 60, 224-231.	1.5	177
75	Generation and analysis of a protein-protein interface data set with similar chemical and spatial patterns of interactions. Proteins: Structure, Function and Bioinformatics, 2005, 61, 6-20.	1.5	44
76	Optimization of multiple-sequence alignment based on multiple-structure alignment. Proteins: Structure, Function and Bioinformatics, 2005, 62, 209-217.	1.5	48
77	From Structure to Function: Methods and Applications. Current Protein and Peptide Science, 2005, 6, 171-183.	0.7	32
78	Combinatorial docking approach for structure prediction of large proteins and multi-molecular assemblies. Physical Biology, 2005, 2, S156-S165.	0.8	44
79	A Comparative Study of Amyloid Fibril Formation by Residues 15â€“19 of the Human Calcitonin Hormone: A Single Î²-Sheet Model with a Small Hydrophobic Core. Journal of Molecular Biology, 2005, 345, 1213-1227.	2.0	71
80	Prediction of Multimolecular Assemblies by Multiple Docking. Journal of Molecular Biology, 2005, 349, 435-447.	2.0	86
81	ARTS: alignment of RNA tertiary structures. Bioinformatics, 2005, 21, ii47-ii53.	1.8	57
82	PatchDock and SymmDock: servers for rigid and symmetric docking. Nucleic Acids Research, 2005, 33, W363-W367.	6.5	2,610
83	Discovery of Protein Substructures in EM Maps. Lecture Notes in Computer Science, 2005, , 423-434.	1.0	4
84	MAPPIS: Multiple 3D Alignment of Protein-Protein Interfaces. Lecture Notes in Computer Science, 2005, , 91-103.	1.0	4
85	Predicting Molecular Interactions in silico: II. Protein-Protein and Protein- Drug Docking. Current Medicinal Chemistry, 2004, 11, 91-107.	1.2	78
86	Predicting Molecular Interactions in silico: I. A Guide to Pharmacophore Identification and its Applications to Drug Design. Current Medicinal Chemistry, 2004, 11, 71-90.	1.2	142
87	BioInfo3D: a suite of tools for structural bioinformatics. Nucleic Acids Research, 2004, 32, W503-W507.	6.5	23
88	Side chain interactions determine the amyloid organization: a single layer Â-sheet molecular structure of the calcitonin peptide segment 15â€“19. Physical Biology, 2004, 1, 89-99.	0.8	19
89	Identification of the N-terminal Peptide Binding Site of Glucose-regulated Protein 94. Journal of Biological Chemistry, 2004, 279, 16543-16552.	1.6	61
90	Protein-Protein Interactions. Structure, 2004, 12, 1027-1038.	1.6	127

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91	A new, structurally nonredundant, diverse data set of protein-protein interfaces and its implications. Protein Science, 2004, 13, 1043-1055.	3.1	185
92	Potential folding-function interrelationship in proteins. Proteins: Structure, Function and Bioinformatics, 2004, 56, 635-649.	1.5	4
93	A method for simultaneous alignment of multiple protein structures. Proteins: Structure, Function and Bioinformatics, 2004, 56, 143-156.	1.5	396
94	FlexProt: Alignment of Flexible Protein Structures Without a Predefinition of Hinge Regions. Journal of Computational Biology, 2004, 11, 83-106.	0.8	64
95	Recognition of Functional Sites in Protein Structures. Journal of Molecular Biology, 2004, 339, 607-633.	2.0	257
96	Protein-Protein Interfaces: Recognition of Similar Spatial and Chemical Organizations. Lecture Notes in Computer Science, 2004, , 194-205.	1.0	25
97	Reducing the computational complexity of protein folding via fragment folding and assembly. Protein Science, 2003, 12, 1177-1187.	3.1	48
98	Hierarchical protein folding pathways: A computational study of protein fragments. Proteins: Structure, Function and Bioinformatics, 2003, 51, 203-215.	1.5	29
99	Conservation and amyloid formation: A study of the gelsolin-like family. Proteins: Structure, Function and Bioinformatics, 2003, 51, 266-282.	1.5	12
100	Taking geometry to its edge: Fast unbound rigid (and hinge-bent) docking. Proteins: Structure, Function and Bioinformatics, 2003, 52, 107-112.	1.5	238
101	SiteLight: Binding-site prediction using phage display libraries. Protein Science, 2003, 12, 1344-1359.	3.1	60
102	Protein structure prediction via combinatorial assembly of sub-structural units. Bioinformatics, 2003, 19, i158-i168.	1.8	44
103	Î²2-Microglobulin Amyloidosis: Insights from Conservation Analysis and Fibril Modelling by Protein Docking Techniques. Journal of Molecular Biology, 2003, 330, 159-174.	2.0	31
104	Protein-protein interactions: Structurally conserved residues distinguish between binding sites and exposed protein surfaces. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5772-5777.	3.3	553
105	Spatial Pattern Detection in Structural Bionformatics. Lecture Notes in Computer Science, 2003, , 35-56.	1.0	0
106	Flexible protein alignment and hinge detection. Proteins: Structure, Function and Bioinformatics, 2002, 48, 242-256.	1.5	113
107	Principles of docking: An overview of search algorithms and a guide to scoring functions. Proteins: Structure, Function and Bioinformatics, 2002, 47, 409-443.	1.5	1,130
108	MultiProt â€" A Multiple Protein Structural Alignment Algorithm. Lecture Notes in Computer Science, 2002, , 235-250.	1.0	42

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109	Principles of docking: An overview of search algorithms and a guide to scoring functions. , 2002, 47, 409.		46
110	Efficient Unbound Docking of Rigid Molecules. Lecture Notes in Computer Science, 2002, , 185-200.	1.0	481
111	Automated multiple structure alignment and detection of a common substructural motif. Proteins: Structure, Function and Bioinformatics, 2001, 43, 235-245.	1.5	60
112	Protein functional epitopes: hot spots, dynamics and combinatorial libraries. Current Opinion in Structural Biology, 2001, 11, 364-369.	2.6	114
113	MUSTA - A General, Efficient, Automated Method for Multiple Structure Alignment and Detection of Common Motifs: Application to Proteins. Journal of Computational Biology, 2001, 8, 93-121.	0.8	62
114	Conservation of polar residues as hot spots at protein interfaces. , 2000, 39, 331-342.		253
115	Geometrical Docking Algorithms A Practical Approach. , 2000, 143, 377-397.		4
116	Conservation of polar residues as hot spots at protein interfaces. , 2000, 39, 331.		3
117	Folding funnels and conformational transitions via hinge-bending motions. Cell Biochemistry and Biophysics, 1999, 31, 141-164.	0.9	85
118	Flexible structural comparison allowing hinge-bending, swiveling motions. , 1999, 34, 232-254.		30
119	Examination of shape complementarity in docking ofUnbound proteins. , 1999, 36, 307-317.		118
120	Efficient Computational Algorithms for Docking and for Generating and Matching a Library of Functional Epitopes II. Computer Vision-Based Techniques for the Generation and Utilization of Functional Epitopes. Combinatorial Chemistry and High Throughput Screening, 1999, 2, 261-269.	0.6	3
121	Efficient Computational Algorithms for Docking and for Generating and Matching a Library of Functional Epitopes I. Rigid and Flexible Hinge-Bending Docking Algorithms. Combinatorial Chemistry and High Throughput Screening, 1999, 2, 249-259.	0.6	5
122	Flexible docking allowing induced fit in proteins: Insights from an open to closed conformational isomers. Proteins: Structure, Function and Bioinformatics, 1998, 32, 159-174.	1.5	110
123	A Method for Biomolecular Structural Recognition and Docking Allowing Conformational Flexibility. Journal of Computational Biology, 1998, 5, 631-654.	0.8	56
124	From computer vision to protein structure and association. New Comprehensive Biochemistry, 1998, , 313-334.	0.1	1
125	Geometric Hashing. IEEE Computational Science and Engineering, 1997, 4, 9-9.	0.6	10
126	Investigation of the enzymatic mechanism of the yeast chorismate mutase by docking a transition state analog. Journal of Molecular Biology, 1997, 271, 838-845.	2.0	11

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127	Studies of proteinâ€protein interfaces: A statistical analysis of the hydrophobic effect. Protein Science, 1997, 6, 53-64.	3.1	361
128	Amino Acid Pair Interchanges at Spatially Conserved Locations. Journal of Molecular Biology, 1996, 256, 924-938.	2.0	35
129	A Dataset of Proteinâ€“Protein Interfaces Generated with a Sequence-order-independent Comparison Technique. Journal of Molecular Biology, 1996, 260, 604-620.	2.0	156
130	Techniques for searching for structural similarities between protein cores, protein surfaces and between protein-protein interfaces. Techniques in Protein Chemistry, 1996, , 419-429.	0.3	2
131	Protein-Protein Interfaces: Architectures and Interactions in Protein-Protein Interfaces and in Protein Cores. Their Similarities and Differences. Critical Reviews in Biochemistry and Molecular Biology, 1996, 31, 127-152.	2.3	110
132	Docking of conformationally flexible proteins. Lecture Notes in Computer Science, 1996, , 271-287.	1.0	5
133	Detection of non-topological motifs in protein structures. Protein Engineering, Design and Selection, 1996, 9, 1103-1119.	1.0	31
134	Context-free attentional operators: The generalized symmetry transform. International Journal of Computer Vision, 1995, 14, 119-130.	10.9	361
135	A 3D sequence-independent representation of the protein data bank. Protein Engineering, Design and Selection, 1995, 8, 981-997.	1.0	49
136	An automated computer vision and roboticsbased technique for 3-D flexible biomolecular docking and matching. Bioinformatics, 1995, 11, 87-99.	1.8	16
137	Molecular Surface Complementarity at Protein-Protein Interfaces: The Critical Role Played by Surface Normals at Well Placed, Sparse, Points in Docking. Journal of Molecular Biology, 1995, 252, 263-273.	2.0	113
138	Threeâ€dimensional, sequence orderâ€independent structural comparison of a serine protease against the crystallographic database reveals active site similarities: Potential implications to evolution and to protein folding. Protein Science, 1994, 3, 769-778.	3.1	90
139	Molecular surface representations by sparse critical points. Proteins: Structure, Function and Bioinformatics, 1994, 18, 94-101.	1.5	104
140	Shape complementarity at protein-protein interfaces. Biopolymers, 1994, 34, 933-940.	1.2	991
141	Molecular surface recognition by a computer vision-based technique. Protein Engineering, Design and Selection, 1994, 7, 39-46.	1.0	102
142	Surface motifs by a computer vision technique: Searches, detection, and implications for protein-ligand recognition. Proteins: Structure, Function and Bioinformatics, 1993, 16, 278-292.	1.5	72
143	A computer vision based technique for 3-D sequence-independent structural comparison of proteins. Protein Engineering, Design and Selection, 1993, 6, 279-287.	1.0	125
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145	Spatial, Sequence-Order-Independent Structural Comparison of Î±/Î² Proteins: Evolutionaiy Implications. Journal of Biomolecular Structure and Dynamics, 1993, 11, 367-380.	2.0	5
146	An Efficient Automated Computer Vision Based Technique for Detection of Three Dimensional Structural Motifs in Proteins. Journal of Biomolecular Structure and Dynamics, 1992, 9, 769-789.	2.0	75
147	3-D substructure matching in protein Molecules. Lecture Notes in Computer Science, 1992, , 136-150.	1.0	9
148	Efficient detection of three-dimensional structural motifs in biological macromolecules by computer vision techniques.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 10495-10499.	3.3	263
149	3â€Ð curve matching using splines. Journal of Field Robotics, 1991, 8, 723-743.	0.7	35
150	Generalizing the generalized hough transform. Pattern Recognition Letters, 1991, 12, 565-573.	2.6	23
151	Model-based object recognition by geometric hashing. Lecture Notes in Computer Science, 1990, , 526-536.	1.0	91
152	3-D curve matching using splines. Lecture Notes in Computer Science, 1990, , 589-591.	1.0	32
153	Affine invariant model-based object recognition. IEEE Transactions on Automation Science and Engineering, 1990, 6, 578-589.	2.4	263
154	On curve matching. IEEE Transactions on Pattern Analysis and Machine Intelligence, 1990, 12, 483-489.	9.7	192
155	Solving jigsaw puzzles by a robot. IEEE Transactions on Automation Science and Engineering, 1989, 5, 752-764.	2.4	52
156	Solving jigsaw puzzles by computer. Annals of Operations Research, 1988, 12, 51-64.	2.6	102
157	Minkowski spaces with extremal distance from the Euclidean space. Israel Journal of Mathematics, 1978, 29, 113-131.	0.4	26
158	Gelsolin. , 0, , 625-634.		0