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1



VISTA

Materials prepared by:
Warren C. Lathe III
Mary E. Mangan
www.openhelix.com

Version_3_1109



VISTA Agenda

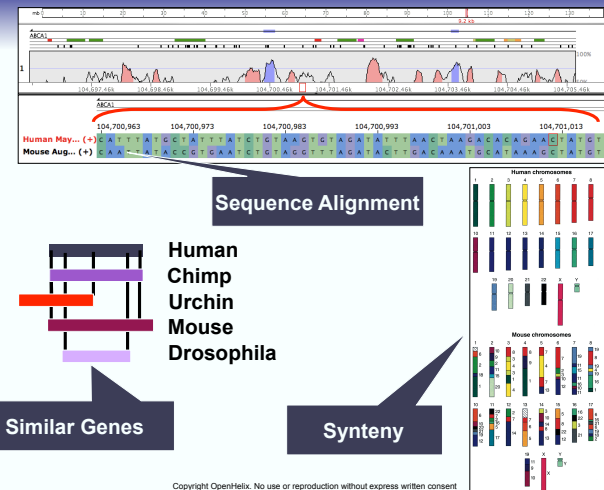
- Introduction and Credits
- VISTA Servers
 - mVISTA
 - rVISTA
 - GenomeVISTA
 - wgVISTA
- VISTA Precomputed Alignments
 - VISTA Browser
 - VISTA-Point
 - Whole Genome rVISTA
- Summary
- Exercises

VISTA resource: <http://genome.lbl.gov/vista>

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3

Comparative Genomics Introduction



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4

Precomputed Alignments

VISTA Browser
Browse through pre-computed whole-genome alignments

VISTA-Point
Browse and obtain sequence and alignment data

Whole Genome rVISTA
Whole genome analysis for conserved TFBS over-represented in upstream regions of genes

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VISTA Overview: Other Projects

Enhancer Browser
Exploration of human enhancer activity

SNP-VISTA
Visualization of mutations in genes and discovery of recombination points

TreeQ-VISTA
Interactive tree visualization tool

Phylo-VISTA
Using phylogenetic relationships to visualize DNA similarity

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VISTA Credits

- Developed & hosted at the Genomics Division of Lawrence Berkeley National Laboratory
- Collaboration & Contribution
 - UC Berkeley
 - Stanford
 - UC Davis
- Supported by the Office of Biological and Environmental Research, US DOE.

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Publications

Nucleic Acids Research, 2004, Vol. 32, Web Server issue: W273–W279
DOI: 10.1093/nar/gkh458

VISTA: computational tools for comparative genomics
Kelly A. Frazer, Lior Pachter^{1,2}, Alexander Poliakov³, Edward M. Rubin^{2,3} and Inna Dubchak^{2,3,*}

Perlegen Sciences, Inc., 2021 Stierlin Court, Mountain View, CA 94043, USA, ¹Department of Mathematics, University of California—Berkeley, Berkeley, CA, 94720, USA, ²Genomics Division, Lawrence Berkeley National Laboratory, MS 84-171, Berkeley, CA 94720, USA and ³Department of Energy Joint Genome Institute, 2800 Mitchell Avenue, Walnut Creek, CA 94598, USA

- Publications and citation information
- Access to downloads

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VISTA Agenda

- Introduction and Credits
- **VISTA Servers**
 - mVISTA
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13

mVISTA: Access

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14

mVISTA: Interface

- Our example will show 3 sequences
- Align up to 100 sequences

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mVISTA: Input of Sequences

- Provide your email address
- Upload your sequences
- Or enter GenBank ID

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16

mVISTA: Input Parameters

Additional options

Alignment program:

- AVID Global pair-wise alignment (sequences can be finished or draft)
- LAGAN Global multiple alignment of finished sequences
- Shuffle-LAGAN Global pair-wise alignment of finished sequences (detects rearrangements)

- AVID
 - multiple pair wise alignments
 - accepts finished or draft sequences
- LAGAN
 - true multiple alignments
- Shuffle-LAGAN
 - multiple pair wise alignments
 - detects sequence rearrangements and inversions

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17

mVISTA: Input Parameters

Additional options

Alignment program:

- AVID Global pairwise alignment (sequences can be finished or draft)
- LAGAN Global multiple alignment of finished sequences
- Shuffle-LAGAN Global pair-wise alignment of finished sequences (detects rearrangements)

Sequence #1
 Name: C1457714 Annotation: (Choose File) no file selected Reverse-complement

RepeatMasker: (one-celled/do not mask)

Sequence #2
 Name: G14328437 Annotation: (Choose File) no file selected Reverse-complement

RepeatMasker: (one-celled/do not mask)

Sequence #3
 Name: G87196504 Annotation: (Choose File) no file selected Reverse-complement

RepeatMasker: (one-celled/do not mask)

Find potential transcription factor binding sites using rVISTA (20Kb max)
 Use translated anchoring in LAGAN/Shuffle-LAGAN (can improve the alignment of distant homologues)

Pairwise phylogenetic tree for the sequences (used by LAGAN):

For example (human baboon) (mouse rat) (chicken). Optional - If you do not enter a tree, it will be calculated by our program.

RankVISTA probability threshold ($0 < p < 1$): 0.5

Reset Submit

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18

mVISTA: Results

You are browsing NM_000230

aligned with:
 NM_008493
 NM_173928
 using the MLAGAN alignment program

[Phylogenetic tree](#)

Download alignments, supplemental information, and visualize your results in the format of dynamic VISTA browser or static VISTA images. You can adjust the default visualization and conservation parameters by clicking the link at the bottom of the table. [Detailed Instructions and Help](#)

Base (reference) sequence	Input and output files (sequences, alignments, etc.)	Dynamic Visualization	VISTA Image
NM_000230	Vista Point	VISTA Browser	PDF
NM_008493	Vista Point	VISTA Browser	PDF
NM_173928	Vista Point	VISTA Browser	PDF

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19

rVISTA: Access

VISTA Tools for Comparative Genomics

VISTA Home Custom Alignment Browser Enhancer DB Downloads Publications Training Help

VISTA is a comprehensive suite of programs and databases for comparative analysis of genomic sequences. There are two ways of using VISTA - you can submit your own sequences and alignments for analysis (VISTA server) or examine pre-computed whole-genome alignments of different species.

Submit Your Sequences

mVISTA

GACAC
T T T T
GACAT

- mVISTA**
Align and compare your sequences from multiple species
- rVISTA**
Locate regulatory sequences in your data using response/regression analysis and transcription factor binding site search
- GenomeVISTA**
Compare your sequences against whole-genome assemblies
- mvVISTA**
Align pair of sequences up to 10Mb long (finished or draft) including microbial whole-genome assemblies

Precomputed Alignments

VISTA Browser

- VISTA Browser**
Examine pre-computed pairwise and multiple alignments of whole genome assemblies
- VISTAPoint**
Access complete data and visual presentation of pairwise and multiple alignments of whole genome assemblies
- Whole Genome rVISTA**
Identify transcription factor binding sites that are conserved between species and overrepresented in upstream regions of groups of genes
- Microbial Genomes**
Access pre-computed list scaffold alignments for microbial genomes through the VISTA component of BED

Training

OpenHelix
VISTA tutorials and training materials from OpenHelix

Updates

October 2009
Added new tool VISTAPoint

June 2009
99 Alignments of 34 genomes sequenced by JGI are added to VISTA Browser. Among these species are plants, fungi, algae, and others

Added whole-genome alignments of the new TAIR8 Arabidopsis genome (TAIR8)

[VISA News Archive](#)

Enhancer DB

Experimentally validated human noncoding fragments and gene enhancer activity as assessed in <http://www.ylab.yale.edu/enhancerdb/>

JGI Genome Portal

Find VISTA alignments for a number of genomes sequenced in the Department of Energy Joint Genome Institute <http://genome.usd.edu/>

Other Projects

Ensembl
NCBI
The ENIGMA
ESD

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20

rVISTA: Interface

Find potential transcription factor binding sites using rVISTA (20Kb max)

- rVISTA sequence submission: set number
- Submit email address, sequences, and set parameters
- Key step: click the box for: Find potential transcription factors

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rVISTA: Select TRANSFAC Matrices

CREB

FOXK

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rVISTA: Mailed Results

display

CREB

FOXK

- Emailed results will provide a link
- Choose which binding sites matrices to display
- You can then choose visualization options

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rVISTA: Results Graphic

sites

sequences

- Blue all transcription factor (TF) binding sites
- Red TF sites which are aligned in both sequences
- Green TF sites which are aligned & in conserved regions

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GenomeVISTA: Access

VISTA Home Custom Alignment Browser Enhancer DB Downloads Publications Training Help

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Submit Your Sequences

mVISTA

GACAC
GACAT

Precomputed Alignments

VISTA Browser

VISTApoint

Training

OpenHelix
VISTA tutorial and training materials from OpenHelix.

Updates

October 2009
Added new tool **VISTApoint**

Updated the design of the VISTA Portal

June 2009
49 Alignments of 34 genomes sequenced by JGI are added to VISTA Browser. Among these species are plants, fungi, algae, and others.

Added whole-genome alignments of the new **TASB** databases genome DBS888.

Added **Vista News Archive**

Other Projects

PhyloVISTA
ENCODE
Transcriptome
ESA

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GenomeVISTA: Input

VISTA Home Custom Alignment Browser Enhancer DB Downloads Publications Training Help

GenomeVISTA

GenomeVISTA Submit:

Submit

About GenomeVISTA

Cite

Query Sequence (choose one of the three options)

Sequence: **paste sequence**

OR

or upload file no file selected

OR

GENBANK Identifier: **or GenBank ID**

Treat lower-case letters as repeats

Target Sequence

Base Genome: **compare to**

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GenomeVISTA: Results

VISTA Home Custom Alignment Browser Enhancer DB Downloads Publications Training Help

You are browsing Human Mar. 2006 aligned with: sequence1 using the AVID alignment program

Chromosome 7

Total Groups: 1 (sorted by alignment size)

chr7:127,679,279-127,684,564 (5285bp) **Vista Point** **VISTA Browser** **VISTA Track**

VISTA-Point

VISTA Browser

VISTA Track

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wgVISTA: Large Scale Sequence Comparison

VISTA Home Custom Alignment Browser Enhancer DB Downloads Publications Training Help

wgVISTA Submit:

Inquiry:

Your email address:

Genome #1: no file selected OR The GENBANK identifier(s):

Genome #2: no file selected OR The GENBANK identifier(s):

Required fields are marked with *

Additional options

Genome #1

Name: genome1 no file selected Soft-masked

Genome #2

Name: genome2 no file selected Soft-masked

Use translated anchoring in Shuffle-LAGAN (can improve the alignment of distant homologues)

RankVISTA probability threshold ($0 < p < 1$): 0.5

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- **wgVISTA: whole genome VISTA**
- Compares 2 sequences (up to 10 Mb)
- Draft or finished microbial assembly sequences can be used

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VISTA Browser: Access

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VISTA Browser: Input Menu

- Choose "base" genome
- Select location
- Determine visualization prefer

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VISTA Browser: Base Genome

- Select a genome
- Note: new versions and species added over time

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VISTA Browser: Position

The screenshot shows the VISTA Browser search interface. The search criteria are set to 'Vertebrate' and 'Human' with the gene 'leptin' entered. A 'Submit' button is highlighted. Below the search bar, a 'Your query "leptin" returned the following results' section lists several RefSeq gene entries. A 'select' button is shown next to the first entry, 'LEP at chr1:127472922-127491632'. A 'symbol' label points to the gene symbol 'LEP' and a 'name' label points to the gene name 'leptin receptor isoform 1'.

- Can be coordinates: chr9:104622838-104769991
- Can be a gene symbol or name
- If multiple matches, select from list

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33

VISTA Browser: Result

The screenshot shows the VISTA Browser result page for the gene 'leptin'. The page displays a graphical display of genome alignments across six different species. A 'Menu & Icons' bar is at the top, and a 'Control Panel' is on the left. A 'Cursor Info' box is visible. A 'Color Legend' is at the bottom left. A 'Curve annotation (species)' is at the bottom right. A '1 row' label points to the first alignment track.

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34

VISTA Browser: Alignment Details

The screenshot shows the VISTA Browser alignment details page for the gene 'leptin'. The page displays a detailed view of the genome alignments, including a 'Color Legend' and a 'Contigs' section. A 'direction' arrow points to the alignment tracks. A 'gene' label points to the gene symbol 'LEP'. A 'repeats' label points to the repeat regions. An 'exon' label points to the exon regions. A 'SNPs' label points to the SNP regions. An 'alignment' label points to the alignment tracks.

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35

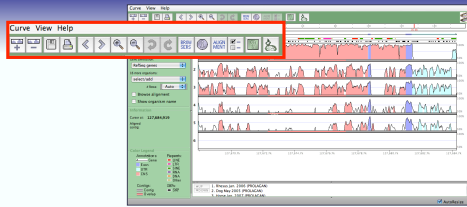
VISTA Browser: Options

The screenshot shows the VISTA Browser options page. The page displays a list of options for the alignment display, including 'Add / Remove selected alignment', 'Print / Save', 'Shift displayed region to left or right', 'Enlarge / Shrink alignment displayed region', and 'Undo / Redo'. Each option is accompanied by a corresponding icon.

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36

VISTA Browser: Options



Access UCSC Genome Browser with VISTA Tracks

Access all alignment-related information and more

Retrieve sequence alignment of displayed region

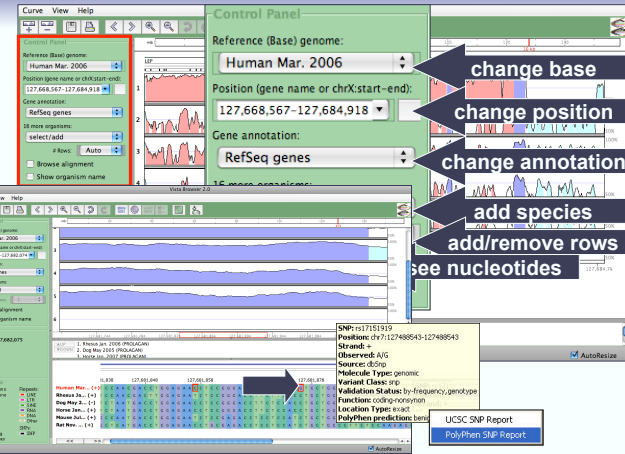
Alter display parameter

Get help

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37

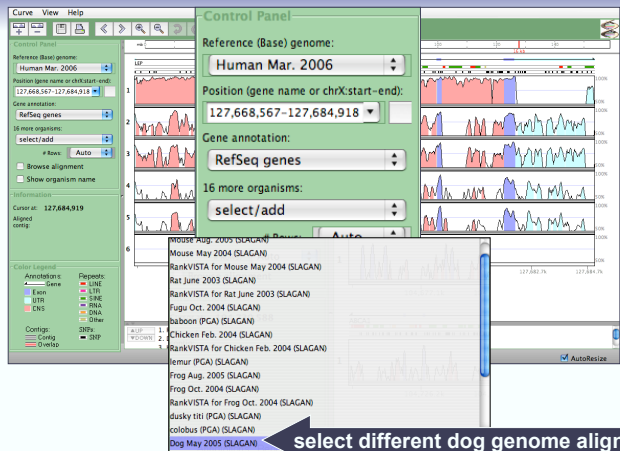
VISTA Browser: Control Panel



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38

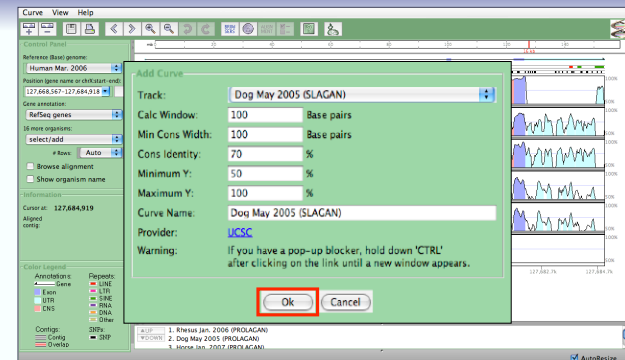
VISTA Browser: Add Species



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39

VISTA Browser: Curve Parameter Panel

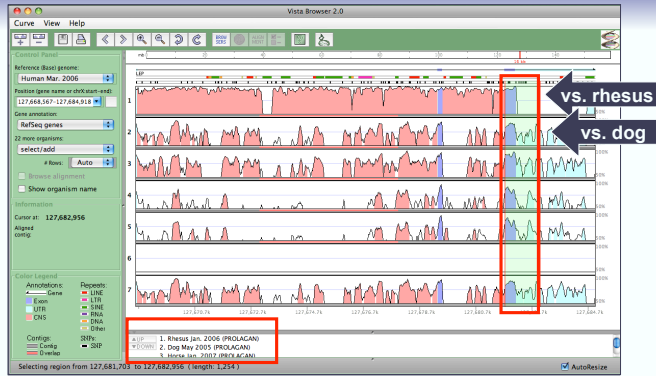


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40

- Default settings for new species curve
- See manual for parameter details
- Change later with "curve parameters" button

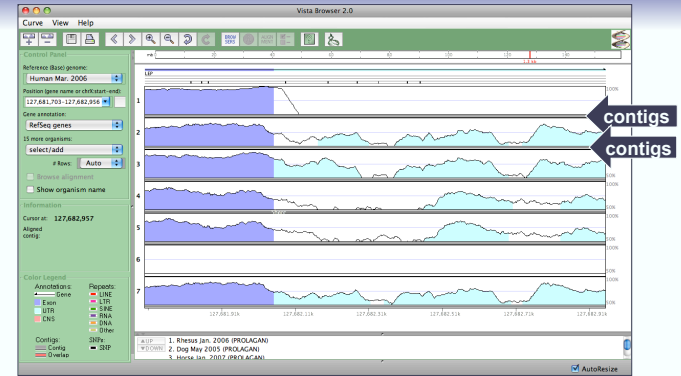
VISTA Browser: Zooming



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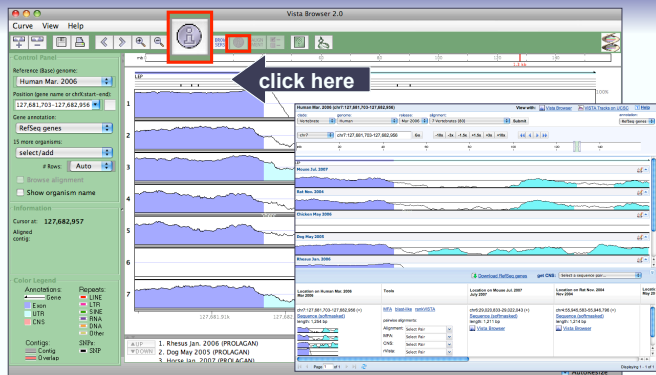
VISTA Browser: Viewing Contigs



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42

VISTA Browser: Alignment Details

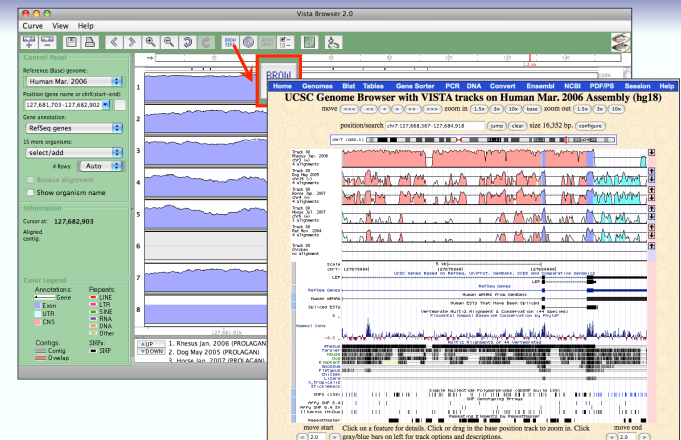


- Click an alignment or annotation to select it
- Then "i" button for information

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43

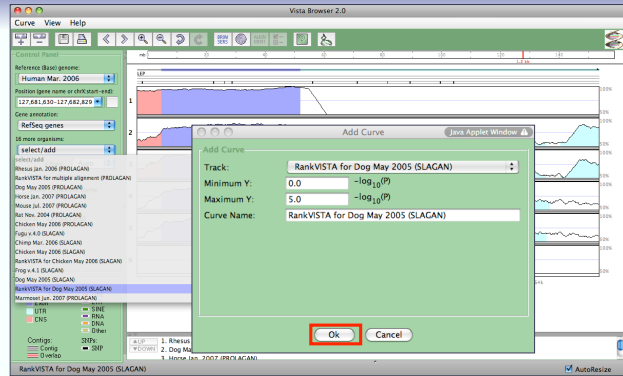
VISTA Browser: Access to UCSC Browser



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44

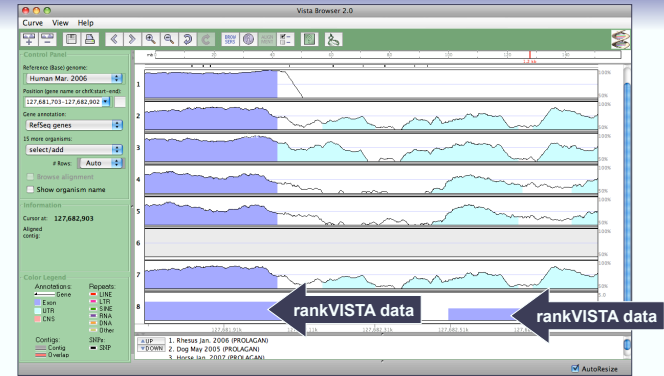
VISTA Browser: rankVISTA Graphic



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45

VISTA Browser: rankVISTA Graphic



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46

VISTA Point: Introduction

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Align and compare your sequences from multiple species
- vVISTA**
Locate regulatory sequences in your data using comparative sequence analysis and transcription factor binding site search
- GenomeVISTA**
Compare your sequences against whole-genome assemblies
- WVISTA**
Align pair of sequences up to 10Mb long (finished or draft) including microbial whole-genome assemblies

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OpenHelix

VISTA tutorials and training materials from OpenHelix

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Added whole-genome alignments of the new TAIR8 Arabidopsis genome

VISTA News Archive

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47

VISTA Point: Access Overview

VISTA

Human Mar. 2006 (127,686,567-127,684,913) View with: VISTA Browser VISTA Tracks on UCSC RefSeq genes

genome: Human Mar. 2006 alignment: 7 Vertebrates (80) Submit

chr7: 127,686,567-127,684,913 Go -10x | -5x | +5x | +10x

VISTA Home Custom Alignment

VISTA Browser (Recommended)
 VISTA Point (New)
 Java 2 installation instructions
 Help

Who Else Genome Comp

From this page you can access:

- the multiple alignments
 - Human Mar. 2006: Callisto
 - Human Mar. 2006: Mouse
- the pairwise alignments of the

Location on Human Mar. 2006	Tools	Location on Mouse Jul. 2007	Location on Rat Nov. 2004
chr7:127,686,567-127,681,250 (+) Sequence (unmasked) length: 12,684 bp	MFA blastlike rankVISTA pairwise alignments: Alignment: Select Pair MFA: Select Pair CNS: Select Pair VISTA: Select Pair	chr6:29,010,220-29,020,462 (+) Sequence (unmasked) length: 10,243 bp VISTA Browser	chr4:55,834,632-45,945,228 (+) Sequence (unmasked) length: 10,697 bp VISTA Browser

Page 1 of 1

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48

VISTA Point: Navigation

Human Mar. 2006 (chr7:127,668,567-127,684,918)

View with: [Vista Browser](#) [VISTA Tracks on UCSC](#) [Help](#)

class: Vertebrate | genome: Human | release: Mar 2006 | alignment: 7 Vertebrates (80) | annotation: UCSC Genes

chr7:127,668,567-127,684,918 | Go | -10x | -3x | -1.5x | +1.5x | +3x | +10x | length: 16,352 bp

7 Vertebrates (80)
 Chicken May 2006 (55)
 Chimp Mar. 2006 (39)
 Dog May 2005 (56)
 Fugu rubripes v.4.0 (675)
 Rhesus,Orangutan and Marmoset (54)
 Trichoplax adhaerens v.1.0 (246)
 Xenopus tropicalis v.4.1 (657)
 Zebrafish Mar. 2006 (6)

Submit

RefSeq genes
 UCSC Genes
 Known Genes

Location on Human Mar. 2006
 chr7:127,668,567-127,681,250 (+)
 Sequence (softmasked)
 length: 12,684 bp

Tools
 MFA: Select Pair
 pairwise alignments: Select Pair
 alignment: Select Pair
 MFA: Select Pair
 CNS: Select Pair
 IVISTA: Select Pair
 PDF: Select Pair

Location on Rat Nov. 2004
 chr4:55,934,532-55,945,228 (+)
 Sequence (softmasked)
 length: 10,997 bp

Location on Marmoset Jun. 2007
 Contig350:431:321-435,454 (+)
 Sequence
 length: 4,134 bp

Location on Rhesus Jan. 2006
 chr3:165,792,114-165,802,027 (-)
 Sequence (softmasked)
 length: 9,914 bp

Download RefSeq genes | get CNS: Select a sequence pair...

Page 1 of 1 | Displaying 1 - 1 of 1

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VISTA Point: Navigation

Human Mar. 2006 (chr7:127,668,567-127,684,918)

View with: [Vista Browser](#) [VISTA Tracks on UCSC](#) [Help](#)

class: Vertebrate | genome: Human | release: Mar 2006 | alignment: Rhesus,Orangutan and Marmoset (54) | annotation: UCSC Genes

chr7:127,668,567-127,684,918 | Go | -10x | -3x | -1.5x | +1.5x | +3x | +10x | length: 16,352 bp

Rhesus,Orangutan and Marmoset (54)
 Trichoplax adhaerens v.1.0 (246)
 Xenopus tropicalis v.4.1 (657)
 Zebrafish Mar. 2006 (6)

Submit

RefSeq genes
 UCSC Genes
 Known Genes

Location on Human Mar. 2006
 chr7:127,668,567-127,678,219 (-)
 Sequence (softmasked)
 length: 9,853 bp

Tools
 MFA: Select Pair
 pairwise alignments: Select Pair
 alignment: Select Pair
 MFA: Select Pair
 CNS: Select Pair
 IVISTA: Select Pair
 PDF: Select Pair

Location on Marmoset Jun. 2007
 Contig350:431:321-435,454 (+)
 Sequence
 length: 4,134 bp

Location on Rhesus Jan. 2006
 chr3:165,792,114-165,802,027 (-)
 Sequence (softmasked)
 length: 9,914 bp

Download UCSC Genes | get CNS: Select a sequence pair...

Page 1 of 1 | Displaying 1 - 2 of 2

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50

VISTA Point: Graphics Table

Human Mar. 2006 (chr7:127,668,567-127,684,918)

View with: [Vista Browser](#) [VISTA Tracks on UCSC](#) [Help](#)

class: Vertebrate | genome: Human | release: Mar 2006 | alignment: Rhesus,Orangutan and Marmoset (54) | annotation: UCSC Genes

chr7:127,668,567-127,684,918 | Go | -10x | -3x | -1.5x | +1.5x | +3x | +10x | length: 16,352 bp

Rhesus Jan. 2006
 Orangutan Jul. 2007

Vista Curve Parameters

Orangutan Jul. 2007

Calc Window, bp: 100
 Min Cons Width, bp: 100
 Cons Identity, %: 70
 Minimum Y, %: 50

apply to all curves

OK

Location on Human Mar. 2006
 chr7:127,668,567-127,681,250 (+)
 Sequence (softmasked)
 length: 12,684 bp

Tools
 MFA: Select Pair
 pairwise alignments: Select Pair
 alignment: Select Pair
 MFA: Select Pair
 CNS: Select Pair
 IVISTA: Select Pair
 PDF: Select Pair

Location on Rat Nov. 2004
 chr4:55,934,532-55,945,228 (+)
 Sequence (softmasked)
 length: 10,997 bp

Location on Marmoset Jun. 2007
 Contig350:426:138-427,397 (+)
 Sequence
 length: 1,260 bp

Location on Rhesus Jan. 2006
 chr3:165,805,340-165,805,905 (-)
 Sequence (softmasked)
 length: 566 bp

Location on Orangutan Jul. 2007
 chr3:125,314,091-125,315,306 (-)
 Sequence (softmasked)
 length: 1,216 bp

Download UCSC Genes | get CNS: Select a sequence pair...

Page 1 of 1 | Displaying 1 - 2 of 2

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51

VISTA Point: Alignments Table

Human Mar. 2006 (chr7:127,681,556-127,682,793)

View with: [Vista Browser](#) [VISTA Tracks on UCSC](#) [Help](#)

class: Vertebrate | genome: Human | release: Mar 2006 | alignment: Rhesus,Orangutan and Marmoset (54) | annotation: UCSC Genes

chr7:127,681,556-127,682,793 | Go | -10x | -3x | -1.5x | +1.5x | +3x | +10x | length: 1,238 bp

Rhesus Jan. 2006
 Orangutan Jul. 2007

sequence

Location on Human Mar. 2006
 chr7:127,681,556-127,682,793 (-)
 Sequence (softmasked)
 length: 9,853 bp

Tools
 MFA: Select Pair
 pairwise alignments: Select Pair
 alignment: Select Pair
 MFA: Select Pair
 CNS: Select Pair
 IVISTA: Select Pair
 PDF: Select Pair

Location on Marmoset Jun. 2007
 Contig350:426:138-427,397 (+)
 Sequence
 length: 1,260 bp

Location on Rhesus Jan. 2006
 chr3:165,805,340-165,805,905 (-)
 Sequence (softmasked)
 length: 566 bp

Location on Orangutan Jul. 2007
 chr3:125,314,091-125,315,306 (-)
 Sequence (softmasked)
 length: 1,216 bp

Download UCSC Genes | get CNS: Select a sequence pair...

Page 1 of 1 | Displaying 1 - 1 of 1

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52

VISTA Point: Alignments Table

Human Mar. 2006 (chr7:127,681,556-127,682,793)

Select Pair: Human - Marmoset, Human - Rhesus, Human - Orangutan, Marmoset - Rhesus, Marmoset - Orangutan, Rhesus - Orangutan

Tools: MFA, blastlike, rankVISTA, align

align

CNS

You are browsing Human Mar. 2006

Please enter a valid Email address to which rVISTA should send the results.

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Whole Genome rVISTA: Access

VISTA Tools for Comparative Genomics

VISTA Home Custom Alignment Browser Enhancer DB Downloads Publications Training Help

Submit Your Sequences

Precomputed Alignments

Training

Whole Genome rVISTA

Enhancer DB

JGI Genome Portal

Other Projects

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Whole Genome rVISTA: Select Alignment

Whole Genome rVista

Whole Genome rVista

Upstream range

IDs or symbols

Submit

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Whole Genome rVISTA: Results

Whole Genome rVista

Results

sites found

family_id	name	number of hits in the submitted regions	total number of hits on genome	log ₁₀ (p-value)
14	AP4	11	41939	3.1193
178	LXR	2	501	3.101
95	ERR1	11	42998	3.049
13	AP2ALPHA	6	13488	3.0432
271	SOX3	6	27100	2.7196
173	LFA1	6	28678	2.6735
321	ZID	6	25502	2.4999
295	TCF4	5	12126	2.4761
140	HIF1	4	8663	2.2437

view genes

Locus Link to	Gene name	Find TFBS over-represented upstream of this gene	Summary of all conserved TFBS upstream of this gene	img
19	ABCA1	90	870w	90
3931	LCA1	90	870w	90

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Whole Genome rVISTA: Gene Results

Number of genes in the set 2
Go to the graphical display of the regions.

Locus Link	Gene name	Find TFBS over-represented upstream of this gene	Summary of all conserved TFBS upstream of this gene	Image
19	ABCA1	go	show	go
3951	LCAT	go	show	go

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The screenshot shows the 'Whole Genome rVISTA' interface. On the left, there is a table with columns for 'Locus Link', 'Gene name', 'Find TFBS over-represented upstream of this gene', 'Summary of all conserved TFBS upstream of this gene', and 'Image'. Two rows are visible: one for ABCA1 (Locus Link 19) and one for LCAT (Locus Link 3951). Below the table, there are 'go' and 'show' buttons for each row. On the right, a graphical display shows the genomic regions for these genes with red bars indicating TFBS. The interface includes a navigation menu at the top with options like 'VISTA Home', 'Custom Alignment', 'Browser', and 'Enhancer DB'.

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VISTA Agenda

- Introduction and Credits
- VISTA Servers
 - mVISTA
 - rVISTA
 - GenomeVISTA
 - wgVISTA
- VISTA Precomputed Alignments
 - VISTA Browser
 - VISTA-Point
 - Whole Genome rVISTA
- Summary
- Exercises

VISTA resource: <http://genome.lbl.gov/vista>

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VISTA Servers

mVISTA: create your own sequence alignments
Download alignments, experimental information, and access our results in the format of GenomeVISTA browser or rankVISTA. You can adjust the default visualization and conservation parameters by clicking the link at the bottom of the table: [Conserved Sites](#) and [mVISTA](#)

rVISTA: identify conserved transcription factor binding sites
aligned with [Human May 2004](#) (Genome Build 35) using the [AYID](#) alignment program

GenomeVISTA: align your sequences with genomes
Identify transcription factor binding sites conserved between species and coded in upstream regions of groups of genes

wgVISTA: to align sequences up to 10 Mb
Access pre-computed full scaffold align microbial genomes through the VISTA of SAS

Enhancer DB
Experimentally validated human transcription fragments with gene enhancer activity as assessed in transgenic mice. <http://webenhancer.lbl.gov/>

JGI Genome Portal
Find VISTA alignments for a genome sequenced in the Energy Joint Genome team. <http://genome.jgi-psf.org/>

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VISTA Browser and rankVISTA

The screenshot shows the VISTA Browser interface. It displays multiple tracks of genome alignments for the rhesus, dog, and horse species. The tracks are labeled 'rhesus', 'dog', and 'horse'. The interface includes a navigation menu at the top with options like 'VISTA Home', 'Custom Alignment', 'Browser', and 'Enhancer DB'. The main display area shows the alignments with red bars indicating TFBS. The interface includes a navigation menu at the top with options like 'VISTA Home', 'Custom Alignment', 'Browser', and 'Enhancer DB'.

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