

Resource Summary Report

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STRIDE Virtual Biospecimen Bank

RRID:SCR_008667

Type: Tool

Proper Citation

STRIDE Virtual Biospecimen Bank (RRID:SCR_008667)

Resource Information

URL: <http://clinicalinformatics.stanford.edu/services/biobank.html>

Proper Citation: STRIDE Virtual Biospecimen Bank (RRID:SCR_008667)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on March 7th, 2023. An online, searchable record of biospecimen attributes and storage location for the following three biobanks at Stanford: * The Bone Marrow Transplant (BMT) program * The Hematology biospecimen bank is a research sample repository focusing on blood, plasma and bone marrow, primarily from leukemia patients. * Cancer Center Pathology Core: The Stanford Comprehensive Cancer Center Tissue Bank stores research samples of both solid tumor and blood from cancer patients, with an emphasis on prostate. As of November 2009, the system contains data on 50,000 biospecimens stored in multiple banks at Stanford. An anonymous Biospecimen Locator allows Stanford researchers to search the STRIDE Virtual Biospecimen Bank for suitable samples without having to know, or expose, any protected patient-specific information. Having determined that suitable specimens exist in one of the constituent biospecimens banks, the researcher can generate a Web-based request form to obtain additional information from the appropriate bank operator(s). Access to specimens is restricted to Stanford Faculty and Staff or affiliates., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: STRIDE Biospecimen Data Repository, STRIDE Biospecimen Locator

Synonyms: STRIDE Anonymous Biospecimen Locator, STRIDE Anonymous Biospecimen Search Tool, STRIDE J2EE-based biospecimen registration management tracking and distribution system

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

Keywords: clinical data, biospecimen, data management, blood, plasma, bone marrow, solid tumor, prostate, tumor, leukemia, cancer

Related Condition: Leukemia, Cancer

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: STRIDE Virtual Biospecimen Bank

Resource ID: SCR_008667

Alternate IDs: nif-0000-33378

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260905T133154+0000

Ratings and Alerts

No rating or validation information has been found for STRIDE Virtual Biospecimen Bank.

No alerts have been found for STRIDE Virtual Biospecimen Bank.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Habibnia M, et al. (2024) Decoding the molecular and structural determinants of the neurokinin A and A β 1-42 peptide cross-interaction in the amyloid cascade pathway. iScience, 27(11), 111187.

Murata H, et al. (2024) Protein superfolds are characterised as frustration-free topologies: A case study of pure parallel β -sheet topologies. PLoS computational biology, 20(8), e1012282.

Guo HB, et al. (2024) AlphaFold2 modeling and molecular dynamics simulations of an intrinsically disordered protein. PLoS one, 19(5), e0301866.

Kaufman BG, et al. (2024) The business case for hospital mobility programs in the veterans health care system: Results from multi-hospital implementation of the STRIDE program. Health services research, 59 Suppl 2(Suppl 2), e14307.

Arnolds O, et al. (2023) Characterization of a fold in TANGO1 evolved from SH3 domains for the export of bulky cargos. Nature communications, 14(1), 2273.

Abu-Hussien M, et al. (2022) The contribution of individual residues of an aggregative hexapeptide derived from the human β D-crystallin to its amyloidogenicity. International journal of biological macromolecules, 201, 182.

Sun D, et al. (2022) STRIDE: accurately decomposing and integrating spatial transcriptomics using single-cell RNA sequencing. *Nucleic acids research*, 50(7), e42.

Bhattacharya S, et al. (2021) In silico screening and exploration into phenotypic alterations of deleterious oncogenic single nucleotide polymorphisms in HSPB1 gene. *Genomics*, 113(4), 2812.

Abbas SG, et al. (2021) Identifying and Mitigating Phishing Attack Threats in IoT Use Cases Using a Threat Modelling Approach. *Sensors (Basel, Switzerland)*, 21(14).

Nguyen H, et al. (2021) Electrostatic Interactions Explain the Higher Binding Affinity of the CR3022 Antibody for SARS-CoV-2 than the 4A8 Antibody. *The journal of physical chemistry. B*, 125(27), 7368.

Li J, et al. (2021) Entropy-Enthalpy Compensations Fold Proteins in Precise Ways. *International journal of molecular sciences*, 22(17).

Uhlemann EE, et al. (2021) At sixes and sevens: cryptic domain in the metal binding chain of the human copper transporter ATP7A. *Biophysical journal*, 120(20), 4600.

Zoma M, et al. (2021) EZH2-induced lysine K362 methylation enhances TMPRSS2-ERG oncogenic activity in prostate cancer. *Nature communications*, 12(1), 4147.

Hastings SN, et al. (2020) Implementation of a stepped wedge cluster randomized trial to evaluate a hospital mobility program. *Trials*, 21(1), 863.

Leisico F, et al. (2020) Multitask ATPases (NBDs) of bacterial ABC importers type I and their interspecies exchangeability. *Scientific reports*, 10(1), 19564.

Bramer D, et al. (2020) Atom-specific persistent homology and its application to protein flexibility analysis. *Computational and mathematical biophysics*, 8(1), 1.

Othoum G, et al. (2018) In silico exploration of Red Sea *Bacillus* genomes for natural product biosynthetic gene clusters. *BMC genomics*, 19(1), 382.