Julian Grandvallet Contreras

Bioinformatics Analyst · Cancer Genomics & Epigenomics

Professional Summary

Bioinformatics analyst with 3+ years of experience in cancer genomics, embedded in a multi-PI shared bioinformatics resource at the University of Colorado Anschutz Medical Campus. Co-author on 6 peer-reviewed journal articles, 7 conference abstracts, and 2 preprints (2023–2026), including *New England Journal of Medicine*, *Leukemia*, *EBioMedicine*, *Brain Pathology*, and *Blood*. Specialized in bulk and single-cell RNA-seq, ATAC-seq, CUT&RUN, ChIP-seq, whole-genome and whole-exome sequencing, and germline and somatic variant and copy-number analysis, applied to pediatric leukemia, neuro-oncology, hematologic disorders, and cancer evolution. Builds reproducible Nextflow and Docker pipelines on HPC and mentors junior analysts.

Academic Appointments

2024–Present Adjunct Member, University of Colorado Comprehensive Cancer Center (UCCCC), Aurora, CO. Appointed member contributing bioinformatics expertise in cancer genomics, epigenomics, and translational oncology research.

Research Experience

julian.g.contreras2025@gmail.com • *julgrandvallet* • *julian-grandvallet*
ORCID: 0000-0001-8021-070X · Google Scholar

Oct 2024–Present **Bioinformatics Analyst**, *University of Colorado Anschutz Medical Campus*, Aurora, CO, Phang Bioinformatics Shared Resource · Department of Pediatrics

Embedded analyst supporting multiple PI laboratories through the institutional bioinformatics core. Lead computational analyses contributing to peer-reviewed publications, including *NEJM* (2025), *Brain Pathology* (2025), *Leukemia* (2026), and *EBioMedicine* (2026).

- **Witkowski Lab (Pediatric Leukemia):** Designed and executed bulk RNA-seq, single-cell RNA-seq, ATAC-seq, CUT&RUN, and whole-genome sequencing analyses investigating CAR-T cell therapy resistance and gene regulatory mechanisms in B-ALL, including a multi-omic study linking the *ARID5B* rs7090445 risk variant to B-ALL incidence in Hispanic/Latino populations (selected lightning talk, CU Anschutz Bioinformatics Symposium 2026).
- **Epigenomics (shared resource):** Established the CUT&RUN analysis workflow now used as the standard across the core: alignment, peak calling, and differential binding for transcription-factor (*CUX1*) and histone-mark (H3K27ac, H3K4me3, H3K9me3, H3K36me3) datasets, including a systematic benchmark of spike-in versus library-size normalization deployed on the institutional HPC cluster.
- **Santos-Cortez Lab (rare disease genomics):** Rare variant analysis of whole-genome sequencing from hereditary hearing loss families. Ran nf-core/Sarek on HPC for alignment, GATK germline calling and CNVkit copy number, then wrote the full downstream workflow: bcftools normalization, ANNOVAR annotation against hg38 (refGene, avsnp147, dbNSFP, gnomAD, ClinVar, COSMIC), and VEP with LOFTEE for high-confidence loss-of-function calls. Prioritization applied rare-variant thresholds per gnomAD v4.1 subpopulation and per GME cohort instead of one global MAF cutoff, preserving candidates in non-European families; required deleteriousness support across SIFT, LRT, MutationTaster, FATHMM, PROVEAN, MetaSVM, MetaLR and DANN; and intersected survivors with per-family curated gene lists and ClinVar assertions. Results delivered as maftools MAF objects alongside Picard coverage, insert-size, GC-bias and per-cycle quality plots.
- **Hemophilia and Thrombosis Research Lab (Manco-Johnson):** Led molecular dynamics simulations and structural docking analyses for a novel gain-of-function Factor VIII variant; analyses contributed directly to publication in *New England Journal of Medicine* (2025).
- **Ernst Lab and Fry Lab:** Contributed transcriptomic and epigenomic analyses to pediatric MLL-rearranged B-ALL modeling and CAR-T resistance projects (*Blood*, 2024 and 2025; *Leukemia*, 2026).
- **Pediatric Neuro-Oncology (Mulcahy Levy and Foreman):** Integrated transcriptomic and tumor microenvironment profiling for low-grade glioma and ganglioglioma cohorts (*Brain Pathology*, 2025).
- Built and documented reproducible analysis pipelines (Nextflow, nf-core, Docker, Git) deployed on HPC under LSF and SLURM for the shared resource, supporting six PI laboratories at once.
- Mentored 4 trainees (1 continuing to a bioinformatics PhD, 1 to industry, 2 undergraduates) in single-cell and bulk transcriptomic and epigenomic analysis.

Nov 2023–Present **Computational Research Collaborator**, *Huang Lab, Icahn School of Medicine at Mount Sinai*, Remote, Center for Transformative Disease Modeling · via Bioinformatics Research Network (BRN)

- Co-author on cancer evolution studies investigating rate-limiting genetic variation in breast and ovarian tumorigenesis (*EBioMedicine*, 2026; bioRxiv preprint, 2024).
- Contributing analyst on tissue-specific BRCA1/2 LOH and aneuploidy study spanning 340,000+ tumor genomes (*bioRxiv*, 2026; manuscript under review).
- Performed statistical analyses on HGSC and TNBC cohorts (group comparisons via t-tests, chi-square, and Fisher's exact tests; multiple-testing correction via Benjamini-Hochberg FDR), SNV visualization, and identification of significant genomic events between patient subgroups using R (`gt`, `ggplot2`, Bioconductor).

Oct 2023–May 2024 **Bioinformatics Analyst (Volunteer)**, *Phang Lab, University of Colorado Anschutz Medical Campus*, Aurora, CO

- Developed an interactive R Shiny application for RNA-seq exploratory analysis enabling non-computational users to generate publication-ready volcano plots, heatmaps, and box plots (see Software).
- Performed gene isoform analyses for the Ernst Lab supporting pediatric leukemia transcriptomic studies.

Jan–Sep 2023 **Bioinformatics Research Intern (Social Service)**, *Population Genomics Department, National Institute of Genomic Medicine (INMEGEN)*, Mexico City, Mexico

- Investigated *IKZF1* dominant-negative isoforms in pediatric B-ALL patients using RASCALL, TOBLERONE, and unsupervised clustering (k-means).
- Built containerized Nextflow workflows (Docker, Git) for reproducible RNA-seq analysis.

Nov 2022–Jan 2023 **Bioinformatics Intern**, *Population Genomics Department, INMEGEN, Cervera Lab*, Mexico City, Mexico

- Detected and characterized fusion genes in pediatric B-ALL RNA-seq cohorts.
- Contributed chromosome-level aberration analyses to a multi-institutional pediatric leukemia consortium.

May 2021–Jul 2022 **Research Intern**, *Solid Tumor Cancer Stem Cells Laboratory, National Cancer Institute (INCan)*, Mexico City, Mexico, Ortiz-Sánchez Lab

- Co-author on circulating gastric cancer stem cells study (*Stem Cells International*, 2024).
- Maintained AGS, HeLa, SiHa, KATO-III, and HaCaT cell lines supporting three concurrent research projects.
- Isolated peripheral blood mononuclear cells (PBMCs) and ran 8-parameter flow cytometry assays.
- Prepared and ran samples on StepOne Real-Time PCR for gene expression quantification.

Education

2018–2023 **B.Sc. in Molecular Biology**, *Universidad Autónoma Metropolitana, Cuajimalpa*, Mexico City, Mexico, GPA: 9.63/10 (3.85/4.0 equivalent).

Thesis: *In vitro evaluation of the cytotoxic activity of compounds LQM 731 and LQM 755 in gastric cancer cell lines.*

Publications

Peer-Reviewed Journal Articles

2026 Garcia, C., Lyons, K. U., **Grandvallet Contreras, J.**, Liu, T., Donnelly, A. J., Novak, A. J., Argabright, A., Anderson, C., Grier, A., Smith, S., et al. (2026). FATP2-mediated lipid metabolism enhances chimeric antigen receptor T-cell therapy resistance in B-cell acute lymphoblastic leukemia. *Leukemia*. Advance online publication.

2026 Houlahan, K. E., Bihie, M., Greatti, Y., **Grandvallet Contreras, J.**, Fulop, D. J., Lopez, G., Williams, M., Huang, H.-H., Van Loo, P., Boutros, P. C., & Huang, K.-l. (2026). Quantifying rate-limiting genetic variation in breast and ovarian tumourigenesis. *EBioMedicine*, 125.

2025 Wischmeyer, J. T., Baird, C. H., **Grandvallet Contreras, J.**, Tran, A., Phang, T., Liu, T., & Manco-Johnson, M. J. (2025). A naturally occurring gain-of-function mutation in Factor VIII. *New England Journal of Medicine*, 393(7), 722–724.

2025 Zahedi, S., Riemondy, K., Liu, T., Griesinger, A. M., Donson, A. M., Apfelbaum, A. A., Fu, R., **Grandvallet Contreras, J.**, Crespo, M., DeSisto, J., et al. (2025). Multi-pronged analysis of pediatric low-grade glioma and ganglioglioma reveals a unique tumor microenvironment associated with BRAF alterations. *Brain Pathology*, 35(6), e70023.

2024 Becerril-Rico, J., **Grandvallet Contreras, J.**, Ruíz-León, M. P., Dorantes-Cano, S., Ramírez-Vidal, L., Tinajero-Rodríguez, J. M., & Ortiz-Sánchez, E. (2024). Circulating gastric cancer stem cells as blood screening and prognosis factor in gastric cancer. *Stem Cells International*, 2024(1), 9999155.

2023 Rodríguez López, M. A., **Grandvallet Contreras, J.**, & Vázquez Contreras, E. (2023). Amiloidosis de inmunoglobulinas: diagnóstico, tratamiento y fisicoquímica. *Ciencia Latina Revista Científica Multidisciplinar*, 7(6), 599–613.

Preprints and Manuscripts Under Review

2026 Wang, X., Sisoudiya, S. D., Bihie, M., Greatti, Y., **Grandvallet Contreras, J.**, Jun, T. W., Sivakumar, S., & Huang, K.-l. (2026). Tissue-specific prevalence and clonal architecture of BRCA1/2 LOH-inducing chromosomal aneuploidy. *bioRxiv* 2026.04.

2024 Houlahan, K. E., Bihie, M., **Grandvallet Contreras, J.**, Fulop, D. J., Lopez, G., Huang, H.-H., Van Loo, P., Curtis, C., Boutros, P. C., & Huang, K.-l. (2024). Deletions rate-limit breast and ovarian cancer initiation. *bioRxiv*.

Peer-Reviewed Conference Abstracts

2026 Vigil, I. G., **Grandvallet Contreras, J.**, DeGolier, K. R., Scott-Browne, J. P., Witkowski, M. T., & Fry, T. J. (2026). Investigating universal mechanisms of leukemic cell resistance to CAR-T cell therapy. *Cancer Immunology Research*, 14(2 Suppl), B014.

2026 Garcia, C., **Grandvallet Contreras, J.**, Phang, T., & Witkowski, M. T. (2026). Investigating gene regulatory mechanisms associated with B-cell acute lymphoblastic leukemia incidence in Hispanic/Latino populations. *Cancer Research*, 86(7 Suppl), 3199.

2025 Garcia, C., Lyons, K., **Grandvallet Contreras, J.**, Liu, T., Donnelly, A., Novak, A., et al. (2025). Lipid uptake via FATP2 enhances CAR-T therapy resistance in B-cell acute lymphoblastic leukemia. *Blood*, 146, 325.

2025 Garcia, C., **Grandvallet, J.**, Iacobucci, I., Yang, J., Mullighan, C. G., Phang, T., & Witkowski, M. T. (2025). Investigating gene regulatory mechanisms associated with B-cell acute lymphoblastic leukemia incidence in Hispanic/Latino populations. *Journal of Clinical and Translational Science*, 9(s1), 22.

2024 Garcia, C., Lyons, K., Liu, T., Iacobucci, I., Novak, A., Argabright, A., Donnelly, A., **Grandvallet Contreras, J.**, Geng, H., Smith, S., et al. (2024). Inhibiting free fatty acid transport to improve CAR-T cell therapy of relapsed B-cell acute lymphoblastic leukemia. *Blood*, 144(Suppl 1), 1446.

2024 Liao, W., Liu, T., **Grandvallet Contreras, J.**, Harris, L. H., Phang, T., Farrar, M. A., Kohler, M. E., Fry, T. J., & Ernst, P. (2024). Developing a pediatric-relevant murine MLL-r B-ALL model to study factors involved in lineage switching. *Blood*, 144, 4129.

2024 Wischmeyer, J., Baird, C., **Grandvallet Contreras, J.**, Tran, A., Phang, T., & Manco-Johnson, M. (2024). A novel Factor VIII mutation with increased activity, severe thrombosis, and resistance to activated protein C. *Blood*, 144, 135.

Software and Reproducible Pipelines

CUT&RUN Normalization Benchmark — Open-source Nextflow pipeline testing which normalization method recovers a genome-wide change in CUT&RUN signal. Validated on simulated data with a known answer: spike-in normalization recovers a true fourfold loss at 98% directional purity, while library-size normalization reports the same loss as a significant *gain* at 480 regions. Docker, Singularity and SLURM profiles, with continuous integration. github.com/julgrandvallet/cutandrun-normalization-benchmark

RNA-seq Explorer — Interactive R Shiny application for exploratory RNA-seq analysis, enabling non-computational users to generate publication-ready volcano plots, heatmaps, and box plots. Deployed across the Phang Bioinformatics Shared Resource.

Analysis Pipelines — Containerized workflows (Nextflow, nf-core, Docker, Git, SLURM) for bulk RNA-seq, ATAC-seq, CUT&RUN, and WGS/WES variant calling, documented for multi-lab reuse.

Code — github.com/julgrandvallet

Awards and Honors

2024 **WillStrong Cancer Foundation Young Investigator Award**

2023 Top GPA, Molecular Biology graduating class 2018–2023, UAM Cuajimalpa

2018 Distinction for Excellence, 6th Student Congress of the Incorporated System, UNAM

Technical Skills

Languages — Python (pandas, NumPy, scikit-learn, Scanpy, Biopython), R (Bioconductor, DESeq2, edgeR, Seurat, ggplot2, Shiny, gt, maftools), Bash, LaTeX.

NGS Analysis	WGS and WES germline and somatic variant calling (nf-core/Sarek, GATK, BWA, bcftools); rare variant annotation and prioritization (ANNOVAR, VEP, LOFTEE, dbNSFP, ClinVar, COSMIC, per-ancestry gnomAD v4.1 and GME filtering, SIFT, PolyPhen, MutationTaster, FATHMM, PROVEAN, MetaSVM, MetaLR, DANN); copy-number and LOH analysis (CNVkit); MAF summarization (maftools); bulk RNA-seq (STAR, HISAT2, Salmon, DESeq2); single-cell RNA-seq (Seurat, Scanpy); ATAC-seq, ChIP-seq and CUT&RUN (Bowtie2, MACS2, SEACR, DiffBind, spike-in and library-size normalization, differential binding); isoform and fusion detection (RASCALL, TOBLERONE); sequencing QC (Picard, MultiQC, FastQC).
Biostatistics	Parametric and non-parametric group comparisons (Student's t-test, Welch's t-test, paired t-test, Mann-Whitney U, Wilcoxon signed-rank, ANOVA, Kruskal-Wallis); categorical analysis (chi-square, Fisher's exact test); correlation (Pearson, Spearman); linear and logistic regression; negative-binomial models for count data (DESeq2, edgeR); survival analysis (Kaplan-Meier, log-rank, Cox proportional hazards); multiple-testing correction (Bonferroni, Benjamini-Hochberg FDR); power and sample-size calculations.
Workflow and Reproducibility	Nextflow (DSL2), nf-core, Docker, Singularity, Git/GitHub, GitHub Actions CI, HPC (SLURM), Quarto, pipeline documentation.
Structural and Systems Biology	Molecular dynamics (NAMD, VMD, GROMACS), molecular docking (AutoDock Vina, HDOCK), protein and nucleic-acid modeling (Modeller, UCSF Chimera, PyMOL), network analysis (Cytoscape, WGCNA), pathway enrichment.
Operating Systems	Linux, macOS.

Teaching and Mentorship

2025–Present **Instructor**, *Análisis de Datos con R para las Ciencias Sociales*. Asynchronous online course in R programming and applied data analysis for social science researchers, delivered through CIICS.

2026 Mentored 4 trainees in bioinformatics and immunogenomics (Phang Lab, CU Anschutz):

- *Lillian Swenson*: CAR-T cell exhaustion gene regulation (now PhD student in bioinformatics).
- *Purvi Patel*: CAR-T cell function (now at TR Consulting).
- *Nandhini Breggin*: undergraduate research in bioinformatics.
- *Michael Oppong*: undergraduate research in RNA-seq and CUT&RUN.

2023 Led introductory workshop on differential gene expression analysis using public datasets at the Cardiogenetics Laboratory, National Pediatric Hospital, Mexico City.

2015–Present Personalized tutoring in calculus, chemistry, and molecular biology for high school and undergraduate students.

Invited Lectures and Workshops

2026 **Invited Faculty Instructor**, *AI-assisted "Vibe Coding" for Physician-Scientists*. American Association for Cancer Research (AACR) 34th Annual Molecular Biology in Clinical Oncology Workshop, Coronado, California, July 2026. Delivered an invited educational workshop on the application of generative artificial intelligence and large language models to scientific programming, bioinformatics, and translational cancer research.

Professional Service

2023–Present **Scientific Outreach and Communications Contributor**, *ASI Childhood Leukemia (Harmonization of Immunophenotyping Systems)*, Remote

- Develop educational and scientific outreach materials to promote evidence-based pediatric leukemia diagnostics.
- Facilitate communication of best practices in flow cytometry and immunophenotyping among healthcare professionals and laboratory specialists.
- Contribute to the harmonization of diagnostic reporting and knowledge-sharing initiatives within the national PRONAII childhood leukemia network.
- Support training, dissemination, and community-engagement activities aimed at improving pediatric leukemia care across Mexico.

asileucemiainfantil.org

Selected Conference Presentations

2026 **Poster**: *2026 Spring Pediatric Research Poster Session*, Children's Hospital Colorado, Aurora, CO. *"Pharmacological, genetic BMI1 inhibition and SMARCB1 re-expression alters PRC1/BMI1 activity in ATRT, significantly prolongs mice survival and decreases tumor growth in vivo."* **Grandvallet Contreras J**, Alimova I, Liu T, Pierce A, Serkova N, Weetel M, Baird J, Phang T, Vibhakar R.

2026 **Lightning talk and poster** (selected): *1st Annual Bioinformatics Symposium*, University of Colorado Anschutz Medical Campus, Aurora, CO. *"Multi-omic analysis reveals epigenetic mechanisms linking ARID5B rs7090445 to B-cell acute lymphoblastic leukemia incidence."*

2023 Oral and poster presentations: XXV Congress of the Mexican Immunology Association, Querétaro, Mexico.

2022 Poster: 7th Symposium of the Bachelor's Degree in Molecular Biology, UAM Cuajimalpa. *A Bioinformatic Analysis of Aging and Menopause*.

2019 Oral and poster presentations: 3rd Symposium of Natural Sciences and Engineering, UAM, Mexico City.

2018 Poster: 6th Student Congress of the Incorporated System, UNAM, Mexico City.

Continuing Education

2023 Creating R/Bioconductor packages for single-cell transcriptomic analysis. Community of Bioinformatics Software Developers (CDSB).

2023 Transcriptome analysis with RNA-seq. INMEGEN.

2021 Advanced Multivariate Statistics with R and Python. SciData.

2021 Principles of Biostatistics. AMCEP.

2019–2020 Cancer biology and metastasis (with Honors), Johns Hopkins University; Molecular Biology of Cancer, Instituto Barbara McClintock.

Memberships

2023–Present Mexican Bioinformatics Network (RMB)

2022–Present Mexican Society of Immunology

Languages

Spanish Native

English Advanced, fluent

French Basic