

Resource Summary Report

Generated by [dkNET](#) on Aug 21, 2026

BorutaShap

RRID:SCR_021696

Type: Tool

Proper Citation

BorutaShap (RRID:SCR_021696)

Resource Information

URL: <https://pypi.org/project/BorutaShap/>

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Description: Software tool as wrapper feature selection method which combines both Boruta feature selection algorithm with shapley values.

Resource Type: software resource

Keywords: Wrapper feature selection method, Boruta feature selection algorithm, shapley values

Availability: Free, Available for download, Freely available

Resource Name: BorutaShap

Resource ID: SCR_021696

Alternate URLs: <https://github.com/Ekeany/Boruta-Shap>

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260815T182701+0000

Ratings and Alerts

No rating or validation information has been found for BorutaShap.

No alerts have been found for BorutaShap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Kong Z, et al. (2026) Unraveling key genes and mitochondrial-related mechanisms of atherosclerosis severity: explorations based on interpretable machine learning. BMC cardiovascular disorders, 26(1).

Fouquier J, et al. (2026) EXPLANA: a user-friendly workflow for EXPLoratory ANALysis and feature selection in cross-sectional and longitudinal microbiome studies. Bioinformatics (Oxford, England), 42(1).

Zheng L, et al. (2025) Development and validation of a hypoxemia prediction model in middle-aged and elderly outpatients undergoing painless gastroscopy. Scientific reports, 15(1), 17965.

DeRosa J, et al. (2024) Neurodevelopmental subtypes of functional brain organization in the ABCD study using a rigorous analytic framework. NeuroImage, 299, 120827.

Schall PZ, et al. (2024) Predictive modeling of oocyte maternal mRNA features for five mammalian species reveals potential shared and species-restricted regulators during maturation. Physiological genomics, 56(1), 9.

Steagall PV, et al. (2023) Fully automated deep learning models with smartphone applicability for prediction of pain using the Feline Grimace Scale. Scientific reports, 13(1), 21584.

Einarsson H, et al. (2022) Promoter sequence and architecture determine expression variability and confer robustness to genetic variants. eLife, 11.