

A wee BLAST

Challenge: Aromatic barley?

Question – is there an ortholog of the rice BAD2 gene in barley?



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Nucleotide Nucleotide rice aroma Search
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Nucleotide

The Nucleotide database is a collection of sequences from several sources, including GenBank, RefSeq, TPA and PDB. Genome, gene and transcript sequence data provide the foundation for biomedical research and discovery.

Using Nucleotide

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- [SRA Home](#)
- [INSDC](#)

You are here: NCBI > DNA & RNA > Nucleotide Database Write to the Help Desk

GETTING STARTED <ul style="list-style-type: none">NCBI EducationNCBI Help ManualNCBI Handbook	RESOURCES <ul style="list-style-type: none">Chemicals & BioassaysData & SoftwareDNA & RNA	POPULAR <ul style="list-style-type: none">PubMedNucleotideBLAST	FEATURED <ul style="list-style-type: none">Genetic Testing RegistryPubMed HealthGenBank	NCBI INFORMATION <ul style="list-style-type: none">About NCBIResearch at NCBINCBI Newsletter
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Windows taskbar: 4:56 PM 2/27/2013

http://www.ncbi.nlm.nih.gov/nuccore

Nucleotide
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Display Settings: Summary, 20 per page, Sorted by Default order

Send to: **Filter your results:**

Results: 11

- [Aspergillus niger supercontig An11](#)
- 1. **2,721,467 bp linear DNA**
Accession: AM270990.1 GI: 134215631
[GenBank](#) [FASTA](#) [Graphics](#)
- [Oryza sativa Indica Group cultivar Kalanamak 3119 betaine aldehyde dehydrogenase \(BADH1\) gene, partial sequence](#)
- 2. **4,214 bp linear DNA**
Accession: EU566863.1 GI: 194399132
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
- [Oryza sativa Japonica Group putative methylcrotonyl-CoA carboxylase beta chain \(O5K17.1\) gene, partial cds; transposons OLO24B and WANDERER, MITE MERMITE, transposon EXPLORER, retrotransposon BAJIE, transposons F770_ORStETNOOT00072, DITTO, and TREP215, complete sequence; putative betaine-aldehyde dehydrogenase \(O5K17.2\) gene, complete cds; transposon F569, complete sequence; putative disease resistance-like protein \(O5K17.3\) and putative disease resistance-like protein \(O5K17.4\) genes, complete cds; and MITE MERMITE18E, complete sequence](#)
- 3. **38,652 bp linear DNA**
Accession: EU155083.1 GI: 161376415
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
- [Oryza sativa Indica Group cultivar Taipei 309 betaine aldehyde dehydrogenase \(BADH1\) gene, partial sequence](#)
- 4. **4,224 bp linear DNA**
Accession: EU566869.1 GI: 194399138
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
- [Oryza sativa Indica Group cultivar Pusa 1121 betaine aldehyde dehydrogenase \(BADH1\) gene, partial sequence](#)
- 5. **4,229 bp linear DNA**
Accession: EU566867.1 GI: 194399136
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
- [Oryza sativa Indica Group cultivar Pokkali betaine aldehyde dehydrogenase \(BADH1\) gene, partial sequence](#)
- 6. **4,220 bp linear DNA**
Accession: EU566865.1 GI: 194399134
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
- [Oryza sativa Indica Group cultivar Java betaine aldehyde dehydrogenase \(BADH1\) gene, partial sequence](#)

- All (11)
- Bacteria (0)
- [INSDC \(GenBank\) \(11\)](#)
- mRNA (0)
- RefSeq (0)
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- Top Organisms** [\[Tree\]](#)
- Oryza sativa Indica Group (9)
 - Oryza sativa Japonica Group (1)
 - Aspergillus niger (1)

Analyze these sequences

Find related data
Database:

Search details

```
("Oryza sativa"[Organism] OR rice[All Fields]) AND ("Aroma"[Organism] OR aroma[All Fields])
```

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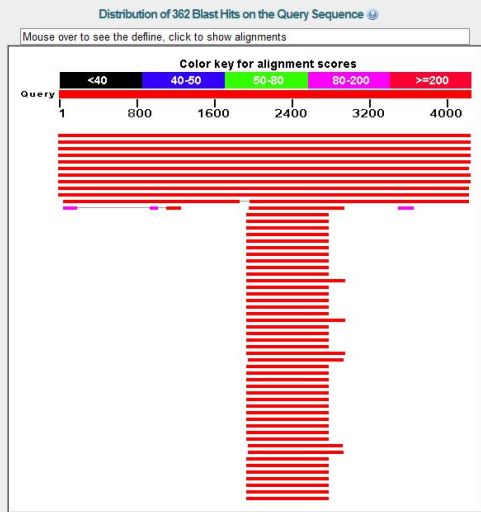
Recent activity

gb|EU566863.1| (4214 letters)

Query ID gi|194399132|gb|EU566863.1|
Description Oryza sativa Indica Group cultivar Kalanamak 3119 betaine aldehyde dehydrogenase (BADH1) gene, partial sequence
Molecule type nucleic acid
Query Length 4214
Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.27+ Citation

Other reports: Search Summary Taxonomy reports Distance tree of results

Graphic Summary



Descriptions

<input type="checkbox"/> Orzya brachyantha isolate BADH_bra_SLE2 betaine aldehyde dehydrogenase (BADH) gene, partial cds	915	915	20%	0.0	85%	JQ414447.1
<input type="checkbox"/> Orzya brachyantha isolate BADH_bra_GUI betaine aldehyde dehydrogenase (BADH) gene, partial cds	911	911	20%	0.0	85%	JQ414443.1
<input type="checkbox"/> Orzya brachyantha isolate BADH_bra_MLI betaine aldehyde dehydrogenase (BADH) gene, partial cds	906	906	20%	0.0	84%	JQ414444.1
<input type="checkbox"/> Orzya brachyantha isolate BADH_bra_NIG betaine aldehyde dehydrogenase (BADH) gene, partial cds	906	906	20%	0.0	84%	JQ414445.1
<input type="checkbox"/> Orzya brachyantha isolate BADH_bra_CMR1 betaine aldehyde dehydrogenase (BADH) gene, partial cds	906	906	20%	0.0	84%	JQ414439.1
<input type="checkbox"/> Orzya brachyantha isolate BADH_bra_CMR2 betaine aldehyde dehydrogenase (BADH) gene, partial cds >qb JQ414441.1 Orzya brachyantha isolate BADH_bra_CMR3 betaine aldehyde dehydrogenase (BADH) gene, partial cds >qb JQ414442.1 Orzya bra	906	906	20%	0.0	84%	JQ414440.1
<input type="checkbox"/> Orzya brachyantha isolate BADH_bra_ZAM betaine aldehyde dehydrogenase (BADH) gene, partial cds	902	902	20%	0.0	84%	JQ414448.1
<input type="checkbox"/> Triticum aestivum cDNA clone: WT003_I14, cultivar: Chinese Spring	277	1539	33%	7e-70	96%	AK332255.1
<input type="checkbox"/> Orzya sativa Japonica Group cDNA clone: J033133A13, full insert sequence	277	2512	33%	7e-70	100%	NM_001059551.1
<input type="checkbox"/> Orzya sativa (indica cultivar-group) BADH (BADH) mRNA, complete cds	277	2512	33%	7e-70	100%	AK103582.1
<input type="checkbox"/> Sorghum bicolor clone BADH15 betaine aldehyde dehydrogenase mRNA, complete cds	273	2441	33%	8e-69	100%	DQ234303.1
<input type="checkbox"/> Sorghum bicolor hypothetical protein, mRNA	223	1570	32%	1e-53	91%	U12196.1
<input type="checkbox"/> Sorghum bicolor hypothetical protein, mRNA	217	951	17%	5e-52	91%	XM_002447933.1
<input type="checkbox"/> PREDICTED: Brachypodium distachyon betaine aldehyde dehydrogenase-like (LOC100826926), mRNA	215	1688	31%	2e-51	98%	XM_003579871.1
<input type="checkbox"/> Zea mays full-length cDNA clone ZM_BFC0104103 mRNA, complete cds	210	1754	33%	8e-50	90%	BT067636.1
<input type="checkbox"/> Zea mays full-length cDNA clone ZM_BFC0031F06 mRNA, complete cds	210	1754	33%	8e-50	90%	BT042732.1
<input type="checkbox"/> Zea mays PCO091899 mRNA sequence	210	483	9%	8e-50	90%	AY108002.1
<input type="checkbox"/> Zea mays betaine aldehyde dehydrogenase (AMADH2), mRNA >qb GQ184594.1 Zea mays aminoaldehyde dehydrogenase 2 (AMADH2) mRNA, complete cds	206	1731	33%	1e-48	90%	NM_001164332.1
<input type="checkbox"/> Zea mays clone 1582776 betaine-aldehyde dehydrogenase mRNA, complete cds	206	1729	33%	1e-48	90%	EU957102.1
<input type="checkbox"/> Sorghum bicolor hypothetical protein, mRNA	205	584	11%	3e-48	90%	XM_002447934.1
<input type="checkbox"/> Zea mays betaine aldehyde dehydrogenase mRNA, partial cds	205	671	12%	3e-48	89%	AF439735.1
<input type="checkbox"/> Levymus chinensis BADH1 mRNA for betaine aldehyde dehydrogenase, complete cds	201	1560	31%	4e-47	94%	AB711137.1
<input type="checkbox"/> Aegropyrion cristatum betaine aldehyde dehydrogenase mRNA, complete cds	201	1520	29%	4e-47	95%	GU181396.1
<input type="checkbox"/> Levymus chinensis LcBADH1 mRNA for betaine aldehyde dehydrogenase, partial cds	201	1560	31%	4e-47	94%	AB183715.1
<input type="checkbox"/> Hordeum vulgare subsp. vulgare mRNA for predicted protein, complete cds, clone: NIA5HV2031D21	196	1542	31%	2e-45	93%	AK365132.1
<input type="checkbox"/> Hordeum brevisubulatum betaine aldehyde dehydrogenase (BADH) mRNA, complete cds	196	1628	32%	2e-45	94%	AY188952.1
<input type="checkbox"/> Hordeum vulgare BBD1 mRNA for betaine aldehyde dehydrogenase, complete cds	196	1545	31%	2e-45	93%	AB063179.1
<input type="checkbox"/> Hordeum vulgare mRNA for betaine aldehyde dehydrogenase, complete cds	196	1382	29%	2e-45	91%	D26448.1
<input type="checkbox"/> Zea mays PCO082010 mRNA sequence	194	899	17%	6e-45	90%	AY104777.1
<input type="checkbox"/> Zovsia tenuifolia mRNA for betaine aldehyde dehydrogenase, complete cds, clone ZBD1	187	1682	32%	9e-43	94%	AB161712.1
<input type="checkbox"/> Zovsia tenuifolia mRNA for betaine aldehyde dehydrogenase, complete cds, clone:10	187	1673	32%	9e-43	94%	AB161708.1
<input type="checkbox"/> Zovsia tenuifolia mRNA for betaine aldehyde dehydrogenase, complete cds, clone:9	183	1678	32%	1e-41	94%	AB161707.1

Alignments

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Display Settings: GenBank Send:

Hordeum vulgare mRNA for betaine aldehyde dehydrogenase, complete cds

GenBank: D26448.1

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Go to:

LOCUS	BLYBAD	1826 bp	mRNA	linear	PLN 18-AUG-2007
DEFINITION	Hordeum vulgare mRNA for betaine aldehyde dehydrogenase, complete cds.				
ACCESSION	D26448				
VERSION	D26448.1 GI:927642				
KEYWORDS	.				
SOURCE	Hordeum vulgare				
ORGANISM	Hordeum vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Pooideae; Triticeae; Hordeum.				
REFERENCE	1 (bases 1 to 1826)				
AUTHORS	Ishitani,M., Nakamura,T., Han,S.Y. and Takabe,T.				
TITLE	Expression of the betaine aldehyde dehydrogenase gene in barley in response to osmotic stress and abscisic acid				
JOURNAL	Plant Mol. Biol. 27 (2), 307-315 (1995)				
PUBMED	7888620				
REFERENCE	2 (bases 1 to 1826)				
AUTHORS	Takabe,T.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-JAN-1994) Tetsuko Takabe, Nagoya University, Department of Bioscience Center; Furoucho, Nagoya, Aichi 464-01, Japan (Tel:81-52-781-5111(ex.6344), Fax:81-52-782-3309)				
FEATURES	Location/Qualifiers				
source	1..1826 /organism="Hordeum vulgare" /mol_type="mRNA" /db_xref="taxon:4513" /clone="pBAD"				
CDS	48..1565 /EC_number="1.2.1.8" /codon_start=1 /product="betaine aldehyde dehydrogenase"				

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Articles about the **LOC548296 gene**

Expression of the betaine aldehyde dehydrogenase gene in bar [Plant Mol Biol. 1995] [See all...](#)

More about the gene **LOC548296**

[LOC548296 gene](#)

Related information

Related Sequences

BioSystems

Gene

Map Viewer

Protein

PubMed

PubMed (Weighted)

Taxonomy

UniGene

Accession	Query	Length	Identical	Positives	Score	E-value	Bits	GI
690	690	67%	0.0	73%	PK242037.1			
690	690	75%	0.0	72%	EF174190.1			
688	688	75%	0.0	71%	JF968601.1			
688	688	66%	0.0	73%	NM_001248061.1			
686	686	63%	0.0	73%	JX050145.1			
682	682	70%	0.0	72%	FQ382859.1			
681	681	80%	0.0	71%	XM_002281948.1			
681	681	64%	0.0	73%	AK060461.1			
677	677	71%	0.0	72%	XM_003608880.1			
673	673	67%	0.0	72%	EF208902.1			
672	672	71%	0.0	71%	BT135083.1			
668	668	76%	0.0	71%	JN192464.1			
668	668	71%	0.0	71%	BT053176.1			
664	664	78%	0.0	71%	JN816361.1			
664	664	67%	0.0	72%	AY083902.1			
663	663	71%	0.0	71%	BT143469.1			
663	663	63%	0.0	73%	JQ067605.1			
663	663	75%	0.0	71%	FJ595952.1			
663	663	63%	0.0	73%	EF541130.1			
663	663	63%	0.0	73%	AY093882.1			
663	663	75%	0.0	71%	M31480.1			
659	659	67%	0.0	72%	AY004192.2			
659	659	78%	0.0	71%	AB043540.1			
657	657	73%	0.0	71%	JX860301.1			
655	655	67%	0.0	72%	AY256971.1			
654	654	64%	0.0	72%	FQ384094.1			
654	654	78%	0.0	70%	XM_002318594.1			
654	654	75%	0.0	71%	AY156694.1			
648	648	60%	0.0	73%	JQ067606.1			
646	646	75%	0.0	71%	GQ381273.1			
645	645	67%	0.0	72%	NM_001198470.1			
645	645	67%	0.0	72%	NM_106150.3			
645	645	67%	0.0	72%	AY093071.1			
645	645	67%	0.0	72%	BX814003.1			
645	645	67%	0.0	72%	AY087395.1			
643	643	55%	2e-180	74%	AY105412.1			
639	639	67%	2e-179	72%	BT008872.1			