Resource Summary Report

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Joint Center for Structural Genomics

RRID:SCR_008251
Type: Tool

Proper Citation

Joint Center for Structural Genomics (RRID:SCR_008251)

Resource Information

URL: http://www.jcsg.org/

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Description: The JCSG is a multi-institutional consortium that aims to explore the expanding protein universe to find new challenges and opportunities to significantly contribute to new biology, chemistry and medicine through development of HT approaches to structural genomics. The mission of JCSG is to to operate a robust HT protein structure determination pipeline as a large-scale production center for PSI-2. A major goal is to ensure that innovative high-throughput approaches are developed that advance not only structural genomics, but also structural biology in general, via investigation of large numbers of high-value structures that populate protein fold and family space and by increasing the efficiency of structure determination at substantially reduced cost. The JCSG centralizes each core activity into single dedicated sites, each handling distinct, but interconnected objectives. This unique approach allows each specialized group to focus on its own area of expertise and provides well-defined interfaces among the groups. In addition, this approach addresses the requirements for the scalability needed to process large numbers of targets at a greatly reduced cost per target. JCSG production groups are: - Administrative Core - Bioinformatics Core - Crystallomics Core - Structure Determination Core - NMR Core JCSG is deeply committed to the development of new technologies that facilitate high throughput structural genomics. The areas of development include hardware, software, new experimental methods, and adaptation of existing technologies to advance genome research. In the hardware arena, their commitment is to the development of technologies that accelerate structure solution by increasing throughput rates at every stage of the production pipeline. Therefore, one major area of hardware development has been the implementation of robotics. In the software arena, they have developed enterprise resource software that track success, failures, and sample histories from target selection to PDB deposition, annotation and target management tools, and helper applications aimed at facilitating and automating multiple steps in the pipeline. Sponsors: The Joint Center for Structural Genomics is funded

by the National Institute of General Medical Sciences (NIGMS), as part of the second phase of the Protein Structure Initiative (PSI) of the National Institutes of Health (U54 GM074898).

Abbreviations: JCSG

Synonyms: JCSG

Resource Type: institution

Keywords: exclusion chromatography, expression, fine-structure spectroscopy, fold, absorption, affinity, bacterial, baculovirus, bioinformatics, biology, biophysical, cell, chemistry, cloning, crystallization, crystallomics, differential scanning calorimetry, diffraction, domain, genomic, gnfuge, growth, hardware, ief gel electrophoresis, macromoleuclar, medicine, microexpression, mouse, nmr, optical density, physicochemical, protein, purification, recombinatorial, robotics, sds-page, sequence, software, structural, structural biology, structure, technology, thermocycler, topoisomerase, tryptic mass spectrometry, uv/vis absorbance scan, x-ray

Funding:

Resource Name: Joint Center for Structural Genomics

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Alternate URLs: https://ror.org/00exr1241

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Ratings and Alerts

No rating or validation information has been found for Joint Center for Structural Genomics.

No alerts have been found for Joint Center for Structural Genomics.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 98 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Yoo R, et al. (2025) Crystallographic, kinetic, and calorimetric investigation of PKA interactions with L-type calcium channels and Rad GTPase. The Journal of biological chemistry, 301(1), 108039.

Yu DS, et al. (2024) The structural repertoire of Fusarium oxysporum f. sp. lycopersici effectors revealed by experimental and computational studies. eLife, 12.

Huang B, et al. (2024) De novo design of miniprotein antagonists of cytokine storm inducers. Nature communications, 15(1), 7064.

McQuarrie S, et al. (2023) Activation of Csm6 ribonuclease by cyclic nucleotide binding: in an emergency, twist to open. Nucleic acids research, 51(19), 10590.

Gubensäk N, et al. (2023) Vibrio cholerae's ToxRS bile sensing system. eLife, 12.

Crouch LI, et al. (2022) Plant N-glycan breakdown by human gut Bacteroides. Proceedings of the National Academy of Sciences of the United States of America, 119(39), e2208168119.

Espaillat A, et al. (2021) Binding of non-canonical peptidoglycan controls Vibrio cholerae broad spectrum racemase activity. Computational and structural biotechnology journal, 19, 1119.

Tan M, et al. (2021) MLL1 is regulated by KSHV LANA and is important for virus latency. Nucleic acids research, 49(22), 12895.

Strohmeier S, et al. (2021) A Novel Recombinant Influenza Virus Neuraminidase Vaccine Candidate Stabilized by a Measles Virus Phosphoprotein Tetramerization Domain Provides Robust Protection from Virus Challenge in the Mouse Model. mBio, 12(6), e0224121.

Salamina M, et al. (2021) Discriminative SKP2 Interactions with CDK-Cyclin Complexes Support a Cyclin A-Specific Role in p27KIP1 Degradation. Journal of molecular biology, 433(5), 166795.

Di Mattia T, et al. (2020) FFAT motif phosphorylation controls formation and lipid transfer function of inter-organelle contacts. The EMBO journal, 39(23), e104369.

Vollmar M, et al. (2020) The predictive power of data-processing statistics. IUCrJ, 7(Pt 2), 342.

Motlova L, et al. (2020) Continuous Assembly of ?-Roll Structures Is Implicated in the Type I-Dependent Secretion of Large Repeat-in-Toxins (RTX) Proteins. Journal of molecular biology, 432(20), 5696.

Chuenchor W, et al. (2020) Different ways to transport ammonia in human and Mycobacterium tuberculosis NAD+ synthetases. Nature communications, 11(1), 16.

Kolich LR, et al. (2020) Structure of MlaFB uncovers novel mechanisms of ABC transporter regulation. eLife, 9.

Cho SY, et al. (2020) Structural basis of serum albumin recognition by SL335, an antibody Fab extending the serum half-life of protein therapeutics. Biochemical and biophysical research communications, 526(4), 941.

Athukoralage JS, et al. (2020) Tetramerisation of the CRISPR ring nuclease Crn3/Csx3 facilitates cyclic oligoadenylate cleavage. eLife, 9.

Zhu X, et al. (2019) Structural Basis of Protection against H7N9 Influenza Virus by Human Anti-N9 Neuraminidase Antibodies. Cell host & microbe, 26(6), 729.

Moroz OV, et al. (2018) Structure of a Talaromyces pinophilus GH62 arabinofuranosidase in complex with AraDNJ at 1.25?Å resolution. Acta crystallographica. Section F, Structural biology communications, 74(Pt 8), 490.

Kroon-Batenburg LM, et al. (2017) Raw diffraction data preservation and reuse: overview, update on practicalities and metadata requirements. IUCrJ, 4(Pt 1), 87.