

[Genome Explore](#)

[Genome Mapping](#)

[Library Mapping](#)

SAGExplore web server tutorial for Module I: Genome Explore

The banner features a dark blue background with a grid of glowing blue circles. On the left, there is a white mouse and a blue frog. In the center, a human silhouette is overlaid with a network of white lines. The background is filled with faint, glowing DNA sequences. A large, stylized 'S' logo is on the right. At the bottom, three orange buttons are visible: 'Genome Explore' (with a red dashed border), 'Genome Mapping', and 'Library Mapping'.

[Genome Explore](#) [Genome Mapping](#) [Library Mapping](#)

I.- Genome Explore Module: This module allows the user to browse and explore a genome, in terms of the context where potential or virtual SAGE tags are found for a given anchoring-tagging enzyme pair.

Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 Organism [?](#)
 Step 2 Anchoring-Tagging Enzyme Pair [?](#)
 Step 3 Odds ratio for confidence class assignments [?](#)

Step 4 TAG categories and genomic mapping contexts to display: [?](#)

TAG Class		Genomic Type		TAG Confidence		TAG Location		Internal Poly-A next?
<input type="radio"/> Platinum	<input type="radio"/> Copper	<input checked="" type="checkbox"/> Known Protein	<input checked="" type="checkbox"/> smRNA	<input checked="" type="checkbox"/> High	<input checked="" type="checkbox"/> ORF	<input checked="" type="checkbox"/> Exon	<input checked="" type="checkbox"/> Yes	
<input type="radio"/> Gold	<input type="radio"/> Iron	<input checked="" type="checkbox"/> Hypothetical Protein	<input checked="" type="checkbox"/> tRNA	<input type="checkbox"/> Low	<input checked="" type="checkbox"/> 3'UTR	<input checked="" type="checkbox"/> Intron	<input type="checkbox"/> No	
<input type="radio"/> Silver	<input type="radio"/> Silicon	<input checked="" type="checkbox"/> rRNA	<input type="checkbox"/> Intergenic A	<input type="checkbox"/> Undefined	<input checked="" type="checkbox"/> 5'UTR			
<input type="radio"/> Aluminum	<input checked="" type="radio"/> All	<input checked="" type="checkbox"/> snoRNA	<input type="checkbox"/> Intergenic B					
		<input checked="" type="checkbox"/> snRNA	<input type="checkbox"/> Intergenic C					

Step 5 Explore SAGE TAGs in the genome by: [?](#)

Gene Name
 Genome Fragment
 Chromosome
 Full Genome

Step 6 Input Data [?](#)

Upload text file

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
 ACT1
 YFR016C
 YPT1

Output Display Options [?](#)

Show
 Sort by

I.- Genome Explore Module Form: The user must follow six sequential steps in this form. Online help with the relevant details is provided for each step.

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Show Sort by

Step 1: The user must select the organism of interest. Currently, only *Saccharomyces cerevisiae* is available. In the near future, other organisms will be added.

Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 **Organism** [?](#) Step 2 **Anchoring-Tagging Enzyme Pair** [?](#) Step 3 **Odds ratio for confidence class assignments** [?](#)

Step 4 TAG categories and genomic mapping contexts to display: [?](#)

TAG Class		Genomic Type		TAG Confidence		TAG Location		Internal Poly-A next?
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Show Sort by

Step 2: The user must select the anchoring-tagging enzyme pair used in SAGE. Currently, only the pair NlaIII-BsmFI is available. In the near future, other enzyme pairs such as the one used in Long-SAGE will be added.

Search Potential TAGs in a Genome

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Output Display Options ?

Show Sort by

Step 3: The user must select the odds ratio used to assign the confidence classes to the different genomic tags. For details see: Malig, R., Varela, C., Agosin, E. and Melo, F. (2006) Accurate and unambiguous tag-to-gene mapping in SAGE by a hierarchical gene assignment procedure. *BMC Bioinformatics*, **7**, 487-507.

Search Potential TAGs in a Genome

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Step 3 Odds ratio for confidence class assignments

Step 4 TAG categories and genomic mapping contexts to display:

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Step 5 Explore SAGE TAGs in the genome by:

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Output Display Options

Show
 Sort by
 Descending

Step 4: The user can choose to display subsets of tags upon a large amount of different features. For details see the help links or: Malig, R., Varela, C., Agosin, E. and Melo, F. (2006) Accurate and unambiguous tag-to-gene mapping in SAGE by a hierarchical gene assignment procedure. *BMC Bioinformatics*, **7**, 487-507.

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Step 5 Explore SAGE TAGs in the genome by: ?

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Output Display Options ?

Show Sort by

Step 5: The user must select the type of input that will be provided in the next step. Four options are available.

Search Potential TAGs in a Genome

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Output Display Options [?](#)

Show Sort by

Step 6: The user must provide the list of genes, genome fragments or chromosomes to explore. In the case of the full genome option, no input is required here. The window in the right explains the input format required for each case.

Search Potential TAGs in a Genome

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Show Sort by Descending

Pre-submit: Before submitting the query, the user can choose the number of rows to display per page and also how to sort the results.

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Output Display Options [?](#)

Show Sort by Descending

Submit: The user is ready to submit the query to the server.

Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

Show

[Download all Results](#) [Graphical View](#)

There are **28,948** records that matched the query.

[Next](#)

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCCAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: Typical output of the Genome Explore Form.

Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

Show

[Download all Results](#) [Graphical View](#)

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Query Results: The total number of records that matched the query are reported.

Search Potential Tags in a Genome: Results

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12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: Only a fraction of the results is displayed. This option can be easily changed by selecting a different number of rows to display or the next button used to go to the next page.

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N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCCAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: The full table can be downloaded as tab-delimited text (compressed file or tar.gzipped).

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N	TC	Seq	GC	TD	DS	BI										
1	Hi	CATGACCTACT														
2	Hi	CATGATATAM														
3	Hi	CATGTTATCT														
4	Hi	CATGTGCAAM														
5	Hi	CATGTATATA														
6	Hi	CATGTTGGAT														
7	Hi	CATGTCGTGT														
8	Hi	CATGAGAGAA														
9	Hi	CATGGACGCA														
10	Hi	CATGTGAGCA														
11	Hi	CATGGTTCTT	1	0.048	Pt	ORF	ORFv	3	1	32390	+	GDH3	YAL062W			
12	Hi	CATGGTGGCTG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W			
13	Hi	CATGTCGGTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W			
14	Hi	CATGAGTACAC	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W			
15	Hi	CATGAGATTAG	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W			
16	Hi	CATGCAATTAG	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W			
17	Hi	CATGTGGGGCC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W			
18	Hi	CATGAAAGAA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W			
19	Hi	CATGTGCTAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W			
20	Hi	CATGAAGCTG	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W			
21	Hi	CATGATTCTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W			

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Query Results: Compressed files for download are kept for 5 hours at the server and then deleted. By clicking on the filename, the file is downloaded.

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N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCAAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGGAGAACTGGA	1	0.018	Pt	ORF	ORFv	6	1	31988	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: Moving the mouse pointer over the table highlights the current row.

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N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCCAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: Online help explaining the meaning of each column is obtained by left-clicking with the mouse over the column headers.

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N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCCAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: These 6 columns contain linked fields.

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N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCAAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: By clicking over the standard gene name, a query to the Saccharomyces Genome Database is launched. Thus, the user can obtain a large amount of data about a given gene.

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1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
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3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCAAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: By clicking over the systematic gene name, a query to the Saccharomyces Genome Database is launched. Thus, the user can obtain a large amount of data about a given gene.



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Interactions

Expression

Protein

[Alternative single page format](#)

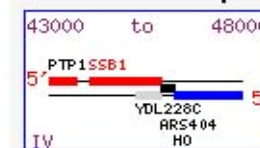
SSB1 BASIC INFORMATION [[View References](#)]

Standard Name	SSB1 (see Nomenclature conflict Note)
Systematic Name	YDL229W
Alias	YG101 ¹
Feature Type	ORF, Verified
Description	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p (2, 3, 4, 5, 6, 7, 8 and see Summary Paragraph)
GO Annotations	SSB1 GO evidence and references
Molecular Function	<ul style="list-style-type: none"> ATPase activity (IDA) unfolded protein binding (IDA, ISS, TAS)
Biological Process	<ul style="list-style-type: none"> cotranslational protein folding (IDA) protein biosynthesis (IMP, IPI, TAS)

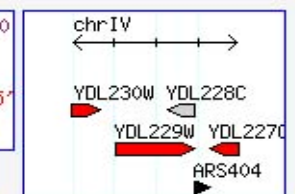
SSB1 RESOURCES

Click on map for expanded view

SGD ORF map



GBrowse



Literature

Literature Guide

Retrieve Sequences

Genomic DNA

SGD Query: An example of the results obtained when querying the Saccharomyces Genome Database by standard or systematic gene name.

Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

Show

[Download all Results](#) [Graphical View](#)

There are **28,948** records that matched the query.

[Next](#)

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCAAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: The genomic context where a tag matches can be obtained by clicking on this field.

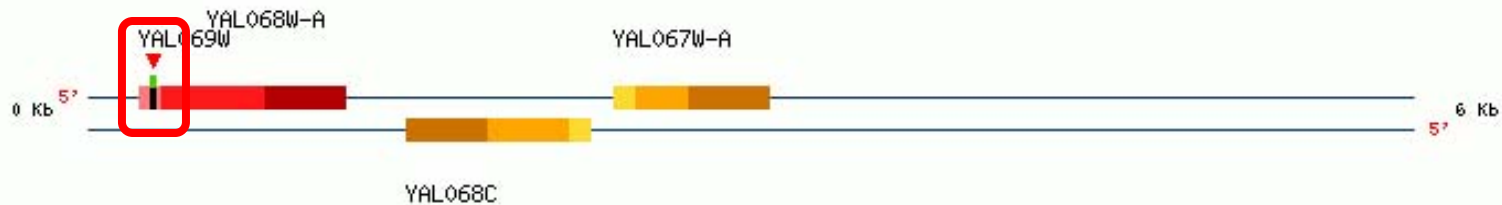
Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- ||| Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- Strand
- Transcript
- Intron
- ↑ TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The selected tag is shown with a vertical arrow head.

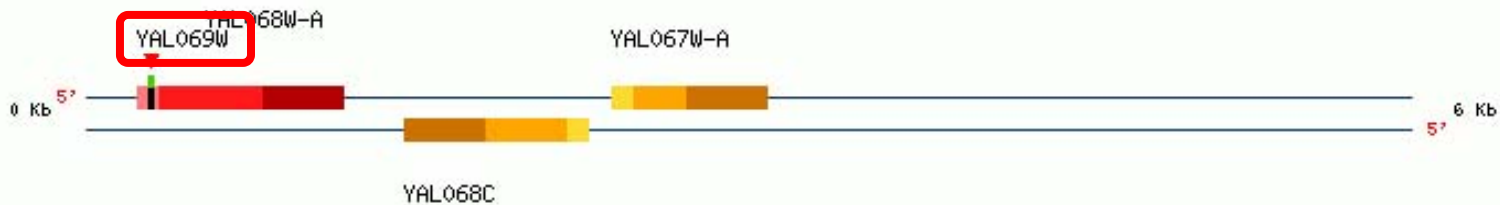
Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

- Watson (+) Strand
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- ||| Fragment Displayed
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- TAG of High Confidence
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Shape:

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- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: Gene names are linked to the Saccharomyces Genome Database.

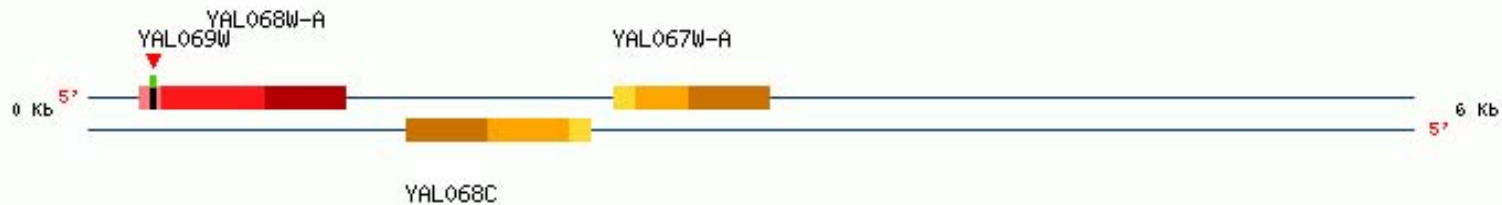
Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- ||| Fragment Displayed
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- TAG of Low Confidence

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- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: Keys of the graphical elements displayed above are provided.

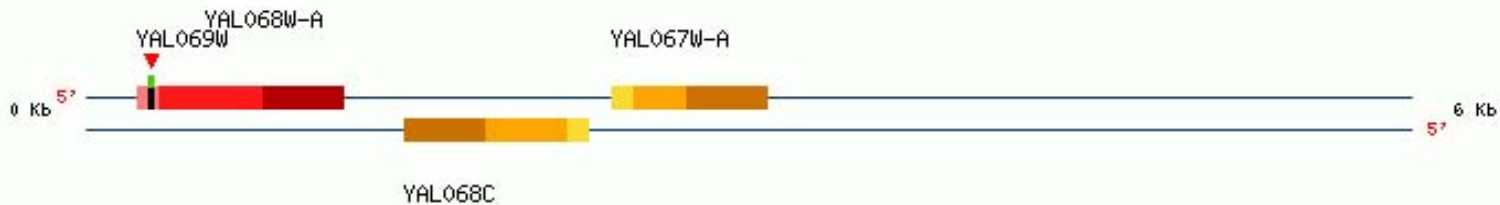
Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- ||| Fragment Displayed
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence
- Centromer

Shape:

- Strand
- Transcript
- Intron
- | TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The fragment of the chromosome being displayed is specified.

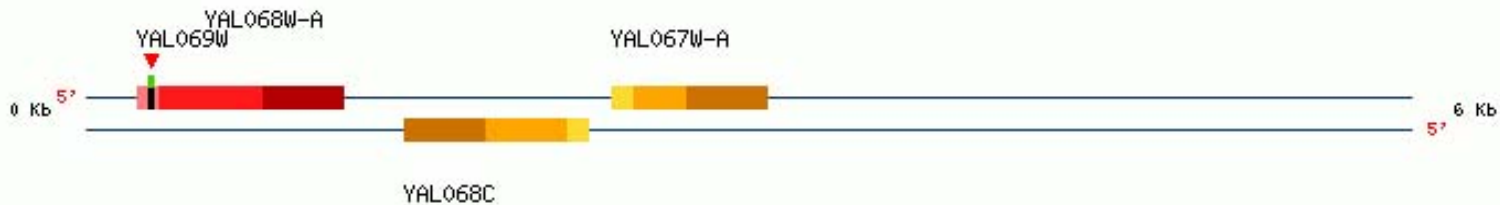
Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- ||| Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- Strand
- Transcript
- Intron
- ↑ TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: In this case corresponds to the 5' end of the chromosome. The user can click on this graphical chromosome to select and display a different region.

Genomic Context

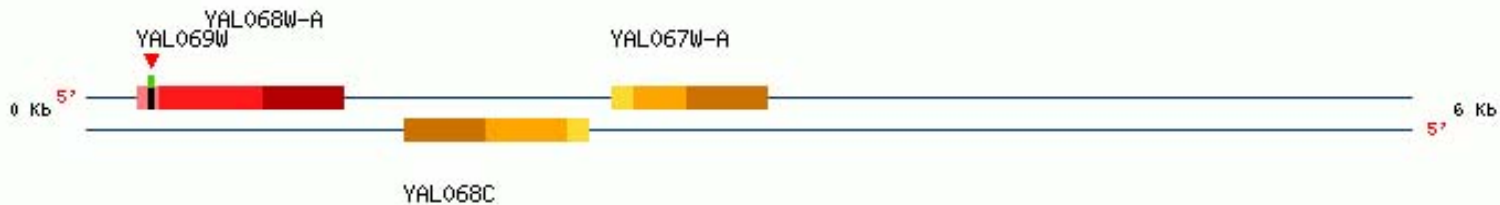
Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb

Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- ||| Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- Strand
- Transcript
- Intron
- ↑ TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The chromosome scale in base pairs is also shown.

Genomic Context

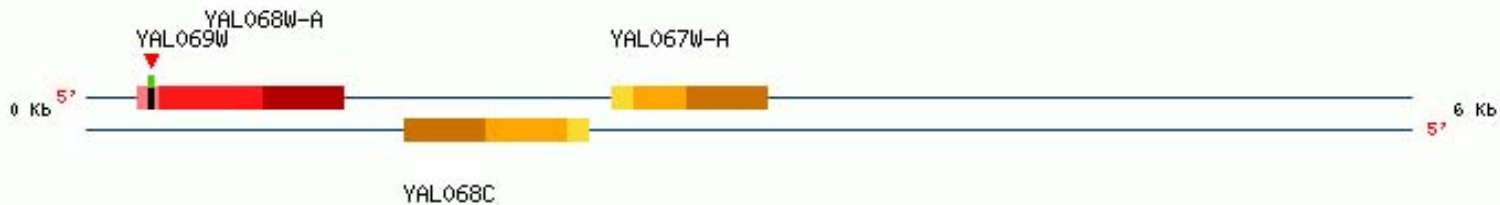
Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb

Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- ||| Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- Strand
- Transcript
- Intron
- ↑ TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The current chromosome number and size are given.

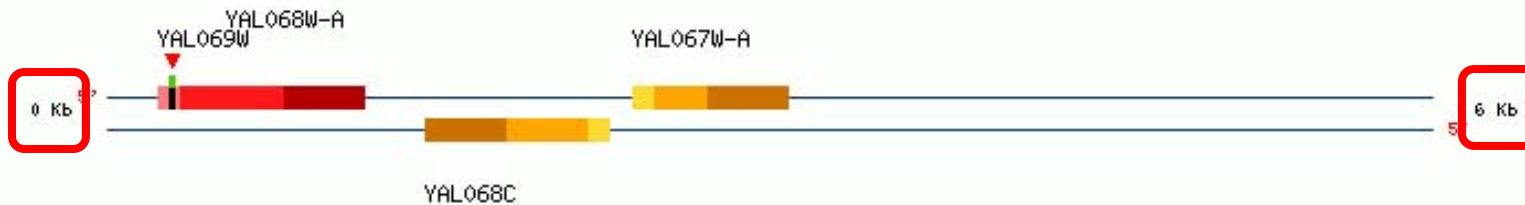
Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- ||| Fragment Displayed
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence
- Centromer

Shape:

- Strand
- Transcript
- Intron
- ↑ TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The 5' and 3' positions of the chromosome fragment displayed are also shown.

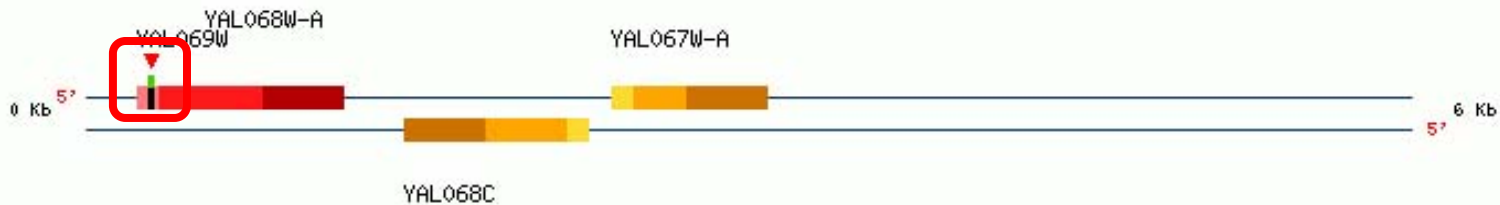
Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- ||| Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- Strand
- Transcript
- Intron
- ↑ TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: Clicking on the tag will display a pop-up window with several details about this tag. This pop-up window can also be launched from the main results table and thus it will be explained next from there.

Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

Show ▼

[Download all Results](#) [Graphical View](#)

There are **28,948** records that matched the query.

[Next](#)

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCAAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: A record with several tag details can be obtained by clicking on this field.

SAGExplore

TAG Detail

TAG: CATGACCTACTCAC

Frequency	Class Score	TAG Class	Odds Ratio
1	0,048	Pt	0,048
Confidence	Chromosome	Start Coord.	End Coord.
Hi	1	282	295
Strand	Location	Intron?	UTR Pred.
+	UTR5	N	P
Type	Position	Distance	Poly-A Next?
2	3	476	N
Distance Poly-A	Length Poly-A	Feature Type	Feature Name
0	0	ORFdu	Dubious
Systematic Name		Standard Name	
YAL069W		N.A.	
Description			
Hypothetical protein			

Tag details: Many details about the tag are provided here. See the online help for an explanation of each field meaning.

Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

Show

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There are **28,948** records that matched the query.

[Next](#)

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCAAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: The genomic sequence context where the tag matches can be downloaded by clicking on this field.

SAGExplore

```
ATCG: UTR  
ATCG: TAG  
ATG ... STOP: ORF
```

```
>scer|chr:4|+|229806-230618  
TTGAATCTGTAAGCCCCTTCGTGATATTTCAAGGTTAAATTACGAATTGCAGTTTTCAGTT  
AATCTTGGACTAACAAAGAAATCAAACAACCTAAGAAGAAAATGTCTGACTCTATTATTTTC  
CTTTGCTGCTTTCATCCTAGCTGATGCTGGTTTGGAAATCACCTCTGACAACCTTATTGAC  
TATCACCAAGGCCGCTGGTGCTAATGTCGACAAACGTATGTACAAAAAATGC AACCTAAAAC  
GACTTTGTGTGACTACGAAGAGAAAGATTAGACAACAATCGTCCCGAGAAATGCGCAATT  
TTGAATAATGGGGGACAGAAAAAATTCATGTAACGTTTCCCTCTAACATGATGAGATACT  
AGGGGGCAATACATGTAGAAATATTTCTCCATTAACGTATTTAACGGAAAGCACAAAGTCA  
GGATCGAATTACTTCTTCAAGGATCTCATTTTACTAACAAACTCAACGAATAACGACTCT  
TCCTATGGAGCTTGTTATATGTATCATTGAATTAGGTCTGGGCTGATGTTTACGCTAAGG  
CTTTGGAAGGTAAGGACTTGAAAGGAAATCCTATCTGGTTTCCATAACGCTGGCCCTGTTG  
CTGGTGCTGGTGCTGCTTCTGGCGCTGCCGCTGCTGGTGGTGACGCTGCTGCTGAAGAAG  
AAAAAGAAAGAAAGCTGCTGAAGAATCTGACGACGACCATGGGTTTCGGTTTATTCGACT  
AAACATACAAGGAAAGTCATTTTTTCTGCAACGTTTTTTTTACCCTTTATGTATATATATT  
TACATATAAAATAAACCTCTAATCAATCAGTAT
```

Download Sequence: If the tag matches an ORF (as it is in this example), the transcript sequence is given. The 5' and 3' UTRs, the start and stop codons, and the tag sequence are all highlighted. If the tag matches an intergenic region, the 500 flanking nucleotides upstream and downstream the tag are provided. In this case, neighbor elements such as UTRs from other genes are also highlighted if present.

SAGExplore

ATCG: UTR

ATCG: TAG

ATG ... STOP: ORF

```
>scer|chr:4|+|229806-230618
```

```
TTGAAATCTGTAAGCCCCCTTCGGGATATTTCAAGGTTAAATTACGAATTGCAGTTTTCAGTT  
AATCTTGGACTAACAAAGAAATCAAACAACCTAAGAAGAAAATGCTCTGACTCTATTATTTTC  
CTTTGCTGCTTTCATCCTAGCTGATGCTGGTTTTGGAAATCACCTCTGACAACCTTATTGAC  
TATCACCAAGGCCGCTGGTGCTAATGTCGACAAACGTATGTACAAAAATGC AACCTAAAAC  
GACTTTGTGTGACTACGAAGAGAAAGATTAGACAACAATCGTCCCGAGAAATGCGCAATT  
TTGAATAATGGGGGACAGAAAAATTCCATGTAACGTTTCCCTCTAACATGATGAGATACT  
AGGGGGCAATACATGTAGAAATATTTCTCCATTAACGTATTTAACGGAAAGCACAAAGTCA  
GGATCGAATTACTTCTTCAAGGATCTCATTTTACTAACAAACTCAACGAATAACGACTCT  
TCCTATGGAGCTTGTTATATGTATCATTGAATTAGGTCTGGGCTGATGTTTACGCTAAGG  
CTTTGGAAGGTAAGGACTTGAAAGGAAATCCTATCTGGTTTCCATAACGCTGGCCCTGTTG  
CTGGTGCTGGTGCTGCTTCTGGCGCTGCCGCTGCTGGTGGTGACGCTGCTGCTGAAGAAG  
AAAAAGAAAGAAAGCTGCTGAAGAATCTGACGACGACCATGGGTTTCGGTTTATTTCGACT  
AAACATACAAGGAAAGTCATTTTTTTCTGCAACGTTTTTTTTACCCTTTATGTATATATATT  
TACATATAAAATAAACCTCTAATCAATCAGTAT
```

Download Sequence: The FASTA header indicates the exact region of the sequence displayed.

Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

Show

[Download all Results](#) [Graphical View](#)

There are **28,948** records that matched the query.

[Next](#)

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCCAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: A query to the BLAST server at the NCBI is launched with the previously described sequence by clicking on this field. In the case of tags matching an intergenic region, this option is very useful to aid the process of gene discovery.

[Search](#)

```

TCACCAGTGTTAGGGTCAAGAACTGCATCAATACCGAAGAAGGGGAATGAGGCAGA
ACCCGGTTTCATTGGTGTAAACACCACCAGCCAGCGGGGTGACCAGATGCGAACCAATT
CTGTTTGCCAGTAGGTGTCTACAATGGGGATTTTCAATTTTACCTATTTTTCAGAGTAC
CACTCCCAAATTCAGCAGCAATTGGCTCACCGACCGAACCCAAAGCAAACGCAAAGATT
TAAGGAATGATTTTCGATGTAGGAATCACCAGCTCTTTTCAACAAACGCAAAGCAGTTG
  
```

[Choose a translation](#)

 TRANSLATED query - PROTEIN database **[blastx]**
[Set subsequence](#)

 From: To:
[Choose database](#)

nr

[Genetic codes](#)

Standard (1)

Now:

 or

BLAST Query: A query to the BLAST server at the NCBI is automatically launched with the flanking sequence that contains the tag. In the case of intergenic tags, BLASTX is launched (this example). In the case of tags matching an ORF, BLASTP is used.

Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

Show

[Download all Results](#)
[Graphical View](#)

There are **28,948** records that matched the query.

[Next](#)

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCCAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
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17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTC	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: A graphical view with all the tags from the results table is also available.

Graphical View

Organism: *Sacharomyces cerevisiae*

100 Kb Chromosome: 1 Length: 230,208 bp



100 Kb Chromosome: 2 Length: 813,178 bp



100 Kb Chromosome: 3 Length: 316,616 bp



100 Kb Chromosome: 4 Length: 1,531,916 bp

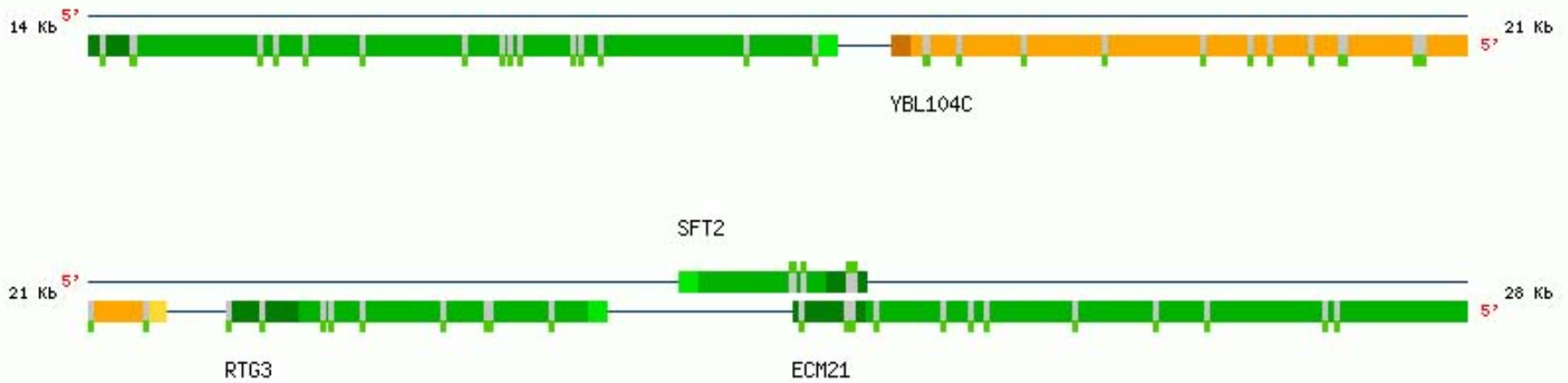


100 Kb Chromosome: 5 Length: 576,869 bp



100 Kb

Graphical View: All chromosomes that contain a tag from the results table are shown. Tags are represented graphically on the chromosomes. By clicking on a chromosome, a new pop-up window will emerge with the details of that chromosome region in the context of the current query.



Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- || Fragment Displayed
- ⌘ Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- Strand
- Transcript
- Intron
- ⌘ TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Graphical View: An example showing all high confidence tags mapping into ORFs is shown here.



The image displays the SAGExplore web server interface. The background is a dark blue grid of DNA sequence characters (A, T, C, G). On the left, there is a glowing white mouse and a glowing blue frog. In the center, a circular genome map is shown with a network of white lines. On the right, a green, glowing, abstract shape resembling a protein or a specific genomic region is highlighted. At the bottom, there are three yellow buttons with black text: "Genome Explore", "Genome Mapping", and "Library Mapping".

***This is the end of the SAGExplore web server tutorial for
module I: Genome Explore
Any comments or inquiries, please contact us***