

Chromosome Analysis Suite (ChAS)

Operating system and hardware requirements

This document provides the minimum and recommended computer system requirements for ChAS 3.1. The software can be installed either as database and browser (workstation) or as database only (server for multiple users).

Note: A 64-bit computer with 8 or more GB of RAM is required for installing and using ChAS 3.1. A previous version of the software (ChAS 2.1) can be used to visualize result files in a 32-bit computer with 3 GB of RAM.

Recommended and minimum system requirements for ChAS 3.1 software

Item	Workstation		Database server	
	Recommended system requirements	Minimum system requirements	Recommended system requirements	Minimum system requirements
Processor	3+ GHz (or greater) Quad Core	3+ GHz (or greater) Quad Core	3.1 GHz (or greater) Quad Core	2.7 GHz (or greater) Quad Core
64-bit operating system	Windows® 7 Professional SP1 or Windows® 8.1	Windows® 7 Professional SP1 or Windows® 8.1	Windows® 2008 Server R2 Standard 64-bit or Windows® 2012 Server R2 Standard 64-bit	Windows® 7 64-bit or Windows® 8.1 64-bit
Recommended web browser	Internet Explorer® 11.0 or above	Internet Explorer® 11.0 or above	N/A	N/A
Available disk space*	250 GB HD + data storage	150 GB HD + data storage	1 TB HD + data storage	512 GB HD + data storage
Free disk space required at install	≥5 GB	≥5 GB	≥5 GB	≥5 GB
RAM	≥16 GB	≥8 GB	≥24 GB	≥16 GB

*The larger file sizes associated with CytoScan® HD Array should be taken into account when calculating the necessary free space requirement. A CytoScan HD Array CYCHP file is ~120 MB.

Compatibility between ChAS software versions and NetAffx® array-type-specific fileset versions*

NetAffx® analysis fileset version	ChAS software version						
	ChAS 3.0 ChAS 3.1	ChAS 2.1	ChAS 2.0	ChAS 1.2.2 ChAS 1.2.1	ChAS 1.2	ChAS 1.1	ChAS 1.0.1 ChAS 1.0
NA33 (hg19)	Yes	Yes	No	No	No	No	No
NA32.3 (hg19)	No	Yes	Yes	No	No	No	No
NA32.1 (hg19)	No	No	No	Yes	No	No	No
NA32 (hg19)	No	No	No	No	Yes	No	No

*NetAffxGenomicAnnotations.Homo_sapiens.hgX.naxx.x.db Browser Annotation files are used by the ChAS browser for displaying reference annotations from the public domain and can be loaded with CHP files of any array type or NA version, as long as the CHP files are of the same human genome (hg) version as the currently loaded ChAS Browser Annotation file.

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