

Resource Summary Report

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CARMA

RRID:SCR_004999

Type: Tool

Proper Citation

CARMA (RRID:SCR_004999)

Resource Information

URL: <http://www.cebitec.uni-bielefeld.de/index.php/2-uncategorised/47-carma?highlight=WyJjYXJtYSJd>

Proper Citation: CARMA (RRID:SCR_004999)

Description: A software pipeline for characterizing the taxonomic composition and genetic diversity of short-read metagenomes. The software was originally designed for the analysis of environmental metagenomes obtained by the ultra-fast 454 pyrosequencing system.

Abbreviations: CARMA

Synonyms: CARMA - Characterizing Short Read Metagenomes

Resource Type: software resource

Defining Citation: [PMID:18285365](#)

Keywords: metagenome, phylogenetic, dna fragment, dna, classification

Availability: Acknowledgement requested

Resource Name: CARMA

Resource ID: SCR_004999

Alternate IDs: OMICS_01451

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260725T190600+0000

Ratings and Alerts

No rating or validation information has been found for CARMA.

No alerts have been found for CARMA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 86 mentions in open access literature.

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

Gautam N, et al. (2025) Mapping the Interactions Among Class IIa Histone Deacetylases and Myocyte Enhancer Factor 2s. Journal of chemical information and modeling, 65(12), 6249.

Manzanilla-Valdez ML, et al. (2025) Antioxidant, Hypotensive, and Antidiabetic Breakthroughs: Bromelain Hydrolysis Unlocks Quinoa's Peptide Potential - In Silico and In Vitro Approach. Journal of agricultural and food chemistry, 73(36), 22877.

Yu T, et al. (2025) Enhanced dynamic coupling in a nuclear receptor underlies ligand activity. The Journal of biological chemistry, 301(2), 108081.

Morgenroth E, et al. (2025) Emo-FilM: A multimodal dataset for affective neuroscience using naturalistic stimuli. Scientific data, 12(1), 684.

Biswas A, et al. (2025) Impact of Replicas and Simulation Length on In Silico Behaviors of a Protein Domain. Chemphyschem : a European journal of chemical physics and physical chemistry, 26(3), e202400783.

Song X, et al. (2025) Lower functional connectivity state transitions during affective processing correlate with subsequent impairment in sustaining positive affect in subthreshold depression. International journal of clinical and health psychology : IJCHP, 25(1), 100560.

Malik A, et al. (2025) Stability of Individual Differences in Social and Nonsocial Visual Attention From Newborn to 14 Months. Developmental psychobiology, 67(4), e70054.

Morales AE, et al. (2025) Bat genomes illuminate adaptations to viral tolerance and disease resistance. Nature, 638(8050), 449.

Lamlom SF, et al. (2025) Cultivar specific nitrogen and potassium recommendations optimize yield and quality attributes in sugar beet. Scientific reports, 15(1), 27550.

Mariasoosai C, et al. (2024) Structural insights into the molecular recognition of integrin α V β 3 by RGD-containing ligands: The role of the specificity-determining loop (SDL). bioRxiv : the preprint server for biology.

Rubiales-Martínez A, et al. (2024) Design of Two New Sulfur Derivatives of Perezone: In Silico Study Simulation Targeting PARP-1 and In Vitro Study Validation Using Cancer Cell Lines. *International journal of molecular sciences*, 25(2).

Carranza-Aranda AS, et al. (2024) Evaluation of Potential Furin Protease Inhibitory Properties of Pioglitazone, Rosiglitazone, and Pirfenidone: An In Silico Docking and Molecular Dynamics Simulation Approach. *Current issues in molecular biology*, 46(8), 8665.

Akgun B, et al. (2024) Genome-wide association analysis and admixture mapping in a Puerto Rican cohort supports an Alzheimer disease risk locus on chromosome 12. *Frontiers in aging neuroscience*, 16, 1459796.

?liwa P, et al. (2024) The Pivotal Distinction between Antagonists' and Agonists' Binding into Dopamine D4 Receptor-MD and FMO/PIEDA Studies. *International journal of molecular sciences*, 25(2).

Díaz-Valdez J, et al. (2024) EhVps35, a retromer component, is involved in the recycling of the EhADH and Gal/GalNac virulent proteins of *Entamoeba histolytica*. *Frontiers in parasitology*, 3, 1356601.

Martínez-Valencia D, et al. (2024) The *Entamoeba histolytica* Vps26 (EhVps26) retromeric protein is involved in phagocytosis: Bioinformatic and experimental approaches. *PloS one*, 19(8), e0304842.

Gavshina AV, et al. (2024) The role of the correlated motion(s) of the chromophore in photoswitching of green and red forms of the photoconvertible fluorescent protein mSAASoti. *Scientific reports*, 14(1), 8754.

Perego E, et al. (2023) Single-photon microscopy to study biomolecular condensates. *Nature communications*, 14(1), 8224.

Dube N, et al. (2023) Identification of an Evolutionarily Conserved Allosteric Network in Steroid Receptors. *Journal of chemical information and modeling*, 63(2), 571.

Rucker G, et al. (2023) Structure, dynamics and free energy studies on the effect of point mutations on SARS-CoV-2 spike protein binding with ACE2 receptor. *PloS one*, 18(10), e0289432.