Resource Summary Report

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CDART

RRID:SCR_006378
Type: Tool

Proper Citation

CDART (RRID:SCR_006378)

Resource Information

URL: https://www.ctsacentral.org/editor/index.php?wg=ps625

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Description: Data management tool designed to support multicenter research studies including key components needed in a full-featured research data management application. It is web based and builds on mysql, xml, and tomcat components. Key features include: * Support for complex, highly customized case report forms (XML based configuration) * Security and access at the site, user, and form levels * User management * Management of multiple studies from a single instance * CDISC Operational Data Model (ODM) data extraction for input to analysis software * Longitudinal data collection They are working on major revisions to improve performance and add important new features. Version 2 should be available by mid-2013. They are making this version available now so that other centers with multisite study and/or complex form needs can leverage CDART for their needs. CDART will have a higher support requirement than REDCap and is not intended to replace REDCap for single site studies. Files are provided to assist in setting up an instance of CDART.

Abbreviations: CDART

Synonyms: Carolina Data Acquisition & Reporting Technology, CDART - Carolina Data Acquisition and Reporting Technology, CDART - Carolina Data Acquisition & Reporting Technology, Carolina Data Acquisition and Reporting Technology

Resource Type: data management software, software application, software resource

Keywords: data management, multicenter

Funding:

Resource Name: CDART

Resource ID: SCR_006378

Alternate IDs: nlx_152158

Record Creation Time: 20220129T080235+0000

Record Last Update: 20250509T055758+0000

Ratings and Alerts

No rating or validation information has been found for CDART.

No alerts have been found for CDART.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 49 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Naveed M, et al. (2025) Exploration of alcohol dehydrogenase EutG from Bacillus tropicus as an eco-friendly approach for the degradation of polycyclic aromatic compounds. Scientific reports, 15(1), 3466.

Hassan MU, et al. (2023) DUF916 and DUF3324 in the WxL protein cluster bind to WxL and link bacterial and host surfaces. Protein science : a publication of the Protein Society, 32(11), e4806.

Kavya N, et al. (2023) Insights on Novel Effectors and Characterization of Metacaspase (RS107_6) as a Potential Cell Death-Inducing Protein in Rhizoctonia solani. Microorganisms, 11(4).

Song P, et al. (2021) Cloning, expression and characterization of metalloproteinase HypZn from Aspergillus niger. PloS one, 16(11), e0259809.

Aragão AO, et al. (2021) Proteins from the core genome of Corynebacterium ulcerans respond for pathogenicity and reveal promising vaccine targets for diphtheria. Microbial pathogenesis, 161(Pt A), 105263.

Matveevsky S, et al. (2021) Heterogeneity in conservation of multifunctional partner enzymes with meiotic importance, CDK2 kinase and BRCA1 ubiquitin ligase. PeerJ, 9, e12231.

Malik A, et al. (2020) Classification and Computational Analysis of Arabidopsis thaliana Sperm Cell-Specific F-Box Protein Gene 3p.AtFBP113. Frontiers in genetics, 11, 609668.

Shahbaaz M, et al. (2020) Functional and Structural Analysis of Predicted Proteins Obtained from Homo sapiens' Minisatellite 33.15-Tagged Transcript pAKT-45 Variants. BioMed research international, 2020, 2562950.

Newing TP, et al. (2020) Molecular basis for RNA polymerase-dependent transcription complex recycling by the helicase-like motor protein HelD. Nature communications, 11(1), 6420.

Guerriero G, et al. (2020) Identification of Callose Synthases in Stinging Nettle and Analysis of Their Expression in Different Tissues. International journal of molecular sciences, 21(11).

Suryawanshi A, et al. (2020) What lies beneath: Hydra provides cnidarian perspectives into the evolution of FGFR docking proteins. Development genes and evolution, 230(3), 227.

Bai Q, et al. (2020) YSIRK-G/S-directed translocation is required for Streptococcus suis to deliver diverse cell wall anchoring effectors contributing to bacterial pathogenicity. Virulence, 11(1), 1539.

Nicolao MC, et al. (2019) Extracellular vesicles from Echinococcus granulosus larval stage: Isolation, characterization and uptake by dendritic cells. PLoS neglected tropical diseases, 13(1), e0007032.

Alviz-Gazitua P, et al. (2019) The Response of Cupriavidus metallidurans CH34 to Cadmium Involves Inhibition of the Initiation of Biofilm Formation, Decrease in Intracellular c-di-GMP Levels, and a Novel Metal Regulated Phosphodiesterase. Frontiers in microbiology, 10, 1499.

Moyano E, et al. (2018) Genome-wide analysis of the NAC transcription factor family and their expression during the development and ripening of the Fragaria × ananassa fruits. PloS one, 13(5), e0196953.

Lu Q, et al. (2018) Genomewide analysis of the lateral organ boundaries domain gene family in Eucalyptus grandis reveals members that differentially impact secondary growth. Plant biotechnology journal, 16(1), 124.

Zhang L, et al. (2018) Divergent evolution of rice blast resistance Pi54 locus in the genus Oryza. Rice (New York, N.Y.), 11(1), 63.

Jain D, et al. (2018) ketu mutant mice uncover an essential meiotic function for the ancient RNA helicase YTHDC2. eLife, 7.

Eckhard U, et al. (2017) Discovery of a proteolytic flagellin family in diverse bacterial phyla that assembles enzymatically active flagella. Nature communications, 8(1), 521.

Baker GJ, et al. (2017) Expression, Purification, and Biochemical Characterization of the Flavocytochrome P450 CYP505A30 from Myceliophthora thermophila. ACS omega, 2(8), 4705.