ProtTrans: Toward Understanding the Language of Life

IEEE Transactions on Pattern Analysis and Machine Intelligenc
44, 7112-7127
DOI: 10.1109/tpami.2021.3095381

Citation Report

#	Article	IF	Citations
1	TALE: Transformer-based protein function Annotation with joint sequenceâ€“Label Embedding. Bioinformatics, 2021, 37, 2825-2833.	1.8	52
4	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	6.5	135
5	Clustering FunFams using sequence embeddings improves EC purity. Bioinformatics, 2021, 37, 3449-3455.	1.8	25
8	TITAN: T-cell receptor specificity prediction with bimodal attention networks. Bioinformatics, 2021, 37, i237-i244.	1.8	73
9	Comparative analysis of molecular fingerprints in prediction of drug combination effects. Briefings in Bioinformatics, 2021, 22, .	3.2	47
10	Protein tertiary structure prediction and refinement using deep learning and Rosetta in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1722-1733.	1.5	40
13	Protein interâ€residue contact and distance prediction by coupling complementary coevolution features with deep residual networks in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1911-1921.	1.5	23
14	iCDI-W2vCom: Identifying the Ion Channelâ€“Drug Interaction in Cellular Networking Based on word2vec and node2vec. Frontiers in Genetics, 2021, 12, 738274.	1.1	6
16	The Transporter-Mediated Cellular Uptake and Efflux of Pharmaceutical Drugs and Biotechnology Products: How and Why Phospholipid Bilayer Transport Is Negligible in Real Biomembranes. Molecules, 2021, 26, 5629.	1.7	14
17	ECNet is an evolutionary context-integrated deep learning framework for protein engineering. Nature Communications, 2021, 12, 5743.	5.8	66
18	CpG Transformer for imputation of single-cell methylomes. Bioinformatics, 2022, 38, 597-603.	1.8	17
19	Computational methods for protein localization prediction. Computational and Structural Biotechnology Journal, 2021, 19, 5834-5844.	1.9	12
20	SPOT-1D2: Improving Protein Secondary Structure Prediction using High Sequence Identity Training Set and an Ensemble of Recurrent and Residual-convolutional Neural Networks. , 2021, , .		1
21	Ensemble of Template-Free and Template-Based Classifiers for Protein Secondary Structure Prediction. International Journal of Molecular Sciences, 2021, 22, 11449.	1.8	1
22	Differentiable biology: using deep learning for biophysics-based and data-driven modeling of molecular mechanisms. Nature Methods, 2021, 18, 1169-1180.	9.0	44
23	Protein matchmaking through representation learning. Cell Systems, 2021, 12, 948-950.	2.9	0
24	FoldHSphere: deep hyperspherical embeddings for protein fold recognition. BMC Bioinformatics, 2021, 22, 490.	1.2	8
25	Understanding mutation hotspots for the SARS-CoV-2 spike protein using Shannon Entropy and K-means clustering. Computers in Biology and Medicine, 2021, 138, 104915.	3.9	31

#	Article	IF	Citations
26	Protein Design with Deep Learning. International Journal of Molecular Sciences, 2021, 22, 11741.	1.8	23
27	The generative capacity of probabilistic protein sequence models. Nature Communications, 2021, 12, 6302.	5.8	28
28	Learning the local landscape of protein structures with convolutional neural networks. Journal of Biological Physics, 2021, 47, 435-454.	0.7	13
29	Light attention predicts protein location from the language of life. Bioinformatics Advances, 2021, 1, .	0.9	57
31	Interpreting Potts and Transformer Protein Models Through the Lens of Simplified Attention. , 2021, , .		4
32	The Power of Universal Contextualized Protein Embeddings in Cross-species Protein Function Prediction. Evolutionary Bioinformatics, 2021, 17, 117693432110626.	0.6	4
33	ProteinBERT: a universal deep-learning model of protein sequence and function. Bioinformatics, 2022, 38, 2102-2110.	1.8	193
34	Predicting Multi-Epitope Vaccine Candidates Using Natural Language Processing and Deep Learning. , 2021, , .		0
36	Ultrafast end-to-end protein structure prediction enables high-throughput exploration of uncharacterized proteins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	26
38	TransDTI: Transformer-Based Language Models for Estimating DTIs and Building a Drug Recommendation Workflow. ACS Omega, 2022, 7, 2706-2717.	1.6	18
39	SignalP 6.0 predicts all five types of signal peptides using protein language models. Nature Biotechnology, 2022, 40, 1023-1025.	9.4	883
40	Using metagenomic data to boost protein structure prediction and discovery. Computational and Structural Biotechnology Journal, 2022, 20, 434-442.	1.9	3
41	ProtPlat: an efficient pre-training platform for protein classification based on FastText. BMC Bioinformatics, 2022, 23, 66.	1.2	2
42	Sequence-based prediction of protein binding regions and drugâ€“target interactions. Journal of Cheminformatics, 2022, 14, 5.	2.8	16
45	Interpreting Potts and Transformer Protein Models Through the Lens of Simplified Attention. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2022, 27, 34-45.	0.7	0
46	An analysis of protein language model embeddings for fold prediction. Briefings in Bioinformatics, 2022, 23, .	3.2	16
47	Ten quick tips for deep learning in biology. PLoS Computational Biology, 2022, 18, e1009803.	1.5	14
48	Mapping Data to Deep Understanding: Making the Most of the Deluge of SARS-CoV-2 Genome Sequences. MSystems, 2022, 7, e0003522.	1.7	5

#	Article	IF	Citations
49	Dropping diversity of products of large US firms: Models and measures. PLoS ONE, 2022, 17, e0264330.	1.1	0
50	Lightweight ProteinUnet2 network for protein secondary structure prediction: a step towards proper evaluation. BMC Bioinformatics, 2022, 23, 100.	1.2	1
51	A Benchmark Dataset for Evaluating Practical Performance of Model Quality Assessment of Homology Models. Bioengineering, 2022, 9, 118.	1.6	1
52	Large-scale design and refinement of stable proteins using sequence-only models. PLoS ONE, 2022, 17, e0265020.	1.1	17
53	Protein design via deep learning. Briefings in Bioinformatics, 2022, 23, .	3.2	33
55	Prediction of RNAâ€“protein interactions using a nucleotide language model. Bioinformatics Advances, 2022, 2, .	0.9	15
56	Recent Advances in Machine Learning Variant Effect Prediction Tools for Protein Engineering. Industrial & Engineering Chemistry Research, 2022, 61, 6235-6245.	1.8	15
57	Learning meaningful representations of protein sequences. Nature Communications, 2022, 13, 1914.	5.8	55
59	rzMLP-DTA: gMLP network with ReZero for sequence-based drug-target affinity prediction. , 2021, , .		7
60	Jointly Learning to Align and Aggregate with Cross Attention Pooling for Peptide-MHC Class I Binding Prediction. , 2021, , .		1
61	Protein embeddings and deep learning predict binding residues for various ligand classes. Scientific Reports, 2021, 11, 23916.	1.6	63
63	NGS read classification using AI. PLoS ONE, 2021, 16, e0261548.	1.1	0
64	Embeddings from protein language models predict conservation and variant effects. Human Genetics, 2022, 141, 1629-1647.	1.8	60
65	DeepLoc 2.0: multi-label subcellular localization prediction using protein language models. Nucleic Acids Research, 2022, 50, W228-W234.	6.5	180
69	RBP-TSTL is a two-stage transfer learning framework for genome-scale prediction of RNA-binding proteins. Briefings in Bioinformatics, 2022, 23, .	3.2	6
70	InterPepScore: a deep learning score for improving the FlexPepDock refinement protocol. Bioinformatics, 2022, 38, 3209-3215.	1.8	1
71	Characterizing and explaining the impact of disease-associated mutations in proteins without known structures or structural homologs. Briefings in Bioinformatics, 2022, 23, .	3.2	18
72	LM-GVP: an extensible sequence and structure informed deep learning framework for protein property prediction. Scientific Reports, 2022, 12, 6832.	1.6	21

#	Article	IF	Citations
73	Reaching alignment-profile-based accuracy in predicting protein secondary and tertiary structural properties without alignment. Scientific Reports, 2022, 12, 7607.	1.6	14
74	Prediction of proteinâ€“protein interaction using graph neural networks. Scientific Reports, 2022, 12, 8360.	1.6	38
75	Deciphering the language of antibodies using self-supervised learning. Patterns, 2022, 3, 100513.	3.1	52
76	Predicting proteinâ€“peptide binding residues via interpretable deep learning. Bioinformatics, 2022, 38, 3351-3360.	1.8	24
77	Protein language-model embeddings for fast, accurate, and alignment-free protein structure prediction. Structure, 2022, 30, 1169-1177.e4.	1.6	52
80	PepNN: a deep attention model for the identification of peptide binding sites. Communications Biology, 2022, 5, .	2.0	16
81	ScanNet: an interpretable geometric deep learning model for structure-based protein binding site prediction. Nature Methods, 2022, 19, 730-739.	9.0	68
82	The structural basis of Cdc7-Dbf4 kinase dependent targeting and phosphorylation of the MCM2-7 double hexamer. Nature Communications, 2022, 13, .	5.8	21
83	ProtTrans-Glutar: Incorporating Features From Pre-trained Transformer-Based Models for Predicting Glutarylation Sites. Frontiers in Genetics, 0, 13, .	1.1	5
84	HIV- Bidirectional Encoder Representations From Transformers: A Set of Pretrained Transformers for Accelerating HIV Deep Learning Tasks. Frontiers in Virology, 0, 2, .	0.7	1
86	Recent Advances in the Prediction of Subcellular Localization of Proteins and Related Topics. Frontiers in Bioinformatics, 2022, 2, .	1.0	3
88	NetSurfP-3.0: accurate and fast prediction of protein structural features by protein language models and deep learning. Nucleic Acids Research, 2022, 50, W510-W515.	6.5	80
89	Contrastive learning on protein embeddings enlightens midnight zone. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	38
91	Deep embeddings to comprehend and visualize microbiome protein space. Scientific Reports, 2022, 12, .	1.6	3
92	Controllable protein design with language models. Nature Machine Intelligence, 2022, 4, 521-532.	8.3	76
93	Identification of Phage Receptor-Binding Protein Sequences with Hidden Markov Models and an Extreme Gradient Boosting Classifier. Viruses, 2022, 14, 1329.	1.5	14
94	DTI-BERT: Identifying Drug-Target Interactions in Cellular Networking Based on BERT and Deep Learning Method. Frontiers in Genetics, 0, 13, .	1.1	7
96	Comparative Analysis on Alignment-Based and Pretrained Feature Representations for the Identification of DNA-Binding Proteins. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-14.	0.7	0

#	Article	IF	Citations
97	Transfer learning in proteins: evaluating novel protein learned representations for bioinformatics tasks. Briefings in Bioinformatics, 2022, 23, .	3.2	8
99	Mitigating cold-start problems in drug-target affinity prediction with interaction knowledge transferring. Briefings in Bioinformatics, 2022, 23, .	3.2	5
100	Artificial intelligence for antibody reading comprehension: AntiBERTa. Patterns, 2022, 3, 100535.	3.1	2
101	Machine Learning Approaches to TCR Repertoire Analysis. Frontiers in Immunology, 0, 13, .	2.2	8
102	Protein sequence profile prediction using ProtAlbert transformer. Computational Biology and Chemistry, 2022, 99, 107717.	1.1	4
105	Accurate prediction of virus-host protein-protein interactions via a Siamese neural network using deep protein sequence embeddings. Patterns, 2022, 3, 100551.	3.1	5
106	ProtGPT2 is a deep unsupervised language model for protein design. Nature Communications, 2022, 13, .	5.8	160
107	Predicting the specific substrate for transmembrane transport proteins using BERT language model. , 2022, , .		1
109	Hierarchical deep learning for predicting GO annotations by integrating protein knowledge. Bioinformatics, 2022, 38, 4488-4496.	1.8	6
111	Transformer Neural Networks for Protein Family and Interaction Prediction Tasks. Journal of Computational Biology, 2023, 30, 95-111.	0.8	3
114	TooT-BERT-M: Discriminating Membrane Proteins from Non-Membrane Proteins using a BERT Representation of Protein Primary Sequences. , 2022, , .		3
115	Fine-tuning of BERT Model to Accurately Predict Drugâ€“Target Interactions. Pharmaceutics, 2022, 14, 1710.	2.0	10
116	TMbed: transmembrane proteins predicted through language model embeddings. BMC Bioinformatics, 2022, 23, .	1.2	24
117	The rise of the machines in chemistry. Magnetic Resonance in Chemistry, 2022, 60, 1044-1051.	1.1	0
118	Reliability of the In Silico Prediction Approach to In Vitro Evaluation of Bacterial Toxicity. Sensors, 2022, 22, 6557.	2.1	4
119	SEMA: Antigen B-cell conformational epitope prediction using deep transfer learning. Frontiers in Immunology, 0, 13, .	2.2	17
120	ProteinGLUE multi-task benchmark suite for self-supervised protein modeling. Scientific Reports, 2022, 12, .	1.6	6
121	DistilProtBert: a distilled protein language model used to distinguish between real proteins and their randomly shuffled counterparts. Bioinformatics, 2022, 38, ii95-ii98.	1.8	13

#	Article	IF	Citations
123	SPRoBERTa: protein embedding learning with local fragment modeling. Briefings in Bioinformatics, 2022, 23, .	3.2	3
124	AMPDeep: hemolytic activity prediction of antimicrobial peptides using transfer learning. BMC Bioinformatics, 2022, 23, .	1.2	8
125	PTG-PLM: Predicting Post-Translational Glycosylation and Glycation Sites Using Protein Language Models and Deep Learning. Axioms, 2022, 11, 469.	0.9	4
126	CollagenTransformer: End-to-End Transformer Model to Predict Thermal Stability of Collagen Triple Helices Using an NLP Approach. ACS Biomaterials Science and Engineering, 2022, 8, 4301-4310.	2.6	13
127	Deciphering microbial gene function using natural language processing. Nature Communications, 2022, 13, .	5.8	13
129	Single-sequence protein structure prediction using a language model and deep learning. Nature Biotechnology, 2022, 40, 1617-1623.	9.4	145
131	Preâ€Training of Equivariant Graph Matching Networks with Conformation Flexibility for Drug Binding. Advanced Science, 2022, 9, .	5.6	10
132	BIONIC: biological network integration using convolutions. Nature Methods, 2022, 19, 1250-1261.	9.0	17
133	Language models for the prediction of SARS-CoV-2 inhibitors. International Journal of High Performance Computing Applications, 2022, 36, 587-602.	2.4	13
135	Alignment-free metal ion-binding site prediction from protein sequence through pretrained language model and multi-task learning. Briefings in Bioinformatics, 2022, 23, .	3.2	15
137	E-SNPs&GO: embedding of protein sequence and function improves the annotation of human pathogenic variants. Bioinformatics, 2022, 38, 5168-5174.	1.8	9
138	PITHIA: Protein Interaction Site Prediction Using Multiple Sequence Alignments and Attention. International Journal of Molecular Sciences, 2022, 23, 12814.	1.8	10
139	SETH predicts nuances of residue disorder from protein embeddings. Frontiers in Bioinformatics, 0, 2, .	1.0	14
140	TooT-BERT-T: A BERT Approach onÂDiscriminating Transport Proteins fromÂNon-transport Proteins. Lecture Notes in Networks and Systems, 2023, , 1-11.	0.5	3
142	Recent Progress in the Discovery and Design of Antimicrobial Peptides Using Traditional Machine Learning and Deep Learning. Antibiotics, 2022, 11, 1451.	1.5	22
144	Improving Protein Function Prediction by Adaptively Fusing Information From Protein Sequences and Biomedical Literature. IEEE Journal of Biomedical and Health Informatics, 2023, 27, 1140-1148.	3.9	0
145	Multiscale Modeling at the Interface of Molecular Mechanics and Natural Language through Attention Neural Networks. Accounts of Chemical Research, 2022, 55, 3387-3403.	7.6	13
146	Computational protein design with dataâ€driven approaches: Recent developments and perspectives. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2023, 13, .	6.2	4

#	Article	IF	Citations
148	Nearest neighbor search on embeddings rapidly identifies distant protein relations. Frontiers in Bioinformatics, 0, 2, .	1.0	13
149	Deep learning for protein secondary structure prediction: Pre and post-AlphaFold. Computational and Structural Biotechnology Journal, 2022, 20, 6271-6286.	1.9	13
150	GOProFormer: A Multi-Modal Transformer Method for Gene Ontology Protein Function Prediction. Biomolecules, 2022, 12, 1709.	1.8	7
151	From sequence to function through structure: Deep learning for protein design. Computational and Structural Biotechnology Journal, 2023, 21, 238-250.	1.9	29
152	RGN: Residue-Based Graph Attention and Convolutional Network for Proteinâ€“Protein Interaction Site Prediction. Journal of Chemical Information and Modeling, 2022, 62, 5961-5974.	2.5	7
154	IPPF-FE: an integrated peptide and protein function prediction framework based on fused features and ensemble models. Briefings in Bioinformatics, 2023, 24, .	3.2	4
155	OrganelX web server for sub-peroxisomal and sub-mitochondrial protein localization and peroxisomal target signal detection. Computational and Structural Biotechnology Journal, 2023, 21, 128-133.	1.9	1
156	Protein Molecular Function Annotation Based onÂTransformer Embeddings. Lecture Notes in Computer Science, 2022, , 210-220.	1.0	0
157	End-to-End Protein Normal Mode Frequency Predictions Using Language and Graph Models and Application to Sonification. ACS Nano, 2022, 16, 20656-20670.	7.3	10
158	A large-scale benchmark study of tools for the classification of protein-coding and non-coding RNAs. Nucleic Acids Research, 2022, 50, 12094-12111.	6.5	2
160	Prediction of polyreactive and nonspecific single-chain fragment variables through structural biochemical features and protein language-based descriptors. BMC Bioinformatics, 2022, 23, .	1.2	3
163	Protein engineering via Bayesian optimization-guided evolutionary algorithm and robotic experiments. Briefings in Bioinformatics, 2023, 24, .	3.2	8
166	Single-sequence protein structure prediction using supervised transformer protein language models. Nature Computational Science, 2022, 2, 804-814.	3.8	46
167	<scp>LambdaPP</scp>: Fast and accessible proteinâ€specific phenotype predictions. Protein Science, 2023, 32, .	3.1	5
170	ManyFold: an efficient and flexible library for training and validating protein folding models. Bioinformatics, 0, , .	1.8	0
172	Integrating unsupervised language model with triplet neural networks for protein gene ontology prediction. PLoS Computational Biology, 2022, 18, e1010793.	1.5	10
174	Novel machine learning approaches revolutionize protein knowledge. Trends in Biochemical Sciences, 2023, 48, 345-359.	3.7	23
176	Convolutional ProteinUnetLM competitive with long shortâ€term memoryâ€based protein secondary structure predictors. Proteins: Structure, Function and Bioinformatics, 2023, 91, 608-618.	1.5	0

#	Article	IF	Citations
177	Tree visualizations of protein sequence embedding space enable improved functional clustering of diverse protein superfamilies. Briefings in Bioinformatics, 2023, 24, .	3.2	2
178	Alignment-free estimation of sequence conservation for identifying functional sites using protein sequence embeddings. Briefings in Bioinformatics, 2023, 24, .	3.2	8
179	CATHe: detection of remote homologues for CATH superfamilies using embeddings from protein language models. Bioinformatics, 2023, 39, .	1.8	8
180	Applications of transformer-based language models in bioinformatics: a survey. Bioinformatics Advances, 2023, 3, .	0.9	22
181	Computational and artificial intelligence-based methods for antibody development. Trends in Pharmacological Sciences, 2023, 44, 175-189.	4.0	29
182	LBCE-XGB: A XGBoost Model for Predicting Linear B-Cell Epitopes Based on BERT Embeddings. Interdisciplinary Sciences, Computational Life Sciences, 0, , .	2.2	0
183	Transformer-based deep learning for predicting protein properties in the life sciences. ELife, 0, 12, .	2.8	29
184	Using machine learning to predict the effects and consequences of mutations in proteins. Current Opinion in Structural Biology, 2023, 78, 102518.	2.6	11
185	MM-StackEns: A new deep multimodal stacked generalization approach for proteinâ€“protein interaction prediction. Computers in Biology and Medicine, 2023, 153, 106526.	3.9	4
186	Exploration of protein sequence embeddings for protein-ligand binding site detection. , 2022, , .		2
187	Gene Ontology based protein functional annotation using pretrained embeddings. , 2022, , .		0
189	Machine learning in computational modelling of membrane protein sequences and structures: From methodologies to applications. Computational and Structural Biotechnology Journal, 2023, 21, 1205-1226.	1.9	3
193	Learning the protein language of proteome-wide protein-protein binding sites via explainable ensemble deep learning. Communications Biology, 2023, 6, .	2.0	11
194	Large language models generate functional protein sequences across diverse families. Nature Biotechnology, 2023, 41, 1099-1106.	9.4	213
195	Deepro-Glu: combination of convolutional neural network and Bi-LSTM models using ProtBert and handcrafted features to identify lysine glutarylation sites. Briefings in Bioinformatics, 2023, 24, .	3.2	6
197	TooT-BERT-C: A study on discriminating ion channels from membrane proteins based on the primary sequenceâ€™s contextual representation from BERT models. , 2022, , .		2
198	Sequence-Structure Embeddings via Protein Language Models Improve on Prediction Tasks. , 2022, , .		0
199	A Study onÂtheÂApplication ofÂProtein Language Models inÂtheÂAnalysis ofÂMembrane Proteins. Lecture Notes in Networks and Systems, 2023, , 147-152.	0.5	1

#	Article	IF	Citations
200	OncoRTT: Predicting novel oncology-related therapeutic targets using BERT embeddings and omics features. Frontiers in Genetics, 0, 14, .	1.1	1
202	Deep language models for interpretative and predictive materials science. , 2023, 1, .		24
203	Machine learning for evolutionary-based and physics-inspired protein design: Current and future synergies. Current Opinion in Structural Biology, 2023, 80, 102571.	2.6	11
204	Phosformer: an explainable transformer model for protein kinase-specific phosphorylation predictions. Bioinformatics, 2023, 39, .	1.8	6
205	MOFormer: Self-Supervised Transformer Model for Metalâ€“Organic Framework Property Prediction. Journal of the American Chemical Society, 2023, 145, 2958-2967.	6.6	27
207	Generative power of a protein language model trained on multiple sequence alignments. ELife, 0, 12, .	2.8	10
211	pLMSNOSite: an ensemble-based approach for predicting protein S-nitrosylation sites by integrating supervised word embedding and embedding from pre-trained protein language model. BMC Bioinformatics, 2023, 24, .	1.2	6
213	Survey of Protein Sequence Embedding Models. International Journal of Molecular Sciences, 2023, 24, 3775.	1.8	3
214	Explainable Deep Hypergraph Learning Modeling the Peptide Secondary Structure Prediction. Advanced Science, 2023, 10, .	5.6	12
215	DeepBIO: an automated and interpretable deep-learning platform for high-throughput biological sequence prediction, functional annotation and visualization analysis. Nucleic Acids Research, 2023, 51, 3017-3029.	6.5	32
216	Low-data interpretable deep learning prediction of antibody viscosity using a biophysically meaningful representation. Scientific Reports, 2023, 13, .	1.6	7
217	Persistent spectral theory-guided protein engineering. Nature Computational Science, 2023, 3, 149-163.	3.8	17
218	Identification of Thermophilic Proteins Based on Sequence-Based Bidirectional Representations from Transformer-Embedding Features. Applied Sciences (Switzerland), 2023, 13, 2858.	1.3	3
219	Uncovering the Interaction Interface Between Harpin (Hpa1) and Rice Aquaporin (OsPIP1;3) Through Proteinâ€“Protein Docking: An In Silico Approach. Molecular Biotechnology, 0, , .	1.3	3
221	Data-driven design of orthogonal protein-protein interactions. Science Signaling, 2023, 16, .	1.6	0
223	Evolutionary-scale prediction of atomic-level protein structure with a language model. Science, 2023, 379, 1123-1130.	6.0	623
226	Align-gram: Rethinking the Skip-gram Model for Protein Sequence Analysis. Protein Journal, 2023, 42, 135-146.	0.7	2
229	Linguistically inspired roadmap for building biologically reliable protein language models. Nature Machine Intelligence, 2023, 5, 485-496.	8.3	13

#	Article	IF	Citations
230	LMNglyPred: prediction of human N-linked glycosylation sites using embeddings from a pre-trained protein language model. Glycobiology, 2023, 33, 411-422.	1.3	6
231	Comment Generator for Java using Deep Learning. , 2023, , .		0
232	DeepSTABp: A Deep Learning Approach for the Prediction of Thermal Protein Stability. International Journal of Molecular Sciences, 2023, 24, 7444.	1.8	10
233	Generative design of de novo proteins based on secondary-structure constraints using an attention-based diffusion model. CheM, 2023, 9, 1828-1849.	5.8	27
241	Theoretical and Data-Driven Approaches for Biomolecular Condensates. Chemical Reviews, 2023, 123, 8988-9009.	23.0	2
266	Deep Learning andÂTransformers inÂMHC-Peptide Binding andÂPresentation Towards Personalized Vaccines inÂCancer Immunology: A Brief Review. Lecture Notes in Networks and Systems, 2023, , 14-23.	0.5	0
267	Neoantigen Detection Using Transformers andÂTransfer Learning inÂtheÂCancer Immunology Context. Lecture Notes in Networks and Systems, 2023, , 97-102.	0.5	0
289	Tutorial: a guide for the selection of fast and accurate computational tools for the prediction of intrinsic disorder in proteins. Nature Protocols, 2023, 18, 3157-3172.	5.5	4
308	DSV: An Alignment Validation Loss forÂSelf-supervised Outlier Model Selection. Lecture Notes in Computer Science, 2023, , 254-269.	1.0	1
319	TeM-DTBA: time-efficient drug target binding affinity prediction using multiple modalities with Lasso feature selection. Journal of Computer-Aided Molecular Design, 2023, 37, 573-584.	1.3	1
320	PEvoLM: Protein Sequence Evolutionary Information Language Model. , 2023, , .		0
322	AcrTransAct: Pre-trained Protein Transformer Models for the Detection of Type I Anti-CRISPR Activities. , 2023, , .		0
323	A Comparative Analysis of Transformer-based Protein Language Models for Remote Homology Prediction. , 2023, , .		0
344	Protein Sorting Prediction. Methods in Molecular Biology, 2024, , 27-63.	0.4	0
389	Is Protein BLAST a thing of the past?. Nature Communications, 2023, 14, .	5.8	0
391	Exploring Bias Evaluation Techniques for Quantifying Large Language Model Biases. , 2023, , .		0
409	De Novo Design ofÂTarget-Specific Ligands Using BERT-Pretrained Transformer. Lecture Notes in Computer Science, 2024, , 311-322.	1.0	0
421	Computer Simulation of Gene Knockout in Bacteria Accelerated by AI. , 2023, , .		0

#	Article	IF	Citations
435	PEST: A General-Purpose Protein Embedding Model for Homology Search. , 2023, , .		0
439	Enhance the recognition of signal peptide domain and transmembrane domain based on transformer. , 2023, , .		0
465	Machine learning for functional protein design. Nature Biotechnology, 2024, 42, 216-228.	9.4	1
472	Transfer-DDG: Prediction of protein-protein binding affinity changes with mutations based on large pre-trained model transfer learning. , 2023, , .		0