Mauno Vihinen

List of Publications by Year in Descending Order

274 papers	11,337 citations	55 h-index	97 g-index
297 ext. papers	12,717 ext. citations	6.3 avg, IF	6.47 L-index

#	Paper	IF	Citations
274	Parkinson's disease and multiple system atrophy patient iPSC-derived oligodendrocytes exhibit alpha-synuclein-induced changes in maturation and immune reactive properties.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, e2111405119	11.5	1
273	Circulating Plasma microRNAs In Systemic Sclerosis-Associated Pulmonary Arterial Hypertension. *Rheumatology*, **2021**,	3.9	2
272	TNF- and -synuclein fibrils differently regulate human astrocyte immune reactivity and impair mitochondrial respiration. *Cell Reports*, **2021**, 34, 108895	10.6	14
271	Measuring and interpreting pervasive heterogeneity, poikilosis. *FASEB BioAdvances*, **2021**, 3, 611-625	2.8	1
270	Prognostic implications of troponin T variations in inherited cardiomyopathies using systems biology. *Npj Genomic Medicine*, **2021**, 6, 47	6.2	0
269	PON-Sol2: Prediction of Effects of Variants on Protein Solubility. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	1
268	Functional effects of protein variants. *Biochimie*, **2021**, 180, 104-120	4.6	4
267	Systematics for types and effects of RNA variations. *RNA Biology*, **2021**, 18, 481-498	4.8	2
266	BTK gatekeeper residue variation combined with cysteine 481 substitution causes super-resistance to irreversible inhibitors acalabrutinib, ibrutinib and zanubrutinib. *Leukemia*, **2021**, 35, 1317-1329	10.7	9
265	Structure-Function Relationships of Covalent and Non-Covalent BTK Inhibitors. *Frontiers in Immunology*, **2021**, 12, 694853	8.4	9
264	Hematologically important mutations: The autosomal forms of chronic granulomatous disease (third update). *Blood Cells, Molecules, and Diseases*, **2021**, 92, 102596	2.1	3
263	Problems in variation interpretation guidelines and in their implementation in computational tools. *Molecular Genetics & Genomic Medicine*, **2020**, 8, e1206	2.3	4
262	Guidelines for systematic reporting of sequence alignments. *Biology Methods and Protocols*, **2020**, 5, bpaa001	2.4	4
261	Strategy for Disease Diagnosis, Progression Prediction, Risk Group Stratification and Treatment-Case of COVID-19. *Frontiers in Medicine*, **2020**, 7, 294	4.9	6
260	Variation benchmark datasets: update, criteria, quality and applications. *Database: the Journal of Biological Databases and Curation*, **2020**, 2020,	5	13
259	Poikilosis - pervasive biological variation. *F1000Research*, **2020**, 9, 602	3.6	3
258	Solubility of proteins.. *ADMET and DMPK*, **2020**, 8, 391-399	1.3	6

257	How good are pathogenicity predictors in detecting benign variants?. *PLoS Computational Biology*, **2019**, 15, e1006481	5	32
256	Benchmarking subcellular localization and variant tolerance predictors on membrane proteins. *BMC Genomics*, **2019**, 20, 547	4.5	10
255	Assessing computational predictions of the phenotypic effect of cystathionine-beta-synthase variants. *Human Mutation*, **2019**, 40, 1530-1545	4.7	3
254	Checklist for gene/disease-specific variation database curators to enable ethical data management. *Human Mutation*, **2019**, 40, 1634-1640	4.7	
253	FGF family members differentially regulate maturation and proliferation of stem cell-derived astrocytes. *Scientific Reports*, **2019**, 9, 9610	4.9	17
252	Combination of Gatekeeper Mutations and Cysteine 481 Replacement Causes Super Resistance to the Irreversible BTK Inhibitors Ibrutinib, Acalabrutinib and Zanubrutinib. *Blood*, **2019**, 134, 5759-5759	2.2	1
251	ProTstab - predictor for cellular protein stability. *BMC Genomics*, **2019**, 20, 804	4.5	7
250	Mu transpososome activity-profiling yields hyperactive MuA variants for highly efficient genetic and genome engineering. *Nucleic Acids Research*, **2018**, 46, 4649-4661	20.1	3
249	PON-tstab: Protein Variant Stability Predictor. Importance of Training Data Quality. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	31
248	Simulation of the Dynamics of Primary Immunodeficiencies in B Cells. *Frontiers in Immunology*, **2018** , 9, 1785	8.4	0
247	Pan-cancer analysis of neoepitopes. *Scientific Reports*, **2018**, 8, 12735	4.9	12
246	NDDVD: an integrated and manually curated Neurodegenerative Diseases Variation Database. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	3
245	Systematics for types and effects of DNA variations. *BMC Genomics*, **2018**, 19, 974	4.5	5
244	Representativeness of variation benchmark datasets. *BMC Bioinformatics*, **2018**, 19, 461	3.6	13
243	Predicting Severity of Disease-Causing Variants. *Human Mutation*, **2017**, 38, 357-364	4.7	23
242	PON-P and PON-P2 predictor performance in CAGI challenges: Lessons learned. *Human Mutation*, **2017**, 38, 1085-1091	4.7	4
241	One Gene, Several Diseases: The Characteristics of Pleiotropic Proteins. *Human Mutation*, **2017**, 38, 241	4.7	
240	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. *Human Mutation*, **2017**, 38, 1042-1050	4.7	9

239	Large differences in proportions of harmful and benign amino acid substitutions between proteins and diseases. *Human Mutation*, **2017**, 38, 839-848	4.7	14
238	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. *Human Mutation*, **2017**, 38, 1182-1192	4.7	28
237	Expanded national database collection and data coverage in the FINDbase worldwide database for clinically relevant genomic variation allele frequencies. *Nucleic Acids Research*, **2017**, 45, D846-D853	20.1	14
236	PON-SC - program for identifying steric clashes caused by amino acid substitutions. *BMC Bioinformatics*, **2017**, 18, 531	3.6	4
235	How to Define Pathogenicity, Health, and Disease?. *Human Mutation*, **2017**, 38, 129-136	4.7	16
234	Simulation of the dynamics of primary immunodeficiencies in CD4+ T-cells. *PLoS ONE*, **2017**, 12, e0176500	3.7	2
233	Establishment of an international database for genetic variants in esophageal cancer. *Annals of the New York Academy of Sciences*, **2016**, 1381, 45-49	6.5	2
232	VariOtator, a Software Tool for Variation Annotation with the Variation Ontology. *Human Mutation*, **2016**, 37, 344-9	4.7	3
231	PON-mt-tRNA: a multifactorial probability-based method for classification of mitochondrial tRNA variations. *Nucleic Acids Research*, **2016**, 44, 2020-7	20.1	28
230	PON-Sol: prediction of effects of amino acid substitutions on protein solubility. *Bioinformatics*, **2016**, 32, 2032-4	7.2	28
229	Variation Interpretation Predictors: Principles, Types, Performance, and Choice. *Human Mutation*, **2016**, 37, 579-97	4.7	75
228	Human Variome Project Quality Assessment Criteria for Variation Databases. *Human Mutation*, **2016**, 37, 549-58	4.7	13
227	Finding our way through phenotypes. *PLoS Biology*, **2015**, 13, e1002033	9.7	144
226	Muddled genetic terms miss and mess the message. *Trends in Genetics*, **2015**, 31, 423-5	8.5	10
225	Specific autoantibody profiles and disease subgroups correlate with circulating micro-RNA in systemic sclerosis. *Rheumatology*, **2015**, 54, 2100-7	3.9	24
224	The Importance of Proper Testing of Predictor Performance. *Human Mutation*, **2015**, 36, iii-iv	4.7	1
223	Types and effects of protein variations. *Human Genetics*, **2015**, 134, 405-21	6.3	22
222	Harmful somatic amino acid substitutions affect key pathways in cancers. *BMC Medical Genomics*, **2015**, 8, 53	3.7	12

221	VariSNP, a benchmark database for variations from dbSNP. *Human Mutation*, **2015**, 36, 161-6	4.7	35
220	Standard development at the Human Variome Project. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015,	5	8
219	Characterization of all possible single-nucleotide change caused amino acid substitutions in the kinase domain of Bruton tyrosine kinase. *Human Mutation*, **2015**, 36, 638-47	4.7	30
218	Classification of Amino Acid Substitutions in Mismatch Repair Proteins Using PON-MMR2. *Human Mutation*, **2015**, 36, 1128-34	4.7	14
217	PON-P2: prediction method for fast and reliable identification of harmful variants. *PLoS ONE*, **2015**, 10, e0117380	3.7	130
216	Genetic Variation in Bruton Tyrosine Kinase. *Rare Diseases of the Immune System*, **2015**, 75-85	0.2	3
215	No more hidden solutions in bioinformatics. *Nature*, **2015**, 521, 261	50.4	17
214	Identification of core T cell network based on immunome interactome. *BMC Systems Biology*, **2014**, 8, 17	3.5	4
213	Variation ontology: annotator guide. *Journal of Biomedical Semantics*, **2014**, 5, 9	2.2	5
212	Performance of protein disorder prediction programs on amino acid substitutions. *Human Mutation* , **2014**, 35, 794-804	4.7	19
211	A systematic analysis of recombination activity and genotype-phenotype correlation in human recombination-activating gene 1 deficiency. *Journal of Allergy and Clinical Immunology*, **2014**, 133, 1099-108	11.5	100
210	Proper reporting of predictor performance. *Nature Methods*, **2014**, 11, 781	21.6	7
209	Novel association of neurofibromatosis type 1-causing mutations in families with neurofibromatosis-Noonan syndrome. *American Journal of Medical Genetics, Part A*, **2014**, 164A, 579-87	2.5	21
208	Clustering of gene ontology terms in genomes. *Gene*, **2014**, 550, 155-64	3.8	12
207	Variation Ontology for annotation of variation effects and mechanisms. *Genome Research*, **2014**, 24, 356-64	9.7	41
206	Majority vote and other problems when using computational tools. *Human Mutation*, **2014**, 35, 912-4	4.7	14
205	Contribution of pseudogenes to sequence diversity. *Methods in Molecular Biology*, **2014**, 1167, 15-24	1.4	3
204	Structure-based prediction of the effects of a missense variant on protein stability. *Amino Acids*, **2013**, 44, 847-55	3.5	29

203	VariBench: a benchmark database for variations. *Human Mutation*, **2013**, 34, 42-9	4.7	87
202	Guidelines for reporting and using prediction tools for genetic variation analysis. *Human Mutation*, **2013**, 34, 275-82	4.7	64
201	Abnormal cerebellar development and ataxia in CARP VIII morphant zebrafish. *Human Molecular Genetics*, **2013**, 22, 417-32	5.6	32
200	Gene expression profiles in human and mouse primary cells provide new insights into the differential actions of vitamin D3 metabolites. *PLoS ONE*, **2013**, 8, e75338	3.7	12
199	copy number variation analysis in familial BRCA1/2-negative Finnish breast and ovarian cancer. *PLoS ONE*, **2013**, 8, e71802	3.7	25
198	Proteomic changes during B cell maturation: 2D-DIGE approach. *PLoS ONE*, **2013**, 8, e77894	3.7	7
197	Nucleolar proteins with altered expression in leukemic cell lines. *Leukemia Research*, **2012**, 36, 232-6	2.7	11
196	How to evaluate performance of prediction methods? Measures and their interpretation in variation effect analysis. *BMC Genomics*, **2012**, 13 Suppl 4, S2	4.5	152
195	Curating gene variant databases (LSDBs): toward a universal standard. *Human Mutation*, **2012**, 33, 291-7	4.7	39
194	Guidelines for establishing locus specific databases. *Human Mutation*, **2012**, 33, 298-305	4.7	42
193	Classification of mismatch repair gene missense variants with PON-MMR. *Human Mutation*, **2012**, 33, 642-50	4.7	24
192	VarioML framework for comprehensive variation data representation and exchange. *BMC Bioinformatics*, **2012**, 13, 254	3.6	14
191	PON-P: integrated predictor for pathogenicity of missense variants. *Human Mutation*, **2012**, 33, 1166-74	4.7	79
190	Conserved and quickly evolving immunome genes have different evolutionary paths. *Human Mutation*, **2012**, 33, 1456-63	4.7	2
189	Human Variome Project country nodes: documenting genetic information within a country. *Human Mutation*, **2012**, 33, 1513-9	4.7	10
188	Flexibility in MuA transposase family protein structures: functional mapping with scanning mutagenesis and sequence alignment of protein homologues. *PLoS ONE*, **2012**, 7, e37922	3.7	4
187	Clarity and claims in variation/mutation databasing. *Nature Biotechnology*, **2011**, 29, 790-2; author reply 792-4	44.5	
186	Screening for BRCA1, BRCA2, CHEK2, PALB2, BRIP1, RAD50, and CDH1 mutations in high-risk Finnish BRCA1/2-founder mutation-negative breast and/or ovarian cancer individuals. *Breast Cancer Research*, **2011**, 13, R20	8.3	85

185	ETS1 mediates MEK1/2-dependent overexpression of cancerous inhibitor of protein phosphatase 2A (CIP2A) in human cancer cells. *PLoS ONE*, **2011**, 6, e17979	3.7	49
184	Mutation (variation) databases and registries: a rationale for coordination of efforts. *Nature Reviews Genetics*, **2011**, 12, 881; discussion 881	30.1	11
183	NMD and microRNA expression profiling of the HPCX1 locus reveal MAGEC1 as a candidate prostate cancer predisposition gene. *BMC Cancer*, **2011**, 11, 327	4.8	7
182	PROlocalizer: integrated web service for protein subcellular localization prediction. *Amino Acids*, **2011**, 40, 975-80	3.5	27
181	Performance of mutation pathogenicity prediction methods on missense variants. *Human Mutation*, **2011**, 32, 358-68	4.7	399
180	Genetic tests need the Human Variome Project. *Genetic Testing and Molecular Biomarkers*, **2011**, 15, 3	1.6	3
179	Different molecular behavior of CD40 mutants causing hyper-IgM syndrome. *Blood*, **2010**, 116, 5867-74	2.2	24
178	Accuracy of protein hydropathy predictions. *International Journal of Data Mining and Bioinformatics*, **2010**, 4, 735-54	0.5	3
177	Performance of protein stability predictors. *Human Mutation*, **2010**, 31, 675-84	4.7	228
176	Systematic classification of primary immunodeficiencies based on clinical, pathological, and laboratory parameters. *Journal of Immunology*, **2009**, 183, 7569-75	5.3	21
175	Identification of candidate disease genes by integrating Gene Ontologies and protein-interaction networks: case study of primary immunodeficiencies. *Nucleic Acids Research*, **2009**, 37, 622-8	20.1	76
174	Evaluation of accuracy and applicability of protein models: retrospective analysis of biological and biomedical predictions. *In Silico Biology*, **2009**, 9, 307-31	2	1
173	Capturing all disease-causing mutations for clinical and research use: toward an effortless system for the Human Variome Project. *Genetics in Medicine*, **2009**, 11, 843-9	8.1	37
172	Prediction of disease-related mutations affecting protein localization. *BMC Genomics*, **2009**, 10, 122	4.5	40
171	Immunome knowledge base (IKB): an integrated service for immunome research. *BMC Immunology*, **2009**, 10, 3	3.7	28
170	Somatic mutation databases as tools for molecular epidemiology and molecular pathology of cancer: proposed guidelines for improving data collection, distribution, and integration. *Human Mutation*, **2009**, 30, 275-82	4.7	12
169	Pathogenic or not? And if so, then how? Studying the effects of missense mutations using bioinformatics methods. *Human Mutation*, **2009**, 30, 703-14	4.7	184
168	A novel mutation in CD40 and its functional characterization. *Human Mutation*, **2009**, 30, 985-94	4.7	5

167	Sharing data between LSDBs and central repositories. *Human Mutation*, **2009**, 30, 493-5	4.7	17
166	Crystal structure of a 1.6-hexanediol bound tetrameric form of Escherichia coli lac-repressor refined to 2.1 A resolution. *Proteins: Structure, Function and Bioinformatics*, **2009**, 75, 748-59	4.2	12
165	Problems with anti-plagiarism database. *Nature*, **2009**, 457, 26	50.4	1
164	Copy number analysis indicates monoclonal origin of lethal metastatic prostate cancer. *Nature Medicine*, **2009**, 15, 559-65	50.5	513
163	Bruton's tyrosine kinase (Btk): function, regulation, and transformation with special emphasis on the PH domain. *Immunological Reviews*, **2009**, 228, 58-73	11.3	344
162	Bioinformatics services related to diagnosis of primary immunodeficiencies. *Current Opinion in Allergy and Clinical Immunology*, **2009**, 9, 531-6	3.3	8
161	Immunodeficiencies and Immunome: Diseases and Information Services **2009**, 71-85		
160	Human Proteinpedia enables sharing of human protein data. *Nature Biotechnology*, **2008**, 26, 164-7	44.5	138
159	PseudoGeneQuest - service for identification of different pseudogene types in the human genome. *BMC Bioinformatics*, **2008**, 9, 299	3.6	13
158	Identification of differentially expressed genes after PPM1D silencing in breast cancer. *Cancer Letters*, **2008**, 259, 61-70	9.9	21
157	Dynamic covariation between gene expression and genome characteristics. *Gene*, **2008**, 410, 53-66	3.8	
156	Model-based prediction of sequence alignment quality. *Bioinformatics*, **2008**, 24, 2165-71	7.2	15
155	Medical Expert Systems. *Current Bioinformatics*, **2008**, 3, 56-65	4.7	12
154	Phylogeny of Tec family kinases identification of a premetazoan origin of Btk, Bmx, Itk, Tec, Txk, and the Btk regulator SH3BP5. *Advances in Genetics*, **2008**, 64, 51-80	3.3	23
153	National research contributions: A case study on Finnish biomedical research. *Scientometrics*, **2008**, 77, 207-222	3	19
152	Expression of sterol regulatory element-binding transcription factor (SREBF) 2 and SREBF cleavage-activating protein (SCAP) in human atheroma and the association of their allelic variants with sudden cardiac death. *Thrombosis Journal*, **2008**, 6, 17	5.6	9
151	Efficiency of the immunome protein interaction network increases during evolution. *Immunome Research*, **2008**, 4, 4		12
150	Genome wide analysis of pathogenic SH2 domain mutations. *Proteins: Structure, Function and Bioinformatics*, **2008**, 72, 779-92	4.2	43

149	Recommendations for locus-specific databases and their curation. *Human Mutation*, **2008**, 29, 2-5	4.7	52
148	The EUROclass trial: defining subgroups in common variable immunodeficiency. *Blood*, **2008**, 111, 77-85	2.2	556
147	Physicochemical feature-based classification of amino acid mutations. *Protein Engineering, Design and Selection*, **2008**, 21, 37-44	1.9	31
146	PhenCode: connecting ENCODE data with mutations and phenotype. *Human Mutation*, **2007**, 28, 554-62	4.7	72
145	A structured simple form for ordering genetic tests is needed to ensure coupling of clinical detail (phenotype) with DNA variants (genotype) to ensure utility in publication and databases. *Human Mutation*, **2007**, 28, 931-2	4.7	8
144	Spectrum of disease-causing mutations in protein secondary structures. *BMC Structural Biology*, **2007**, 7, 56	2.7	62
143	ImmTree: database of evolutionary relationships of genes and proteins in the human immune system. *Immunome Research*, **2007**, 3, 4		16
142	IDR knowledge base for primary immunodeficiencies. *Immunome Research*, **2007**, 3, 6		21
141	Molecular characterization of the immune system: emergence of proteins, processes, and domains. *Immunogenetics*, **2007**, 59, 333-48	3.2	27
140	The structural basis of hyper IgM deficiency - CD40L mutations. *Protein Engineering, Design and Selection*, **2007**, 20, 133-41	1.9	35
139	Immunity genes and their orthologs: a multi-species database. *International Immunology*, **2007**, 19, 1361-70	4.9	12
138	High-precision mapping of protein protein interfaces: an integrated genetic strategy combining en masse mutagenesis and DNA-level parallel analysis on a yeast two-hybrid platform. *Nucleic Acids Research*, **2007**, 35, e103	20.1	14
137	Immunological systems biology: gene expression analysis of B-cell development in Ramos B-cells. *Molecular Immunology*, **2007**, 44, 3537-51	4.3	3
136	Detection of Pathogenic Mutation Prone Locations from Protein Sequences using Solvent Accessibility Measurements **2007**,		1
135	Immunome, Immtree and Immunity: Databases for Systems Biology of Immune System **2007**,		1
134	Immunome: a reference set of genes and proteins for systems biology of the human immune system. *Cellular Immunology*, **2006**, 244, 87-9	4.4	44
133	Immunodeficiency mutation databases (IDbases). *Human Mutation*, **2006**, 27, 1200-8	4.7	101
132	Bioinformatic analysis of protein structure-function relationships: case study of leukocyte elastase (ELA2) missense mutations. *Human Mutation*, **2006**, 27, 1230-43	4.7	42

131	BTKbase: the mutation database for X-linked agammaglobulinemia. *Human Mutation*, **2006**, 27, 1209-17	4.7	147
130	Profiling genetic variation along the androgen biosynthesis and metabolism pathways implicates several single nucleotide polymorphisms and their combinations as prostate cancer risk factors. *Cancer Research*, **2006**, 66, 743-7	10.1	51
129	A statistical score for assessing the quality of multiple sequence alignments. *BMC Bioinformatics*, **2006**, 7, 484	3.6	35
128	Primary Immunodeficiencies: Genotype-Phenotype Correlations **2006**, 443-460		2
127	Proteome analysis of B-cell maturation. *Proteomics*, **2006**, 6, 5152-68	4.8	13
126	B cells. *International Journal of Biochemistry and Cell Biology*, **2005**, 37, 518-23	5.6	35
125	Genome-wide selection of unique and valid oligonucleotides. *Nucleic Acids Research*, **2005**, 33, e115	20.1	5
124	Characterization of CA XV, a new GPI-anchored form of carbonic anhydrase. *Biochemical Journal*, **2005**, 392, 83-92	3.8	140
123	On exact string matching of unique oligonucleotides. *Computers in Biology and Medicine*, **2005**, 35, 173-84	1.7	11
122	Bruton's tyrosine kinase: cell biology, sequence conservation, mutation spectrum, siRNA modifications, and expression profiling. *Immunological Reviews*, **2005**, 203, 200-15	11.3	159
121	Dynamic covariation between gene expression and proteome characteristics. *BMC Bioinformatics*, **2005**, 6, 215	3.6	9
120	Distribution of immunodeficiency fact files with XML--from Web to WAP. *BMC Medical Informatics and Decision Making*, **2005**, 5, 21	3.6	4
119	KinMutBase: a registry of disease-causing mutations in protein kinase domains. *Human Mutation*, **2005**, 25, 435-42	4.7	53
118	Statistical methods for identifying conserved residues in multiple sequence alignment. *Statistical Applications in Genetics and Molecular Biology*, **2004**, 3, Article28	1.2	6
117	Characterization of CA XIII, a novel member of the carbonic anhydrase isozyme family. *Journal of Biological Chemistry*, **2004**, 279, 2719-27	5.4	187
116	Structure-function analysis of PrsA reveals roles for the parvulin-like and flanking N- and C-terminal domains in protein folding and secretion in Bacillus subtilis. *Journal of Biological Chemistry*, **2004**, 279, 19302-14	5.4	83
115	Conservation and covariance in PH domain sequences: physicochemical profile and information theoretical analysis of XLA-causing mutations in the Btk PH domain. *Protein Engineering, Design and Selection*, **2004**, 17, 267-76	1.9	36
114	Different gene expression in immunoglobulin-mutated and immunoglobulin-unmutated forms of chronic lymphocytic leukemia. *Cancer Genetics and Cytogenetics*, **2004**, 153, 69-72		30

113	Online registry of genetic and clinical immunodeficiency diagnostic laboratories, IDdiagnostics. *Journal of Clinical Immunology*, **2004**, 24, 53-61	5.7	15
112	Probing the alpha-complementing domain of E. coli beta-galactosidase with use of an insertional pentapeptide mutagenesis strategy based on Mu in vitro DNA transposition. *Proteins: Structure, Function and Bioinformatics*, **2004**, 54, 681-92	4.2	42
111	Virtual bioinformatics distance learning suite*. *Biochemistry and Molecular Biology Education*, **2004**, 32, 156-60	1.3	12
110	APECED-causing mutations in AIRE reveal the functional domains of the protein. *Human Mutation*, **2004**, 23, 245-57	4.7	90
109	Fast Iterative Gene Clustering Based on Information Theoretic Criteria for Selecting the Cluster Structure. *Journal of Computational Biology*, **2004**, 11, 660-682	1.7	3
108	cDNA microarray analysis of gene expression in coeliac disease jejunal biopsy samples. *Journal of Autoimmunity*, **2004**, 22, 249-65	15.5	30
107	Fast iterative gene clustering based on information theoretic criteria for selecting the cluster structure. *Journal of Computational Biology*, **2004**, 11, 660-82	1.7	6
106	RankViaContact: ranking and visualization of amino acid contacts. *Bioinformatics*, **2003**, 19, 2161-2	7.2	23
105	Autoinhibition of Jak2 tyrosine kinase is dependent on specific regions in its pseudokinase domain. *Molecular Biology of the Cell*, **2003**, 14, 1448-59	3.5	170
104	Signal transduction-related bioinformatics services. *Briefings in Bioinformatics*, **2003**, 4, 325-31	13.4	
103	The diverse genetic basis of immunodeficiencies **2003**, 45-76		
102	On Postprocessing of Neural Network Prediction of Polyproline Type II Secondary Structures: Network Spectrum, Response Analysis, and Scattering. *Neural Computing and Applications*, **2003**, 11, 238-243	4.8	4
101	Changes in apoptosis-related pathways in acute myelocytic leukemia. *Cancer Genetics and Cytogenetics*, **2003**, 146, 89-101		41
100	Stimulation-induced gene expression in Ramos B-cells. *Genes and Immunity*, **2003**, 4, 343-50	4.4	12
99	Efficient estimation of emission probabilities in profile hidden Markov models. *Bioinformatics*, **2003** , 19, 2359-68	7.2	6
98	Bioinformatics in Proteomics **2003**, 419-428		
97	Interaction between Btk TH and SH3 domain. *Biopolymers*, **2002**, 63, 325-34	2.2	14
96	Novel insertions of Bruton tyrosine kinase in patients with X-linked agammaglobulinemia. *Human Mutation*, **2002**, 20, 480-1	4.7	6

95	Pattern of somatic androgen receptor gene mutations in patients with hormone-refractory prostate cancer. *Laboratory Investigation*, **2002**, 82, 1591-8	5.9	55
94	IDR: the ImmunoDeficiency Resource. *Nucleic Acids Research*, **2002**, 30, 232-4	20.1	13
93	Structural basis of ICF-causing mutations in the methyltransferase domain of DNMT3B. *Protein Engineering, Design and Selection*, **2002**, 15, 1005-14	1.9	11
92	Microarray analysis of B-cell stimulation. *Vitamins and Hormones*, **2002**, 64, 77-99	2.5	12
91	Mobile access to biological databases on the Internet. *IEEE Transactions on Biomedical Engineering*, **2002**, 49, 1477-9	5	9
90	V(D)J recombination defects in lymphocytes due to RAG mutations: severe immunodeficiency with a spectrum of clinical presentations. *Blood*, **2001**, 97, 81-8	2.2	278
89	Coevolution of the domains of cytoplasmic tyrosine kinases. *Molecular Biology and Evolution*, **2001**, 18, 312-21	8.3	14
88	Analysis of Btk mutations in patients with X-linked agammaglobulinaemia (XLA) and determination of carrier status in normal female relatives: a nationwide study of Btk deficiency in Greece. *Scandinavian Journal of Immunology*, **2001**, 54, 321-7	3.4	13
87	Bioinformatics in proteomics. *New Biotechnology*, **2001**, 18, 241-8		34
86	Mutations in severe combined immune deficiency (SCID) due to JAK3 deficiency. *Human Mutation*, **2001**, 18, 255-63	4.7	83
85	The Tec family of cytoplasmic tyrosine kinases: mammalian Btk, Bmx, Itk, Tec, Txk and homologs in other species. *BioEssays*, **2001**, 23, 436-46	4.1	227
84	On preprocessing of protein sequences for neural network prediction of polyproline type II secondary structures. *Computers in Biology and Medicine*, **2001**, 31, 385-98	7	8
83	Molecular dynamics simulation of the effects of cytosine methylation on structure of oligonucleotides. *Computational and Theoretical Chemistry*, **2001**, 546, 51-62		21
82	Intermolecular interactions between the SH3 domain and the proline-rich TH region of Bruton's tyrosine kinase. *FEBS Letters*, **2001**, 489, 67-70	3.8	31
81	Primary immunodeficiency mutation databases. *Advances in Genetics*, **2001**, 43, 103-88	3.3	58
80	Structure-function effects in primary immunodeficiencies. *Scandinavian Journal of Immunology*, **2000**, 52, 226-32	3.4	9
79	Novel immunodeficiency data servers. *Immunological Reviews*, **2000**, 178, 177-85	11.3	26
78	Of genes and phenotypes: the immunological and molecular spectrum of combined immune deficiency. Defects of the gamma(c)-JAK3 signaling pathway as a model. *Immunological Reviews*, **2000**, 178, 39-48	11.3	84

77	Structural basis of Wiskott-Aldrich syndrome causing mutations in the WH1 domain. *Journal of Molecular Medicine*, **2000**, 78, 530-7	5.5	29
76	Bruton tyrosine kinase BTK in X-linked agammaglobulinemia XLA. *Frontiers in Bioscience - Landmark*, **2000**, 5, d917-928	2.8	2
75	Structural Basis of Bloom Syndrome (BS) Causing Mutations in the BLM Helicase Domain. *Molecular Medicine*, **2000**, 6, 155-164	6.2	33
74	The autoimmune regulator protein has transcriptional transactivating properties and interacts with the common coactivator CREB-binding protein. *Journal of Biological Chemistry*, **2000**, 275, 16802-9	5.4	168
73	Six X-linked agammaglobulinemia-causing missense mutations in the Src homology 2 domain of Bruton's tyrosine kinase: phosphotyrosine-binding and circular dichroism analysis. *Journal of Immunology*, **2000**, 164, 4170-7	5.3	28
72	Structural basis for SH2D1A mutations in X-linked lymphoproliferative disease. *Biochemical and Biophysical Research Communications*, **2000**, 269, 124-30	3.4	26
71	Identification of novel transcription factor-like gene from human intestinal cells. *Biochemical and Biophysical Research Communications*, **2000**, 276, 660-6	3.4	35
70	Molecular modeling of the Jak3 kinase domains and structural basis for severe combined immunodeficiency. *Clinical Immunology*, **2000**, 96, 108-18	9	21
69	Isolation and initial characterization of a novel zinc finger gene, DNMT3L, on 21q22.3, related to the cytosine-5-methyltransferase 3 gene family. *Genomics*, **2000**, 65, 293-8	4.3	221
68	Rational design and purification of human Bruton's tyrosine kinase SH3-SH2 protein for structure-function studies. *Protein Expression and Purification*, **2000**, 20, 365-71	2	4
67	Bruton tyrosine kinase (BTK) in X-linked agammaglobulinemia (XLA). *Frontiers in Bioscience - Landmark*, **2000**, 5, D917-28	2.8	28
66	KinMutBase, a database of human disease-causing protein kinase mutations. *Nucleic Acids Research*, **1999**, 27, 362-4	20.1	16
65	A novel family of DNA-polymerase-associated B subunits. *Trends in Biochemical Sciences*, **1999**, 24, 14-6	10.3	56
64	Mutations of the human BTK gene coding for bruton tyrosine kinase in X-linked agammaglobulinemia. *Human Mutation*, **1999**, 13, 280-5	4.7	76
63	Pleckstrin homology domains of tec family protein kinases. *Biochemical and Biophysical Research Communications*, **1999**, 265, 151-7	3.4	31
62	Mapping and cloning of FAD2 gene to develop allele-specific PCR for oleic acid in spring turnip rape (Brassica rapa ssp. oleifera). *Molecular Breeding*, **1998**, 4, 543-550	3.4	54
61	SH3-Domain binding function of HIV-1 Nef is required for association with a PAK-related kinase. *Virology*, **1998**, 250, 273-82	3.6	93
60	Androgen-sensitive human prostate cancer cells, LNCaP, produce both N-terminally mature and truncated prostate-specific antigen isoforms. *FEBS Journal*, **1998**, 255, 329-35		14

59	Thermal unfolding of small proteins with SH3 domain folding pattern. *Proteins: Structure, Function and Bioinformatics*, **1998**, 31, 309-19	4.2	49
58	Determination and analysis of antigenic epitopes of prostate specific antigen (PSA) and human glandular kallikrein 2 (hK2) using synthetic peptides and computer modeling. *Protein Science*, **1998**, 7, 259-69	6.3	51
57	X-linked agammaglobulinemia: lack of mature B lineage cells caused by mutations in the Btk kinase. *Seminars in Immunopathology*, **1998**, 19, 369-81		18
56	Mutation screening of the BTK gene in 56 families with X-linked agammaglobulinemia (XLA): 47 unique mutations without correlation to clinical course. *Pediatrics*, **1998**, 101, 276-84	7.4	98
55	Solution structure of the SH3 domain from Bruton's tyrosine kinase. *Biochemistry*, **1998**, 37, 2912-24	3.2	68
54	Interactions between SH2 and SH3 domains. *Biochemical and Biophysical Research Communications*, **1998**, 242, 351-6	3.4	5
53	Stimulation of B and T cells activates expression of transcription and differentiation factors. *Biochemical and Biophysical Research Communications*, **1998**, 249, 475-80	3.4	17
52	BTKbase, mutation database for X-linked agammaglobulinemia (XLA). *Nucleic Acids Research*, **1998**, 26, 242-7	20.1	60
51	Delta3,5-delta2,4-dienoyl-CoA isomerase from rat liver. Molecular characterization. *Journal of Biological Chemistry*, **1998**, 273, 349-55	5.4	46
50	BTKbase, mutation database for X-linked agammaglobulinemia (XLA). *Nucleic Acids Research*, **1997**, 25, 166-71	20.1	39
49	Identification of csk tyrosine phosphorylation sites and a tyrosine residue important for kinase domain structure. *Biochemical Journal*, **1997**, 322 (Pt 3), 927-35	3.8	12
48	Missense mutations affecting a conserved cysteine pair in the TH domain of Btk. *FEBS Letters*, **1997**, 413, 205-10	3.8	28
47	Structural analysis of an anti-estradiol antibody. *Molecular Immunology*, **1997**, 34, 1215-26	4.3	20
46	Molecular and Structural Characterization of Five Novel Mutations in the Bruton Tyrosine Kinase Gene from Patients with X-Linked Agammaglobulinemia. *Molecular Medicine*, **1997**, 3, 477-485	6.2	18
45	Registries of immunodeficiency patients and mutations. *Human Mutation*, **1997**, 10, 261-7	4.7	8
44	BTKbase, mutation database for X-linked agammaglobulinemia (XLA). *Nucleic Acids Research*, **1996**, 24, 160-5	20.1	51
43	Sequence specificity in CpG mutation hotspots. *FEBS Letters*, **1996**, 396, 119-22	3.8	56
42	Structural aspects of signal transduction in B-cells. *Critical Reviews in Immunology*, **1996**, 16, 251-75	1.8	20

41	Structural consequences of neopullulanase mutations. *BBA - Proteins and Proteomics*, **1996**, 1295, 195-200		2
40	Aromatic interactions define the binding of the alphavirus spike to its nucleocapsid. *Structure*, **1996**, 4, 519-29	5.2	95
39	X-linked agammaglobulinemia (XLA): a genetic tyrosine kinase (Btk) disease. *BioEssays*, **1996**, 18, 825-34	4.1	56
38	Immunodeficiency mutation databases a new research tool. *Trends in Immunology*, **1996**, 17, 495-496		
37	BTKbase: XLA-mutation registry. *Trends in Immunology*, **1996**, 17, 502-506		37
36	CD40Lbase: a database of CD40L gene mutations causing X-linked hyper-IgM syndrome. *Trends in Immunology*, **1996**, 17, 511-516		84
35	BTKbase: XLA-mutation registry. *Trends in Immunology*, **1996**, 17, 502-6		20
34	CD40lbase: a database of CD40L gene mutations causing X-linked hyper-IgM syndrome. *Trends in Immunology*, **1996**, 17, 511-6		56
33	Immunodeficiency mutation databases--a new research tool. *Trends in Immunology*, **1996**, 17, 495-6		16
32	BTKbase: a database of XLA-causing mutations. International Study Group. *Trends in Immunology*, **1995**, 16, 460-5		76
31	Representative selection of proteins based on nuclear families. *Protein Engineering, Design and Selection*, **1995**, 8, 501-3	1.9	10
30	Accurate prediction of protein secondary structural class with fuzzy structural vectors. *Protein Engineering, Design and Selection*, **1995**, 8, 505-12	1.9	10
29	Structural basis for pleckstrin homology domain mutations in X-linked agammaglobulinemia. *Biochemistry*, **1995**, 34, 1475-81	3.2	57
28	Identification of Btk mutations in 20 unrelated patients with X-linked agammaglobulinaemia (XLA). *Human Molecular Genetics*, **1995**, 4, 693-700	5.6	54
27	Deletion within the Src homology domain 3 of Bruton's tyrosine kinase resulting in X-linked agammaglobulinemia (XLA). *Journal of Experimental Medicine*, **1994**, 180, 461-70	16.6	78
26	Accuracy of protein flexibility predictions. *Proteins: Structure, Function and Bioinformatics*, **1994**, 19, 141-9	4.2	241
25	Modeling of prostate specific antigen and human glandular kallikrein structures. *Biochemical and Biophysical Research Communications*, **1994**, 204, 1251-6	3.4	27
24	Tec homology (TH) adjacent to the PH domain. *FEBS Letters*, **1994**, 350, 263-5	3.8	85

23	C-terminal truncations of a thermostable Bacillus stearothermophilus alpha-amylase. *Protein Engineering, Design and Selection*, **1994**, 7, 1255-9	1.9	28
22	Structural basis for chromosome X-linked agammaglobulinemia: a tyrosine kinase disease. *Proceedings of the National Academy of Sciences of the United States of America*, **1994**, 91, 12803-7	11.5	68
21	Structural similarity of the binding sites of cyclophilin A-cyclosporin A and FKBP-FK506 systems. *Biochemical and Biophysical Research Communications*, **1993**, 192, 912-7	3.4	13
20	HYDRO: a program for protein hydropathy predictions. *Computer Methods and Programs in Biomedicine*, **1993**, 41, 121-9	6.9	2
19	Modelling of the 3D structure of Bacillus circulant var. alkalophilus cyclomaltodextrin glucanotransferase and comparison with □amylase **1993**, 433-434		
18	MULTICOMP: a program package for multiple sequence comparison. *Bioinformatics*, **1992**, 8, 35-8	7.2	4
17	Computer modeling of two inorganic pyrophosphatases. *Biochemical and Biophysical Research Communications*, **1992**, 186, 122-8	3.4	5
16	Selection of a representative set of structures from Brookhaven Protein Data Bank. *Proteins: Structure, Function and Bioinformatics*, **1992**, 14, 265-76	4.2	47
15	Site-directed mutagenesis of putative active-site residues of Bacillus stearothermophilus □amylase. *Molecular Engineering*, **1991**, 1, 267-273		8
14	Simultaneous comparison of several sequences. *Methods in Enzymology*, **1990**, 183, 447-56	1.7	10
13	Conservation of functional residues between yeast and E. coli inorganic pyrophosphatases. *BBA - Proteins and Proteomics*, **1990**, 1038, 338-45		37
12	Site-directed mutagenesis of a thermostable alpha-amylase from Bacillus stearothermophilus: putative role of three conserved residues. *Journal of Biochemistry*, **1990**, 107, 267-72	3.1	69
11	Conserved residues of liquefying alpha-amylases are concentrated in the vicinity of active site. *Biochemical and Biophysical Research Communications*, **1990**, 166, 61-5	3.4	11
10	Microbial amylolytic enzymes. *Critical Reviews in Biochemistry and Molecular Biology*, **1989**, 24, 329-418	8.7	306
9	An algorithm for simultaneous comparison of several sequences. *Bioinformatics*, **1988**, 4, 89-92	7.2	2
8	Relationship of protein flexibility to thermostability. *Protein Engineering, Design and Selection*, **1987**, 1, 477-80	1.9	234
7	Poikilosis □pervasive biological variation. *F1000Research*,9, 602	3.6	0
6	Strategy for Disease Diagnosis, Progression Prediction, Risk Group Stratification and Treatment – Case of COVID-19		2

List of Publications

5	How good are pathogenicity predictors in detecting benign variants?		1
4	Variation Benchmark Datasets: Update, Criteria, Quality and Applications		2
3	Mixed T- and B-Lymphocyte Deficiency Disorders1-7		
2	Immunodeficiency, Primary: Affecting the Adaptive Immune System1-6		1
1	Generic model for biological regulation. *F1000Research*,11, 419	3.6	0