

Resource Summary Report

Generated by [kravitz2](#) on Aug 8, 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: 20260801T190723+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 [kravitz2](#) .

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).

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).

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.