

Resource Summary Report

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GSDS - Golden State Donor Services

RRID:SCR_004605

Type: Tool

Proper Citation

GSDS - Golden State Donor Services (RRID:SCR_004605)

Resource Information

URL: <http://www.gsds.org/Home%20Page>

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Description: Golden State Donor Services (GSDS) is the nonprofit, federally designated transplant donor network serving two and a half million people in the greater Sacramento area. We are committed to saving and improving lives by connecting one life to another through donation and transplantation. We support potential donor families in their time of loss, provide care for them through the donation process and coordinate the recovery of organs and tissues for transplant. We also provide after-care support to donor families while at the same time working to inspire universal acceptance of donation to ensure every person in need receives the "Gift of Life." GSDS' designated service area includes 11 counties in Northern California, (Amador, Calaveras, Colusa, El Dorado, Nevada, Placer, Sacramento, Sierra, Sutter, Yolo, and Yuba), as well as the communities of Santa Rosa and Reno. Currently GSDS has agreements with 30 hospitals. In Golden State Donor Services' area, more than 1000 people now wait for an organ transplant, (heart, liver, lungs, kidneys, intestine or pancreas).

Abbreviations: GSDS

Synonyms: Golden State Donor Services

Resource Type: biomaterial supply resource, material resource, tissue bank

Resource Name: GSDS - Golden State Donor Services

Resource ID: SCR_004605

Alternate IDs: nlx_60283

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260905T133125+0000

Ratings and Alerts

No rating or validation information has been found for GSDS - Golden State Donor Services.

No alerts have been found for GSDS - Golden State Donor Services.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Jiang Q, et al. (2025) Two leucine-rich repeat receptor-like kinases initiate herbivory defense responses in tea plants. *Horticulture research*, 12(1), uhae281.

Fu C, et al. (2024) Genome-wide identification and molecular evolution of Dof transcription factors in *Cyperus esculentus*. *BMC genomics*, 25(1), 667.

Kr?pski T, et al. (2023) Identification and characteristics of wheat Lr orthologs in three rye inbred lines. *PloS one*, 18(7), e0288520.

Bai MZ, et al. (2023) Bioinformatics Analysis of MSH1 Genes of Green Plants: Multiple Parallel Length Expansions, Intron Gains and Losses, Partial Gene Duplications, and Alternative Splicing. *International journal of molecular sciences*, 24(17).

Filyushin MA, et al. (2023) DREB1 and DREB2 Genes in Garlic (*Allium sativum* L.): Genome-Wide Identification, Characterization, and Stress Response. *Plants (Basel, Switzerland)*, 12(13).

Liu FF, et al. (2022) CTL10 has multiple functions in the innate immune responses of the silkworm, *Bombyx mori*. *Developmental and comparative immunology*, 127, 104309.

Hurali DT, et al. (2022) Analysis of NIA and GSNOR family genes and nitric oxide homeostasis in response to wheat-leaf rust interaction. *Scientific reports*, 12(1), 803.

Xia J, et al. (2021) Genome-Wide Analysis of the YABBY Transcription Factor Family in Rapeseed (*Brassica napus* L.). *Genes*, 12(7).

Wang H, et al. (2021) Genome-wide identification, characterization, and expression analysis of tea plant autophagy-related genes (CsARGs) demonstrates that they play diverse roles during development and under abiotic stress. *BMC genomics*, 22(1), 121.

Filyushin MA, et al. (2021) Genome-Wide Identification and Expression of Chitinase Class I Genes in Garlic (*Allium sativum* L.) Cultivars Resistant and Susceptible to *Fusarium proliferatum*. *Plants (Basel, Switzerland)*, 10(4).

Anisimova OK, et al. (2021) Pathogenesis-Related Genes of PR1, PR2, PR4, and PR5 Families Are Involved in the Response to Fusarium Infection in Garlic (*Allium sativum* L.). *International journal of molecular sciences*, 22(13).

Zheng L, et al. (2020) Genome-Wide Study of the GATL Gene Family in *Gossypium hirsutum* L. Reveals that GhGATL Genes Act on Pectin Synthesis to Regulate Plant Growth and Fiber Elongation. *Genes*, 11(1).

Meng J, et al. (2020) Genome-Wide Analysis of the Cyclin Gene Family and Their Expression Profile in *Medicago truncatula*. *International journal of molecular sciences*, 21(24).

Meng J, et al. (2020) Genome-Wide Characterization, Evolution, and Expression Analysis of the Leucine-Rich Repeat Receptor-Like Protein Kinase (LRR-RLK) Gene Family in *Medicago truncatula*. *Life (Basel, Switzerland)*, 10(9).

Cao JF, et al. (2020) Genome-wide characterization of the GRF family and their roles in response to salt stress in *Gossypium*. *BMC genomics*, 21(1), 575.

Hao Z, et al. (2019) Cloning, Characterization and Functional Analysis of the LtuPTOX Gene, a Homologue of *Arabidopsis thaliana* IMMUTANS Derived from *Liriodendron tulipifera*. *Genes*, 10(11).

Sabbione A, et al. (2019) Genome-wide analysis of AGO, DCL and RDR gene families reveals RNA-directed DNA methylation is involved in fruit abscission in *Citrus sinensis*. *BMC plant biology*, 19(1), 401.

Bartholomew ES, et al. (2019) Comprehensive Analysis of the Chitinase Gene Family in Cucumber (*Cucumis sativus* L.): From Gene Identification and Evolution to Expression in Response to *Fusarium oxysporum*. *International journal of molecular sciences*, 20(21).

Ding S, et al. (2019) Identification of Maize CC-Type Glutaredoxins That Are Associated with Response to Drought Stress. *Genes*, 10(8).

Chen YW, et al. (2018) Coll(Chromomycin)? Complex Induces a Conformational Change of CCG Repeats from i-Motif to Base-Extruded DNA Duplex. *International journal of molecular sciences*, 19(9).