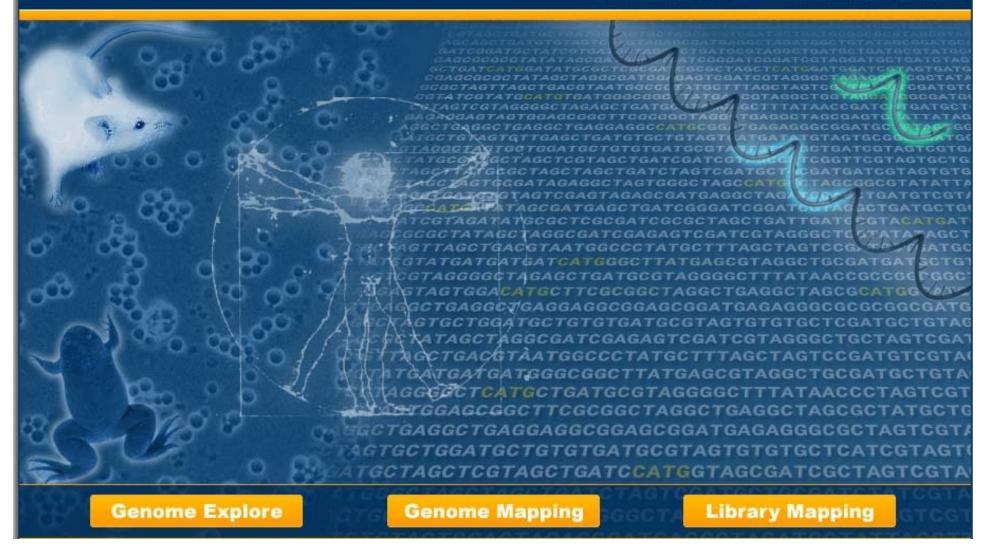
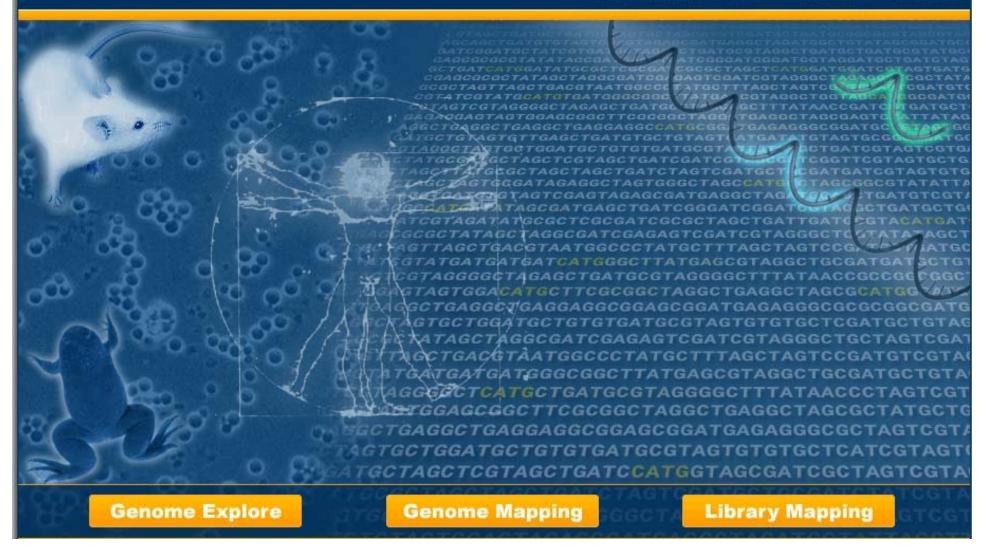
ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD



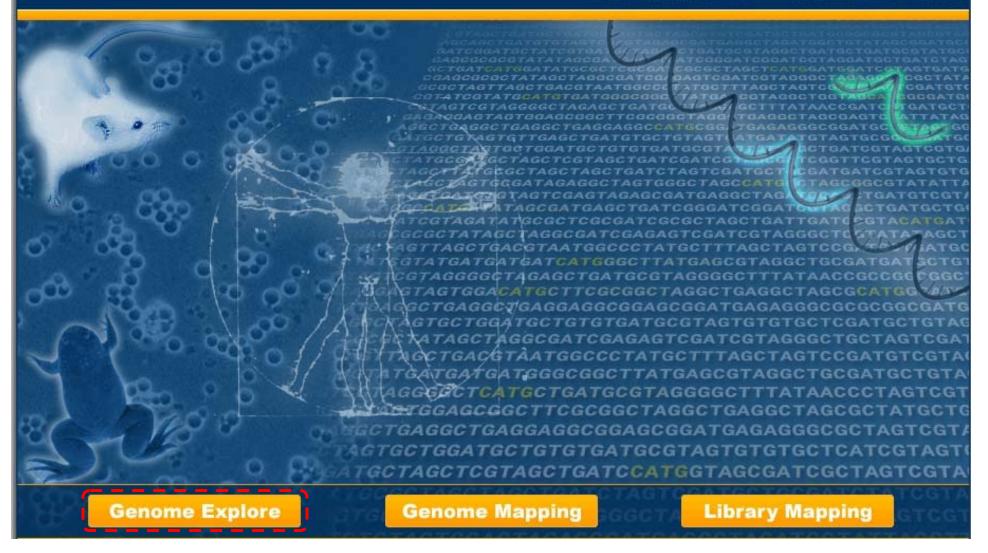
SAGExplore web server tutorial

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD



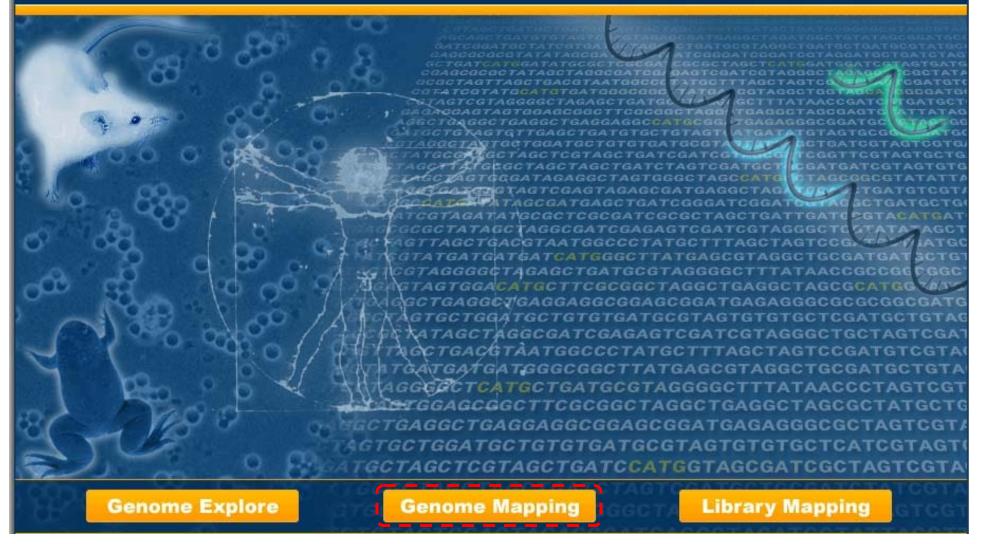
The SAGExplore server has three different modules ...

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD



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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD



II.- Genome Mapping Module:

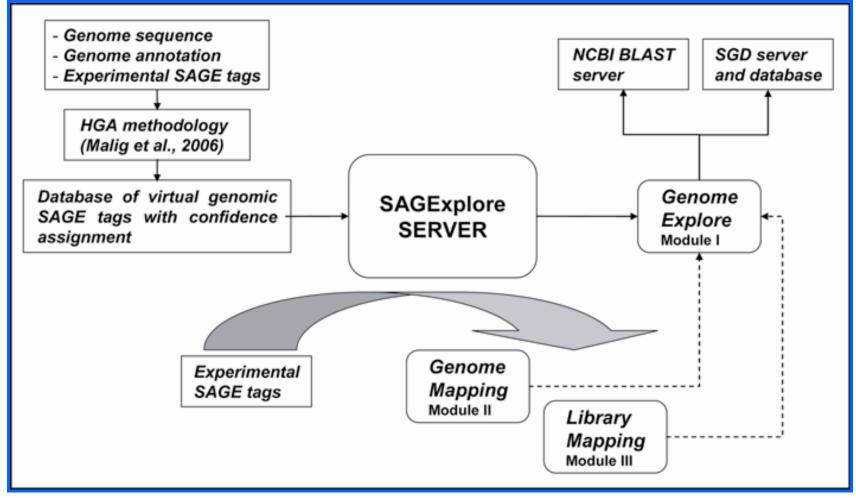
This module allows the user to map experimental tags against the genome.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD



III.- Library Mapping Module:

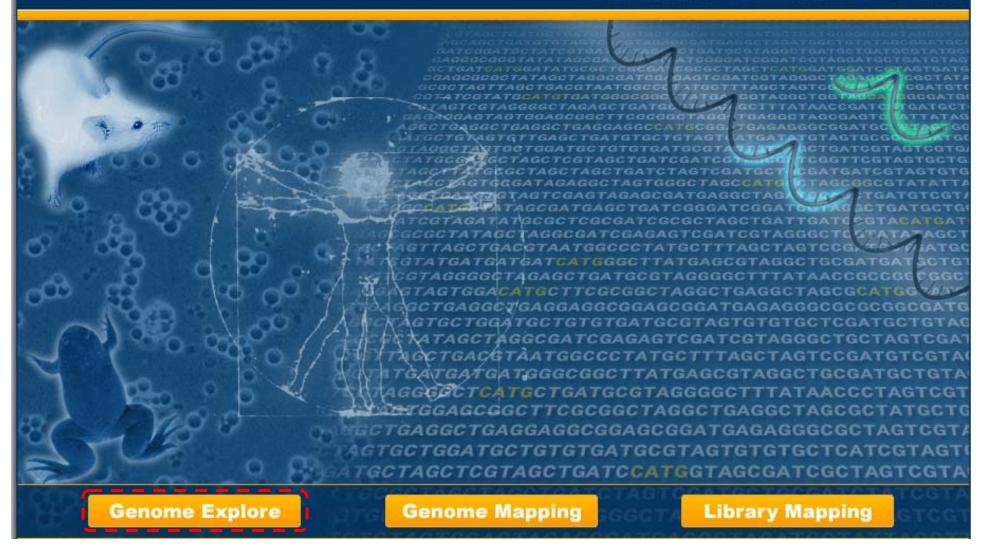
This module allows the user to map experimental tags against known experimental libraries of SAGE tags.



Layout and flowchart of the SAGExplore server.

The core of the server is a MySQL database of virtual genomic SAGE tags with confidence assignments The module I is linked to NCBI BLAST server and to the Saccharomyces Genome Database (SGD) and does not require any input from the user. The modules II and III requires experimental tag sequences and their counts (optional) as input, and are linked to the module I and, through this, to the external servers and databases.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD



I.- Tutorial Genome Explore Module.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Explore
2	Search Poten	itial TAGs in	a Genome					
PLOF	This item allows	to extract the p	otential SAGE TAGs from t	he entire or regions o	f a genome.			
GENOME EXPLORE	Step 1 Organi Saccharomyces	ism ? : cerevisiae 🗸	Step 2 Anchoring-Tag NlaIII - BsmFI 💌	gging Enzyme Pair	Step 3 Odd 5 ✓	ds ratio for o	onfidence c	lass assignments ?
	Step 4 TAG ca	ategories and	genomic mapping conte	xts to display: 🕐				
S.	TAG Class		Genomic Type		TAG Confidence	TAG Location	•	Internal Poly-A next?
IAP 9	🔘 Platinum	O Copper	🗹 Known Protein	🗹 smRNA	🗹 High	ORF	🗹 Exon	🗹 Yes
ų.	O Gold	O Iron	🗹 Hypothetical Protein	🗹 tRNA	Low	3'UTR	🗹 Intron	🗹 No
No.	🔿 Silver	🔘 Silicon	🗹 rRNA	🔲 Intergenic A	🔲 Undefined	S'UTR		
ē	O Aluminum		🗹 snoRNA	🔲 Intergenic B				
u.			🗹 snRNA	🔲 Intergenic C				
ARIES MAPPING LIBRARIES EXPLO	 Gene Name Genome Fra Chromosom Full Genome 	gment e	in the genome by: ?	Step 6 Input Data Upload text file OR Fill in Gene Nat	Browse	<	The Gene r format (inp textarea bo should be l ACT1 YFR016C YPT1	ut file or x)
LIBR	Output Display Op Show 50	Sort by	Confidence 💌 I	Descending 💌				ubmit Reset
				ersidad Católica de Ch 2006 SAGExplore, All 1		ns of Use		

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Explore
	Search Poter	ntial TAGs in	a Genome					
GENOME EXPLORE	This item allows	to extract the p	otential SAGE TAGs from t	he entire or regions o	f a genome.			
EX	Step 1 Organi	ism ?	Step 2 Anchoring-Ta	gging Enzyme Pair	? Step 3 Odd	ls ratio for i	confidence c	lass assignments ?
OME	Saccharomyces		NlaIII - BsmFI	gging chaynic i dh	5 🗸	is rucio tor .	connucince c	
GEN								
-	Step 4 TAG ca	ategories and	genomic mapping conte	exts to display: 👔				
2	TAG Class		Genomic Type		TAG Confidence	TAG Location	n	Internal Poly-A next ?
APP	🔿 Platinum	O Copper	🗹 Known Protein	smRNA	🗹 High	ORF	🗹 Exon	Ves Yes
	🔿 Gold	🔘 Iron	🗹 Hypothetical Protein	🔽 trna	Low	S'UTR	🗹 Intron	🗹 No
NON	🔘 Silver	🔘 Silicon	🗹 rRNA	🔲 Intergenic A	🔲 Undefined	S'UTR		
8	🔿 Aluminum		🗹 snoRNA	📃 Intergenic B				
			🗹 snRNA	📃 Intergenic C				
LGR.								
EX	and the second	e SAGE TAGS	in the genome by: ?	Step 6 Input Data Upload text file			The Gene r	
RIES	Gene Name				Browse		format (inp textarea bo	x)
BRA	 Genome Fra Chromosom 						should be l	ike:
Ξ.	O Full Genome			OR Fill in Gene Na	ne list	1001	YFR016C YFT1	
믳	O rui Genome					~	- IFTT	
Ida								
S NU						~		
ARIE								
IBRU	Output Display O	ptions ?						
-	Show 50	Sort by	Confidence 🔽	Descending 🔽			S	ubmit Reset
			Pontificia Unive	ersidad Católica de Cl	nile MBL Tern	ns of Use		
			©2	2006 SAGExplore, All (rights reserved.			

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Explore
	Search Poter	tial TAGs in	a Genome					
LOR	This item allows	to extract the p	potential SAGE TAGs from t	he entire or regions o	f a genome.			
EXE	Step 1 Organi	iem 2	Step 2 Anchoring-Ta	gging Enzyme Pair	? Step 3 Odd	de ratio for d	confidence c	lass assignments 👔
GENOME EXPLORE	Saccharomyces		NlaIII - BsmFI	gging chaynic i dh	5 🗸		confidence c	
GEN	Cardeenaren 1969		Midili - Domit -					
	Step 4 TAG ca	ategories and	genomic mapping conte	exts to display: 🕐				
S.	TAG Class		Genomic Type		TAG Confidence	TAG Location	n	Internal Poly-A next ?
APP	🔘 Platinum	O Copper	🗹 Known Protein	🗹 smRNA	🗹 High	ORF	🗹 Exon	🗹 Yes
E.	O Gold	🔘 Iron	🗹 Hypothetical Protein	🗹 tRNA	Low	3'UTR	🗹 Intron	🗹 No
N.	O Silver	🔘 Silicon	🗹 rRNA	🔲 Intergenic A	🔲 Undefined	S'UTR		
8	O Aluminum		🗹 snoRNA	🔲 Intergenic B				
			🗹 snRNA	🔲 Intergenic C				
5	Euploy	A PACE TACA	in the genome by: ?	Step 6 Input Data	ি			
EX	Step 5 Explor	C SAGE TAUS	in the genome by.	Upload text file	· 🖽		The Gene r	
RIE	Gene Name	ament			Browse		format (inp textarea bo	x)
BRA	O Chromosom	- T					should be l	ike:
=	O Full Genome			OR Fill in Gene Na	me list	~	YFRO15C YPT1	
2	O rai conome							
APP								
S N						~		
ARIE		the second second		C.				
E B	Output Display O	ptions ?						
	Show 50	Sort by	Confidence 💌	Descending 💌				ubmit Reset
				ersidad Católica de Cl		ns of Use		
			02	2006 SAGExplore, All	rights reserved.			

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Explore
	Search Poten	itial TAGs in	a Genome					
LOR	This item allows	to extract the p	otential SAGE TAGs from t	he entire or regions o	f a genome,			
EX	Step 1 Organi	ism 2	Step 2 Anchoring-Ta	gging Enzyme Pair	? Step 3 Od	ds ratio for o	onfidence c	lass assignments ?
GENOME EXPLORE	Saccharomyces		NlaIII - BsmFI	gging cite/inc i di	5 🗸			
GEN								
	Step 4 TAG ca	ategories and	genomic mapping conte	exts to display: ?				
S.	TAG Class		Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next ?
A P P	🔘 Platinum	🔘 Copper	🗹 Known Protein	smRNA	🗹 High	ORF	🗹 Exon	Ves Yes
E N	O Gold	O Iron	🗹 Hypothetical Protein	🗹 trna	Low	S'UTR	🗹 Intron	🗹 No
N.	🔿 Silver	🔘 Silicon	🗹 rRNA	🔲 Intergenic A	🔲 Undefined	S'UTR		
8	O Aluminum	All	🗹 snoRNA	🔲 Intergenic B				
			🗹 snRNA	🔲 Intergenic C				
	Fueles	- CACE TAC-	is the second buy 🗵	Step 6 Input Data	. [9]			
EX	and the second	e SAGE TAGS	in the genome by: ?	Step 6 Input Data Upload text file			The Gene r	
RIES	 Gene Name Genome Fra 				Browse		format (inp textarea bo	x)
BRA	Chromosom	- T					should be l	ike:
Ξ.	O Full Genome			OR Fill in Gene Na	me list		YFR016C YPT1	
2	O rail octionite	·						
APPI								
S M						~		
ARIE								
LIBR.	Output Display Op	ptions ?						
	Show 50	Sort by	Confidence 💌	Descending 🔛				ubmit Reset
				ersidad Católica de Cl		ns of Use		
			©2	2006 SAGExplore, All	rights reserved.			

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Explore
W	Search Poten	tial TAGs in	a Genome					
PLOF	This item allows	to extract the p	otential SAGE TAGs from t	he entire or regions o	f a genome.			
	Step 1 Organi	sm ?	Step 2 Anchoring-Ta	gging Enzyme Pair	? Step 3 Odd	ds ratio for o	onfidence c	lass assignments ?
GENOME EXPLORE	Saccharomyces		NlaIII - BsmFI 💌		5 🗸			
B								
	Step 4 TAG ca	itegories and	genomic mapping conte	exts to display: 🕐				
PING	TAG Class		Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next?
IAP	🔘 Platinum	O Copper	🗹 Known Protein	smRNA	🗹 High	ORF	🗹 Exon	🗹 Yes
ų.	O Gold	O Iron	🗹 Hypothetical Protein	🗹 tRNA	Low	S'UTR	🗹 Intron	🗹 No
R	O Silver	O Silicon	🗹 rRNA	🔲 Intergenic A	🔲 Undefined	S'UTR		
9	🔘 Aluminum		🗹 snoRNA	🔲 Intergenic B				
			🗹 snRNA	🔲 Intergenic C				
5	Euglan	- CACE TACA	in the genome by: ?	Step 6 Input Data				
EX	and the second	e sage lags	in the genome by: [1]	Upload text file			The Gene r	
RIES	Gene Name Gene See				Browse		format (inp textarea bo	x)
BRA	 Genome Fra Chromosom 	7.5.5.5.5.5					should be l	ike:
Ξ.	O Full Genome			OR Fill in Gene Na	ne list	-	YFR015C YPT1	
9	O Tall Genome						IIII	
Ida								
S NU						~		
ARIE				1.2				
BR	Output Display Op	tions ?						
-	Show 50	Sort by	Confidence 💌	Descending 🔽			S	ubmit Reset
				ersidad Católica de Cl		ns of Use		
			©2	2006 SAGExplore, All	rights reserved.			

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Explore
W	Search Poten	tial TAGs in	a Genome					
PLOF	This item allows	to extract the p	otential SAGE TAGs from t	he entire or regions o	^f a genome.			
EX	Step 1 Organi	sm ?	Step 2 Anchoring-Tag	gging Enzyme Pair	? Step 3 Odd	ls ratio for o	onfidence c	lass assignments ?
GENOME EXPLORE	Saccharomyces		NIaIII - BsmFI 💌		5 🗸			
GE								
	Step 4 TAG ca	tegories and	genomic mapping conte	xts to display: ?				
PING	TAG Class		Genomic Type	_	TAG Confidence	TAG Location		Internal Poly-A next?
NAP	O Platinum	O Copper	Known Protein	smRNA	High	ORF	🗹 Exon	Yes
닅	O Gold	O Iron	Hypothetical Protein	trna	Low	3'UTR	🗹 Intron	🗹 No
R.	O Silver	O Silicon	🗹 rRNA	Intergenic A	Undefined	S'UTR		
	O Aluminum		SNORNA snoRNA	📃 Intergenic B				
2			🗹 snRNA	🔲 Intergenic C				
P.	Step 5 Explor	e SAGE TAGE	in the genome by: ?	Step 6 Input Data	2			
S EX	 Gene Name 	c shut mus	in the genome by.	Upload text file			The Gene r format (inp	
IRIE	Genome Fra	ament			Browse		textarea bo	x)
IBR/	O Chromosom	T		OR Fill in Gene Na	no list		should be l	ike:
-	O Full Genome			OK FIII III Gene Na	ne list	~	YFRO15C YFT1	
NG.							-	
APP								
ES						1		
UARI				ita -				
E.	Output Display Op	and a second						
	Show 50	Sort by	Confidence 💌 🛛	Descending 💌			LSU	ubmit Reset
				ersidad Católica de Cl		ns of Use		
			02	006 SAGExplore, All 1	ights reserved.			

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

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Explore
ш	Search Poten	ntial TAGs in	a Genome					
PLOF	This item allows	to extract the p	otential SAGE TAGs from th	ne entire or regions o	f a genome.			
GENOME EXPLORE	Step 1 Organi Saccharomyces	ism ? s cerevisiae 🗸	Step 2 Anchoring-Tag NlaIII - BsmFI 💌	gging Enzyme Pair	Step 3 Odd 5 ✓	ds ratio for (onfidence c	lass assignments ?
	Step 4 TAG ca	ategories and	genomic mapping conte	sts to display: 🙎				
2	TAG Class		Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next ?
Idde	O Platinum	O Copper	🗹 Known Protein	smRNA	V High	ORF	🗹 Exon	Ves
	O Gold	O Iron	🗹 Hypothetical Protein	TRNA	Low	S'UTR	🗹 Intron	🔽 No
NON	🔿 Silver	🔿 Silicon	🗹 rRNA	🔲 Intergenic A	Undefined	S'UTR		
98	🔿 Aluminum	All	🗹 snoRNA	🔲 Intergenic B				
w			🗹 snRNA	🔲 Intergenic C				
RARIES MAPPING LIBRARIES EXPLO	 Gene Name Genome Fra Chromosom Full Genome 	igment ie 9	in the genome by: ?	Step 6 Input Data Upload text file OR Fill in Gene Nat	Browse	2	The Gener format (inp textarea bo should be l ACT1 YFR016C YPT1	ut file or ox)
LIB.	Output Display Op Show 50	Sort by	Confidence 💌 [Descending 🔽				ubmit Reset
				ersidad Católica de Cl 006 SAGExplore, All		ns of Use		

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Explore
2	Search Poten	itial TAGs in	a Genome					
PLOF	This item allows	to extract the p	otential SAGE TAGs from t	he entire or regions o	f a genome.			
EEX	Step 1 Organi	ism ?	Step 2 Anchoring-Tag	gging Enzyme Pair	? Step 3 Odd	ls ratio for o	onfidence c	lass assignments ?
GENOME EXPLORE	Saccharomyces	; cerevisiae 🗸	NIaIII - BsmFI 💌		5 🗸			
	Step 4 TAG ca	ategories and	genomic mapping conte	exts to display: 🕐				
N.	TAG Class		Genomic Type		TAG Confidence	TAG Location	1	Internal Poly-A next ?
IAP	🔘 Platinum	O Copper	🗹 Known Protein	SmRNA	🗹 High	ORF	🗹 Exon	Ves Yes
-	O Gold	O Iron	🗹 Hypothetical Protein	🗹 trna	Low	3'UTR	🗹 Intron	🗹 No
No.	O Silver	🔿 Silicon	🗹 rRNA	🔲 Intergenic A	🔲 Undefined	S'UTR		
9	O Aluminum	All	🗹 snoRNA	🔲 Intergenic B				
#			🗹 snRNA	🔲 Intergenic C				
PLOF	Step 5 Explor	A SACE TACE	in the genome by: 👔	Step 6 Input Data	2			
SEX	Gene Name	C SHUE THUS	in the genome by.	Upload text file			The Gene r format (inp	
RIE	Genome Fra	ament			Browse		textarea bo	x)
IBR/	O Chromosom			OR Fill in Gene Na	nalist		should be l	ike;
-	O Full Genome			UK FIII III Gelle Nai	nenst	~	YFRO15C YPT1	
BN	-						-	
IAPP								
IES N						~		
RAR	Output Display Op	ptions ?						
1	Show 50	Sort by	Confidence 💌 🛛	Descending 🔽				ubmit Reset
		00100)		bootoniding in				
			Poptificia Unive	ersidad Católica de Cl	ile MBL Term	of lise		
				2006 SAGExplore, All I		13 01 030		
_								

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Explore
	Search Poten	ntial TAGs in	a Genome					
PLOF	This item allows	to extract the p	otential SAGE TAGs from t	he entire or regions o	^f a genome.			
EEX	Step 1 Organi	ism ?	Step 2 Anchoring-Ta	gging Enzyme Pair	? Step 3 Odd	ls ratio for	confidence c	lass assignments ?
GENOME EXPLORE	Saccharomyces		NlaIII - BsmFI 💌		5 🗸			
9								
		ategories and	genomic mapping conte	exts to display: ?				
NId	TAG Class	0.0	Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next ?
M	O Platinum	O Copper	Known Protein	smRNA	High	ORF	🗹 Exon	Yes
¥	O Gold	O Iron	Hypothetical Protein	✓ tRNA	Low	3'UTR	🗹 Intron	✓ No
Ĩ.	O Silver	 Silicon All 	rrna	Intergenic A	Undefined	S'UTR		
<u> </u>	Aldinindin	I All	SNORNA	Intergenic B				
쁥			🗹 snRNA	📃 Intergenic C				
E.	Step 5 Explor	e SAGE TAGS	in the genome by: ?	Step 6 Input Data	?			
3 5	(Gene Name			Upload text file			The Gene r format (inp	
ARIE	O Genome Fra	igment			Browse		textarea bo should be l	
IBR	O Chromosom	ie		OR Fill in Gene Na	ne list		ACT1 YFR016C	
-	O Full Genome	•				~	YPT1	
Na la							1	
IAPS								
8						~		
RAR								
=	Output Display Op	and a second	Confidence 💌 🛙	Deserved to a state				
	Show 50	Sort by	Confidence 💌 🛛	Descending 🔽				ubmit Reset
				ersidad Católica de Cl 2006 SAGExplore, All i		ns of Use		
			02	.000 SAGEXPIORE, All I	ignes reserved.			

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

													G	enon	ie t	×
		Potential Tags in shows a detail outpu					tiple links t	o impor	tant ir	nformatio	n.					
Sho	w 5	io 🔽										Down	load all Results	Grap	ohic	al
The	re are	28,948 records tha	t matche	d the qu	ery.											
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	Sy <i>s</i> Name	GC	тр	D
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W		i	â
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	a
з	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	A
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	đ
5	Hi	C AT GT AT AT AG A A A	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	A
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	đ
7	Hi	CATGTOGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B		i	A
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFV	6	1	31966	+	GDH3	YAL062W		i	a
9	Hī	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W		i	A
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFV	4	1	32477	+	GDH3	YAL062W		i	A
11	Hī	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	з	1	32590	+	GDH3	YAL062W		i	A
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFV	2	1	32899	+	GDH3	YAL062W		i	đ
13	Hī	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	A
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	A
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	A
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	A
17	Hī	CATGTEGEGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	A
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	A
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	2
20	Hi	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	đ
21	Hi	CATGATTGTGATTG	4	0.863	D+	ORE	OREdu	4	1	34698	1	NΔ	Y 81 86 1W			Le.

Query Results: Typical output of the Genome Explore Form.

													G	enome Expl
Sea	arch	Potential Tags in	n a Geno	ome: Re	esul	ts								
This	page	shows a detail output	ut table o	f your qu	Jery	with mult	iple links t	o import	ant i	nformatio	n.			
	-											All rest of the local division of the local		-
Sho	w 5	0										Down	load all Results	Graphical Vi
The	ro aro	28,948 records tha	t matcha	d the qui	-									
ine		20,940 records the	ic matche		51 9 1									
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS
1	Hī	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W	I AI
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W	1 AI
з	Hī	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W	ES 1
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W	ES I
5	HT	C AT GT AT AT AG A A A	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W	I AI
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B	1 AI
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B	E 1 83
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W	1 A
9	Hī	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W	ES I
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W	1 AI
11	Hī	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	з	1	32590	+	GDH3	YAL062W	I AI
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W	I AI
13	Hī	CATGTCGGTAATTA	1	0,863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W	i a
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W	i Ag
15	Hī	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W	i a
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W	i Ag
17	Hī	CATGTGGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W	i AT
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W	i Au
19	Hī	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W	i AT
20	Hi	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W	1 AI
21	Hi	CATGATTGTGATTG	4	0.863	D+	ORE	OREdu	4	-1	34698	1	NA	YAL061W	

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

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

													G	enome Expl
		Potential Tags in shows a detail outpu					iple links t	o import	ant ir	nformatio	n.			
Show	v 5	0 🖌										Down	load all Results	Graphical Vi
There	e are	28,948 records tha	t matche	d the qu	ery.									C
N	тс	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W	I AI
2	Hi	C AT G AT AT A AT A AC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W	1 AI
з	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W	1 A
4	Hi	CATGTGCAAATCAG	1	0,048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W	1 A
5	Hī	C AT GT AT AT AG A A A	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W	i AT
6	ні	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B	1 A
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B	📑 🚺 🔠
8	ні	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W	i &
9	Hī	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W	1 A
10	ні	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFV	4	1	32477	+	GDH3	YAL062W	1 A
11	Hī	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	з	1	32590	+	GDH3	YAL062W	1 AI
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W	1 A
13	Hī	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W	1 A
14	ні	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W	1 A
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W	1 A
16	ні	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W	i a
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W	I A
18	ні	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W	IS 1
19	Hİ	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W	IS I E
20	ні	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W	IS I EI
21	HT	CATGATTGTGATTG	4	0.863	D+	ORE	OREdu	4	1	34698	+	NA	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.

Sho	w :	50 💌										Down	ioad all Results	Grap	hica	11
The	re are	e 28,948 records that	t matche	d the qu	ery.											
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Star	StdName	SysName	GC	то	0
1	Hî	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W		i	A
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	A
з	Hī	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	A
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	A
5	Hī	C AT GT AT AT AGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	A
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	A
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B		i	A
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFV	6	1	31966	+	GDH3	YAL062W		i	A
9	Hī	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFV	5	1	32469	+	GDH3	YAL062W		i	A
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFV	4	1	32477	+	GDH3	YAL062W		i	A
11	Hī	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFV	з	1	32590	+	GDH3	YAL062W		i	A
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFV	2	1	32899	+	GDH3	YAL062W		i	A
13	Hi	CATGTCGGTAATTA	1	0,863	Pt	UTR3	ORFV	1	1	33100	+	GDH3	YAL062W		i	A
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	A
15	Hī	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	A
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	A
17	Hī	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	A
18	Hi	CAT GAAAGAAAGT A	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	A
19	Hî	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	A
20	Hi	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	AC
21	LIT	CATGATTGTGATTG	4	0.963	D+	ORE	OREdu	4	1	34698	+	NΔ	YAL061W		1	Te

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

														G	enome Exp
Sear	rch I	Potential Tag	s in a	a Gen	ome: Re	esul	ts								
This p	page	shows a detail o	utput	table o	of your qu	ery	with mult	tiple links to	impor	tant i	nformation	1.			
Show	, 5	0 💌											Down	ioad all Results	Graphical V
There	e are	28,948 records	that r	matche	ed the que	ery.									
N 1	TC	Seq	040	Explo										y <i>s</i> Name	GC TD DS
1 1	Hī	CATGACCTAC	эны	схрю	ne									11069W	1 AI
2 1	Hi	CATGATATAA	(Income of				or env							11066W	1 A
3 1	Hi	CATGTTATCT	Dow	nload	I All Res	sult	5							11066W	1 AI
4 1	ні	CATGTGCAAA												1066W	I 63
5 1	Hī	C AT GT AT AT A	SAC		DE 127	2507	2006	May-18.tar						11066W	1 ei
6 1	Hi	CATGTTGGAT	SAG	EAPL	JRE-127.	5507	-2006-1	na)-ioilai	.yz					L064W-B	i 81
7 1	Hi	CATGTCGTGT			en	84								L064W-B	1 A
8 1	ні	CATGAGAGAA	Note	: This	file will	stay	at this	site for 5 l	nrs.					1L062W	I 63
9 1	Hī	CATGGACGCA												1062W	1 ei
10 1	ні	CATGTGAGCA												11062W	1 ei
11	Hī	CATGGGTTCTACA	c.	T	0.048	Ρt	OKF	OKEV	3	Т	32390	Ŧ	GDH3	TAL062W	1 AT
12 1	ні	CATGGTGGCTGAC	G	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W	1 A
13 1	Hī	CATGTCGGTAATT	A	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W	i AT
14 1	Hi	CATGAGTACACAG	A	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W	1 ei
15 1	Hī	CATGAGATTAGTC	A	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W	1 AT
16 1	ні	CATGCAATTAGAG	т	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W	1 A
17 1	Hī	CATGTGGGGCCAT	с	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W	1 AI
18 H	ні	CATGAAAGAAAGT	A	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W	1 A
19 1	Hī	CATGTGCTACACA	c	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W	1 AI
20 1	ні	CATGAAGCTGATA	A	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W	I I AI
21 1		CATGATTGTGATT	c.	4	0.863	D+	ORE	OREdu	84	4	34698	100	NΔ	YAL061W	

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

													G	enon	ne t	хp	R
		Potential Tags in shows a detail outpu					tiple links t	o impor	tant ir	nformatio	n.						
Sho	w 5	io 🖌										Down	load all Results	Grap	hic	al V	ł
The	re are	28,948 records tha	it matche	d the qu	ery.												
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	то	DS	
1	Hī	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W		i	AT	
2	ні	CATGATATAATAAC	1	0,021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	AT]
з	Hī	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	AT	1
4	ні	CATGTGCAAATCAG	1	0,048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	AT	
5	Hī	C AT GT AT AT AGAAA	1	0,863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	AT	-
6	Hi	CATGTTGGATAGAC	4	0.021	Pt	UTR5	OREdu	4	1	11993	+	N. A.	YA1064W-B		1	AI	1
7	Hī	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B		i	AT	
8	н	CAIGAGAGAACIGA	1	0.018	PC	OKF	OKEV	ь	T	31366	+	GDH3	TAL002W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W		i	AT	
10	Hi	CATGTGAGCAACGT	1	0,021	Pt	ORF	ORFV	4	1	32477	+	GDH3	YAL062W		i	ÂŢ	
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFV	з	1	32590	+	GDH3	YAL062W		i	AT CG	
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFV	2	1	32899	+	GDH3	YAL062W		i	ĉĞ	
13	Hi	CATGTCGGTAATTA	1	0,863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	ĉŢ	
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	
16	Hi	CATGCAATTAGAGT	1	0,018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	ĉŢ	
17	Hī	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	ĉĞ	
19	Hī	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	AT CG	
20	Hi	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	AT CG	
21	Hi	CATGATTGTGATTG		0.863	D+	ORE	OREdu		1	34698	+	NΔ	YA1061W	-	1	AT	ĺ

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

	w 5	io 💌										Down	ioad all Results	Gra	phic	al V	R
Гhei	re are	28,948 records tha	it matche	d the qu	ery.												3
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Star	StdName	SysName	GC	то	DS	
1	HI	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W			ĉŝ	
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	AT CG]
з	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	AT]
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	AT CG]
5	Hi	C AT GT AT AT AGAAA	1	0,863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	AT]
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	ÂŢ]
7	Hi	CATGTEGTGTATTE	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B		i	AT]
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFV	6	1	31966	+	GDH3	YAL062W		i	AT]
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFV	5	1	32469	+	GDH3	YAL062W		i	AT]
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W		i	AT]
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	з	1	32590	+	GDH3	YAL062W		i	AT	
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W		i	AT]
13	Hī	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	AT	
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	1
16	Hi	CAT GCAATT AGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	AT CG	
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	ĺ
18	ні	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	AT	
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	AT	-
20	Hi	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	AT	T
21	1.1+	CATGATTGTGATTG	104	0.963	D+	ORE	OREdu	<u></u>	4	34698	194	NΔ	Y 41 05 1W			AT	ł

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

Sho		50 🔽										Down	load all Results	Gra	abire	31 M	Tota
SHO	w											DOWN	ivau all Results	ena	onner	100.4	
Гhе	re are	28,948 records tha	t matche	d the que	ery.											2	N
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Ste	StdName	SysName	GC	то	DS	
1	Hī	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W		i	AT	Į
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	AT	1
з	Hī	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	AT	
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	AT	
5	Hī	C AT GT AT AT AG A A A	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	AT	Ē
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	AT	Ē
7	Hi	CATGTOGTGTATTC	1	0.048	Pt	ORF	ORFdu	З	1	12146	+	N.A.	YAL064W-B		i	AT	Ē
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFV	6	1	31966	+	GDH3	YAL062W		i	ÂŢ	
9	Hī	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFV	5	1	32469	+	GDH3	YAL062W		i	AT	Ē
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFV	4	1	32477	+	GDH3	YAL062W		i	AT	Ē
11	Hī	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	з	1	32590	+	GDH3	YAL062W		i	AT	Ē
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W		i	AT	
13	Hī	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	Ē
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	AT	
15	Hī	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	Ī
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	AT	
17	HÌ	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	Ē
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	AT	
19	HÌ	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	AT	Ī
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	AT	Ī
21	LIT	CATCATTCTCATTC	4	0.963	D+	ORE	OREdu	4	1	34698	+	NΔ	Y 41 05 1W			AT	E

Query Results: These 6 columns contain linked fields.

	_													G	enon	ne t	Expl	ore
2	Sea	arch	Potential Tags in	n a Geno	ome: Re	esul	ts											
GENOME EXPLORE	This	page	shows a detail outp	ut table o	f your qu	Jery	with mult	tiple links t	o import	ant ir	nformatio	n.						
	Cha												Design	load all Results	-	altica	al Vi	-
	Sho	W	50										LIGHT	ioau all Results	Gra	anne		
	The	re are	28,948 records that	at matche	d the que	ery.												Nex
	N	тс	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Star	StdName	SysName	GC	то	DS	BI
1	1000	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W		i	ÂŢ	
	2	ні	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	ÊĞ	
I	з	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	AT	
1	4	ні	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	ÊĞ	
-	5	Hi	C AT GT AT AT AGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	ÂŢ	
	6	ні	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	ĉŢ	m
	7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B		i	AT	
I	8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFV	6	1	31966	+	GDH3	YAL062W		i	ÂŢ	
	9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W		i	AT	
	10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W		i	AT CG	
	11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFV	з	1	32590	+	GDH3	YAL062W		i	AT	
1	12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W		i	AT	m
	13	Hi	C AT GT C G GT A ATT A	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	
	14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	AT	
	15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	
	16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	AT	
	17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	I
	18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	AT	
	19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	AT	
	20	Hi	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	AT CG	
																	Land I	

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.

_														G	lenon	ne t	Expl	ore
S	ea	irch	Potential Tags in	n a Geno	ome: R	esul	ts											
т	his	page	e shows a detail outp	ut table o	f your qu	Jery	with mul	tiple links t	o import	tant ir	nformatio	n.						
~	ho		50 🔽										Down	ioad all Results	Gra	ahie	allav	low.
2	110	w [3	50										- COMPANY	ioau an results	Gra	anne	-110-4	
т	her	re are	e 28,948 records tha	at matche	d the qu	ery.												Nex
	N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	10	DS	BI
	0	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W		i		
	2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YALOGOW		i		
	3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YALOSSW		i	1.11	
	4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i		
	5	Hī	CAT GT AT AT AGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i		
	6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i		
	7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B		i	-	
1	8	ні	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W		i		
	9	Hī	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W		i	ÂŢ	
1	LO	ні	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W		i	ÂŢ	m
1	11	Hī	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFV	з	1	32590	+	GDH3	YAL062W		i	AT	
1	12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFV	2	1	32899	+	GDH3	YAL062W		i	ÂŢ	m
1	13	Hī	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	
1	14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	ÂŢ	
1	15	Hî	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	
1	16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	AT	I
1	17	Hī	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	
1	18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	ÂŢ	
1	19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	ÂŢ	
2	20	Hi	CAT GAAGCT GAT AA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i		

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.

Quick	Search:	Submit	Site Map Full Search Helj	p <u>Contact SGD</u> <u>Hor</u>	ne
Community Info Sub	omit Data <u>BLAST</u>	Primers PatMatch	Gene/Seq Resources	Advanced Search	<u>Virtual Library</u>
		SSB1/YDL22	9W Summary		Help
Summary Locus History	Literature Gene Onto	ology Phenotype Inte	eractions Expression Protei	n	
Alternative single page fo	ormat				
SSB1 BASIC INFORM	ATION [<u>View Refere</u>	ences]		SSB1 RES	OURCES
Standard Name	SSB1 (see <u>Nomen</u>	clature conflict Note)		Click on map for	
Systematic Name	YDL229W			SGD ORF map 43000 to 48000	GBrowse
Alias	YG101 ¹			5'	$\longleftrightarrow \rightarrow $
Feature Type	ORF, Verified			YDL228C 57 ARS404	YDL230W YDL228C
Description	chaperone, function folding of newly-mac	de polypeptide chains; h phosphatase subunit	essociated molecular r Zuo1p; may be involved in member of the HSP70 Reg1p (2, 3, 4, 5, 6, 7, 8 and		ARS404
GO Annotations	SSB1 GO evidence	e and references		Literature Guide	View
Molecular Function	 <u>ATPase activity</u> (<u>II</u> <u>unfolded protein b</u>)	 Retrieve Sequence 	es	
Biological Process	 cotranslational pro- protein biosynthese 	otein folding (IDA) sis (IMP_IPL_TAS)		Genomic DNA	View

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

		Potential Tags in shows a detail outpu					tiplo lipks t	o import	tant ir	formatio				Senon	ne t	zxpi	Ure
Sho	-		ut table o	r your qu	Jery	with high	uple links (nonnado		Down	load all Results	Gra	phic	al V	iew
The	re are	28,948 records tha	it matche	d the qu	ery.												Ne:
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	то	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W		i	ÂŢ	
2	Hi	CATGAT AT AAT AAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	AT CG	
з	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	AT	I
4	Hi	CATGTGCAAATCAG	1	0,048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	AT	I
5	Hi	C AT GT AT AT AGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	AT	
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	ÂŢ	
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B		i	AT	
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W		i	AT	I
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W		i	AT	
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W		i	AT	I
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFV	з	1	32590	+	GDH3	YAL062W		i	AT	I
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W		i	AT	I
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	AT	
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	AT	
17	Hİ	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	AT	I
19	Hİ	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	AT	
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	AT CG	I
21	LIT	CATCATTCTCATTC	4	0 060	D+	ORE	OREdu	4	-	24690	1	N A	YAL061W			AT	TTT

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

Genomic Context

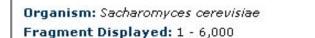
Organism: Sacharomyces cerevisiae





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

Genomic Context





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

Genomic Context

Organism: Sacharomyces cerevisiae

Fragment Displayed: 1 - 6,000



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



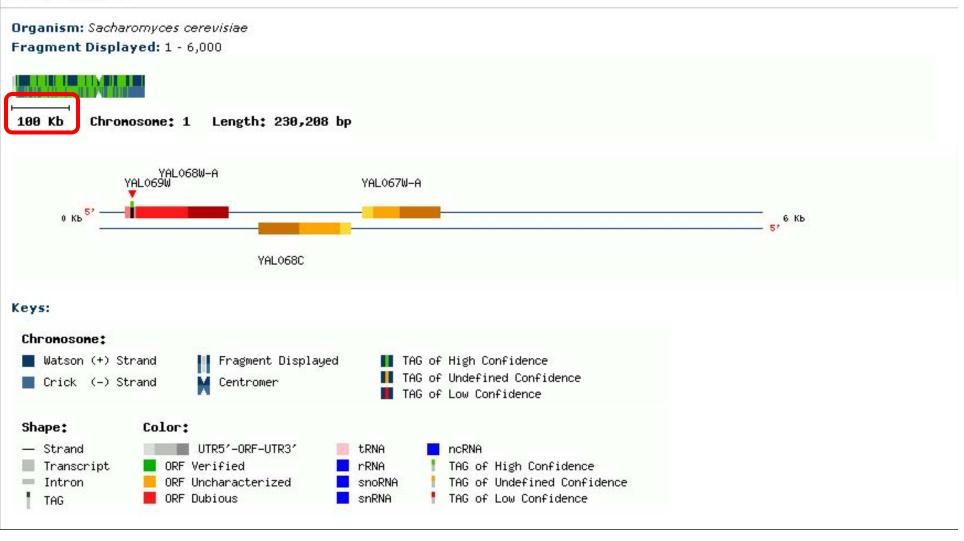
Genomic Context: The fragment of the chromosome being displayed is specified.

Genomic Context



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



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

Genomic Context



Fragment Displayed: 1 - 6,000

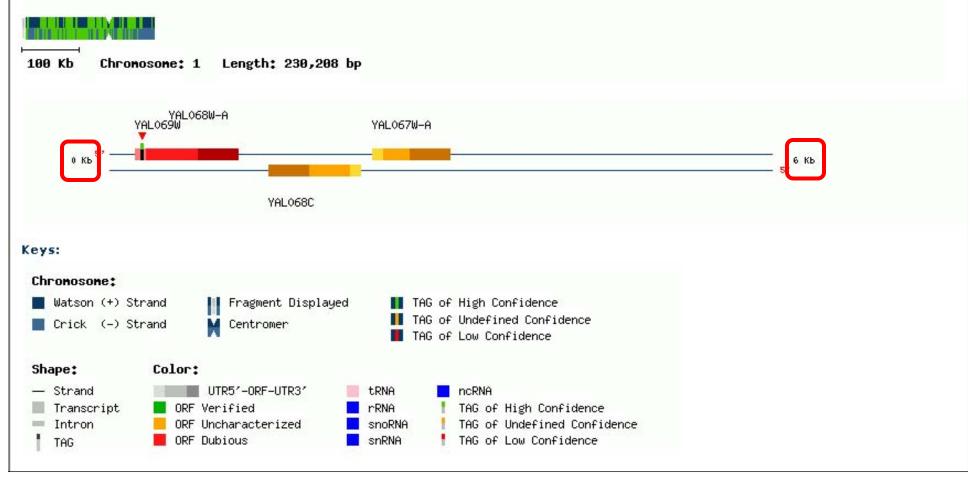


Genomic Context: The current chromosome number and size are given.

Genomic Context

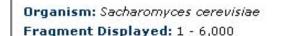
Organism: Sacharomyces cerevisiae





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

Genomic Context





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.

	w 5	50 💌										Down	load all Results	Gra	phic	al Vi	lew
Гhe	re are	28,948 records tha	t matche	d the qu	ery.												Ne>
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	то	DS	BI
1	Hī	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W		i	AT	
2	Hi	CATGAT AT AAT AAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	AT	I
з	Hī	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	AT	I
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	ÂŢ	m
5	Hī	C AT GT AT AT AGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	AT	
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	ĉŢ	I
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B		i	AT CG	
8	ні	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W		i	ÂŢ	m
9	Hī	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W		i	AT	
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W		i	AT	Ш
11	Hī	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	з	1	32590	+	GDH3	YAL062W		i	AT	
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W		i	AT	I
13	Hī	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	ÂŢ	m
15	Hī	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	I
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	AT	I
17	Hī	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	I
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	ĉŢ	I
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	ÂŢ	I
20	Hi	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	ĉŢ	
21	Hi	CATGATTGTGATTG	4	0.863	Dt	ORE	OREdu	-	1	34698	+	NΔ	YAL061W		11	AT	TTT

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

TAG Detail

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	Р			
Туре	Position	Distance	Poly-A Next?			
2	3	476	N			
Distance Poly-A	Length Poly-A	Feature Type	Feature Name			
0	0	ORFdu	Dubious			
Systemat	ic Name	Standa	rd Name			
YALO	59W	N.A.				

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

		Potential Tags in shows a detail outpu					tiple links t	o import	ant ir	nformatio	n.						
Sho	w s	io 💌										Down	ioad all Results	Gra	phic	al Vi	ew
The	re are	28,948 records tha	t matche	d the que	ery.												Next
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	то	DS	BI
1	Hī	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W		i	AT	
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	ÊĞ	
з	Hī	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	AT	
4	Hi	CATGTGCAAATCAG	1	0,048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	ÂŢ	
5	Hī	C AT GT AT AT AGAAA	1	0,863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	AT	
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	ÊĨ	
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B		i	AT .	
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFV	6	1	31966	+	GDH3	YAL062W		i	ÊĞ	
9	Hī	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W		i	AT	
10	Hi	CATGTGAGCAACGT	1	0,021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W		i	<u>AT</u>	
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFV	з	1	32590	+	GDH3	YAL062W		i	AT	
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W		i	AT	m
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	AT	m
15	Hī	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	
16	Hi	CATECAATTAGAET	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	AT CG	m
17	Hī	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	
18	ні	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	âŢ	m
19	Hī	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	AT	
20	ні	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	ÂŢ	
21	-	CATCATTCTCATTC	1	0.040	D+	ORE	OREdu	4	4	24690	1	N A	YA1061W			AT	[TTT]

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

SAGExplore

ATCG: UTR <u>ATCG</u>: TAG **ATG ... STOP**: ORF

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 downstrem the tag are provided. In this case, neighbor elements such as UTRs from other genes are also highlighted if present.

ATCG: UTR <u>ATCG</u>: TAG **ATG** ... **STOP**: ORF

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

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

														G	enon	ne E	Expl	ore
GENOME EXPLORE	This Sho	page w	Potential Tags in shows a detail outpu	ut table o	f your qu	Jery		tiple links t	o import	ant ir	nformatio	n.	Down	ioad all Results	Graj	hic	al Vi	
Ľ	The	re are	28,948 records tha	t matche	d the que	ery.												Next
2	N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Star	StdName	SysName	GC	то	DS	BI
APP	1	Hī	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W		i	AT	
E S	2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	AT	
NON	з	Hī	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	AT	
8	4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	AT CG	
-	5	Hī	C AT GT AT AT AG A A A	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	AT	
ORE	6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	AT	
E X PI	7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	З	1	12146	+	N.A.	YAL064W-B		i	AT	
ES	8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFV	6	1	31966	+	GDH3	YAL062W		i	ÂŢ	
RAR	9	Hī	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W		i	AT	I
LIBE	10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W		i	AT	
	11	Hī	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	з	1	32590	+	GDH3	YAL062W		i	AT	
PING	12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W		i	ÂŢ	
AAP	13	Hī	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	
Es	14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	AT CG	
UARI	15	Hī	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	
LIBE	16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	ÂŢ	
	17	Hī	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	
	18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	AT	
	19	Hī	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	AT	
	20	Hi	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	AT CG	

Query Results: A query to the BLAST server at the NCBI is launched with the previosuly 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.

Nucleotide	Protein	<i>translat</i> Translations	Retrieve results for an RID	
				-22
тс	ACCAGTGTTAGGGTCAAGA	ACAACTGCATCAATACC	GAAGAAGGGGGAATGAGGCAGA	
D26373			TGACCAGATGCGAACCAGATT	10 P
A DECEMBER OF THE OWNER OWNE			TTACCTATTTTTTCAGAGTAC	
E43366			ACCCAAGCAACGCAAAGATTT TCAACAAACGCAAAGCAGTTG	
	AUGAAIGAI III COAIGIA		I CARONARO CONARCONO I I C	
Choose a				
Choose a translation	ANSLATED query - PROT	EIN database <mark>[blastx]</mark>	×	
	ANSLATED query - PROT	EIN database <mark>[blastx]</mark>		
		EIN database <mark>[blastx]</mark>		
translation TR		EIN database <mark>[blastx]</mark>		
translation TR		EIN database <mark>[blastx]</mark>		
translation IR	n: To:	EIN database <mark>[blastx]</mark>		
translation TR et subsequence From hoose database nr	n: To:	EIN database [blastx]		
translation TR et subsequence From hoose database nr	n: To:			

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.

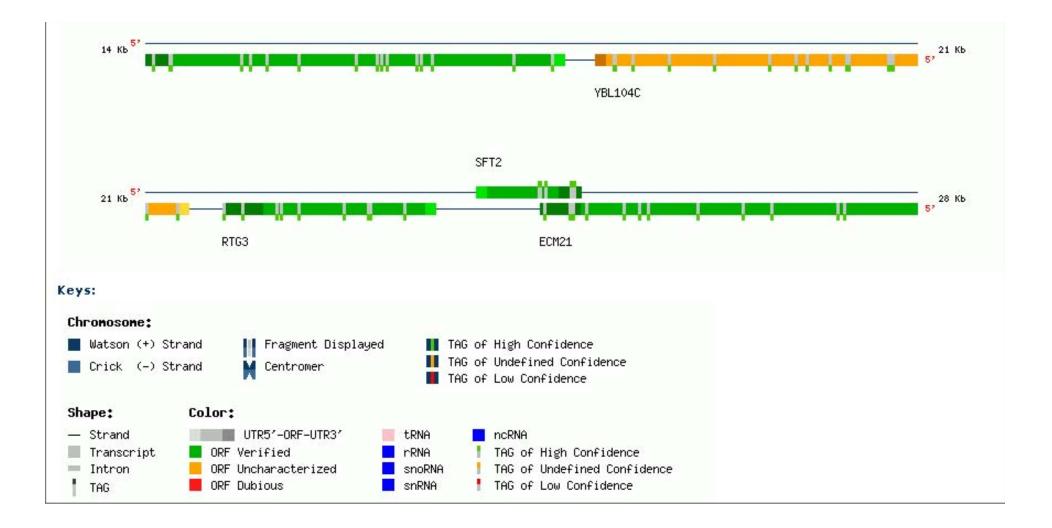
Sho	w [50 💌										Down	load all Results	Gra	hic	al Vi	ew
The	re ar	e 28,948 records tha	it matche	d the que	ery.												Ne
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	то	DS	B
1	HÌ	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	з	1	282	+	N.A.	YAL069W		i	AT	
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W		i	ÂŢ	I
З	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W		i	AT	I
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	з	1	10182	+	N.A.	YAL066W		i	AT	I
5	Hİ	C AT GT AT AT AG A A A	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W		i	AT	I
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B		i	ÂŢ	I
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	з	1	12146	+	N.A.	YAL064W-B		i	AT	
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W		i	ÂŢ	I
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W		i	AT	I
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W		i	ÂŢ	I
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	з	1	32590	+	GDH3	YAL062W		i	AT	
12	Hi	CATGGTGGCTGACG	1	0,140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W		i	ÂŢ	I
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W		i	AT	I
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W		i	ĉŢ	m
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W		i	AT	I
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W		i	ÂŢ	
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W		i	AT	
18	ні	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W		i	AT	m
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	з	1	34396	+	N.A.	YAL061W		i	AT	I
20	ні	CATGAAGCTGATAA	1	0,140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W		i	ÂŢ	m
21	LU1	CATGATTGTGATTG	4	0.863	Dt	ORE	OREdu	4	1	34698	+	NΔ	YAL061W			AT	TTT

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

SAGExplore

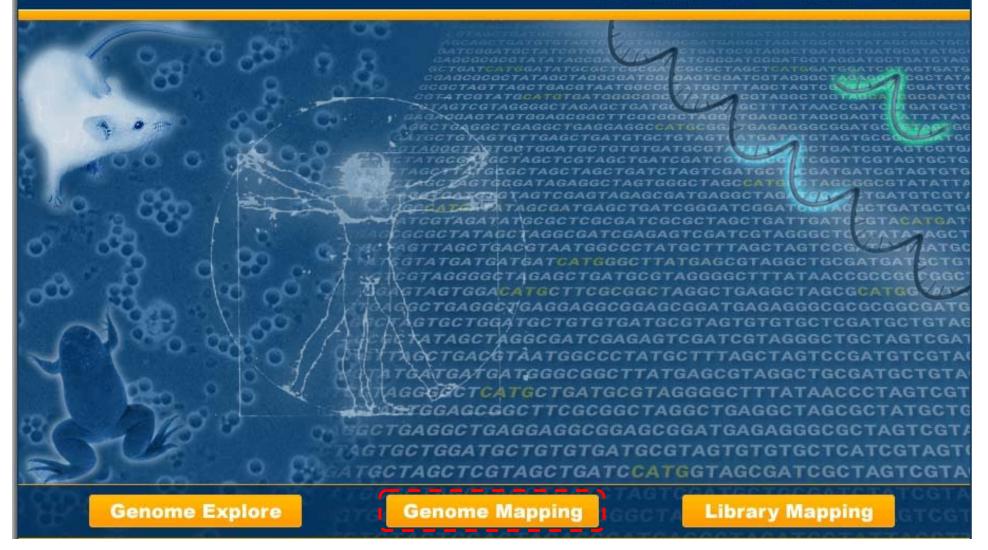
SAGExplo	re	
Graphical	View	
Organism	: Sacharomyces cei	revisiae
100 Kb	Chronosone: 1	Length: 230,208 bp
100 Kb	Chronosone: 2	Length: 813,178 bp
100 Kb	Chronosone: 3	Length: 316,616 bp
100 Kb	Chronosone: 4	Length: 1,531,916 bp
100 KD	cill unusune, 4	
100 Kb	Chronosone: 5	Length: 576,869 bp

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.



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

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD



II.- Tutorial Genome Mapping Module.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

							Genome Mapping
Map your TAC	Gs within a G	enome					
This section allo	ws to find TAGs	within a Genome.					
Step 1 Organi	ism ?	Step 2 Anchoring-Tag	ging Enzyme Pair	? Step 3 Od	ds ratio for	confidence c	lass assignments 🕐
Saccharomyces	s cerevisiae 💌	NlaIII - BsmFI 💌		5 🛩			
Step 4 TAG ca	ategories and	genomic mapping conte	xts to display: 🕐				
TAG Class		Genomic Type		TAG Confidence	TAG Locatio	n	Internal Poly-A next ?
O Platinum	O Copper	🗹 Known Protein	smRNA	High	ORF	Exon	Yes
O Gold	O Iron	🗹 Hypothetical Protein	🗹 trna	Low	3'UTR	🗹 Intron	No No
O Silver	O Silicon	🗹 rRNA	🗹 Intergenic A	🗹 Undefined	S'UTR		
O Aluminum		🗹 snoRNA	🗹 Intergenic B				
		🗹 snRNA	🗹 Intergenic C				
Step 5 Input Upload text fil OR Fill in TAG	Browse						
Output Display Op Show 50	ptions ? Sort by	Confidence 💌 🛙	escending 💌				ubmit Reset
			rsidad Católica de Cl 006 SAGExplore. All		ms of Use		

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

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Mapping
	Map your TA	Gs within a G	lenome					
2	This section allo	ws to find TAGs	within a Genome.					
GENOME EX	Step 1 Organ Saccharomyces		Step 2 Anchoring-Tag NlaIII - BsmFI 💌	jging Enzyme Pair	? Step 3 Odd	ds ratio for	confidence c	lass assignments ?
_	Step 4 TAG ca	ategories and	genomic mapping conte	xts to display: 🕐				
9N	TAG Class		Genomic Type		TAG Confidence	TAG Locatio	n	Internal Poly-A next ?
APP	🔘 Platinum	🚫 Copper	🗹 Known Protein	smRNA	🗹 High	🗹 ORF	Exon	🗹 Yes
	🔘 Gold	🔘 Iron	🗹 Hypothetical Protein	🗹 trna	Low	🗹 3'UTR	🗹 Intron	🗹 No
GENOME MAPPING	O Silver	🔘 Silicon	🗹 rRNA	🗹 Intergenic A	Undefined	🗹 S'UTR		
5	🔿 Aluminum		🗹 snoRNA	🗹 Intergenic B				
u.			🗹 snRNA	🗹 Intergenic C				
RIES MAPPING LIBRARIES EXPL	Step 5 Input Upload text fil OR Fill in TAG	Browse	k					
LIBRA	Output Display O Show 50	ptions ? Sort by	Confidence 💌 [Descending 💌			S	ubmit Reset
				rsidad Católica de Cl 006 SAGExplore, All		ns of Use		

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

-								Genome Mapping
		Gs within a G						
This :	section allo	ws to find TAGs	within a Genome.					
Step	1 Organi	ism ?	Step 2 Anchoring-Tag	iging Enzyme Pair	? Step 3 Od	ds ratio for	confidence c	lass assignments 🕐
Saco	charomyces	s cerevisiae 💌	NlaIII - BsmFI 💌		5 💌			
Step	TAG ca	ategories and	genomic mapping conte	xts to display: ?				
TAG	Class		Genomic Type		TAG Confidence	TAG Locatio	n	Internal Poly-A next ?
OF	latinum	🚫 Copper	📝 Known Protein	💌 smRNA	🗹 High	🗹 ORF	🗹 Exon	Ves
00	Gold	🔘 Iron	🗹 Hypothetical Protein	🗹 trna	Low	🗹 3'UTR	🗹 Intron	🗹 No
	Silver	O Silicon	🗹 rRNA	🗹 Intergenic A	🗹 Undefined	🗹 S'UTR		
	luminum	All	🗹 snoRNA	🗹 Intergenic B				
9			🗹 snRNA	🗹 Intergenic C				
a star	5 Input	Data 2						
	ad text fil							
		Browse						
	ill in TAG	lict						
	III III TAU	list		~				
				~				
Oute	ut Display Oj	ptions ?						
Show	-	Sort by	Confidence 🔽 🛛	Descending 🔽				ubmit Reset
Chiow	00	00.009		seconding 1			<u></u>	abrine Keset
			Poptificia Unive	rsidad Católica de Cl	bila I MRI I Torr	nc of Uca		
				006 SAGExplore, All		ns or use		
					and the second se			

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

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

							Genome Mapping
Map your TA	Gs within a G	enome					
This section allo	ws to find TAGs	within a Genome.					
Step 1 Organ Saccharomyce:	ism ? s cerevisiae 💌	Step 2 Anchoring-Tag NlaIII - BsmFI 💌	iging Enzyme Pair	Step 3 Od	ds ratio for	confidence c	lass assignments ?
Step 4 TAG c	ategories and	genomic mapping conte	xts to display: 🕐				
TAG Class		Genomic Type		TAG Confidence	TAG Locatio	n	Internal Poly-A next ?
🔘 Platinum	🚫 Copper	🗹 Known Protein	🗹 smRNA	III High	🗹 ORF	Exon	🕑 Yes
O Gold	🔘 Iron	🗹 Hypothetical Protein	🗹 trna	Low	🗹 3'UTR	🗹 Intron	Vo No
O Silver	🔘 Silicon	🗹 rRNA	🗹 Intergenic A	🗹 Undefined	S'UTR		
Aluminum		🗹 snoRNA	🗹 Intergenic B				
		🗹 snRNA	🗹 Intergenic C				
Step 5 Input Upload text fil OR Fill in TAG	le Browse						
Output Display O Show 50	ptions ? Sort by	Confidence 💌 [Descending 💌				ubmit Reset
			rsidad Católica de Cl 006 SAGExplore. All		ms of Use		

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

-							Genome Mapping
Map your TA	Gs within a G	enome					
This section allo	ws to find TAGs	within a Genome.					
Step 1 Organ Saccharomyces		Step 2 Anchoring-Ta NlaIII - BsmFI 💌	gging Enzyme Pair	? Step 3 Odd	ds ratio for	confidence c	ass assignments ?
	ategories and	genomic mapping conte	exts to display: 🥐				
TAG Class	-	Genomic Type	_	TAG Confidence	TAG Locatio	10.000	Internal Poly-A next ?
O Platinum	O Copper	Known Protein	smRNA	High	ORF	Exon	Yes
O Gold	O Iron	Hypothetical Protein	✓ tRNA	Low	3'UTR	Intron	Vo No
TAG Class Platinum Gold Silver Aluminum	O Silicon	🗹 rRNA	Intergenic A	Undefined	S'UTR		
Aluminum	 All 	snoRNA	Intergenic B				
		🗹 snRNA	🗹 Intergenic C				
Upload text fil	Browse						
OR Fill in TAG	list						
Output Display Of Show 50	ptions ? Sort by	Confidence 💌	Descending 💌				ubmit Reset
			ersidad Católica de Cl 2006 SAGExplore, All		ns of Use		

Step 4: The user can choose to map the experimental tags against a subset of genomic 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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

_								Genome Mapping
	Map your TA	Gs within a G	enome					
	This section allo	ws to find TAGs	within a Genome.					
GENOME EX	Step 1 Organ Saccharomyce:	ism ? s cerevisiae 💌	Step 2 Anchoring-Tag NlaIII - BsmFI 💌	gging Enzyme Pair	? Step 3 Odd	ds ratio for	confidence c	lass assignments ?
	Step 4 TAG ca	ategories and	genomic mapping conte	xts to display: 🕐				
2 No	TAG Class		Genomic Type		TAG Confidence	TAG Locatio	n	Internal Poly-A next ?
	🔘 Platinum	🚫 Copper	🗹 Known Protein	🗹 smRNA	🗹 High	🗹 ORF	🗹 Exon	Ves Yes
	🔘 Gold	🔘 Iron	🗹 Hypothetical Protein	🗹 tRNA	Low	🗹 3'UTR	🗹 Intron	🗹 No
ENOME MAPPING	🔘 Silver	🔘 Silicon	🗹 rRNA	🗹 Intergenic A	🗹 Undefined	🗹 S'UTR		
3	O Aluminum		🗹 snoRNA	🗹 Intergenic B				
			🗹 snRNA	🗹 Intergenic C				
LIBRARIES MAPPING LIBRARIES EXPLO	Step 5 Input Upload text fil OR Fill in TAG Output Display 0 Show 50	Browse		Descending M			<u></u> Si	Jbmit Reset
				rsidad Católica de Cl 006 SAGExplore, All		ns of Use		

Step 5: The user must provide a list of experimental tags to map against the genome-based annotation of virtual or potential tags. A text file can be uploaded or the data directly pasted into the textarea. The input format is explained in the help link for this step. Full tag sequences must be provided (ie. including CATG).

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

							Genome Mapping
Map your	TAGs within a (Genome					
This section	allows to find TAGs	; within a Genome.					
	ganism ? nyces cerevisiae 🔽	Step 2 Anchoring-Tag NlaIII - BsmFI 💌	iging Enzyme Pair	? Step 3 Odd	ds ratio for	confidence c	lass assignments ?
Step 4 TA	G categories and	genomic mapping conte	xts to display: 🕐				
TAG Class		Genomic Type		TAG Confidence	TAG Locatio	n	Internal Poly-A next ?
TAG Class	m 🔿 Copper	🗹 Known Protein	smRNA	III High	🗹 ORF	Exon	🗹 Yes
	🔘 Iron	🗹 Hypothetical Protein	🗹 trna	Low	🗹 3'UTR	🗹 Intron	Vo No
O Gold O Silver	🔘 Silicon	🗹 rRNA	🗹 Intergenic A	🗹 Undefined	🗹 S'UTR		
O Alumin	um 💿 All	🗹 snoRNA	🗹 Intergenic B				
		🗹 snRNA	🗹 Intergenic C				
Step 5 In Upload tes OR Fill in 7 Output Disp Show 50	TAG list		Descending V				ubmit Reset
511011 30	- Sole by		rescending T			<u>_</u>	
			rsidad Católica de Cl 006 SAGExplore. All		ns of Use		

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

								Genome Mapping
	Map your TA	Gs within a G	enome					
	This section allo	ws to find TAGs	within a Genome.					
GENOME EX	Step 1 Organ Saccharomyces	Arrest Arrest Arrest	Step 2 Anchoring-Tag NlaIII - BsmFI 💌	iging Enzyme Pair	? Step 3 Odd	ds ratio for	confidence c	lass assignments ?
-	Step 4 TAG ca	ategories and	genomic mapping conte	xts to display: 🕐				
	TAG Class		Genomic Type		TAG Confidence	TAG Locatio	n	Internal Poly-A next ?
	🔿 Platinum	🚫 Copper	🗹 Known Protein	🗹 smRNA	🗹 High	🗹 ORF	Exon	🗹 Yes
	O Gold	O Iron	🗹 Hypothetical Protein	🗹 trna	Low	🗹 3'UTR	🗹 Intron	🗹 No
GENOME	O Silver	🔿 Silicon	🗹 rRNA	🗹 Intergenic A	🗹 Undefined	🗹 S'UTR		
5	🔿 Aluminum	All	🗹 snoRNA	🗹 Intergenic B				
			🗹 snRNA	🗹 Intergenic C				
LIBRARIES MAPPING LIBRARIES LAFL	Step 5 Input Upload text fil OR Fill in TAG Output Display Of Show 50	le Browse		Descending				ubmit Reset
				rsidad Católica de Cl 006 SAGExplore, All		ms of Use		

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

Ma	n ur	our TAGs within	a Co	nome	· P.	oculte									поте Мар	
100																
Inis	sect	tion allows to find	TAGS	vitnin a	Ger	iome.										
Sho	ωĪ	50											Downloa	d all Results	Expression	
The	re ar	e 1,657 records t	hat ma	atched t	he c	uery.3	49 NIDs ou	t of 1,6	22	submitted	TAG	s were foun	d.			
N	тс	Seq	Freq	Odds	CI	LocD	LocT	TrPos	ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	1
1		CATGGTCAACAAAG	2		Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C		340	
	Un	CATGACACCACCAG	3		Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C		3010	
	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W		006	
	Un	CATGGCGCAGTTGG	5	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A		340	
	Un	CATGCTGCATCCTA	4	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C		006	
6	Un	CATGCAAAAGACTG	4	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W		12 0 13	
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.			1283	
8	Un	CATGTACACACACA	2	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i 21 m	340	
9	Un	C AT GGT AT AT GT GT	2	1,000	Fe	Int	int	0	2	236361	+	N.A.		i 🔠 🎹	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	i & 🛄	046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFV	2	2	478942	+	TEF2	YBR118W	i 🔠 🏛	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	i & 🔳	303	
13	Un	CATGTAAAAAAAAA	2	1,000	Fe	Int	int	0	2	622839	+	N.A.		i 🔠 🎹	640	
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	i & 🎹	600	
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	i 🔠 🏛	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		i & 🛄	9 17 0	
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	з	90077	+	N.A.	575		1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W		6 12 0	
19	Un	CATGTACATACATC	2	1,000	Al	UTR3	ORFV	1	4	99277	+	MRPL11	YDL202W		6 17 0	
1 m 1 m 1	Un	CATGATATCAAAAA	2	0.375	A	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	🛋 i 🔠 🎹	6 17 0	

Query Results: Typical output of the Genome Mapping Form.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

														Gei	поте Мар	opi
Maj	p yc	our TAGs within	n a Ge	enome	9: R	esults										
This	sect	tion allows to find	TAGS (within a	Ger	nome.										
Sho		50											Downlo	ad all Results	Expression	
3110	••• [30											- Comme		Expression	diada
Ther	re ar	e 1,657 records t	hat ma	atched t	he c	query.3	49 NIDs ou	t of 1,	622	submitted	TAG	s were found	±.			P
			1					1							in the second second second second second second second second second second second second second second second	
	TC	Seq	Freq	Odds	CI		LocT	TrPos		Ini	Str	StdName	SysName	GC TD DS BI	Cn	I
1		CATGGTCAACAAAG	2		Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C		340	
	Un	CATGACACCACCAG	3	1,000		Int	int,opORF	0	1	140213	+	N.A.	YAL005C		3010	
	Un	CATGGAGGAGATTT	2	1,239	Au	ORF	ORFdu	2	1	141074	+	N. A.	YAL004W		006	
	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	trna	1	1	166273	+	N.A.	tA(UGC)A		340	
5	Un	CATGCTGCATCCTA	4		Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C		006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W		12 0 13	
7	Un	CATGCACTTCAACT	20	1,000	Fe	Int	int	0	2	34908	+	N.A.	575		1283	
8	Un	CATGTACACACACA	2	1,239		UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W		340	
9	Un	CATGGTATATGTGT	2	1.000		Int	int	0	2	236361	+	N.A.			603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	З	2	478284	+	TEF2	YBR118W		046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W		61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C		303	
13	Un	C AT GT AAAAAAAAA	2	1,000	Fe	Int	int	0	2	622839	+	N.A.			640	
14	Un	CATGGCGTTTGAGG	2	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W		600	
15	Un	CATGCTCTGGTTCT	2	2,667	Al	ORF	ORFdu	З	2	704693	+	N.A.	YBR242W		340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.			9 17 0	
17	Un	CATGCACTTCAACT	20	1,000	Fe	Int	int	0	З	90077	+	N.A.			1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W		6 12 0	
19	Un	CATGTACATACATC	2	1,000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W		6 17 0	
00	Un	CATGATATCAAAAA	2	0.375	A	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	🖬 i 🔠 🎹	6 17 0	

Query Results: The total number of records that matched the query are reported. Also, the total number of unmatched tags (NIDs or Non-Identified Tags) out of the total number of submitted tags is given.

														Gei	поте Мар	ping
Ma	р у	our TAGs within	n a Ge	enome	:: R	esults										
This	s sec	tion allows to find	TAGS 1	within a	Ger	nome.										
_																
Sho	W	50											Downloa	ad all Results	Expression	Map
The	re a	re 1,657 records t	that ma	atched t	he r	werk 3		t of 1	622	submitted	TAG	s were foun	d			Next
1110		1,007 1000103 (ande me	100100		1001)			JEE	Sabinicea	ino	s more roan	u.			NOAC
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	Info
1	Un	CATGGTCAACAAAG	2	0,807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	🖹 🔝 🎞	340	17
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	i & 🎹	3010	-
з	Un	CATGGAGGAGATTT	2	1,239	Au	ORF	ORFdu	2	1	141074	+	N. A.	YAL004W	📑 🖬 🔠 🎹	006	
4	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	i & 🎹	340	-
5	Un	CATGCTGCATCCTA	4	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	🖬 🔝 🎹	006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	i & III	12 0 13	-
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.		📑 🖬 🔠 🎹	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i & 🎞	340	-
9	Un	C AT GGT AT AT GT GT	2	1.000	Fe	Int	int	0	2	236361	+	N.A.	575	📑 🖬 🚮 🎹	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	🖬 🖬 🖬 🎹	046	-
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	🖬 🖬 🖬	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	🖬 🔝 🎹	303	-
13	Un	CATGTAAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.	575	📑 🖬 🖬 🎹	640	
14	Un	CATGGCGTTTGAGG	2	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	i & 🛄	600	-
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	📑 🖬 🖬 🎹	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		📑 i 🔠 🎹	9 17 0	-
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	з	90077	+	N.A.	575	i 🗟 🏛	1283	17
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i 🗟 🏛	6 12 0	-
19	Un	CATGTACATACATC	2	1.000	Al	UTR3	ORFV	1	4	99277	+	MRPL11	YDL202W	i 🔠 🏛	6 17 0	
20	Un	CATGATATCAAAAA	2	0,375	Al	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	📰 🔝 🔳	6 17 0	-
823	121	0 MR C C C T T T O C C T T	14	1 000		ODE	ODE.	100	1.0	000500	- 197	00040	UDIADOW		45 40 0	

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.

64		un TACc mithis				o culto								Gei	поте Мар	эрн
		our TAGs within														
Ihis	sect	tion allows to find	TAGS	within a	Ger	nome.										
Shov	ωĒ	50 🔽											Downloa	nd all Results	Expression	м
	·· • • •															
Ther	re ar	e 1,657 records t	that ma	atched t	he d	query.3	349 NIDs ou	t of 1,	622	submitted	TAG	s were foun	d.			1
		10-1047-1	low							10-00-0					Frank Control of Contr	
N		Seq	Freq	Odds	CI		LocT	TrPos		Ini	Str		SysName	GC TD DS BI	Cn	1
1		CATGGTCAACAAAG	2		Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C		340	
	Un		3	1,000		Int	int,opORF	0	1	140213	+	N.A.	YALOOSC	Active Control of the second	3010	
	Un	CATGGAGGAGATTT	2		Au	ORF	ORFdu	2	1	141074	+	N.A.	YALOO4W		006	
	Un	CATGGCGCAGTTGG	5	1,000	A	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A		340	
	Un	CATGCTGCATCCTA	4		Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C		006	
	Un	CATECAAAAGACTE	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W		12 0 13	
	Un	CATGCACTTCAACT	20		Fe	Int	int	0	2	34908	+	N.A.			1283	
	Un	CATGTACACACACA	2		Au		ORFdu	2	2	119235	+	N.A.	YBL054W		340	
	Un	C AT GGT AT AT GT GT	2		Fe	Int	int	0	2	236361	+	N.A.			603	
10 1		CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	З	2	478284	+	TEF2	YBR118W		046	
11		CATGAGACAAACTG	2	0.402		ORF	ORFv	2	2	478942	+	TEF2	YBR118W		61 55 193	
12		CATGGAAATCCGGT	2		Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C		303	
13		C AT GT AAAAAAAAA	2	1,000		Int	int	0	2	622839	+	N.A.			640	
14		CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W		600	
15		CATGCTCTGGTTCT	2	2,667		ORF	ORFdu	3	2	704693	+	N.A.	YBR242W		340	
16 1		CATGCGTCAGTGTG	9	0,807		Int	int	0	2	812205	+	N.A.			9170	
17 1	Un	CATGCACTTCAACT	20	1,000		Int	int	0	з	90077	+	N.A.	575		1283	
18		CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W		6 12 0	
19 1	Un	CATGTACATACATC	2	1,000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W		6 17 0	
	Un	CATGATATCAAAAA	2	0.375	A	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	i & 🎹	6 17 0	

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

													Gei	поте Мар	ping
	your TAGs withi														
This se	ection allows to find	TAGS	within a	Ger	iome.										
Show	50											Downloa	ad all Results	Expression	Map
There	are 1,657 records	that m	atched t	he a	uery.3	49 NIDs out	of 1,	622	submitted	TAG	s were foun	d.			Ne
N TC	Seq	040	Fundar										TD DS BI	Cn	Inf
1 Ur	CATGGTCAACAAA	SAG	Explor	e									i 🔠 🎹	340	1.7
2 Ur	n CATGACACCACCA												i 🛃 🎹	3010	-
3 Ur	n CATGGAGGAGATT	Dow	nload	All	Result	ts							1 EI 🎹	006	
4 Ur	n CATGGCGCAGTTG												i & III	340	-
5 Ur	CATGCTGCATCCT			1000				57.000					1 EI 🎹	006	1.7
6 Ur	n CATGCAAAAGACT	SAG	EXPLO	(E-1	127350	17-2006-May	-18.t	ar.g	z				i & III	12 0 13	-
7 Ur	CATGCACTTCAAC		12.000 12		NUMBER	1000 Mar. 100							i 🔠 🎹	1283	
8 Ur	n CATGTACACACAC	Note	: This f	ile (will sta	y at this site	for !	5 hrs	;.				i 61 🎹	340	-
9 Ur	CATGGTATATGTG												1 EI 🎹	603	
10 Ur	n CATEGTACAAGGG												i 🔠 🎹	046	-
11 Ur	n CATGAGACAAACT												1 6J 🎹	61 55 193	
12 Ur	n CATEGAAATCCEET	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	i 🔠 🎹	303	-
13 Ur	CATGTAAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.		📑 🔝 🛄	640	-
14 Ur	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	🖬 🔝 🛄	600	-
15 Ur	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	🖬 🔝 🛄	340	
16 Ur	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		📰 🔝 🔝	9 17 0	-
17 Ur	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	з	90077	+	N.A.		i 🔠 🏛	1283	
18 Ur	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i & 🛄	6 12 0	-
19 Ur	CATGTACATACATC	2	1.000	Al	UTR3	ORFV	1	4	99277	+	MRPL11	YDL202W	i 🔠 🏛	6 17 0	-
	CATGATATCAAAAA	2	0,375	Al	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	📰 🔝 🏛	6 17 0	1.12

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.

														Gei	поте Мар	pin
Ma	p yo	our TAGs within	n a Ge	enome	: Ri	esults										
This	sec	tion allows to find	TAGS V	within a	Ger	nome.										
oL -		F.0. [44]												ad all Results	Environmenter	
Sho	w	50 💌											Downio	ad all Results	Expression	and the second
The	re ar	e 1,657 records t	that ma	atched t	he c	uery. 3	49 NIDs ou	t of 1.6	522	submitted	TAG	s were foun	d.			P
-																
N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	I
1	Un	CATEGICAACAAAE	2	0.807	51	Int	Int,opOKF	0	T.	43989	+	N.A.	YALU54C		340	
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	🖬 🖬 🖬 🎹	3010	
з	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	📰 🖬 🎹	006	
4	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	i & 🎞	340	
5	Un	CATGCTGCATCCTA	4	1,000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	i 🔠 🎹	006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	i & 🎹	12 0 13	
7	Un	CATGCACTTCAACT	20	1,000	Fe	Int	int	0	2	34908	+	N.A.		🖬 🖬 🖬	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	🖬 🖬 🖬 🎹	340	
9	Un	C AT GGT AT AT GT GT	2	1,000	Fe	Int	int	0	2	236361	+	N.A.		📑 🖬 🔠 🎹	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	🖹 i 🔠 🎹	046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	🖹 i 🔠 🎹	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	i & III	303	
13	Un	CATGTAAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.		🖹 🖬 🛄	640	
14	Un	CATGGCGTTTGAGG	2	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	i 🔠 🎹	600	
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	i 🔠 🎹	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		📰 🔝 📰	9170	
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	з	90077	+	N.A.		i & III	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	AI	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i & m	6 12 0	
19	Un	CATGTACATACATC	2	1.000	A	UTR3	ORFV	1	4	99277	+	MRPL11	YDL202W	i & III	6 17 0	
20	Un	CATGATATCAAAAA	2	0,375	A	ORF	ORFV	7	4	179499	+	MSH5	YDL154W		6 17 0	
		0 MT C C CTTTT C C CTTT		1 000		ODE	ODE	100	100	000500	197	00010	VDLLOOW		15 10 0	

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

														Gei	поте Мар	pin
Ma	p y	our TAGs within	n a Ge	enome	:: R	esults										
This	s sec	tion allows to find	TAGS	within a	Ger	nome.										
															the local design of the lo	
Sho	W	50											Downloa	ad all Results	Expression	Ma
The	re a	re 1,657 records t	that ma	atched t	he c	wery S		t of 1 f	522	submitted	TAG	: were foun	а			N
1110	10 0	1,037 1000103 1	and the			1001 7.1				Sabinicea	ino.	s were roun	u.			1.4
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	In
1	Un	CATGGTCAACAAAG	2	0,807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	= i 📾 📖	340	
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	i & 🎹	3010	
з	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	🖬 🔝 🎹	006	
4	Un	CATGGCGCAGTTGG	5	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	i 🔠 🎹	340	4
5	Un	CATGCTGCATCCTA	4	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	i 🔠 🎹	006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	i & 🎞	12 0 13	4
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.		🖬 🖬 🛄	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i & 🎹	340	4
9	Un	C AT GGT AT AT GT GT	2	1.000	Fe	Int	int	0	2	236361	+	N.A.	575	🖬 🔝 🎹	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	i & 🎞	046	4
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	🖬 🖬 🖬	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	🖬 🖬 🖬 🎹	303	4
13	Un	CATGTAAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.	575	📑 🖬 🖬 🎹	640	1
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	i & 🎞	600	j.
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	📑 🖬 🔠 🎹	340	1
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		📑 🖬 🔠 🎹	9 17 0	4
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	з	90077	+	N.A.	575	i 🗟 🏛	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i 🗟 🎹	6 12 0	1
19	Un	CATGTACATACATC	2	1.000	A	UTR3	ORFV	1	4	99277	+	MRPL11	YDL202W	i 🔠 🏛	6 17 0	
20	Un	CATGATATCAAAAA	2	0,375	Al	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	🖬 🔝 🏛	6 17 0	
~	11-	0 MT C C C T T T C C C T T		1 000	0.1	ODE	ODE	1 Q		000500	- 92	00010	VDLIDAW		45 40 0	

Query Results: These 6 columns contain linked fields.

														Gei	поте Мар	ping
Ma	рус	our TAGs within	n a Ge	enome	: R	esults										
This	sec	tion allows to find	TAGS	within a	Ger	nome.										
	1												and the second second second		- providence of the	11 T 10
Sho	W	50											Downloa	nd all Results	Expression	LUE:
The	re ar	e 1,657 records t	hat m	atched t	he c	uerv. 3	49 NIDS our	t of 1.6	522	submitted	TAG	s were foun	d.			N
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	I
1	Un	CATGGTCAACAAAG	2	0,807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C		340	
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	i 🔠 🎹	3010	
з	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	🖹 🔝 🎹	006	
4	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	🖹 🖬 🛄	340	
5	Un	CATGCTGCATCCTA	4	1,000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	i 🔠 🎹	006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	i & 🎹	12 0 13	
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.		🖬 🔝 🎹	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	🖬 🔝 🎹	340	
9	Un	C AT GGT AT AT GT GT	2	1.000	Fe	Int	int	0	2	236361	+	N.A.		🖬 🔝 🏧	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	🖹 🔝 🎹	046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	i 🔠 🎹	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	i 🔠 🎹	303	
13	Un	CATGTAAAAAAAAA	2	1,000	Fe	Int	int	0	2	622839	+	N.A.	575	i 🔠 🎹	640	
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N. A.	YBR206W	🖹 🔝 🎹	600	
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	i 🔠 🎹	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		🖹 🖬 🎹	9 17 0	
17	Un	CATGCACTTCAACT	20	1,000	Fe	Int	int	0	з	90077	+	N.A.	575	📑 🖬 🔠 🎹	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i 🔠 🏛	6 12 0	
19	Un	CATGTACATACATC	2	1.000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W	📑 🖬 🔠 🎹	6 17 0	
20	Un	CATGATATCAAAAA	2	0,375	A	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	🖬 🖬 🛄	6 17 0	
665		0 3 m c c c m m n c c c m m	124	No second		ODE	OD F.	101	100	000500		00040	UD1 100W		15 10 0	

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.

our TAGs withir tion allows to find [•] 50 • re 1,657 records t														
50 💌	TAGS	within a	Ger	nome.										
re 1,657 records t											Downioa	id all Results	Expression	ALC: N
	hat m	atched t	he c	query.3	349 NIDs out	t of 1,0	622	submitted	TAG	s were foun	d.			N
192														
Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName		Cn	In
CATGGTCAACAAAG	2	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C		340	
CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	Actual Control of Control of Control	3010	
CATGGAGGAGATTT	2	1,239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W		006	
CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A		340	
CATGCTGCATCCTA	4	1,000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	i 🔠 🎹	006	
CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N. A.	YAR075W	i & 🛄	12 0 13	
CATGCACTTCAACT	20	1,000	Fe	Int	int	0	2	34908	+	N.A.		i 🔠 🎹	1283	
CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i & 🛄	340	
C AT GGT AT AT GT GT	2	1.000	Fe	Int	int	0	2	236361	+	N.A.	- 1 -	i 🔠 🎹	603	
CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	📑 🖬 🔠 🎹	046	
CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	i 🔠 🎹	61 55 193	
CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N. A.	YBR170C	i 🔠 🏛	303	
CATGTAAAAAAAAA	2	1,000	Fe	Int	int	0	2	622839	+	N.A.		i 🔠 🎹	640	
CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	i 🔠 🎹	600	
CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	i 🔠 🎹	340	
CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N. A.		📑 🖬 🔠 🎹	9 17 0	
CATGCACTTCAACT	20	1.000	Fe	Int	int	0	з	90077	+	N.A.	575	📰 🔝 🎹	1283	
CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	📰 🔝 🎞	6 12 0	
CATGTACATACATC	2	1.000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W	📑 i 🔠 🎹	6 17 0	
CATGATATCAAAAA	2	0,375	Al	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	i & III	6 17 0	
	Seq CATGGTCAACAAAG CATGGACACCACCAG CATGGACACCACCAG CATGGCGCAGTTGG CATGGCGCAGTTGG CATGCTGCATCCTA CATGCACACACAC CATGCACACACACA CATGCACACACACA CATGGTACAACACACA CATGGTACAAAGGGT CATGGTACAAAGGGT CATGGAAAACCGGT CATGGAAAACCGGT CATGGCACTTGAAGGGT CATGGCTCTGGTTCT CATGCACTTCAACT CATGCACTTCAGTGTGT CATGCACTTCAACT CATGCACTTCAGTGTGT CATGCACTTCAGTGTGT CATGCACTTCAGTGTGT CATGCACTTCAGTGTGT	Seq Freq CATGETCAACAAAG 2 CATGETCAACAAAG 2 CATGEACACCACAG 3 CATGEACACCACAG 3 CATGEACACCACAG 3 CATGEACACCACAG 2 CATGEAGEAGATTT 2 CATGEACACACACAG 4 CATGCACACTCAACT 20 CATGCACATCAACAC 2 CATGCACACACACAC 2 CATGEACACACACAC 2 CATGETACAAGEGET 2 CATGEACACACACAC 2 CATGEACACACACACA 2 CATGEACACACACACA 2 CATGEACACACACACAC 2 CATGEACACACACACAC 2 CATGEACACACACACACAC 2 CATGEACATTGEAGEGT 2 CATGEACATTGEAGETGT 2 CATGCACTTCAGETTCACACT 20 CATGEACATTCAACT 20 CATGEACATTCAACT 20 CATGEACATTCACATC 20 CATGEACATTCAACATC 20 CATGEACATTCAACATCACATC 20 CATGATACAATAT	Seq Freq Odds CATGETCAACAAAG 2 0.807 CATGACACCACCAG 3 1.000 CATGACACCACCAG 3 1.000 CATGEACACCACCAG 3 1.000 CATGEAGGAGATTT 2 1.239 CATGECGCAGTGEG 5 1.000 CATGCTGCATCCTA 4 1.000 CATGCACACACAC 2 1.239 CATGCACATCCTA 4 1.000 CATGCACATCCAAC 4 1.000 CATGCACATCACACA 2 1.239 CATGCACATCAACACA 2 1.000 CATGGAATATGTGT 2 0.343 CATGGAAATCCGGT 2 0.402 CATGGAAATCCGGT 2 1.000 CATGGAAATCGGGT 2 1.000 CATGGCACTTGAAGA 2 1.000 CATGGCACTTGAGTGT 2 1.000 CATGGCACTTGAAGT 2 1.000 CATGGCACTTGAACT 2 1.000 CATGGCACTTCAACT 2 1.000	Seq Freq Odds Cl CATGETCAACAAAG 2 0.807 Si CATGACACCACCAG 3 1.000 Fe CATGGACACCACCAG 3 1.000 Fe CATGGACACCACCAG 3 1.000 Au CATGGAGGGAGATTT 2 1.239 Au CATGGCGCAGTCGA 4 1.000 Fe CATGCTGCATCCTA 4 1.000 Fe CATGCACACACACA 2 1.239 Au CATGCAACACACACA 2 1.000 Fe CATGGAACACACACA 2 1.000 Fe CATGGTACAACACACA 2 0.343 Au CATGGTACAAAGGGT 2 0.340 Si CATGGAAATCGGGT 2 0.402 Au CATGGAAATCGGGT 2 0.402 Au CATGGAAATCGGGT 2 0.402 Au CATGGAAATCGGGT 2 0.402 Au CATGGAAATCGGGT 2 0.400 Fe	SeqFreqOddsClLocdCATGGTCAACAAAG20.807SiIntCATGACACCACCAG31.000FeIntCATGGAGGGAGATTT21.239AuORFCATGGCGCAGTGGG51.000AIORFCATGCTGCATCCTA41.000FeIntCATGCAAAAAGACTG41.000AIORFCATGCACATCAACA201.000FeIntCATGCACACACACA21.239AuUTR3CATGTACACACACA21.000FeIntCATGGTACAAGAGGT20.343AIORFCATGGAAAACAGAGA20.402AIORFCATGGAAAACAGAGA20.807SiIntCATGGAAAAAAAAA21.000FeIntCATGGCACTTGAGGT22.667AIORFCATGGCACTGGGTTG21.000SiIntCATGCACTGAGTGGT21.000SiIntCATGCACTGAGTGGT21.000AIORFCATGCACTTCAACT21.000AIORFCATGCACTTCAACT21.000AIORFCATGTACAAAAAAA21.000AIORFCATGCACTTCAACT21.000AIORFCATGCACTTCAACT21.000AIORFCATGCACTTCAACT21.000AIORFCATGCACTTCAACT21.000AIORFCATGCACTTCAACT21.000AI <td>Seq Freq Odds Cl LocD LocT CATGGTCAACAAAG 2 0.807 Si Int int,opORF CATGGACACCACCAG 3 1.000 Fe Int int,opORF CATGGACACCACCAG 3 1.000 Fe Int int,opORF CATGGAGGAGATTT 2 1.239 Au ORF ORFdu CATGGCGCAGTTGG 5 1.000 Al ORF TRNA CATGCACACCACT 4 1.000 Fe Int int,opORF CATGCAAAAGACTG 4 1.000 Al ORF ORFdu CATGCACACACACA 2 1.239 Au UTR3 ORFdu CATGGTACACACACA 2 1.239 Au UTR3 ORFdu CATGGTACACACACA 2 1.000 Fe Int int CATGGTACAAAAGGGT 2 0.402 Al ORF ORFv CATGGTACAAAAAAAAA 2 0.402 Al ORF ORFv</td> <td>Seq Freq Odds Cl LocD LocT TrPos CATGGTCAACAAAG 2 0.807 Si Int int.opORF 0 CATGGACACCACCAG 3 1.000 Fe Int int.opORF 0 CATGGAGAGATTT 2 1.239 Au ORF ORFdu 2 CATGGCGCAGTTGG 5 1.000 Al ORF tRNA 1 CATGGCAGCATCTA 4 1.000 Fe Int int.opORF 0 CATGGCAAAAAGACTG 4 1.000 Fe Int int.opORF 0 CATGGCAACTCAACACA 20 1.000 Fe Int int 0 CATGGCAACACACA 2 1.239 Au UTR3 ORFdu 2 CATGGTACACACACA 2 1.239 Au UTR3 ORFdu 2 CATGGTACAAAGGGT 2 1.000 Fe Int int 0 CATGGAAAATCGGGT 2 0.402</td> <td>SeqFreqOddsClLocDLocTTrPosChCATGGTCAACAAAG20.807SiIntint,opORF01CATGGACACCAG31.000FeIntint,opORF01CATGGAGCACCAGG31.000FeIntint,opORF01CATGGAGCAGTTGG51.000AlORFTRNA11CATGCACACCACA41.000FeIntint,opORF001CATGCACACACACA41.000AlORFORFdu11CATGCACATCAACT41.000FeIntint,opORF01CATGCACATCAACA41.000FeIntint,opORF01CATGCACATCAACA21.239AuUTR3ORFdu11CATGCACATCAACA21.239AuUTR3ORFdu22CATGTACACACACA21.239AuUTR3ORFdu22CATGGAACACACACA21.239AuUTR3ORFdu22CATGGAACACACACA21.000FeIntint02CATGGAACACACACA20.402AlORFORFv32CATGGAAACAGAGGT20.402AlORFORFv12CATGGAAAACAGAG20.807SiIntint,opORF02CATGGAAAAAAAAAA21.000AlUTR3ORFdu<t< td=""><td>SeqFreqOddsClLoCJInPosChIniCATGETCAACAAAG20.807SiIntint,opORF0143989CATGEACACCACGA31.000FeIntint,opORF01140213CATGEAGEAGATTT21.239AuORFORFdu21141074CATGECEACTCGA41.000AlORFtRNA11217023CATGCTGCATCCTA41.000FeIntint,opORF001229005CATGCACACTCAACT201.000FeIntint0234908CATGCACATCAACA21.239AuUTR3ORFdu11229005CATGCATATACACACA21.209AuUTR3ORFdu2234908CATGGTATAACACACA21.239AuUTR3ORFdu112CATGGTATAACACACA21.239AuUTR3ORFdu2234908CATGGTACAACACACA21.239AuUTR3ORFdu2234908CATGGTACAACACACA21.000FeIntint0234908CATGGTAAAAGAGA20.343AlORFORFv2247824CATGGAAAACGGG20.3007SiIntint,opORF02576616CATGGAAAACGGG21.000AlORFORFdu12635140<</td><td>Seq Freq Odds Cl LocD LocT TrPes Ch Init Str CATGGTCAACAAAG 2 0.807 Si Int int,opORF 0 1 43989 + CATGGACACCACAG 3 1.000 Fe Int int,opORF 0 1 140213 + CATGGACACCACCAG 3 1.000 Fe Int int,opORF 0 1 140213 + CATGGACACCACCAG 3 1.000 Al ORF ORFdu 10 1 166273 + CATGGCAAACCACACA 4 1.000 Fe Int int,opORF 0 1 217023 + CATGCACATCAACA 4 1.000 Fe Int int,opORFdu 1 2 34908 + CATGCACATCAACA 2 1.239 Au UTR3 ORFdu 1 2 34908 + CATGGAAAACAACA 2 0.343 Al ORF<</td><td>Seq Freq Odds Cl LocD LocT TrPos Ch Ini Str StdName CATGGTCAACAAAG 2 0.807 Si Int int,opORF 0 1 43989 + N.A. CATGGACACCACGA 3 1.000 Fe Int int,opORF 0 1 140213 + N.A. CATGGACACCACGAG 3 1.000 Fe Int int,opORF 0 1 140213 + N.A. CATGGACACCACGAG 3 1.000 Al ORF ORFdu 1 1 166273 + N.A. CATGGCACATCTA 4 1.000 Fe Int int,opORF 0 1 217023 + N.A. CATGCACACACAC 4 1.000 Fe Int int 0 2 34908 + N.A. CATGCACACACAC 2 1.239 Au UTR3 ORFdu 2 2 19235</td><td>CATGGTCAACAAAG 2 0.807 Si Int Int,opORF 0 1 43989 + N.A. YAL054C CATGACACACACA 3 1.000 Fe Int int,opORF 0 1 140213 + N.A. YAL05C CATGGACACACACA 3 1.239 Au ORF ORFdu 2 1 141074 + N.A. YAL05C CATGGCACATGG 5 1.000 Al ORF trint 1 1 166273 + N.A. YAL054U CATGCGCAGTTGA 4 1.000 Fe Int int,opORF 0 1 217023 + N.A. YAR050C CATGCACATCAA 4 1.000 Fe Int int 0 2 34908 + N.A. YAR050C CATGCACACACAC 2 1.000 Fe Int int 0 2 34908 + N.A. YBL054W CATGCACACACACA</td><td>Seq Freq Odds Cl LocD TrPos Ch Tai St StdName SysName CC TD St CATGGTCAACAACAA 2 0.807 Si Int int,opORF 0 1 43989 + N.A. YAL054C Image: Image</td><td>Seq Free Odds Cl LoCD LoCT TrPos Ch Jai Sto Stolkame SysName GC TD DS B Cn CATGGTCACACAG 2 0.807 Si Int int.opORF 0 1 4399 + N.A. YAL054C Image: Similar Simila</td></t<></td>	Seq Freq Odds Cl LocD LocT CATGGTCAACAAAG 2 0.807 Si Int int,opORF CATGGACACCACCAG 3 1.000 Fe Int int,opORF CATGGACACCACCAG 3 1.000 Fe Int int,opORF CATGGAGGAGATTT 2 1.239 Au ORF ORFdu CATGGCGCAGTTGG 5 1.000 Al ORF TRNA CATGCACACCACT 4 1.000 Fe Int int,opORF CATGCAAAAGACTG 4 1.000 Al ORF ORFdu CATGCACACACACA 2 1.239 Au UTR3 ORFdu CATGGTACACACACA 2 1.239 Au UTR3 ORFdu CATGGTACACACACA 2 1.000 Fe Int int CATGGTACAAAAGGGT 2 0.402 Al ORF ORFv CATGGTACAAAAAAAAA 2 0.402 Al ORF ORFv	Seq Freq Odds Cl LocD LocT TrPos CATGGTCAACAAAG 2 0.807 Si Int int.opORF 0 CATGGACACCACCAG 3 1.000 Fe Int int.opORF 0 CATGGAGAGATTT 2 1.239 Au ORF ORFdu 2 CATGGCGCAGTTGG 5 1.000 Al ORF tRNA 1 CATGGCAGCATCTA 4 1.000 Fe Int int.opORF 0 CATGGCAAAAAGACTG 4 1.000 Fe Int int.opORF 0 CATGGCAACTCAACACA 20 1.000 Fe Int int 0 CATGGCAACACACA 2 1.239 Au UTR3 ORFdu 2 CATGGTACACACACA 2 1.239 Au UTR3 ORFdu 2 CATGGTACAAAGGGT 2 1.000 Fe Int int 0 CATGGAAAATCGGGT 2 0.402	SeqFreqOddsClLocDLocTTrPosChCATGGTCAACAAAG20.807SiIntint,opORF01CATGGACACCAG31.000FeIntint,opORF01CATGGAGCACCAGG31.000FeIntint,opORF01CATGGAGCAGTTGG51.000AlORFTRNA11CATGCACACCACA41.000FeIntint,opORF001CATGCACACACACA41.000AlORFORFdu11CATGCACATCAACT41.000FeIntint,opORF01CATGCACATCAACA41.000FeIntint,opORF01CATGCACATCAACA21.239AuUTR3ORFdu11CATGCACATCAACA21.239AuUTR3ORFdu22CATGTACACACACA21.239AuUTR3ORFdu22CATGGAACACACACA21.239AuUTR3ORFdu22CATGGAACACACACA21.000FeIntint02CATGGAACACACACA20.402AlORFORFv32CATGGAAACAGAGGT20.402AlORFORFv12CATGGAAAACAGAG20.807SiIntint,opORF02CATGGAAAAAAAAAA21.000AlUTR3ORFdu <t< td=""><td>SeqFreqOddsClLoCJInPosChIniCATGETCAACAAAG20.807SiIntint,opORF0143989CATGEACACCACGA31.000FeIntint,opORF01140213CATGEAGEAGATTT21.239AuORFORFdu21141074CATGECEACTCGA41.000AlORFtRNA11217023CATGCTGCATCCTA41.000FeIntint,opORF001229005CATGCACACTCAACT201.000FeIntint0234908CATGCACATCAACA21.239AuUTR3ORFdu11229005CATGCATATACACACA21.209AuUTR3ORFdu2234908CATGGTATAACACACA21.239AuUTR3ORFdu112CATGGTATAACACACA21.239AuUTR3ORFdu2234908CATGGTACAACACACA21.239AuUTR3ORFdu2234908CATGGTACAACACACA21.000FeIntint0234908CATGGTAAAAGAGA20.343AlORFORFv2247824CATGGAAAACGGG20.3007SiIntint,opORF02576616CATGGAAAACGGG21.000AlORFORFdu12635140<</td><td>Seq Freq Odds Cl LocD LocT TrPes Ch Init Str CATGGTCAACAAAG 2 0.807 Si Int int,opORF 0 1 43989 + CATGGACACCACAG 3 1.000 Fe Int int,opORF 0 1 140213 + CATGGACACCACCAG 3 1.000 Fe Int int,opORF 0 1 140213 + CATGGACACCACCAG 3 1.000 Al ORF ORFdu 10 1 166273 + CATGGCAAACCACACA 4 1.000 Fe Int int,opORF 0 1 217023 + CATGCACATCAACA 4 1.000 Fe Int int,opORFdu 1 2 34908 + CATGCACATCAACA 2 1.239 Au UTR3 ORFdu 1 2 34908 + CATGGAAAACAACA 2 0.343 Al ORF<</td><td>Seq Freq Odds Cl LocD LocT TrPos Ch Ini Str StdName CATGGTCAACAAAG 2 0.807 Si Int int,opORF 0 1 43989 + N.A. CATGGACACCACGA 3 1.000 Fe Int int,opORF 0 1 140213 + N.A. CATGGACACCACGAG 3 1.000 Fe Int int,opORF 0 1 140213 + N.A. CATGGACACCACGAG 3 1.000 Al ORF ORFdu 1 1 166273 + N.A. CATGGCACATCTA 4 1.000 Fe Int int,opORF 0 1 217023 + N.A. CATGCACACACAC 4 1.000 Fe Int int 0 2 34908 + N.A. CATGCACACACAC 2 1.239 Au UTR3 ORFdu 2 2 19235</td><td>CATGGTCAACAAAG 2 0.807 Si Int Int,opORF 0 1 43989 + N.A. YAL054C CATGACACACACA 3 1.000 Fe Int int,opORF 0 1 140213 + N.A. YAL05C CATGGACACACACA 3 1.239 Au ORF ORFdu 2 1 141074 + N.A. YAL05C CATGGCACATGG 5 1.000 Al ORF trint 1 1 166273 + N.A. YAL054U CATGCGCAGTTGA 4 1.000 Fe Int int,opORF 0 1 217023 + N.A. YAR050C CATGCACATCAA 4 1.000 Fe Int int 0 2 34908 + N.A. YAR050C CATGCACACACAC 2 1.000 Fe Int int 0 2 34908 + N.A. YBL054W CATGCACACACACA</td><td>Seq Freq Odds Cl LocD TrPos Ch Tai St StdName SysName CC TD St CATGGTCAACAACAA 2 0.807 Si Int int,opORF 0 1 43989 + N.A. YAL054C Image: Image</td><td>Seq Free Odds Cl LoCD LoCT TrPos Ch Jai Sto Stolkame SysName GC TD DS B Cn CATGGTCACACAG 2 0.807 Si Int int.opORF 0 1 4399 + N.A. YAL054C Image: Similar Simila</td></t<>	SeqFreqOddsClLoCJInPosChIniCATGETCAACAAAG20.807SiIntint,opORF0143989CATGEACACCACGA31.000FeIntint,opORF01140213CATGEAGEAGATTT21.239AuORFORFdu21141074CATGECEACTCGA41.000AlORFtRNA11217023CATGCTGCATCCTA41.000FeIntint,opORF001229005CATGCACACTCAACT201.000FeIntint0234908CATGCACATCAACA21.239AuUTR3ORFdu11229005CATGCATATACACACA21.209AuUTR3ORFdu2234908CATGGTATAACACACA21.239AuUTR3ORFdu112CATGGTATAACACACA21.239AuUTR3ORFdu2234908CATGGTACAACACACA21.239AuUTR3ORFdu2234908CATGGTACAACACACA21.000FeIntint0234908CATGGTAAAAGAGA20.343AlORFORFv2247824CATGGAAAACGGG20.3007SiIntint,opORF02576616CATGGAAAACGGG21.000AlORFORFdu12635140<	Seq Freq Odds Cl LocD LocT TrPes Ch Init Str CATGGTCAACAAAG 2 0.807 Si Int int,opORF 0 1 43989 + CATGGACACCACAG 3 1.000 Fe Int int,opORF 0 1 140213 + CATGGACACCACCAG 3 1.000 Fe Int int,opORF 0 1 140213 + CATGGACACCACCAG 3 1.000 Al ORF ORFdu 10 1 166273 + CATGGCAAACCACACA 4 1.000 Fe Int int,opORF 0 1 217023 + CATGCACATCAACA 4 1.000 Fe Int int,opORFdu 1 2 34908 + CATGCACATCAACA 2 1.239 Au UTR3 ORFdu 1 2 34908 + CATGGAAAACAACA 2 0.343 Al ORF<	Seq Freq Odds Cl LocD LocT TrPos Ch Ini Str StdName CATGGTCAACAAAG 2 0.807 Si Int int,opORF 0 1 43989 + N.A. CATGGACACCACGA 3 1.000 Fe Int int,opORF 0 1 140213 + N.A. CATGGACACCACGAG 3 1.000 Fe Int int,opORF 0 1 140213 + N.A. CATGGACACCACGAG 3 1.000 Al ORF ORFdu 1 1 166273 + N.A. CATGGCACATCTA 4 1.000 Fe Int int,opORF 0 1 217023 + N.A. CATGCACACACAC 4 1.000 Fe Int int 0 2 34908 + N.A. CATGCACACACAC 2 1.239 Au UTR3 ORFdu 2 2 19235	CATGGTCAACAAAG 2 0.807 Si Int Int,opORF 0 1 43989 + N.A. YAL054C CATGACACACACA 3 1.000 Fe Int int,opORF 0 1 140213 + N.A. YAL05C CATGGACACACACA 3 1.239 Au ORF ORFdu 2 1 141074 + N.A. YAL05C CATGGCACATGG 5 1.000 Al ORF trint 1 1 166273 + N.A. YAL054U CATGCGCAGTTGA 4 1.000 Fe Int int,opORF 0 1 217023 + N.A. YAR050C CATGCACATCAA 4 1.000 Fe Int int 0 2 34908 + N.A. YAR050C CATGCACACACAC 2 1.000 Fe Int int 0 2 34908 + N.A. YBL054W CATGCACACACACA	Seq Freq Odds Cl LocD TrPos Ch Tai St StdName SysName CC TD St CATGGTCAACAACAA 2 0.807 Si Int int,opORF 0 1 43989 + N.A. YAL054C Image: Image	Seq Free Odds Cl LoCD LoCT TrPos Ch Jai Sto Stolkame SysName GC TD DS B Cn CATGGTCACACAG 2 0.807 Si Int int.opORF 0 1 4399 + N.A. YAL054C Image: Similar Simila

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.

Quick	Search:	Submit	<u>Site Map Full S</u>	Search Help	<u>Contact SGD</u> <u>Ho</u> i	<u>ne</u>			
Community Info Sub	bmit Data <u>BLAST</u>	Primers PatMat	ch <u>Gene/Seq R</u>	esources	Advanced Search	<u>Virtual Library</u>			
		SSB1/YDI	.229W Summar	ъ		Help			
Summary Locus History	Literature Gene Onto	ology Phenotype	Interactions Expres	ssion Protein					
Alternative single page fo	ormat								
SSB1 BASIC INFORM	ATION [<u>View Refer</u>	ences]			SSB1 RES	OURCES			
Standard Name	SSB1 (see <u>Nomer</u>	clature conflict No	ite)		Click on map for				
Systematic Name	YDL229W				SGD ORF map	GBrowse chrIV			
Alias	YG101 ¹				5 ⁷	$\longleftrightarrow \rightarrow $			
Feature Type	ORF, Verified				YDL228C 51 ARS4.04	YDL220W YDL228C			
Description	chaperone, function folding of newly-ma	ns with J-protein pa de polypeptide cha h phosphatase sub	ne-associated molec irtner Zuo1p; may be ains; member of the l iunit Reg1p (2, 3, 4, 5	involved in HSP70	• Literature	ARS404			
GO Annotations	SSB1 GO evidence		Literature Guide	View					
Molecular Function	 <u>ATPase activity</u> (<u>unfolded protein b</u> 			 Retrieve Sequences 					
Biological Process	 cotranslational pr protein biosynthe 	otein folding (IDA) sis (IMP_IPI_TAS)			Genomic DNA	View			

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

														Gei	поте Мар	pir
Ма	p yo	our TAGs within	n a Ge	enome	: R	esults										
This	sec	tion allows to find	TAGs (within a	Ger	nome.										
	1															
Sho	w	50											Downloa	ad all Results	Expression	M
The	re ar	re 1,657 records t	hat ma	atched t	he r	werk 3		t of 1 f	522	submitted	TAG	: were foun	4			r
	10 01	0 1,007 1000105 0	ande me	icono a		1001) . 0	.49 11103 00			Sabrincea	180.	, were roan.				
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	1
1	Un	CATGGTCAACAAAG	2	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	📑 🖬 🔠 🎹	340	
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	i & 🎹	3010	
з	Un	CATGGAGGAGATTT	2	1,239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	📑 🖬 🔠 🎹	006	
4	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	🖬 🖬 🔛	340	
5	Un	CATGCTGCATCCTA	4	1,000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	📑 🖬 🔠 🎹	006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	i & 🎞	12 0 13	
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.		📑 🔝 🔝 🎹	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i & 🎞	340	
9	Un	C AT GGT AT AT GT GT	2	1,000	Fe	Int	int	0	2	236361	+	N.A.		📰 🔝 🔳	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	📰 🔝 🔳	046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	📰 🔝 🛄	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	i & III	303	
13	Un	CATGTAAAAAAAAA	2	1,000	Fe	Int	int	0	2	622839	+	N.A.	575	🖬 🖬 🖬 🎹	640	
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	🖬 🔝 🛄	600	
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	i 🔠 🎹	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		🖬 🖬 🖬	9170	
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	з	90077	+	N.A.	575	i 🔠 🏛	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	🖬 🔝 🛄	6 12 0	
19	Un	CATGTACATACATC	2	1,000	Al	UTR3	ORFV	1	4	99277	+	MRPL11	YDL202W	i 🔠 🏛	6 17 0	
20	Un	CATGATATCAAAAA	2	0,375	Al	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	📰 🔝 🛄	6 17 0	
2.5		0 Mm C C C 7 7 7 0 C C 7 7 7		1 000	. 1	ODE	ODE.			000500		00010	VDL 100W		45 40 0	

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

Genomic Context

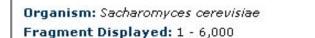
Organism: Sacharomyces cerevisiae





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

Genomic Context





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

Genomic Context

Organism: Sacharomyces cerevisiae

Fragment Displayed: 1 - 6,000



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



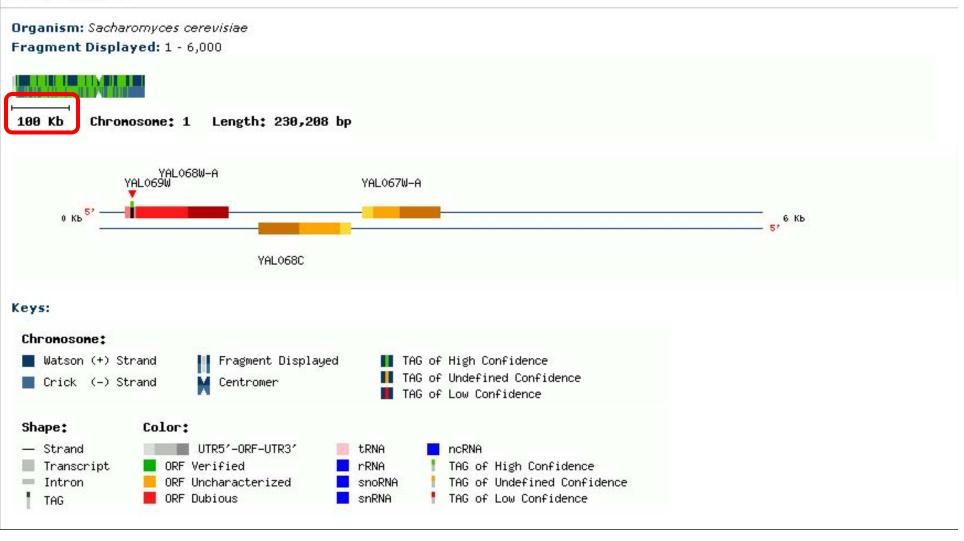
Genomic Context: The fragment of the chromosome being displayed is specified.

Genomic Context



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



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

Genomic Context



Fragment Displayed: 1 - 6,000

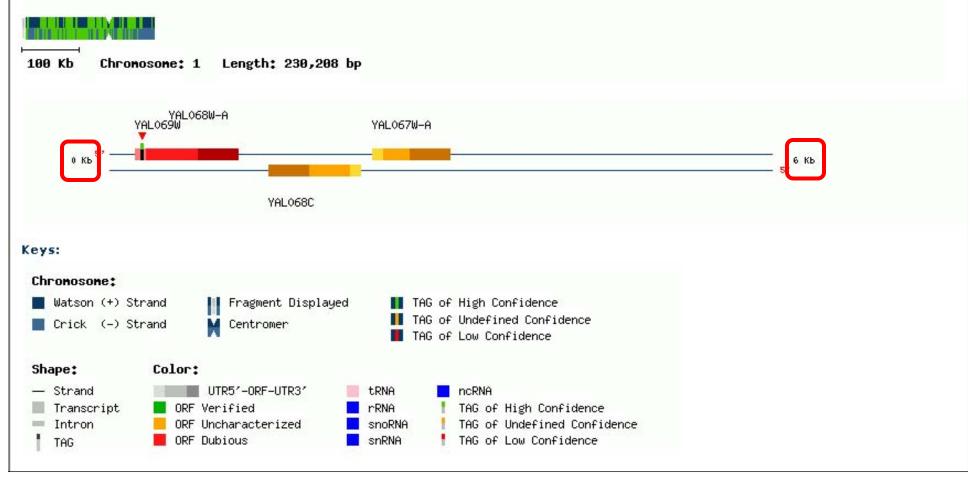


Genomic Context: The current chromosome number and size are given.

Genomic Context

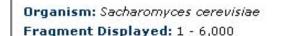
Organism: Sacharomyces cerevisiae





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

Genomic Context





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.

														Gei	поте Мар	ping
Мa	рус	our TAGs within	n a Ge	enome	: R	esults										
This	s sec	tion allows to find ⁻	TAGS	within a	Ger	ome.										
Sho	w	50											Downloa	nd all Results	Expression	Ma
Th a		e 1,657 records t	h		h					au basitta d	тас		4			
me	rear	e 1,637 records t	nacin	atoneu t	ne u	juery. a	149 NIDS 00		DZZ	sabinittea	TAG:	s were roun	u.			N
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	In
1	Un	CATGGTCAACAAAG	2	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	🔚 🔝 🛄	340	
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	🖬 🔝 🛄	3010	
з	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	🖬 🔝 🎹	006	
4	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	🖹 🔝 🎹	340	
5	Un	CATGCTGCATCCTA	4	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C		006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	🖹 🔝 🎞	12 0 13	
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.		🖹 🔝 🛄	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i & 🏧	340	
9	Un	C AT GGT AT AT GT GT	2	1.000	Fe	Int	int	0	2	236361	+	N.A.		i 🔠 🎹	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	🖬 🔝 🏧	046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFV	2	2	478942	+	TEF2	YBR118W	🖬 🖬 🛄	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	i & 🏧	303	
13	Un	CATGTAAAAAAAAA	2	1,000	Fe	Int	int	0	2	622839	+	N.A.	575	i 🔠 🎹	640	
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	i 🔠 🎹	600	
15	Un	CATGCTCTGGTTCT	2	2,667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	🖬 🖬 🛄	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N. A.		i & 🛄	9 17 0	
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	з	90077	+	N.A.		📑 🖬 🔠 🎹	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i & 🛄	6 12 0	
19	Un	CATGTACATACATC	2	1.000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W	🖹 🔝 🎞	6 17 0	
20	Un	CATGATATCAAAAA	2	0,375	Al	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	🖬 🔝 🎹	6 17 0	
~ .			1	+	2.27			105						End (a) (a) Free		

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

DDD1D

TAG Detail

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	Р
Туре	Position	Distance	Poly-A Next?
2	3	476	N
Distance Poly-A	Length Poly-A	Feature Type	Feature Name
0	0	ORFdu	Dubious
Systemat	ic Name	Standa	rd Name
YALO	59W	N	.A.

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

														Gei	поте Мар	фh
Maj	p yo	our TAGs within	n a Ge	enome	: R	esults										
This	sec	tion allows to find	TAGs v	within a	Ger	nome.										
	T														and the local design of the local data	
Sho	w	50											Downloa	nd all Results	Expression	14
The	re ar	re 1,657 records t	hat ma	atched t	he c	werk 3		t of 1 f	:22	submitted	TAG	: were foun	а			r
11101	u,	c 1,00 7 (ccords c	ande me	icono a		1001) 1 0		,.		Sabrincea	180.	, were roan				
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	I
1	Un	CATGGTCAACAAAG	2	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	📰 🔝 🎹	340	
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	i & 🎹	3010	
з	Un	CATGGAGGAGATTT	2	1,239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	📑 🖬 🔠 🎹	006	
4	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	i 🔠 🎹	340	
5	Un	CATGCTGCATCCTA	4	1,000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	📑 🖬 🛄	006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	i 🔠 🎹	12 0 13	
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.			1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i & 🎹	340	
9	Un	C AT GGT AT AT GT GT	2	1,000	Fe	Int	int	0	2	236361	+	N.A.		📑 🔝 🏛	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	🖬 🔝 🏛	046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	🖬 🔝 🏛	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	🖬 🖬 🖬	303	
13	Un	CATGTAAAAAAAAA	2	1,000	Fe	Int	int	0	2	622839	+	N.A.		i 🔠 🏛	640	
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	i 🔠 🏛	600	
15	Un	CATGCTCTGGTTCT	2	2,667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	i 🔠 🎹	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		🖬 i 🔠 🎹	9 17 0	
17	Un	CATGCACTTCAACT	20	1,000	Fe	Int	int	0	з	90077	+	N.A.	575	🖹 i 🔠 🎹	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i & 🏛	6 12 0	
19	Un	CATGTACATACATC	2	1,000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W	📑 🖬 🔠 🎹	6 17 0	
20	Un	CATGATATCAAAAA	2	0,375	AI	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	🖹 i 🔠 🎹	6 17 0	
		0 MPCCC000000CC000	1	1 000		ODE		1			100	00010	VDL100W		15 10 0	

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

ATCG: UTR <u>ATCG</u>: TAG **ATG ... STOP**: ORF

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 downstrem the tag are provided. In this case, neighbor elements such as UTRs from other genes are also highlighted if present.

ATCG: UTR <u>ATCG</u>: TAG **ATG** ... **STOP**: ORF

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

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

														Gei	поте Мар	ping
Ma	p yo	our TAGs within	n a Ge	enome	: R	esults										
This	s sec	tion allows to find ⁻	TAGs	within a	Ger	nome.										
	1															
Sho	w	50											Downloa	ad all Results	Expression	Мар
The	re a	e 1,657 records t	bat m	atched t	he r	werk 3		t of 1 f	522	submitted	TAG	s were foun	d			Ne:
		c 1,00 7 (ccolds c	and c m			1001)				Sabinicea	180.	s more roun	u.			110.
N	тс	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	Inf
1	Un	CATGGTCAACAAAG	2	0,807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	🖹 🔝 🎹	340	1.7
2	Un	CATGACACCACCAG	3	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	i 🔠 🎹	3010	-
з	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	📑 🖬 🔠 🎹	006	-
4	Un	CATGGCGCAGTTGG	5	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	i 🔠 🎹	340	-
5	Un	CATGCTGCATCCTA	4	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	🖹 🔝 🛄	006	-
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	🖬 🔝 🏛	12 0 13	-
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.		🖹 🔝 🛄	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	📰 🔝 🛄	340	-
9	Un	C AT GGT AT AT GT GT	2	1,000	Fe	Int	int	0	2	236361	+	N.A.		📰 🔝 🛄	603	
10	Un	CATGGTACAAGGGT	2	0,343	A	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	i & 🏛	046	-
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	🖬 🔝 🏛	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	i & III	303	-
13	Un	C AT GT AAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.		📰 🔝 🛄	640	-
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	📰 🔝 🔳	600	-
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	i 🔠 🎹	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		📰 🔝 🔳	9170	-
17	Un	CATGCACTTCAACT	20	1,000	Fe	Int	int	0	з	90077	+	N.A.	575	🖬 🔝 🛄	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i 🔠 🏛	6 12 0	-
19	Un	CATGTACATACATC	2	1.000	Al	UTR3	ORFV	1	4	99277	+	MRPL11	YDL202W	🖬 🔝 🏛	6 17 0	
20	Un	CATGATATCAAAAA	2	0,375	Al	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	i 🔠 🎹	6 17 0	-
		e am c c c mm e c c mm	1	1 000		ODE	ODE	1112		000500		00010	VDI 100W		45 40 0	

Query Results: A query to the BLAST server at the NCBI is launched with the previosuly 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.

Nucleotide	Protein	<i>translat</i> Translations	Retrieve results for an RID	
				-22
тс	ACCAGTGTTAGGGTCAAGA	ACAACTGCATCAATACC	GAAGAAGGGGGAATGAGGCAGA	
D26373			TGACCAGATGCGAACCAGATT	10 P
A DECEMBER OF THE OWNER OWNE			TTACCTATTTTTTCAGAGTAC	
E43366			ACCCAAGCAACGCAAAGATTT TCAACAAACGCAAAGCAGTTG	
	AUGAAIGAI III COAIGIA		I CARONARO CONARCONO I I C	
Choose a				
Choose a translation	ANSLATED query - PROT	EIN database <mark>[blastx]</mark>	×	
	ANSLATED query - PROT	EIN database <mark>[blastx]</mark>		
		EIN database <mark>[blastx]</mark>		
translation TR		EIN database <mark>[blastx]</mark>		
translation TR		EIN database <mark>[blastx]</mark>		
translation IR	n: To:	EIN database <mark>[blastx]</mark>		
translation TR et subsequence From hoose database nr	n: To:	EIN database [blastx]		
translation TR et subsequence From hoose database nr	n: To:			

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.

														Ger	поте Мар	deta.
Maj	p yo	our TAGs within	n a Ge	enome	e: Ri	esults										
This	sect	tion allows to find	TAGs V	within a	Ger	nome.										
-		F0														
Sho	W	50											Downloa	ad all Results	Expression	and the second
Ther	re ar	e 1,657 records t	hat ma	atched t	he c	uery.3	49 NIDs ou	t of 1.6	522	submitted	TAG	s were foun	d.			
					ر: محمد مع											
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	1
1	Un	CATGGTCAACAAAG	2	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	i & III	340	
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	i & 🛄	3010	
з	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	📰 🖬 🎹	006	
4	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	🖬 🖬 🖬	340	
5	Un	CATGCTGCATCCTA	4	1,000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	📑 🖬 🔠 🎹	006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	i & 🛄	12 0 13	
7	Un	CATGCACTTCAACT	20	1,000	Fe	Int	int	0	2	34908	+	N.A.		📑 🖬 👪 🎹	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i & 🎹	340	
9	Un	C AT GGT AT AT GT GT	2	1,000	Fe	Int	int	0	2	236361	+	N.A.		📑 🔝 🏛	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	i & III	046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	📰 🔝 🏛	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	🖬 🖬 🖬	303	
13	Un	CATGTAAAAAAAAA	2	1,000	Fe	Int	int	0	2	622839	+	N.A.	575	📑 🖬 🖬 🎹	640	
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N. A.	YBR206W	🖬 🔝 🎹	600	
15	Un	CATGCTCTGGTTCT	2	2,667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	i 🔠 🎹	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N. A.		🖬 i 🔠 🎹	9 17 0	
17	Un	CATGCACTTCAACT	20	1,000	Fe	Int	int	0	з	90077	+	N.A.	575	📑 i 🔠 🎹	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i & 🏛	6 12 0	
19	Un	CATGTACATACATC	2	1,000	A	UTR3	ORFV	1	4	99277	+	MRPL11	YDL202W	i 🔠 🏛	6 17 0	
														🖹 i 🔠 🎹		

Query Results: The tag counts provided by the user are shown here (in case the user provided this information). In this case, the counts of three independent experiments were provided and shown.

														Gei	поте Мар	pin
Ma	p ye	our TAGs within	n a Ge	enome	: R	esults										
This	sec	tion allows to find ⁻	TAGS	within a	Ger	nome.										
	1															
Sho	w	50											Downloa	ad all Results	Expression	ILLE I
The	re ar	e 1,657 records t	hat m	atched t	he r	merv. 3		t of 1.	622	submitted	TAG	s were foun	d.			Ν
		c 1,00 , 1000103 (inde init			4001) . 0			ULL	Sabinicea	180.	s more roan	<u>.</u>			
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	I
1	Un	CATGGTCAACAAAG	2	0,807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	🖹 🖬 🛄	340	
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	i 🔠 🎹	3010	
з	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	📑 🖬 🔠 🎹	006	
4	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	i 🔠 🎹	340	
5	Un	CATGCTGCATCCTA	4	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	🖬 🖬 🛄	006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	i 🔠 🎹	12 0 13	C
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.		📑 🔝 🛄	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i 🔠 🎹	340	
9	Un	C AT GGT AT AT GT GT	2	1.000	Fe	Int	int	0	2	236361	+	N.A.		📑 🖬 🔠 🎹	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	🖬 🔝 🛄	046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	📰 🔝 🛄	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	i & III	303	
13	Un	CATGTAAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.	777	📑 🖬 🔠 🎹	640	
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTRS	ORFdu	1	2	635140	+	N.A.	YBR206W	i 🔠 🎹	600	
15	Un	CATGCTCTGGTTCT	2	2.667	Al.	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	i 🔠 🏛	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		i & 🎹	9 17 0	
17	Un	CATGCACTTCAACT	20	1,000	Fe	Int	int	0	з	90077	+	N.A.	555	i 🔠 🏛	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	i & 🎹	6 12 0	
19	Un	CATGTACATACATC	2	1,000	Al	UTR3	ORFV	1	4	99277	+	MRPL11	YDL202W	i 🔠 🏛	6 17 0	
20	Un	CATGATATCAAAAA	2	0,375	Al	ORF	ORFV	7	4	179499	+	MSH5	YDL154W	i & III	6 17 0	
22.5			1.1		1.122	23222	10 10 10 10 10 10 10 10 10 10 10 10 10 1	100	11233							

Query Results: Each tag can have a label (if the user provided it), which is displayed in this field. This could be useful to highlight some specific tags of interest, or for example, to see the cluster group number of each tag. The user can provide any label here. This field is optional and can be empty (as it is this example case).

														Gei	nome Map	opir
Maj	р ус	our TAGs within	n a Ge	enome	: R	esults										
This	sect	tion allows to find ⁻	TAGS	within a	Ger	nome.										
	T															
Sho	w	50											Downloa	ad all Results	Expression	Húi
The	re ar	e 1,657 records t	hat m	atched t	he c	werk 3		t of 1	622	submitted	TAG	: were foun	а			P
		c 1,007 (ccords d	nac m		no c	1001) . 0			ULL	Sabinicea	110.	, were roan.				
N	TC	Seq	Freq	Odds	CI	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC TD DS BI	Cn	I
1	Un	CATGGTCAACAAAG	2	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	🖹 🖬 🏧	340	
2	Un	CATGACACCACCAG	3	1,000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	i & 🎹	3010	
з	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	🖬 🖬 🏧	006	
4	Un	CATGGCGCAGTTGG	5	1,000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	i 🔠 🎹	340	
5	Un	CATGCTGCATCCTA	4	1,000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	i 🔠 🎹	006	
6	Un	CATGCAAAAGACTG	4	1,000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	i 🔠 🎹	12 0 13	
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.		📑 🖬 🔠 🎹	1283	
8	Un	CATGTACACACACA	2	1,239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	i & 🎹	340	
9	Un	C AT G GT AT AT GT GT	2	1.000	Fe	Int	int	0	2	236361	+	N.A.		i 🔠 🎹	603	
10	Un	CATGGTACAAGGGT	2	0,343	Al	ORF	ORFV	з	2	478284	+	TEF2	YBR118W	i 🔠 🎹	046	
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	i 🔠 🎹	61 55 193	
12	Un	CATGGAAATCCGGT	2	0,807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	i & III	303	
13	Un	CATGTAAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.		🖬 🔝 🛄	640	
14	Un	CATGGCGTTTGAGG	2	1,000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	i 🔠 🎹	600	
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	з	2	704693	+	N.A.	YBR242W	📰 🔝 🔝	340	
16	Un	CATGCGTCAGTGTG	9	0,807	Si	Int	int	0	2	812205	+	N.A.		📰 🔝 🔝	9 17 0	
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	з	90077	+	N.A.		📰 🔝 🔝	1283	
18	Un	CATGTCTTCTCGTT	2	1,000	Al	ORF	ORFV	1	4	45892	+	SSB1	YDL229W	📰 🔝 🔝	6 12 0	
19	Un	CATGTACATACATC	2	1.000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W	🖬 🔝 🛄	6 17 0	
		CATGATATCAAAAA		0.375		ORF	ORFV	7	4	179499	+	MSH5	YDL154W	🖬 🖬 🖬	6 17 0	

Query Results: An expression map with the counts of all the mapped tags onto the genome is available by following the highlighted button.



Expression Map: An expression map with the counts of all the mapped tags onto the genome is displayed. This is useful to detect transcriptionally active regions in a chromosome.



Expression Map: The user can select a single experimental condition or to display all of them simultaneously (as it is the case in this example). The 'show' button on the right must be clicked to make effective any change of parameters.



Expression Map: The user can select a range of expression level. Only the tags which counts belong to this expression range will be displayed. The 'show' button on the right must be clicked to make effective any change of parameters.



Expression Map: The user can select two types of scale for the Y axis of the graph: linear or logarithmic. The 'show' button on the right must be clicked to make effective any change of parameters.

SAGExplore	
Expression Map	
Experimental Condition: All 💌 Expression Level: 0 to 1000 (range: 0-1000) Y-Axis Scale: Logarithmic 💌 Show	
Organism: Sacharomyces cerevisiae Fragment Displayed: 490,001 - 497,000	
100 Kb Chronosone: 2 Length: 813,178 bp	
1000	
100	(+) Strand
i0	÷
10 10 10 10	
2 10	and
100	(-) Strand
1000	
491000 492000 493000 494000 495000 496000 Sequence (bp)	
Keys:	
Chronosone:	
Watson (+) Strand 📕 Fragment Displayed 📕 TAG of High Confidence	
Crick (-) Strand Centromer	

Expression Map: The tags mapped are graphically shown in the chromosome.

SAGExplore
Expression Map
Experimental Condition: All 💌 Expression Level: 0 to 1000 (range: 0-1000) Y-Axis Scale: Logarithmic 💌 Show
Organism: Sacharomyces cerevisiae Fragment Displayed: 490,001 - 497,000
100 Kb Chromosome: 2 Length: 813,178 bp
100
100 G
1000 491000 492000 493000 494000 495000 496000 Sequence (bp)
Chronosone:
Watson (+) Strand Fragment Displayed TAG of High Confidence Crick (-) Strand Centromer TAG of Undefined Confidence

Expression Map: The start and end coordinates of the chromosome fragment displayed are given. Also, in the chromosome, the selected region is highlighted. The graph below shows the counts of each tag for each experimental condition, as supplied by the user.

SAGExplore	
Expression Map	
Experimental Condition: All 💌 Expression Level: 0 to 1000 (range: 0-1000) Y-Axis Scale: Logarithmic 💌 Show	
Organism: Sacharomyces cerevisiae Fragment Displayed: 490,001 - 497,000 100 Kb Chronosone: 2 Length: 813,178 bp	
	(-) Strand (+) Strand
1000 491000 492000 493000 494000 495000 496000 491000 5equence (bp)	
Keys:	
Chronosone: Watson (+) Strand Fragment Displayed Crick (-) Strand Centromer TAG of High Confidence TAG of Undefined Confidence TAG of Undefined Confidence	

Expression Map: By clicking on a given tag count, several tag details are given in a pop-up window.

TAG Detail

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	Р
Туре	Position	Distance	Poly-A Next?
2	3	476	N
Distance Poly-A	Length Poly-A	Feature Type	Feature Name
0	0	ORFdu	Dubious
Systemat	ic Name	Standa	rd Name
YALO	59W	N	.A.

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

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD



III.- Tutorial Library Mapping Module.

			Library Mapp
Map your TAGs within a SA	GE library		
This section allows to find TAGs w	ithin a SAGE library.		
Step 1 Organism ?	Step 2 Anchoring-Tagging Enzyme Pair	? Step 3 Libraries ?	
Saccharomyces cerevisiae 💌	NlaIII - BsmFI 💌	All libraries	×
Step 4 Input Data 👔			
Upload text file			
Browse			
OR Fill in TAG list			
Output Display Options			
	User order 💌 Descending 🗸		
Show 50 💽 Sort by	User order 💌 Descending ⊻		Submit Reset
	Pontificia Universidad Católica de Chile	I MBL I Terms of Use	
	©2007 SAGExplore, All righ	a second a second second second second second second second second second second second second second second s	

III.- Library Mapping Module Form: The user must follow four sequential steps in this form. Online help with the relevant details is provided for each step.

			Libra	ry Mapping
	Map your TAGs within a SAGE library			
	This section allows to find TAGs within a SAGE library.			
IE EX6	Step 1 Organism ? Step 2 Anchoring-Tagging Enzyme Pair ?	Step 3 Libraries ?		
IENON	Saccharomyces cerevisiae 💌 🛛 NIaIII - BsmFI 💌	All libraries		
•	Step 4 Input Data ?			
SNIE	Upload text file			
MAP	OR Fill in TAG list			
OME				
GEN				
0				
MAPPING	Output Display Options			
	Show 50 Sort by User order V Descending V		Submit	Reset
LIBRARY			(oddinic)	(Kesee)
3				
	Pontificia Universidad Católica de Chile M	1BL L Terms of Lise		
	©2007 SACEvolore All rights re			

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.

		Library Mapping
Map your TAGs within a SAGE library		
This section allows to find TAGs within a SAGE library.		
Step 1 Organism Step 2 Anchoring-Tagging Enzyme Pair ?	Step 3 Libraries ?	
Saccharomyces cerevisiae 💌 🛛 🛛 NlaIII - BsmFI 💌	All libraries	×
Step 4 Input Data Upload text file Browse OR Fill in TAG list Input Data		
Output Display Options ? Show 50 v Sort by User order v Descending v	<u></u> St	ubmit Reset
Pontificia Universidad Católica de Chile Mi ©2007 SAGExplore. All rights res		

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.

			Library Mapping
Map your TAGs within a SA	GE library		
This section allows to find TAGs w	ithin a SAGE library.		
Step 1 Organism ?	Step 2 Anchoring-Tagging Enzyme Pair 🕐	Step 3 Libraries ?	
Saccharomyces cerevisiae 🗸	NlaIII - BsmFI 💌	All libraries	
Step 4 Input Data 🥐			
Upload text file			
Browse			
OR Fill in TAG list			
Output Display Options			
Show 50 💽 Sort by	User order 💽 Descending 😒		Submit Reset
Show 50 💉 Sort by			
	Pontificia Universidad Católica de Chile ©2007 SAGExplore, All rights		

Step 3: The user must select an experimental library of SAGE tags. By default, all libraries will be selected. In the case of Saccharomyces cerevisiae, eight independent libraries have been reported and are included in the server.

			Library Mapping
Map your TAGs within a SA	AGE library		
This section allows to find TAGs v	within a SAGE library.		
Step 1 Organism 🥐	Step 2 Anchoring-Tagging Enzyme Pair	? Step 3 Libraries ?	
Saccharomyces cerevisiae 💌	NlaIII - BsmFI 💌	All libraries	×
Step 4 Input Data ?			
Upload text file			
Browse			
OR Fill in TAG list			
Output Display Options			
A CONTRACTOR OF A CONTRACTOR OF	Uses and an and Descention		
Show 50 💽 Sort by	User order 💉 Descending 😪		Submit Reset
	Pontificia Universidad Católica de Chil ©2007 SACEvolore, All ric		

Step 4: The user must provide a list of experimental tags to map against the known experimental libraries of tags. A text file can be uploaded or the data directly pasted into the textarea. The input format is explained in the help link for this step. The full tag sequence must be provided (ie. including the CATG at the 5' end).

			Library Mapping
Map your TAGs within a SA	GE library		
This section allows to find TAGs w	vithin a SAGE library.		
Step 1 Organism ?	Step 2 Anchoring-Tagging Enzyme Pair	? Step 3 Libraries ?	
Saccharomyces cerevisiae 💌	NlaIII - BsmFI 💌	All libraries	
Step 4 Input Data ? Upload text file Browse OR Fill in TAG list			
Dutput Display Options ? Show 50 Sort by	User order 💌 Descending ⊻		Submit Reset
	Pontificia Universidad Católica de Chile	MBL Terms of Use	
	©2007 SAGExplore. All righ	a second a second second second second second second second second second second second second second second s	

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.

				Library Mapping
Map your TAGs within a SA	AGE library			
This section allows to find TAGs	within a SAGE library.			
Step 1 Organism 🥐	Step 2 Anchoring	J-Tagging Enzyme Pair 🕐	Step 3 Libraries ?]
Saccharomyces cerevisiae 💌	NlaIII - BsmFI 💌		All libraries	
Step 4 Input Data ?				
Upload text file				
Browse				
OR Fill in TAG list				
Output Display Options				
A CONTRACT OF A				
Show 50 Sort by	User order 💉	Descending ⊻		Submit Reset
	Pontificia Ur	iiversidad Católica de Chile M	IBL Terms of Use	
		©2007 SAGExplore. All rights re	eserved.	

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

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

Library Mapping

Show 5	50									Download al	l Results
'ou subm	itted 1,622 TAGs.										Nex
N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900	52
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	043	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	7.1
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	340	-
9	CATGCAACTTGTGA	3	0	6	З	2	1	0	0	306	53
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0010	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0010	7.1
12	CATGAAAAGATCAT	3	4	3	5	19	з	0	0	343	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	7.1
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	600	+ :
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	з	0	686	+:
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	+ 1
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	7.1
20	CATGGAACTCCACA	3	4	0	0	1	з	0	0	340	-

Query Results: Typical output of the Library Mapping Form.

	ur TAGs within a SAGE on allows to find TAGs with										
Show 5	i0 💌									Download al	Result
You subm	itted 1,622 TAGs.										Ne
N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900	53
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	043	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	52
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	5
8	CATGATTCTCTTT	з	4	0	0	0	0	4	5	340	-
9	CATGCAACTTGTGA	3	0	6	З	2	1	0	0	306	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0010	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0010	-
12	CATGAAAAGATCAT	3	4	з	5	19	з	0	0	343	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	5
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	600	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	
16	CATGCGAAGTCAAA	6	8	6	1	2	0	з	0	686	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	з	0	0	340	-

Query Results: The total number of records that matched the query are reported. Also, the total number of tags that did not match any record in the known libraries out of the total number of submitted tags is given.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

Library Mapping

-	YOUR TAGS within a SAGE ction allows to find TAGs with										
Show	50									Download al	
0	bmitted 1,622 TAGs.				1						Next
<u> </u>	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
2 1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900	53
2 3	CATGAGACCAATCC	0	4	3	0	0	0	0	0	043	-
	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	-
4 5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
9 7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	
8	CATGATTCTCTTT	З	4	0	0	0	0	4	5	340	+
W 9	CATECAACTIETA	з	0	6	З	2	1	0	0	306	
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0010	-
7 8 9 10 11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	
12	CATGAAAAGATCAT	3	4	З	5	19	3	0	0	343	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATECCATACAGET	6	0	0	0	14	2	0	0	600	+:
15	CATGCCTGTTTGAG	з	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	з	0	686	
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	з	4	0	0	1	з	0	0	340	-

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.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

Library Mapping

	50 💉 Mitted 1,622 TAGs.									Download all	Resu
N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Int
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	043	
з	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	340	
9	CATGCAACTTGTGA	з	0	6	З	2	1	0	0	306	
10	CATECAGATCTGAG	0	0	10	0	0	0	0	0	0010	
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	
12	CATGAAAAGATCAT	3	4	з	5	19	з	0	0	343	
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATECCATACAGET	6	0	0	0	14	2	0	0	600	
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	
16	CATGCGAAGTCAAA	6	8	6	1	2	0	З	0	686	
17	CATGOGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	
18	CATECTCATTATCT	0	0	6	0	0	0	0	0	006	
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	340	

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

										Library /	Happing
	ur TAGs within a SA										
This section	on allows to find TAGs w	ithin a SAGE lib	rary.								
Show 5	0									Download all	Results
You subm	itted 1,622 TAGs.										Next
N	Seque	-A2	879	14: 	A) (A	50 V			Counts	Info
1		xplore								900	
2	CATGAGAC									043	-
3	CATGAGAG Down	load All Resu	ılts							12 0 76	53
4	CATGAGAG									0017	-
5	CATGATAA	VDLODE 1979	07 2006	May 10 4						0 4 10	52
6	CATGATAT	XPLORE-1273	507-2006-	-May-10.0	ar.yz					6 17 0	-
7	CATGATGG Note:	This file will st	tay at this	site for 5	brs					0810	52
8	CATGATTO	1113 110 1111 3	tay at ano	. 5100 101 0						340	÷
9	CATGCAAC									306	7.1
10	CATGCAGA									0010	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0010	7.1
12	CATGAAAAGATCAT	3	4	З	5	19	3	0	0	343	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	7.1
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	600	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	72
16	CATGCGAAGTCAAA	6	8	6	1	2	0	з	0	686	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	52
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	51
20	CATGGAACTCCACA	3	4	0	0	1	з	0	0	340	- 1

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.

Show 5	50									Download al	Results	
You subm	nitted 1,622 TAGs.									Ne		
N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info	
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900		
2	CATGAGACCAATCC	0	4	з	0	0	0	0	0	043	-	
з	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-	
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	- 1	
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0410	-	
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-	
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-	
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	340	-	
9	CATGCAACTTGTGA	3	0	6	З	2	1	0	0	306		
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0010	-	
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0010	53	
12	CATGAAAAGATCAT	3	4	З	5	19	з	0	0	343	-	
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	53	
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	600	-	
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	52	
16	CATGCGAAGTCAAA	6	8	6	1	2	0	з	0	686	-	
17	CATGOGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	52	
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	-	
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	7.0	
20	CATGGAACTCCACA	3	4	0	0	1	з	0	0	340	1.0	

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

Library Mapping

Show 5	50 💌									Download al	l Results
You subm	itted 1,622 TAGs.										Ne
N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900	51
2	CATGAGACCAATCC	0	4	з	0	0	0	0	0	043	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	50
8	CATGATTCTCTTT	3	4	0	0	0	0	4	5	340	-
9	CATGCAACTTGTGA	3	0	6	З	2	1	0	0	306	50
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0010	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	70
12	CATGAAAAGATCAT	3	4	З	5	19	З	0	0	343	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	50
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	600	-
15	CATGCCTGTTTGAG	з	0	27	42	14	31	5	1	3 0 27	30
16	CATGCGAAGTCAAA	6	8	6	1	2	0	з	0	686	
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	53
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	5
20	CATGGAACTCCACA	3	4	0	0	1	з	0	0	340	-

Query Results: By clicking on the tag sequence, a query with this tag sequence against the genome is carried out (ie. the Genome Mapping Module is invoked). The results displayed correspond to the same described previously for that module.

	ur TAGs within a SAGI										
	50 💉 itted 1,622 TAGs.									Download al	l Result Ne
N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Inf
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900	5
2	CATGAGACCAATCC	0	4	З	0	0	0	0	0	043	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	7
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	7
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	7
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	340	-
9	CATGCAACTTGTGA	3	0	6	З	2	1	0	0	306	7
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0010	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	з	5	19	з	0	0	343	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	5
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	600	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	з	0	686	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	7
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	
20	CATGGAACTCCACA	3	4	0	0	1	з	0	0	340	-

ABOUT

Query Results: The observed counts of this tag for each known experimental library.are displayed. In those cases where a tag does not match any library, the row is highlighted in red color.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

Library Mapping

	ur TAGs within a SAGE on allows to find TAGs with										
	50									Download all	
You subm	nitted 1,622 TAGs. Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	N Inf
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	043	
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0410	
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	340	
9	CATGCAACTTGTGA	3	0	6	З	2	1	0	0	306	
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0010	
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0010	
12	CATGAAAAGATCAT	3	4	3	5	19	з	0	0	343	
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	600	
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	
16	CATGCGAAGTCAAA	6	8	6	1	2	0	З	0	686	
17	CATGOGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	з	0	0	340	

Query Results: The observed counts of this tag provided by the user are shown in this field.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD

Library Mapping

	ur TAGs within a SAGE on allows to find TAGs with										
Show :	50 💌									Download al	Resul
You subm	nitted 1,622 TAGs.										N
N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Inf
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900	5
2	CATGAGACCAATCC	0	4	З	0	0	0	0	0	043	-
з	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	340	-
9	CATGCAACTTGTGA	3	0	6	З	2	1	0	0	306	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0010	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	з	0	0	343	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	600	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	з	0	686	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	з	0	0	340	

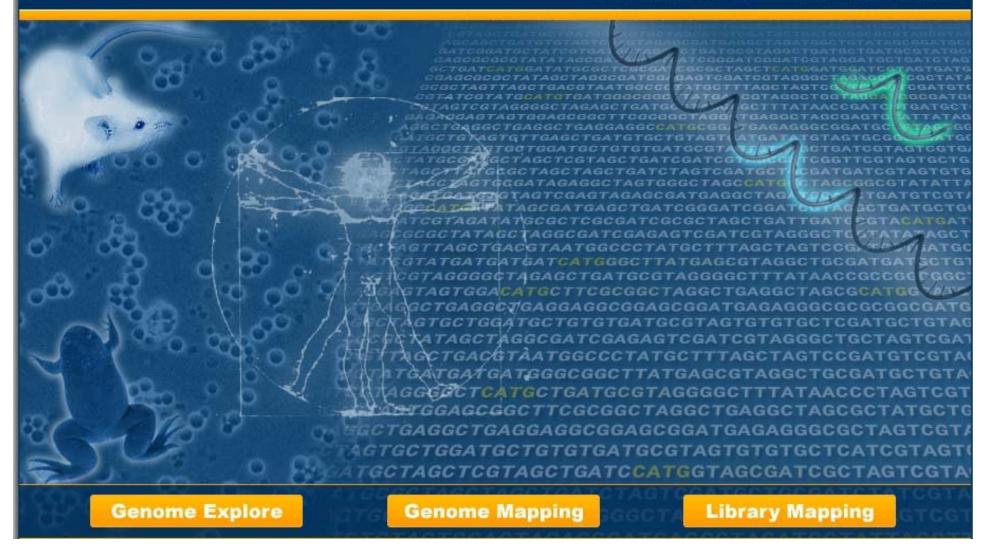
Query Results: A custom label for each tag is displayed here, if it was provided by the user.

Library Mapping

Show 5	50 💌									Download all Resu		
rou subm	itted 1,622 TAGs.										Ne	
N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info	
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	900	-	
2	CATGAGACCAATCC	0	4	З	0	0	0	0	0	043	-	
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76		
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0017	-	
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0410		
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-	
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	7.0	
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	340	-	
9	CATGCAACTTGTGA	3	0	6	З	2	1	0	0	306	7.0	
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0010	-	
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0010	52	
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	343	-	
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	50	
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	600	-	
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	7.1	
16	CATGCGAAGTCAAA	6	8	6	1	2	0	з	0	686	-	
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-	
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	006	-	
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-	
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	340	-	

Query Results: The tags that did not match any known tag in the libraries are highlighted in red. These tags could represent unknown genes.

ABOUT TUTORIAL HISTORY USEFULLINKS DOWNLOAD



This is the end of the SAGExplore web server tutorial Any comments or inquiries, please contact us