

23 documenti

search details

Fariselli p[Author] OR (Benvenuta S[Author]) AND ("2016/01/01"[PDAT] : "2019/08/19"[PDAT]) AND ("2016/01/01"[PDAT] : "2019/12/31"[PDAT])

1: Benevenuta S, Fariselli P. On the Upper Bounds of the Real-Valued Predictions.

Bioinform Biol Insights. 2019 Aug 23;13:1177932219871263. doi: 10.1177/1177932219871263. eCollection 2019. PubMed PMID: 31488948; PubMed Central PMCID: PMC6710671.

2: Montanucci L, Capriotti E, Frank Y, Ben-Tal N, Fariselli P.

DDGun: an untrained method for the prediction of protein stability changes upon single and multiple point variations. BMC Bioinformatics. 2019 Jul 3;20(Suppl 14):335. doi: 10.1186/s12859-019-2923-1. PubMed PMID: 31266447; PubMed Central PMCID: PMC6606456.

3: Savojardo C, Petrosino M, Babbi G, Bovo S, Corbi-Verge C, Casadio R, Fariselli

P, Folkman L, Garg A, Karimi M, Katsonis P, Kim PM, Lichtarge O, Martelli PL, Pasquo A, Pal D, Shen Y, Strokach AV, Turina P, Zhou Y, Andreoletti G, Brenner SE, Chiaraluce R, Consalvi V, Capriotti E. Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Hum Mutat. 2019 Jun 17. doi: 10.1002/humu.23843. [Epub ahead of print] PubMed PMID: 31209948.

4: Capriotti E, Montanucci L, Profiti G, Rossi I, Giannuzzi D, Aresu L, Fariselli

P. Fido-SNP: the first webserver for scoring the impact of single nucleotide variants in the dog genome. Nucleic Acids Res. 2019 Jul 2;47(W1):W136-W141. doi: 10.1093/nar/gkz420. PubMed PMID: 31114899; PubMed Central PMCID: PMC6602425.

5: Milan M, Maroso F, Dalla Rovere G, Carraro L, Ferrareso S, Patarnello T,

Bargelloni L, Cardazzo B, Fariselli P. Tracing seafood at high

spatial resolution
using NGS-generated data and machine learning: Comparing microbiome
versus SNPs.
Food Chem. 2019 Jul 15;286:413–420. doi: 10.1016/j.foodchem.
2019.02.037. Epub
2019 Feb 15. PubMed PMID: 30827626.

6: Giannuzzi D, Marconato L, Elgendy R, Ferrareso S, Scarselli E,
Fariselli P,
Nicosia A, Pegolo S, Leoni G, Laganga P, Leone VF, Giantin M, Troise
F, Dacasto
M, Aresu L. Longitudinal transcriptomic and genetic landscape of
radiotherapy
response in canine melanoma. Vet Comp Oncol. 2019 Sep;17(3):308–316.
doi:
10.1111/vco.12473. Epub 2019 Mar 27. PubMed PMID: 30805995.

7: Montanucci L, Savojardo C, Martelli PL, Casadio R, Fariselli P.
On the biases
in predictions of protein stability changes upon variations: the
INPS test case.
Bioinformatics. 2018 Nov 29. doi: 10.1093/bioinformatics/bty979.
[Epub ahead of
print] PubMed PMID: 30496382.

8: Montanucci L, Martelli PL, Ben-Tal N, Fariselli P. A natural
upper bound to
the accuracy of predicting protein stability changes upon mutations.
Bioinformatics. 2019 May 1;35(9):1513–1517. doi: 10.1093/
bioinformatics/bty880.
PubMed PMID: 30329016.

9: De Liguoro M, Riga A, Fariselli P. Synergistic toxicity of some
sulfonamide
mixtures on *Daphnia magna*. Ecotoxicol Environ Saf. 2018 Nov
30;164:84–91. doi:
10.1016/j.ecoenv.2018.08.011. Epub 2018 Aug 8. PubMed PMID:
30098509.

10: KoÁillari L, Fariselli P, Trovato A, Seno F, Maritan A.
Signature of Pareto
optimization in the *Escherichia coli* proteome. Sci Rep. 2018 Jun
14;8(1):9141.
doi: 10.1038/s41598-018-27287-3. PubMed PMID: 29904084; PubMed
Central PMCID:
PMC6002381.

11: Savojardo C, Martelli PL, Fariselli P, Profiti G, Casadio R.

BUSCA: an integrative web server to predict subcellular localization of proteins. *Nucleic Acids Res.* 2018 Jul 2;46(W1):W459–W466. doi: 10.1093/nar/gky320. PubMed PMID: 29718411; PubMed Central PMCID: PMC6031068.

12: Magro M, Zaccarin M, Miotto G, Da Dalt L, Baratella D, Fariselli P, Gabai G, Vianello F. Analysis of hard protein corona composition on selective iron oxide nanoparticles by MALDI–TOF mass spectrometry: identification and amplification of a hidden mastitis biomarker in milk proteome. *Anal Bioanal Chem.* 2018 May;410(12):2949–2959. doi: 10.1007/s00216-018-0976-z. Epub 2018 Mar 12. PubMed PMID: 29532191.

13: Savojardo C, Martelli PL, Fariselli P, Casadio R. DeepSig: deep learning improves signal peptide detection in proteins. *Bioinformatics.* 2018 May 15;34(10):1690–1696. doi: 10.1093/bioinformatics/btx818. PubMed PMID: 29280997; PubMed Central PMCID: PMC5946842.

14: Milan M, Carraro L, Fariselli P, Martino ME, Cavalieri D, Vitali F, Boffo L, Patarnello T, Bargelloni L, Cardazzo B. Microbiota and environmental stress: how pollution affects microbial communities in Manila clams. *Aquat Toxicol.* 2018 Jan;194:195–207. doi: 10.1016/j.aquatox.2017.11.019. Epub 2017 Nov 27. PubMed PMID: 29202271.

15: Capriotti E, Fariselli P. PhD–SNPg: a webserver and lightweight tool for scoring single nucleotide variants. *Nucleic Acids Res.* 2017 Jul 3;45(W1):W247–W252. doi: 10.1093/nar/gkx369. PubMed PMID: 28482034; PubMed Central PMCID: PMC5570245.

16: Carraro M, Minervini G, Giollo M, Bromberg Y, Capriotti E, Casadio R, Dunbrack R, Elefanti L, Fariselli P, Ferrari C, Gough J, Katsonis P, Leonardi E, Lichtarge O, Menin C, Martelli PL, Niroula A, Pal LR, Repo S, Scaini

MC, Vihinen
M, Wei Q, Xu Q, Yang Y, Yin Y, Zaucha J, Zhao H, Zhou Y, Brenner SE,
Moult J,
Tosatto SCE. Performance of in silico tools for the evaluation of
p16INK4a
(CDKN2A) variants in CAGI. Hum Mutat. 2017 Sep;38(9):1042–1050. doi:
10.1002/humu.23235. Epub 2017 May 16. PubMed PMID: 28440912; PubMed
Central
PMCID: PMC5561474.

17: Savojardo C, Martelli PL, Fariselli P, Casadio R. SChloro:
directing
Viridiplantae proteins to six chloroplastic sub-compartments.
Bioinformatics.
2017 Feb 1;33(3):347–353. doi: 10.1093/bioinformatics/btw656. PubMed
PMID:
28172591; PubMed Central PMCID: PMC5408801.

18: Savojardo C, Fariselli P, Martelli PL, Casadio R. ISPRED4:
interaction sites
PREDiction in protein structures with a refining grammar model.
Bioinformatics.
2017 Jun 1;33(11):1656–1663. doi: 10.1093/bioinformatics/btx044.
PubMed PMID:
28130235.

19: Capriotti E, Martelli PL, Fariselli P, Casadio R. Blind
prediction of
deleterious amino acid variations with SNPs&GO. Hum Mutat. 2017
Sep;38(9):1064–1071. doi: 10.1002/humu.23179. Epub 2017 May 2.
PubMed PMID:
28102005; PubMed Central PMCID: PMC5522651.

20: Bovo S, Di Lena P, Martelli PL, Fariselli P, Casadio R. NET-GE:
a web-server
for NETwork-based human gene enrichment. Bioinformatics. 2016 Nov
15;32(22):3489–3491. Epub 2016 Aug 2. PubMed PMID: 27485441.

21: Menichetti G, Fariselli P, Remondini D. Network measures for
protein folding
state discrimination. Sci Rep. 2016 Jul 28;6:30367. doi: 10.1038/
srep30367.
PubMed PMID: 27464796; PubMed Central PMCID: PMC4964642.

22: Martelli PL, Fariselli P, Savojardo C, Babbi G, Aggazio F,
Casadio R. Large
scale analysis of protein stability in OMIM disease related human
protein

variants. BMC Genomics. 2016 Jun 23;17 Suppl 2:397. doi:
10.1186/s12864-016-2726-y. PubMed PMID: 27356511; PubMed Central
PMCID:
PMC4928156.

23: Savojardo C, Fariselli P, Martelli PL, Casadio R. INPS-MD: a web
server to
predict stability of protein variants from sequence and structure.
Bioinformatics. 2016 Aug 15;32(16):2542-4. doi: 10.1093/
bioinformatics/btw192.
Epub 2016 Apr 10. PubMed PMID: 27153629.