

## Applications\_Compatibility

Last Updated: 5. Jul. 2007  
BCG Version 1.5

OPERATING SYSTEM	Solaris 9 SPARC 04/03	Solaris 10 on x86		RHEL WS 4.0 x86_64	ROCKS 3.3.0 i386	ROCKS 3.3.0 x86_64
		32-bit x86	X64			
COMPILER	Sun Studio 9	Sun Studio 12	Sun Studio 12	Gcc in the RHEL 4		
GLIBC Version	Not Applicable	Not Applicable	Not Applicable	Not Applicable		
# of Apps	27	19	14 + 5	23 + 1		
Application Name	Version	Version	Version	Version	Version	Version
ACT	3	7	Use 32-bit version	Yes		
Artemis	6	9	Use 32-bit version	Yes		
Biojava	1.3	1.5	Use 32-bit version	Yes		
Bioperl	1.4	Not Available	Not Available	Yes		
Biopython	1.4b	Not Available	Not Available	Yes		
Blast	2.2.10	2.2.16	2.2.16	Yes		
Clustalw	1.83	1.83	1.83	Yes		
Cn3D	4.1	Not Available	Not Available	Yes		
Dowser	3.00	April 2003	April 2003	Yes		
Emboss	2.10.0	3.0.0	3.0.0	Not Available		
Fasta	V34t0	V35t0	V35t0	Only 32-bit		
FastDNAmI	1.22	1.22	1.22	Yes		
GlimmerM	2.51	Not Available	Not Available	Yes		
Gromacs	3.2.1	3.2.1	3.2.1	Not Available		
HMMER	2.3.2	2.3.2	2.3.2	Yes		
Image	3.10	3.10b	3.10b	Yes		
LOOPP	LOOPP 2000	LOOPP 2000	LOOPP 2000	Yes		
NAB	5.1.2	5.1.2	5.1.2	Yes		
NAMD	2.5	Not Available	Not Available	Yes		
NMRView	6.2.10	Not Available	Not Available	Yes		
PAML	3.14	3.15	3.15	Yes		
PHYLIP	3.6.3	3.66	3.66	Yes		
Rasmol	2.7.2.1	Not Available	Not Available	Not Available		
Readseq	2.1.20	2.1.24	Use 32-bit version	Yes		
T-Coffee	2.03	5.03	5.03	Yes		
TribeMCL	05-090	05-118	05-118	Not Available		
VMD	1.83	Not Available	Not Available	Yes		
Wise2	2-2-0	2-2-0	2-2-0	Yes		

## NOTE:

Sometimes Java is not installed in Redhat installations. So it needs to be installed separately.

## Description

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Application Name	Category	Description
ACT	Viewer	
Artemis		Artemis is a free genome viewer and annotation tool
Biojava	Development Tools	The BioJava Project is an open-source project dedicated to providing Java tools for processing biological data.
Bioperl	Development Tools	The Bioperl Project is an international association of developers of open source Perl tools for bioinformatics, genomics and life science research.
Biopython	Development Tools	The Biopython Project is an international association of developers of freely available Python tools for computational molecular biology.
Blast	Homology and Similarity Search	Finds the degree of similarity of a given nucleotide or protein sequence against a database, also performs alignment with the sequences in the database
Clustalw	Sequence Analysis	Multiple Sequence Alignment
Cn3D	Viewer	To view 3-dimensional structures from the NCBI Entrez retrieval service
Dowser	Structural Analysis	Surveys the structure of a protein molecule to locate internal cavities and assess the hydrophilicity of these cavities
Emboss	Application Suite	European Molecular Biology Open Software Suite
Fasta	Homology and Similarity Search	Fast protein comparison or a fast nucleotide comparison.
FastDNAmI	Phylogeny	Estimating maximum likelihood phylogenetic trees from nucleotide sequences
GlimmerM	Gene Finder	A gene finder derived from Glimmer, but developed specifically for eukaryotes.
Gromacs	Molecular Dynamics Simulations	GROMACS is a versatile package to perform molecular dynamics for systems with hundreds to millions of particles.
HMMER	Sequence Analysis	Sequence Analysis using profile Hidden Markov Models
Image	Gel Image Processing	Package of analysis algorithms for processing gel images
LOOPP	Protein Analysis	Learning, Observing and Outputting Protein Patterns
NAB	Molecular Modeling	A computer language for structural exploration
NAMD	Molecular Modeling	High-performance simulation of large biomolecular systems
NMRView	Visualisation	Visualization and Analysis of Nuclear Magnetic Resonance Data
PAML	Phylogeny	Phylogenetic analyses of DNA or protein sequences using maximum likelihood
PHYLIP	Phylogeny	A free package of programs for inferring phylogenies
Rasmol	Visualisation	Molecular Graphics Visualization Tool
Readseq	Sequence Format Conversion	Reads and writes nucleic/protein sequences in various formats. Data files may have multiple sequences.
T-Coffee	Sequence Analysis	Multiple Sequence Alignment
TribeMCL	Protein Analysis	An efficient algorithm for large-scale detection of protein families
VMD	Visualisation	Molecular visualization program for displaying, animating, and analyzing large biomolecular systems
Wise2	Homology and Similarity Search	Comparisons of DNA sequence and protein sequence.

Website

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Application Name	Website
ACT	
Artemis	<a href="http://www.sanger.ac.uk/Software/Artemis/">http://www.sanger.ac.uk/Software/Artemis/</a>
Biojava	<a href="http://www.biojava.org/">http://www.biojava.org/</a>
Bioperl	<a href="http://bio.perl.org/">http://bio.perl.org/</a>
Biopython	<a href="http://www.biopython.org/">http://www.biopython.org/</a>
Blast	<a href="http://www.ncbi.nlm.nih.gov/BLAST/">http://www.ncbi.nlm.nih.gov/BLAST/</a>
Clustalw	<a href="http://www.ebi.ac.uk/clustalw/">http://www.ebi.ac.uk/clustalw/</a>
Cn3D	<a href="http://www.ncbi.nih.gov/Structure/CN3D/cn3d.shtml">http://www.ncbi.nih.gov/Structure/CN3D/cn3d.shtml</a>
Dowser	<a href="http://femto.med.unc.edu/DOWSER/Dowser.htm">http://femto.med.unc.edu/DOWSER/Dowser.htm</a>
Emboss	<a href="http://www.hgmp.mrc.ac.uk/Software/EMBOSS/">http://www.hgmp.mrc.ac.uk/Software/EMBOSS/</a>
Fasta	<a href="http://fasta.bioch.virginia.edu/fasta/home.html">http://fasta.bioch.virginia.edu/fasta/home.html</a>
FastDNAMl	<a href="http://geta.life.uiuc.edu/~gary/programs/fastDNAMl.html">http://geta.life.uiuc.edu/~gary/programs/fastDNAMl.html</a>
GlimmerM	<a href="http://www.tigr.org/software/glimmer/">http://www.tigr.org/software/glimmer/</a>
Gromacs	<a href="http://www.gromacs.org/">http://www.gromacs.org/</a>
HMMER	<a href="http://hmmer.wustl.edu/">http://hmmer.wustl.edu/</a>
Image	<a href="http://www.sanger.ac.uk/Software/Image/">http://www.sanger.ac.uk/Software/Image/</a>
LOOPP	<a href="http://cbsu.tc.cornell.edu/software/loopp/index.htm">http://cbsu.tc.cornell.edu/software/loopp/index.htm</a>
NAB	<a href="http://www.scripps.edu/mb/case">http://www.scripps.edu/mb/case</a>
NAMD	<a href="http://www.ks.uiuc.edu/Research/namd/">http://www.ks.uiuc.edu/Research/namd/</a>
NMRView	<a href="http://onemoonscientific.com/nmrview/">http://onemoonscientific.com/nmrview/</a>
PAML	<a href="http://abacus.gene.ucl.ac.uk/software/paml.html">http://abacus.gene.ucl.ac.uk/software/paml.html</a>
PHYLIP	<a href="http://evolution.genetics.washington.edu/phylip.html">http://evolution.genetics.washington.edu/phylip.html</a>
Rasmol	<a href="http://www.umass.edu/microbio/rasmol/index2.htm">http://www.umass.edu/microbio/rasmol/index2.htm</a>
Readseq	<a href="http://iubio.bio.indiana.edu/soft/molbio/readseq/java/">http://iubio.bio.indiana.edu/soft/molbio/readseq/java/</a>
T-Coffee	<a href="http://igs-server.cnrs-mrs.fr/~cnotred/Projects_home_page/t_coffee_home_page.html">http://igs-server.cnrs-mrs.fr/~cnotred/Projects_home_page/t_coffee_home_page.html</a>
TribeMCL	<a href="http://www.ebi.ac.uk/research/cgg/tribe/">http://www.ebi.ac.uk/research/cgg/tribe/</a>
VMD	<a href="http://www.ks.uiuc.edu/Research/vmd/">http://www.ks.uiuc.edu/Research/vmd/</a>
Wise2	<a href="http://www.ebi.ac.uk/Wise2/">http://www.ebi.ac.uk/Wise2/</a>