|  |  |  |  |
| --- | --- | --- | --- |
|  | **MMPatho** |  | **mrmbert** |
| **Category**: [Genome-wide variants] | **Category**: [RNA modifications] |
| **Description**: Prediction of pathogenicity and function impact of missense mutation. | **Description**: Prediction of multiple types of RNA modifications via biological language model |
| **Journal**:**Sumbitted** | **Journal**: **IEEE TCBB** |
| [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667) XXX | [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667) 10.1109/TCBB.2023.3283985 |
| **Year**: **2023** | **Year**: **2023** |
| **http://202.119.84.36:3079/mmpatho/** | **http://csbio.njust.edu.cn/bioinf/mrmbert/** |
|  | **VPatho** |  | [**FFMSRes-MutP**](http://csbio.njust.edu.cn/bioinf/ffmsresmutp) |
| **Category**: [Genome-wide variants] | **Category**: [Mutations prediction] |
| **Description**: Prediction of pathogenicity and function impact of variants. | **Description**: Prediction of disease-related nsSNPs by integrating deep feature fusion and multi-scale ResNet. |
| **Journal**: **Briefings in Bioinformatics** | **Journal**: **Briefings in Bioinformatics.** |
| [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667) XXX | [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667) 10.1093/bib/bbab530 |
| **Year**: **2022** | **Year**: **2022** |
| **http://csbio.njust.edu.cn/bioinf/vpatho/** | **http://csbio.njust.edu.cn/bioinf/ffmsresmutp/** |
|  | **MutTMPredctor** |  | **csORF-finder** |
| **Category**: [Mutations prediction] | **Category**:[ identification of [coding sORFs](javascript:;)] |
| **Description**: Disease-related mutations prediction in transmembrane protein. | **Description**: an effective ensemble learning framework for accurate identification of multi-species coding short open reading frames |
| **Journal**: **Computational and Structural Biotechnology Journal.** | **Journal**: Briefings in Bioinformatics |
| [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667) 10.1016/j.csbj.2021.11.024 | [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667) 10.1093/bib/bbac392 |
| **Year**: **2021** | **Year**: **2022** |
| **http://csbio.njust.edu.cn/bioinf/muttmpredictor/** | http://202.119.84.36:3079/csorffinder/ |
|  | **PROST** |  | |  | | --- | | SSCpred | |
| **Category**:  [Mutations upon protein stability] | **Category**: [Protein Contact Map] |
| **Description**: AlphaFold2-aware Sequence-Based Predictor to Estimate Protein Stability Changes upon Missense Mutations | **Description**: Single-Sequence-Based Protein Contact Prediction Using Deep Fully Convolutional Network |
| **Journal**: Journal of Chemical Information and Modeling | **Journal**: Journal of Chemical Information and Modeling |
| [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667)10.1021/acs.jcim.2c00799 | [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667)10.1021/acs.jcim.9b01207 |
| **Year**: 2022 | **Year**: 2020 |
| http://202.119.84.36:3079/prost/ | http://csbio.njust.edu.cn/bioinf/sscpred/ |
|  | [**DCFCrystal**](http://csbio.njust.edu.cn/bioinf/dcfcrystal/) |  | **mrmbert** |
| **Category**: [Protein Crystallization] | **Category**: [RNA modifications types] |
| **Description**: Predicting Protein Crystallization. | **Description**: Prediction of multiple types of RNA modifications via biological language model |
| **Journal**: **Briefings in Bioinformatics** | **Journal**: IEEE-ACM Transactions on Computational Biology and Bioinformatics |
| [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667)**10.1093/bib/bbaa076** | [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667)**XXX** |
| **Year**: 2021 | **Year**: 2022 |
| **http://csbio.njust.edu.cn/bioinf/dcfcrystal/** | <http://csbio.njust.edu.cn/bioinf/mrmbert>  [http://csbio.njust.edu.cn/bioinf/\*\*\*\*](http://csbio.njust.edu.cn/bioinf/****) **（先用这个，等录用之后，再换地址）** |
|  | **DeepnsSNPs** |  | TargetMM |
| **Category**: [Mutations prediction] | **Category**: [Mutations prediction] |
| **Description**: Accurate Prediction of Non-synonymous Single-nucleotide Polymorphisms by Combining Multi-scale Convolutional Neural Network and Residue Environment Information | **Description**: Accurate Missense Mutation Prediction by Utilizing Local and Global Sequence Information with Classifier Ensemble |
| **Journal**: Chemometrics and Intelligent Laboratory Systems | **Journal**: Combinatorial Chemistry & High Throughput Screening |
| [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667)**10.1016/j.chemolab.2021.104326** | [**DOI:**](https://doi.org/10.1093/bioinformatics/btab667)[10.2174/1386207323666201204140438](https://doi.org/10.2174/1386207323666201204140438) |
| **Year**: 2021 | **Year**: 2022 |
| **https://github.com/sera0616/gefang-DeepnsSNPs.git** |  | **https://github.com/sera616/TargetMM.git** |