

# 1 - cysteine endopeptidase (EC 3.4.22.-) precursor - castor bean gb|AAC62396.1| cysteine endopeptidase precursor [Ricinus communis]

Details for BARLEY1:CONTIG5626\_S\_AT  
 Full Screen

NetAffx Links [Cluster Members](#)  
[Consensus/Exemplar](#)  
[Group Members](#)

## GeneChip Array Information

Probe Set ID Contig5626\_s\_at  
 GeneChip Array Affymetrix Barley Genome Array  
 Organism Name Barley

## Probe Design Information

Transcript ID(Array Design) Contig5626  
 Sequence Type Exemplar sequence  
 Representative Public ID Contig5626 [NCBI](#)  
 Target Description BEST BLASTX NR: 10/29/02 T08122 1e-74 cysteine endopeptidase (EC 3.4.22.-) precursor - castor bean gb|AAC62396.1| cysteine endopeptidase precursor [Ricinus communis]

## Annotation Method Description

Annotation Description Contig5626\_s\_at was annotated using the Design Representative Id based pipeline to a UniGene identifier using 1 transcript(s).

Annotation Grade This is a grade R annotation.

Annotation Transcript Cluster (# of Matching Probes) Contig5626

Transcript	Representative Transcript	Description	Matching Probes	Related Probesets by Grade
------------	---------------------------	-------------	-----------------	----------------------------

<b>Assignments</b>	Contig5626	None																																																												
<b>Annotation Notes</b>	There are no noteworthy cross hybridizing mRNAs found for this probe set.																																																													
<b>Sequence</b>																																																														
<b>Target Sequence</b>	>BARLEY1:CONTIG5626_S_AT aacaagaagccgtccgcccgtgggtcaccatcgacgggtatgaggacgtgcccgccaacgacg aaaccgcgctgaagaaggcgggtggctgcacagccagtgccgctggccatcgaggctagc gggtcgcacttccagttctactcggaggggggtgttcgcgggcaagtgcgggacggagctg gaccatggcgtggcggcggtgggggtacggcaccaccgtggacggcaccaagtattggatc gtgaaaaactcatgggggcccggagtggggtgagaagggatacatccgcatgaagcgcgat g																																																													
	<a href="#">BLASTn GenBank NR</a>																																																													
<b>Probe Info</b>	<table border="1"> <thead> <tr> <th>Probe Sequence(5'-3')</th> <th>Probe X</th> <th>Probe Y</th> <th>Probe Interrogation Position</th> <th>Target Strandedness</th> </tr> </thead> <tbody> <tr> <td>AACAAGAAGCCGTCCGCCGTGGTCA</td> <td>543</td> <td>157</td> <td>483</td> <td>Antisense</td> </tr> <tr> <td>CCGTGGTCACCATCGACGGGTATGA</td> <td>632</td> <td>271</td> <td>499</td> <td>Antisense</td> </tr> <tr> <td>GGTATGAGGACGTGCCGCCAACGA</td> <td>570</td> <td>509</td> <td>517</td> <td>Antisense</td> </tr> <tr> <td>GCCAACGACGAAACCGCGCTGAAGA</td> <td>288</td> <td>281</td> <td>534</td> <td>Antisense</td> </tr> <tr> <td>GAAGAAGGCGGTGGCTGCACAGCCA</td> <td>575</td> <td>343</td> <td>554</td> <td>Antisense</td> </tr> <tr> <td>GCCATCGAGGCTAGCGGGTCCGCACT</td> <td>103</td> <td>285</td> <td>588</td> <td>Antisense</td> </tr> <tr> <td>CTAGCGGGTCGCACTTCCAGTTCTA</td> <td>253</td> <td>211</td> <td>598</td> <td>Antisense</td> </tr> <tr> <td>CACCGTGGACGGCACCAAGTATTGG</td> <td>295</td> <td>125</td> <td>695</td> <td>Antisense</td> </tr> <tr> <td>GTGGACGGCACCAAGTATTGGATCG</td> <td>691</td> <td>475</td> <td>699</td> <td>Antisense</td> </tr> <tr> <td>GTGAGAAGGGATACATCCGCATGAA</td> <td>414</td> <td>479</td> <td>751</td> <td>Antisense</td> </tr> <tr> <td>GGATACATCCGCATGAAGCGCGATG</td> <td>393</td> <td>519</td> <td>759</td> <td>Antisense</td> </tr> </tbody> </table>	Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Target Strandedness	AACAAGAAGCCGTCCGCCGTGGTCA	543	157	483	Antisense	CCGTGGTCACCATCGACGGGTATGA	632	271	499	Antisense	GGTATGAGGACGTGCCGCCAACGA	570	509	517	Antisense	GCCAACGACGAAACCGCGCTGAAGA	288	281	534	Antisense	GAAGAAGGCGGTGGCTGCACAGCCA	575	343	554	Antisense	GCCATCGAGGCTAGCGGGTCCGCACT	103	285	588	Antisense	CTAGCGGGTCGCACTTCCAGTTCTA	253	211	598	Antisense	CACCGTGGACGGCACCAAGTATTGG	295	125	695	Antisense	GTGGACGGCACCAAGTATTGGATCG	691	475	699	Antisense	GTGAGAAGGGATACATCCGCATGAA	414	479	751	Antisense	GGATACATCCGCATGAAGCGCGATG	393	519	759	Antisense	
Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Target Strandedness																																																										
AACAAGAAGCCGTCCGCCGTGGTCA	543	157	483	Antisense																																																										
CCGTGGTCACCATCGACGGGTATGA	632	271	499	Antisense																																																										
GGTATGAGGACGTGCCGCCAACGA	570	509	517	Antisense																																																										
GCCAACGACGAAACCGCGCTGAAGA	288	281	534	Antisense																																																										
GAAGAAGGCGGTGGCTGCACAGCCA	575	343	554	Antisense																																																										
GCCATCGAGGCTAGCGGGTCCGCACT	103	285	588	Antisense																																																										
CTAGCGGGTCGCACTTCCAGTTCTA	253	211	598	Antisense																																																										
CACCGTGGACGGCACCAAGTATTGG	295	125	695	Antisense																																																										
GTGGACGGCACCAAGTATTGGATCG	691	475	699	Antisense																																																										
GTGAGAAGGGATACATCCGCATGAA	414	479	751	Antisense																																																										
GGATACATCCGCATGAAGCGCGATG	393	519	759	Antisense																																																										
<b>Sequence Source</b>	Affymetrix Proprietary Database																																																													

## 2-nuclear transcription factor SLN1 [Hordeum vulgare]

Details for BARLEY1:CONTIG3135\_AT  
[Full Screen](#)

<b>NetAffx Links</b>	<a href="#">Cluster Members</a> <a href="#">Consensus/Exemplar</a>
<b>GeneChip Array Information</b>	
<b>Probe Set ID</b>	Contig3135_at
<b>GeneChip Array</b>	Affymetrix Barley Genome Array
<b>Organism Common Name</b>	Barley
<b>Probe Design Information</b>	
<b>Transcript ID(Array Design)</b>	Contig3135
<b>Sequence Type</b>	Exemplar sequence

<b>Representative Public ID</b>	Contig3135 <a href="#">NCBI</a>				
<b>Target Description</b>	BEST BLASTX NR: 11/04/02 AAL66734.1 6e-88 nuclear transcription factor SLN1 [Hordeum vulgare]				
<b>Annotation Method Description</b>					
<b>Annotation Description</b>	Contig3135_at was annotated using the Design Representative Id based pipeline to a UniGene identifier using 1 transcript(s).				
<b>Annotation Grade</b>	This is a grade R annotation.				
<b>Annotation Transcript Cluster (# of Matching Probes)</b>	Contig3135				
<b>Transcript Assignments</b>	<b>Representative Transcript</b>	<b>Description</b>	<b>Matching Probes</b>	<b>Related Probesets by Grade</b>	
	Contig3135			None	
<b>Annotation Notes</b>	There are no noteworthy cross hybridizing mRNAs found for this probe set.				
<b>Sequence</b>					
<b>Target Sequence</b>	<pre>&gt;BARLEY1:CONTIG3135_AT ggctccaatgcctacaagcaggcgagcacgctgctggccctcttcgccggcgggcga cggg tacaaggtggaagagaaggaaggggtgcctgactctcgggtggcacacgcgcccgct gatac gccacttccgcatggcgctcgcgcgcccgtgatcgcgagtttgaacgctgtaag taga catcgtgagagcatggagcgtacgacacaacccccggccgcccggccccggct ctcc ggcgcacgcacacgcacttgaagaagaagaagatgaagaagaagctaaatgtcagt gata cgctgaattgcagcgaccggctaggatcgatcgggttaccactctacggtttggtt ctgc gtccggcgtgaagacatggacacgaccaactccgaccagaccgcccggcatgtaatg taat ccctccttcggtcccagttcaccatcacccgtaaaactccttattaagccctatta ctat tattattatgtttaaagtctattactattgctatgtgtaattcctccaatcgctc atat tgaaataagcacgggcccggactttgtagcagctgctccattgagaatt</pre>				
	<a href="#">BLASTn GenBank NR</a>				
<b>Probe Info</b>	<b>Probe Sequence(5'-3')</b>	<b>Probe X</b>	<b>Probe Y</b>	<b>Probe Interrogation Position</b>	<b>Target Strandedness</b>
	GGCTCCAATGCCTACAAGCAGGCGA	55	545	1866	Antisense
	AGAGAAGGAAGGGTGCCTGACTCTC	277	93	1937	Antisense
	GCCGTGATCGCGAGTTTTGAACGCT	671	287	2012	Antisense
	TGAGAGCATGGAGCGCTACGACACA	592	581	2051	Antisense
	GCACGCACACGCCTTGAAGAAGAA	552	325	2109	Antisense
	CTGAATTGCAGCGACCGCTAGGAT	618	251	2168	Antisense
	ACCACTCTACGGTTTGGTTCTGCGT	392	111	2203	Antisense
	TCTGCGTCCGGCGTGAAGACATGGA	8	617	2221	Antisense
	AAATGCTATTACTATTGCTATGTG	622	149	2359	Antisense
	ACGGCCCGGACTTTGTTAGCAGCTG	200	127	2416	Antisense
	GTTAGCAGCTGCTCCATTGAGAATT	318	437	2430	Antisense

**Sequence Source** Affymetrix Proprietary Database

### 3- putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]

Details for BARLEY1:HVSMEA0013F14R2\_AT  
[Full Screen](#)

<b>NetAffx Links</b>	<a href="#">Cluster Members</a> <a href="#">Consensus/Exemplar</a>			
<b>GeneChip Array Information</b>				
<b>Probe Set ID</b>	HVSMEa0013F14r2_at			
<b>GeneChip Array</b>	Affymetrix Barley Genome Array			
<b>Organism Common Name</b>	Barley			
<b>Probe Design Information</b>				
<b>Transcript ID (Array Design)</b>	HVSMEa0013F14r2			
<b>Sequence Type</b>	Exemplar sequence			
<b>Representative Public ID</b>	HVSMEa0013F14r2 <a href="#">NCBI</a>			
<b>Target Description</b>	BEST BLASTX NR: 11/08/02 BAB19089.1 2e-80 (AP002744) putative cytochrome P450 [Oryza sativa (japonica cultivar-group)]			
<b>Annotation Method Description</b>				
<b>Annotation Description</b>	HVSMEa0013F14r2_at was annotated using the Design Representative Id based pipeline to a UniGene identifier using 1 transcript(s).			
<b>Annotation Grade</b>	This is a grade R annotation.			
<b>Annotation Transcript Cluster (# of Matching Probes)</b>	HVSMEa0013F14r2			
<b>Transcript Assignments</b>	<b>Representative Transcript</b>	<b>Description</b>	<b>Matching Probes</b>	<b>Related Probesets by Grade</b>
	HVSMEa0013F14r2			None
<b>Annotation Notes</b>	There are no noteworthy cross hybridizing mRNAs found for this probe set.			
<b>Sequence</b>				
<b>Target Sequence</b>	>BARLEY1:HVSMEA0013F14R2_AT gtatgaagttctccggtgtaccaccggctaccgcattcaccggaaaacgtaca agga gatcgagggtcgggggcatcacgtaccagccggcgtgatgt <b>tcgagatgccggtgc</b> <b>tgta</b> catccaccatgacacgggcatttgggga <b>gaagatgcgaccgattca</b> agccggaca ggtt cgccgagggggtctccaaggcgtccaaggaccggccgcttcttcccgttcggtt gggg gccacggatctgcatcgccagaacttcgcgttgcttgaggccaagatggccttgt gcat gatccttcagcgctttgagtttgagctcgcgccgctcgtacgccatacaccgcata			

	<pre>gcgt gatgatggttgcgtcccatgcatggtgctcagatcaggcttcacgctatctcttctcct agta tcgtacgcatggcattcacttcctatgtgatatgcatgtagtctttaattaccatc cggc t</pre>																																																												
	<a href="#">BLASTn GenBank NR</a>																																																												
<b>Probe Info</b>	<table border="1"> <thead> <tr> <th style="background-color: #d9e1f2;">Probe Sequence(5'-3')</th> <th style="background-color: #d9e1f2;">Probe X</th> <th style="background-color: #d9e1f2;">Probe Y</th> <th style="background-color: #d9e1f2;">Probe Interrogation Position</th> <th style="background-color: #d9e1f2;">Target Strandedness</th> </tr> </thead> <tbody> <tr><td>GTATGAAGTTCTCCGGTTGTACCCA</td><td>551</td><td>447</td><td>127</td><td>Antisense</td></tr> <tr><td>TACCCAGCCGGCGTGATGTTTCGAGA</td><td>351</td><td>647</td><td>209</td><td>Antisense</td></tr> <tr><td>GATGTTTCGAGATGCCGGTGCTGTAC</td><td>282</td><td>403</td><td>223</td><td>Antisense</td></tr> <tr><td>TGTACATCCACCATGACACGGGCAT</td><td>686</td><td>563</td><td>243</td><td>Antisense</td></tr> <tr><td>AGAAGATGCGCACCATTCAAGCCG</td><td>602</td><td>99</td><td>274</td><td>Antisense</td></tr> <tr><td>GATTCGAAGCCGGACAGGTTCCGCCA</td><td>610</td><td>421</td><td>288</td><td>Antisense</td></tr> <tr><td>GATCCTTCAGCGCTTTGAGTTTGAG</td><td>136</td><td>409</td><td>427</td><td>Antisense</td></tr> <tr><td>TGCATGGTGCTCAGATCAGGCTTCA</td><td>441</td><td>591</td><td>504</td><td>Antisense</td></tr> <tr><td>TATCTCTTCTAGTATCGTACGCAT</td><td>304</td><td>659</td><td>532</td><td>Antisense</td></tr> <tr><td>TACGCATGGCATTCACTTCCTATGT</td><td>554</td><td>645</td><td>550</td><td>Antisense</td></tr> <tr><td>TGTAGTCTTTAATTACCATCCGGTT</td><td>585</td><td>569</td><td>583</td><td>Antisense</td></tr> </tbody> </table>	Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Target Strandedness	GTATGAAGTTCTCCGGTTGTACCCA	551	447	127	Antisense	TACCCAGCCGGCGTGATGTTTCGAGA	351	647	209	Antisense	GATGTTTCGAGATGCCGGTGCTGTAC	282	403	223	Antisense	TGTACATCCACCATGACACGGGCAT	686	563	243	Antisense	AGAAGATGCGCACCATTCAAGCCG	602	99	274	Antisense	GATTCGAAGCCGGACAGGTTCCGCCA	610	421	288	Antisense	GATCCTTCAGCGCTTTGAGTTTGAG	136	409	427	Antisense	TGCATGGTGCTCAGATCAGGCTTCA	441	591	504	Antisense	TATCTCTTCTAGTATCGTACGCAT	304	659	532	Antisense	TACGCATGGCATTCACTTCCTATGT	554	645	550	Antisense	TGTAGTCTTTAATTACCATCCGGTT	585	569	583	Antisense
	Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Target Strandedness																																																								
	GTATGAAGTTCTCCGGTTGTACCCA	551	447	127	Antisense																																																								
	TACCCAGCCGGCGTGATGTTTCGAGA	351	647	209	Antisense																																																								
	GATGTTTCGAGATGCCGGTGCTGTAC	282	403	223	Antisense																																																								
	TGTACATCCACCATGACACGGGCAT	686	563	243	Antisense																																																								
	AGAAGATGCGCACCATTCAAGCCG	602	99	274	Antisense																																																								
	GATTCGAAGCCGGACAGGTTCCGCCA	610	421	288	Antisense																																																								
	GATCCTTCAGCGCTTTGAGTTTGAG	136	409	427	Antisense																																																								
	TGCATGGTGCTCAGATCAGGCTTCA	441	591	504	Antisense																																																								
	TATCTCTTCTAGTATCGTACGCAT	304	659	532	Antisense																																																								
TACGCATGGCATTCACTTCCTATGT	554	645	550	Antisense																																																									
TGTAGTCTTTAATTACCATCCGGTT	585	569	583	Antisense																																																									
<b>Sequence Source</b>	Affymetrix Proprietary Database																																																												

#### 4- glutathione-S-transferase Cla47 [Triticum aestivum]

Details for BARLEY1:CONTIG21968\_AT  
[Full Screen](#)

<b>NetAffx Links</b>	<a href="#">Cluster Members</a> <a href="#">Consensus/Exemplar</a>
<b>GeneChip Array Information</b>	
<b>Probe Set ID</b>	Contig21968_at
<b>GeneChip Array</b>	Affymetrix Barley Genome Array
<b>Organism Common Name</b>	Barley
<b>Probe Design Information</b>	
<b>Transcript ID(Array Design)</b>	Contig21968
<b>Sequence Type</b>	Exemplar sequence
<b>Representative Public ID</b>	Contig21968 <a href="#">NCBI</a>
<b>Target Description</b>	BEST BLASTX NR: 11/08/02 AAL47687.1 6e-23 glutathione-S-transferase Cla47 [Triticum aestivum]
<b>Annotation Method Description</b>	
<b>Annotation Description</b>	Contig21968_at was annotated using the Design Representative Id based pipeline to a UniGene identifier using 1 transcript(s).
<b>Annotation Grade</b>	This is a grade R annotation.

<b>Annotation Transcript Cluster (# of Matching Probes)</b>	Contig21968				
<b>Transcript Assignments</b>	<b>Representative Transcript</b>	<b>Description</b>	<b>Matching Probes</b>	<b>Related Probesets by Grade</b>	
	Contig21968			None	
<b>Annotation Notes</b>	There are no noteworthy cross hybridizing mRNAs found for this probe set.				
<b>Sequence</b>					
<b>Target Sequence</b>	<pre>&gt;BARLEY1:CONTIG21968_AT gactccatcgggtacgtggacctcgcgctcgggtgcaacctcttctggatcgaggc gctg cgccacatgttcggcatcaactgtcatcgacgccggcaggacccccgcctggccgc ctgg gctgagagggttcgtggagacggaggctgcaaagaaggcggcgcacccatggaaag catg ttggaggaggccgagaagctgcgggctatgtgggctgcggcggctgc caagtaatt attg gctagctcggag gagcttctttatTTTTcggctcgtcacttctgtttgagggtttg cagt cgtcacctTTTTTTTtacattagcgtcagtcgtcacgttaattattactttatgagt atta gttacctatatgaagtactgtgaatttcactcctctaagttgta</pre>				
	<a href="#">BLASTn GenBank NR</a>				
<b>Probe Info</b>	<b>Probe Sequence(5'-3')</b>	<b>Probe X</b>	<b>Probe Y</b>	<b>Probe Interrogation Position</b>	<b>Target Strandedness</b>
	GACTCCATCGGGTACGTGGACCTCG	202	363	101	Antisense
	TCGGGTGCAACCTCTTCTGGATCGA	71	611	129	Antisense
	ACATGTTTCGGCATCACTGTCAFCGA	350	139	165	Antisense
	GGCGCCACCCATGGAAAGCATGTTG	490	547	259	Antisense
	GCTGCGGCGGCTGCCAAGTAATTAT	227	305	314	Antisense
	TAATTATTGGCTAGCTCGGAGGAGC	709	631	332	Antisense
	GAGCTTCTTTATTTTCGGTCGTCA	508	377	353	Antisense
	CGGTCGTCACTTCTGTTTGGAGGTT	1	255	369	Antisense
	TTGGAGGTTTTGCAGTCGTACCTT	431	707	385	Antisense
	CATTAGCGTCAGTCGTACGTTAAT	468	235	417	Antisense
	GTGAATTCCTCCTCTAAGTTGTA	515	479	480	Antisense
<b>Sequence Source</b>	Affymetrix Proprietary Database				

## 5- asparaginase [*Hordeum vulgare*] [*Hordeum vulgare* subsp. *vulgare*]

Details for BARLEY1:CONTIG8739\_AT  
[Full Screen](#)

[NetAffx Cluster Members](#)  
[Links Consensus/Exemplar](#)

### GeneChip Array Information

**Probe Set ID** Contig8739\_at

<b>GeneChip Array</b>	Affymetrix Barley Genome Array
<b>Organism Common Name</b>	Barley

### Probe Design Information

<b>Transcript ID (Array Design)</b>	Contig8739
<b>Sequence Type</b>	Exemplar sequence
<b>Representative Public ID</b>	Contig8739 <a href="#">NCBI</a>
<b>Target Description</b>	BEST BLASTX NR: 11/08/02 AAG28786.1 2e-99 (AF308474) asparaginase [Hordeum vulgare] [Hordeum vulgare subsp. vulgare]

### Annotation Method Description

**Annotation Description** Contig8739\_at was annotated using the Design Representative Id based pipeline to a UniGene identifier using 1 transcript(s).

**Annotation Grade** This is a grade R annotation.

**Annotation Transcript Cluster (# of Matching Probes)** Contig8739

Transcript Assignments	Representative Transcript	Description	Matching Probes	Related Probesets by Grade
	Contig8739			None

**Annotation Notes** There are no noteworthy cross hybridizing mRNAs found for this probe set.

### Sequence

**Target Sequence**

```
>BARLEY1:CONTIG8739_AT
gacgtggccgcgcgtgatggaatacaaggggctgcctctgcaggaggccgtggacttctgc
gtcaaggagcggctcgacgaggggttcgccgggctcatcgccgtgtccggcaccggcgag
gtggcatacgggttcaactgcaccggcatgttcagaggctgcgccaccgaggacggattca
tggaggctcggcatctgggagtgagcgcgcgcaggcagatgtcgctgtggctggcctgaac
tttgaagatagtgcgtgtgtgtgtgtgcatttggccatcctgcgattgccatgtggatct
agtctgagatcctggtttagtagcagtactagtggatcgggagattgggtgatgggtggaat
aattatgatggccgtgaaa
```

<u>BLASTn GenBank NR</u>					
	<b>Probe Sequence(5'-3')</b>	<b>Probe X</b>	<b>Probe Y</b>	<b>Probe Interrogation Position</b>	<b>Target Strandedness</b>
<b>Probe Info</b>	GACGTGGCCCGCGTGATGGAATACA	584	367	881	Antisense
	CGATGTCGCTGTGGCTGGCCTGAAC	364	263	1096	Antisense
	GTGGCTGGCCTGAACTTTGAAGATA	351	493	1106	Antisense
	CTTTGAAGATAGTGCCTGTGTGTGT	79	243	1120	Antisense
	GTGTGTGCATTTGGCCATCCTGCGA	128	489	1141	Antisense
	GGCCATCCTGCGATTGCCATGTGGA	7	551	1153	Antisense
	ATTGCCATGTGGATCTAGTCTGAGA	570	7	1165	Antisense
	TCTAGTCTGAGATCCTGGTTTAGTA	690	619	1178	Antisense
	GAGATCCTGGTTTAGTAGCAGTACT	631	385	1186	Antisense
	GTAGCAGTACTAGTGGATCGGAGAT	635	451	1200	Antisense
	GGAATAATTATGATGGCCGTGAAA	335	533	1236	Antisense
<b>Sequence Source</b>	Affymetrix Proprietary Database				