

The leading genetic data analysis software that evolves with your lab



Chromosome Analysis Suite (ChAS) software

Applied Biosystems™ Chromosome Analysis Suite (ChAS) software is an intuitive and flexible software for cytogenetic research analysis that enables you to view and summarize chromosomal aberrations across the genome. It is available for free to all customers who own Applied Biosystems™ CytoScan™ and OncoScan™ products.

Key features:

- Analyze copy number, mosaicism, and loss of heterozygosity (LOH) segment data at different levels of resolution
- Automatically prioritize segment data using scoring inspired by the American College of Medical Genetics and Genomics
- Customize and load your own annotations and regions for focused analysis
- Store, query, and display historic sample data and annotations for streamlined analysis
- Application programming interfaces (APIs) to push and pull segment coordinates in and out of ChAS software
- Automatic generation of a results file with zero manual setup required

ChAS software is a powerful tool that enables customized visualization and analysis of the following data file types:

- Applied Biosystems™ CytoScan™ arrays (CYCHP)
- Applied Biosystems™ OncoScan™ FFPE arrays (OSCHP)

- Applied Biosystems™ CytoScan™ XON arrays (XNCHP)
- Browser extensible data (BED), Applied Biosystems™ Affymetrix™ extensible data (AED), and variant call format (VCF) files

With ChAS software, you can directly access multiple data sources, such as the NCBI, UCSC Genome Browser, OMIM®, DECIPHER, ClinVar, ClinGen, and Ensembl™ databases.

[Request a demo](#)

CytoScan Automated Interpretation and Reporting (AIR) solution

Streamline genetic data analysis to increase productivity with consistent interpretation and reporting. Franklin by Genoox™ is an end-to-end research solution for genetic data analysis with advanced AI-driven interpretation. With the Applied Biosystems™ CytoScan™ Automated Interpretation and Reporting (AIR) solution, our customers can combine the power of ChAS and Franklin to augment the visualizations of LOH and copy number variation (CNV) gains and losses, with key clinical research interpretation information.

[View CytoScan AIR flyer](#)

ChAS—8 years of continuous innovation

Developed by scientists, for scientists

ChAS software was developed with input from leading cytogeneticists and customized for copy number (CN) and cytogenetics research analysis and reporting. We work with our

customers, listen to their valuable feedback, and continually empower them with enhanced features to make data analysis simpler and more intuitive.

2015	2016	2018	2020	2021	2022	2023
ChAS 3.0	ChAS 3.2	ChAS 3.3	ChAS 4.1	ChAS 4.3	CytoScan AIR	ChAS 4.4
<ul style="list-style-type: none"> ChAS database (DB) Trio analysis OncoScan analysis 	<ul style="list-style-type: none"> B-allele frequency Direct links to ClinVar database Usability updates hg38 support 	<ul style="list-style-type: none"> CytoScan XON assay support Whole Genome View (WGV) improvements Automatic results summary 	<ul style="list-style-type: none"> Manual re-centering for CytoScan assays Exon numbering for RefSeq and Ensembl databases 	<ul style="list-style-type: none"> New mosaic algorithm Updates to automatic CHP file generation Full VCF support Laboratory information management system (LIMS) API 	<ul style="list-style-type: none"> AI-driven, automated data interpretation and reporting with Franklin by Genoox 	<ul style="list-style-type: none"> Whole-genome support of CytoScan XON arrays CN state for CytoScan XON arrays LIMS APIs
ChAS 3.1		ChAS 4.0	ChAS 4.2			
<ul style="list-style-type: none"> ChAS DB improvements Manual re-centering for OncoScan analysis 		<ul style="list-style-type: none"> Multisample viewer Aneuploidy analysis updates Show original segment in "Edit" mode Assign >1 CytoRegion file 	<ul style="list-style-type: none"> Segment prioritization Add CN to LOH segment calls for proper International System for Human Cytogenomic Nomenclature (ISCN) Automatic CHP file generation 			

Enhance your genetic data analysis with the new ChAS 4.4 software

- Seamless integration with Franklin by Genoox using the CytoScan AIR Solution
- Whole-genome segmentation for large copy number aberrations on the CytoScan XON array
- Flag segments to bypass filter settings
- Display different LOH segment colors based on median copy number
- pHaplo and pTripto scores
- ClinGen curated regions in a recurrent/curated regions track
- Download library files from the NetAffx™ server securely via <https>



ChAS software training videos

We offer on-demand training videos for you to compare your analysis pipeline and see new and enhanced features you may want to incorporate into your training regimen.

[Browse modules](#)



Customer support

With comprehensive onboarding services and support offerings for ChAS software, our team of experienced professionals, including technical sales specialists, field service engineers (FSEs), field application scientists (FASs), and clinical application consultants (CACs), can provide the technical assistance and peace of mind you need to stay focused on what matters—your research.

[Access support brochure](#)

Learn more at thermofisher.com/chas

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