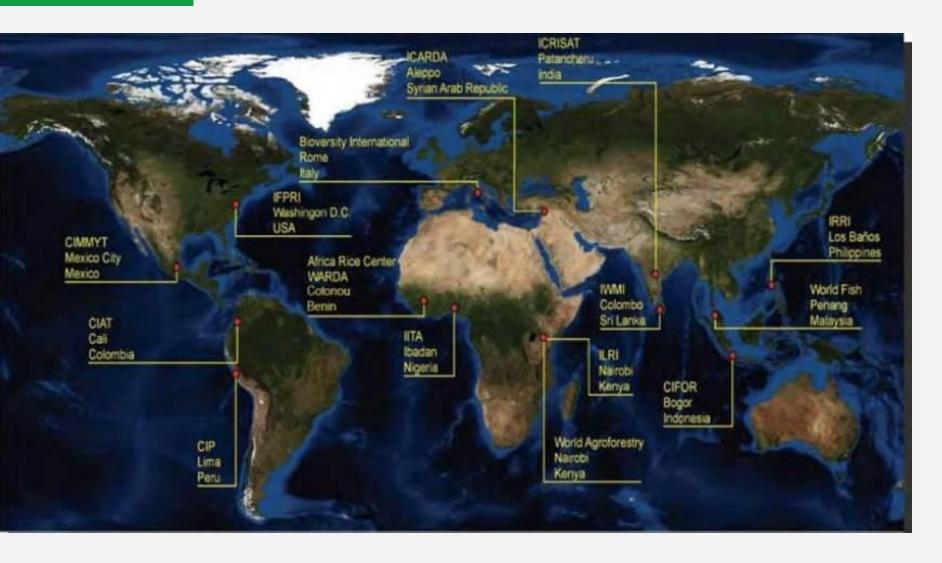
CGIAR's Big Data Platform



Medha Devare (m.devare@cgiar.org)
CAPSELLA Open Data Workshop, Chania | June 2, 2017

Who?



GOALS

Reduced poverty

Improved food and nutrition security for health

Improved natural resource systems and ecosystem services

15 Centers; >8000 scientists; fundamental to applied, multi-scale, multi-disciplinary research





"The data and knowledge products generated by CGIAR arguably are assets of comparable social value to the content of the genebanks, which strongly suggests that CGIAR has dramatically underinvested in the curation and maintenance.

CGIAR Research Programs Second Call Guidance for Pre-Proposals

Companion to the 2016 – 2030 CGIAR Strategy and Results Framework

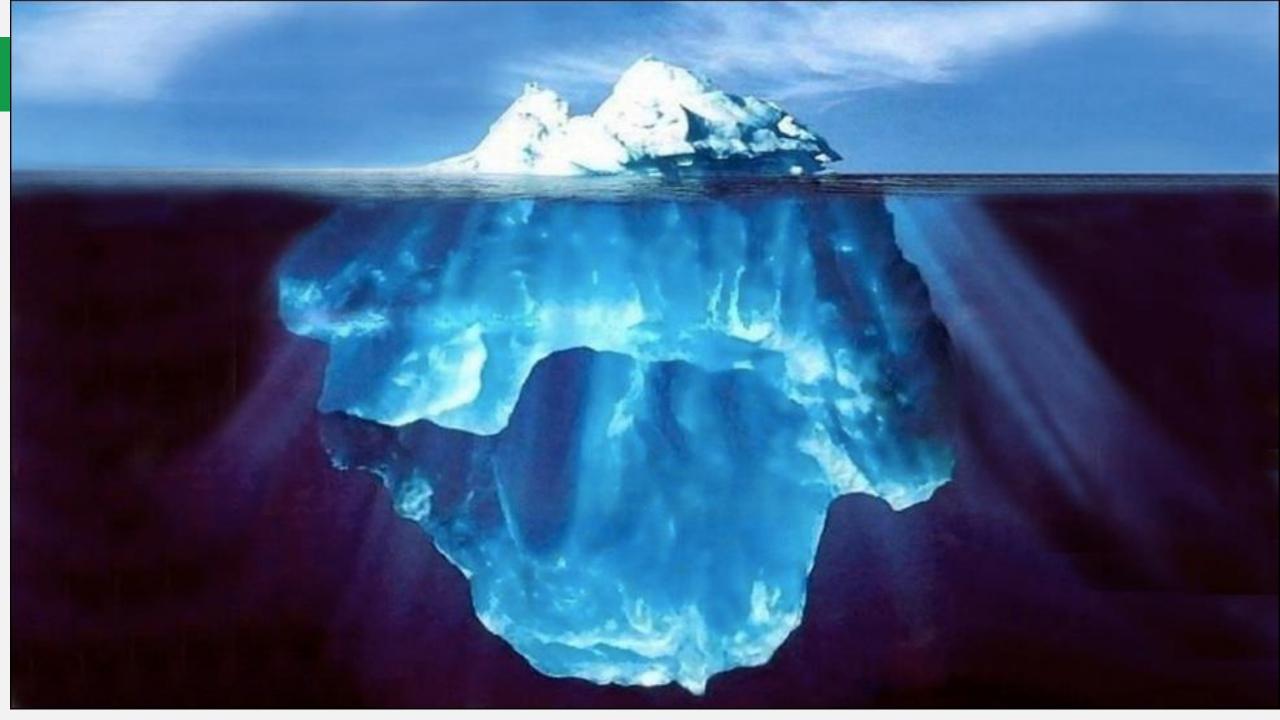
> 15 June 2015 GIAR Consortium Office

dramatically underinvested in the curation and maintenance of these assets.

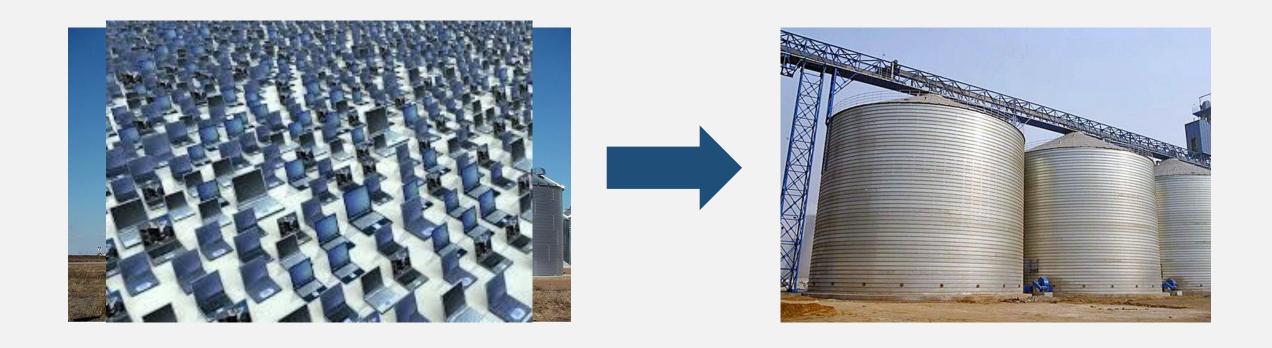
"The field is changing so fast that the only way to stay on the edge is to be invested and involved in these processes, which occur outside the CGIAR.

"...growing amount of frustration...on lack of data transparency and discoverability on breeding, remote sensing, soil agronomy, etc."









Requires FAIR datasets -> harmonization on tools/platforms/standards, and... incentives/culture

Organize

Convene

Inspire







Support data generation and management, practices, enable FAIR data

Bring together big data practitioners, private sector, academia, (I)NGOs++ to produce innovative solutions

Employ analytics and ICTs to deliver info to farmers, monitor ag and food security, and inform policy



Issues: Culture, technical...business model...

- Address standardization at data collection not at data storage stage (AMS)
- Support adoption of minimum metadata standard (CG Core)
- Establish and foster uptake of interoperability standards and protocols through Communities of Practice where needed (controlled vocabularies, ontologies)
- Develop easy workflows, and data documentation, curation, QA/QC processes
- Ensure ease of use, value proposition for databases and tools
- Provide continuous support for researchers (advocacy, training, DMP help...)
- Incentivize data sharing (annual evals, "data sprints" with rewards, dataset citations, funding consequences...)



Organize

Support and improve data generation, management, access

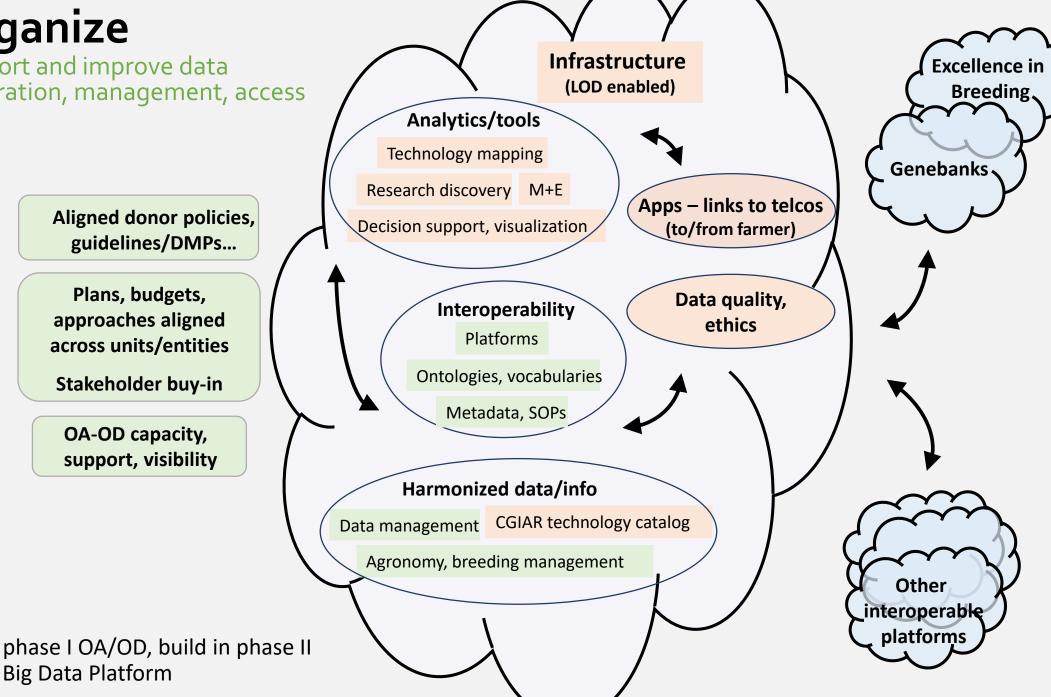
> Aligned donor policies, guidelines/DMPs...

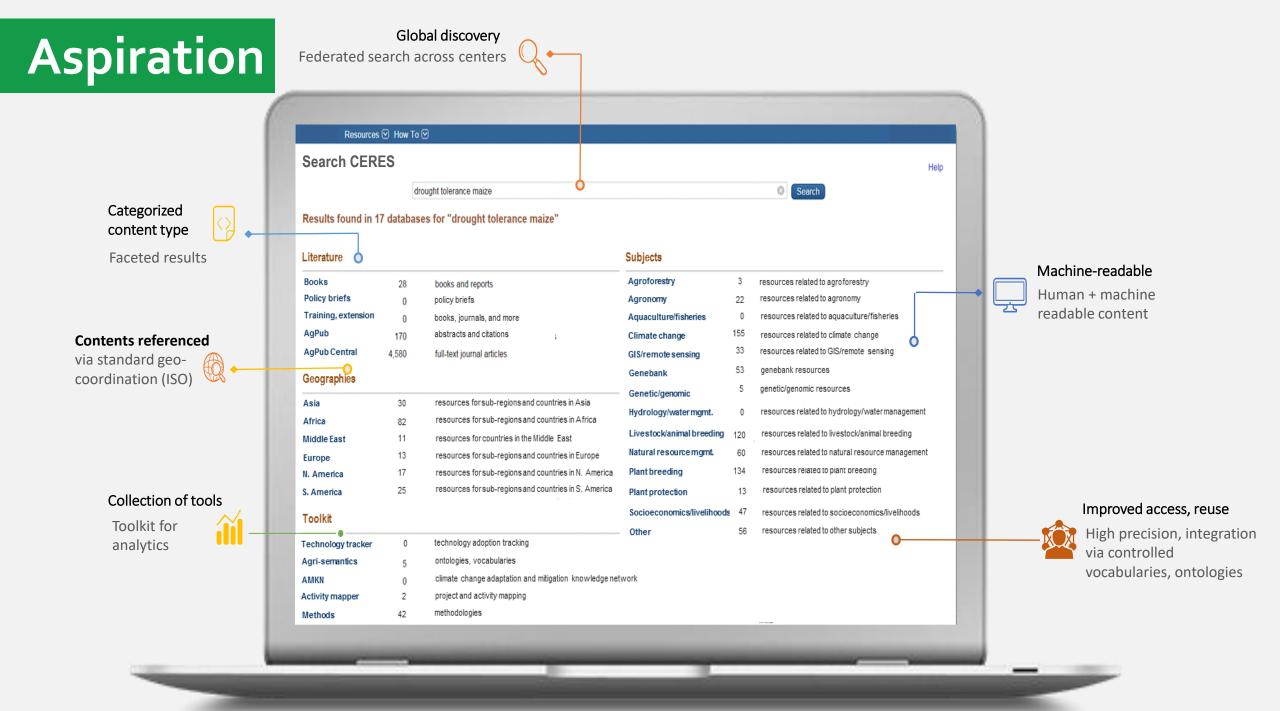
Plans, budgets, approaches aligned across units/entities

Stakeholder buy-in

OA-OD capacity, support, visibility

Big Data Platform





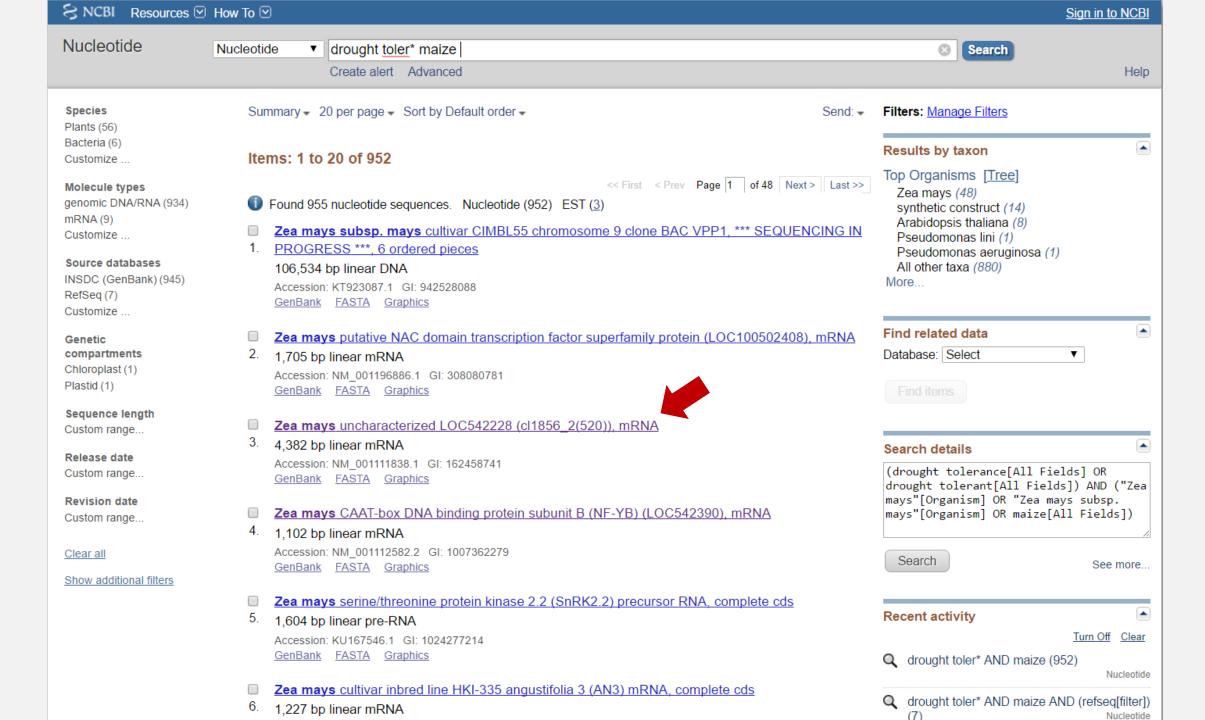
Help

Search NCBI databases

drought toler* maize

Results found in 13 databases for "drought toler* maize"

Literature			Genes						
Books	24	books and reports	EST	3	expressed sequence tag sequences				
MeSH	0	ontology used for PubMed indexing	Gene	7	collected information about gene loci				
NLM Catalog	0	books, journals and more in the NLM Collections	GEO DataSets	7	functional genomics studies				
PubMed	197	scientific & medical abstracts/citations	GEO Profiles	0	gene expression and molecular abundance profiles				
PubMed Central	4,058	full-text journal articles	HomoloGene	0	homologous gene sets for selected organisms				
Health			PopSet	0	sequence sets from phylogenetic and population studies				
ClinVar	0	human variations of clinical significance	UniGene	0	clusters of expressed transcripts				
dbGaP	0	genotype/phenotype interaction studies	Proteins						
GTR	0	genetic testing registry							
MedGen	0	medical genetics literature and links	Conserved Domains	0	conserved protein domains				
OMIM	0	online mendelian inheritance in man	Protein	47	protein sequences				
PubMed Health	1	clinical effectiveness, disease and drug reports	Protein Clusters	0	sequence similarity-based protein clusters				
		,	Structure	0	experimentally-determined biomolecular structures				
Genomes			- Chemicals						
Assembly	0	genome assembly information							
BioProject	10	biological projects providing data to NCBI	BioSystems	26	molecular pathways with links to genes, proteins and chemicals				
BioSample	10	descriptions of biological source materials	PubChem BioAssay	0	bioactivity screening studies				
Clone	0	genomic and cDNA clones	1 aboliciii bioAssay	O	chemical information with structures, information and				
dbVar	0	genome structural variation studies	PubChem Compound	0	links				
Genome	0	genome sequencing projects by organism	PubChem Substance	0	deposited substance and chemical information				
GSS	0	genome survey sequences			•				
Nucleotide	952	DNA and RNA sequences							
Probe	0	sequence-based probes and primers							



Zea mays uncharacterized LOC542228 (cl1856_2(520)), mRNA NCBI Reference Sequence: NM 001111838.1 FASTA Graphics Go to: ✓ LOCUS NM 001111838 4382 bp mRNA linear PLN 23-APR-2017 Zea mays uncharacterized LOC542228 (cl1856 2(520)), mRNA. DEFINITION ACCESSION NM 001111838 VERSION NM 001111838.1 KEYWORDS RefSeq. SOURCE Zea mays ORGANISM Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea. 1 (bases 1 to 4382) REFERENCE Lu Y, Li Y, Zhang J, Xiao Y, Yue Y, Duan L, Zhang M and Li Z. **AUTHORS** TITLE Overexpression of Arabidopsis molybdenum cofactor sulfurase gene confers drought tolerance in maize (Zea mays L.) PLoS ONE 8 (1), E52126 (2013) **JOURNAL** PUBMED 23326325 REMARK GeneRIF: Data indicate that overexpression of Arabidopsis molybdenum cofactor sulfurase gene (LOS5) in maize markedly enhanced the expression of ZmAO and aldehyde oxidase (AO) activity, leading to abscisic acid (ABA) accumulation and increased drought tolerance. 2 (bases 1 to 4382) REFERENCE Sekimoto H, Seo M, Dohmae N, Takio K, Kamiya Y and Koshiba T. AUTHORS Cloning and molecular characterization of plant aldehyde oxidase TITLE JOURNAL J. Biol. Chem. 272 (24), 15280-15285 (1997) PUBMED 9182554 3 (bases 1 to 4382) REFERENCE Koshiba T, Saito E, Ono N, Yamamoto N and Sato M. **AUTHORS** TITLE Purification and Properties of Flavin- and Molybdenum-Containing Aldehyde Oxidase from Coleoptiles of Maize Plant Physiol. 110 (3), 781-789 (1996) JOURNAL PUBMED 12226218 COMMENT PROVISIONAL REFSEO: This record has not yet been subject to final NCBI review. The reference sequence was derived from D88451.1. ##Evidence-Data-START## Transcript exon combination :: D88451.1, SRR3147030.20297.1

Customize view Analyze this sequence Run BLAST Pick Primers Highlight Sequence Features Find in this Sequence Articles about the cl1856_2(520) gene Overexpression of Arabidopsis molybdenum cofactor sulfurase gene confers [PLoS One. 2013] Sequencing, mapping, and analysis of 27,455 maize full-length cDNAs. [PLoS Genet. 2009] Anchoring 9,371 maize expressed sequence tagged unigenes to the bact [Plant Physiol, 2004] See all.. Pathways for the cl1856_2(520) gene Tryptophan metabolism Reference sequence information RefSea protein product See the reference protein sequence for indole-3acetaldehyde oxidase (NP 001105308.1). More about the gene cl1856_2(520) cl1856 2(520) gene Also Known As: ZEAMMB73 Zm00001d034387...

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Zea mays uncharacterized LOC542228 (cl1856_2(520)), mRNA

NCBI Reference Sequence: NM_001111838.1

FASTA Graphics

Go to: ✓

LOCUS NM_001111838 4382 bp mRNA linear PLN 23-APR-2017

DEFINITION Zea mays uncharacterized LOC542228 (cl1856_2(520)), mRNA.

ACCESSION NM_001111838 VERSION NM_001111838.1

KEYWORDS RefSeq.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae;

Zea.

REFERENCE 1 (bases 1 to 4382)

AUTHORS Lu Y, Li Y, Zhang J, Xiao Y, Yue Y, Duan L, Zhang M and Li Z.

TITLE Overexpression of Arabidopsis molybdenum cofactor sulfurase gene

confers drought tolerance in maize (Zea mays L.)

JOURNAL PLoS ONE 8 (1), E52126 (2013)

PUBMED 23326325

REMARK GeneRIF: Data indicate that overexpression of Arabidopsis molybdenum cofactor sulfurase gene (LOS5) in maize markedly enhanced the expression of ZmAO and aldehyde oxidase (AO) activity,

leading to abscisic acid (ABA) accumulation and increased drought

tolerance.

REFERENCE 2 (bases 1 to 4382)

AUTHORS Sekimoto H, Seo M, Dohmae N, Takio K, Kamiya Y and Koshiba T.
TITLE Cloning and molecular characterization of plant aldehyde oxidase

JOURNAL J. Biol. Chem. 272 (24), 15280-15285 (1997)

PUBMED <u>9182554</u>

REFERENCE 3 (bases 1 to 4382)

AUTHORS Koshiba T, Saito E, Ono N, Yamamoto N and Sato M.

TITLE Purification and Properties of Flavin- and Molybdenum-Containing

Aldehyde Oxidase from Coleoptiles of Maize

JOURNAL Plant Physiol. 110 (3), 781-789 (1996)

PUBMED 12226218

COMMENT PROVISIONAL <u>REFSEQ</u>: This record has not yet been subject to final

NCBI review. The reference sequence was derived from D88451.1.

##Evidence-Data-START##

Transcript exon combination :: D88451.1, SRR3147030.20297.1

Customize view

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Articles about the cl1856_2(520) gene



Overexpression of Arabidopsis molybdenum cofactor sulfurase gene confers [PLoS One. 2013]

Sequencing, mapping, and analysis of 27,455 maize full-length cDNAs. [PLoS Genet. 2009]

Anchoring 9,371 maize expressed sequence tagged unigenes to the bacte [Plant Physiol. 2004]

See all...

Pathways for the cl1856_2(520) gene



Tryptophan metabolism

Reference sequence information



RefSeq protein product

See the reference protein sequence for indole-3-acetaldehyde oxidase (NP_001105308.1).

More about the gene cl1856_2(520)



cl1856_2(520) gene Also Known As: ZEAMMB73_Zm00001d034387...

Sequences producing significant alignments:

Select: All None Selected:0

2010	AT								
ÃĮ.	Alignments Download GenBank Graphics Distance tree of results								
	Description	Max score		Query cover	E value	Ident	Accession		
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	Zea mays full-length cDNA clone ZM_BFc0067H14 mRNA, complete cds	4992	4992	62%	0.0	99%	BT063475.1		
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	PREDICTED: Zea mays indole-3-acetaldehyde oxidase-like (LOC103644157), mRNA	3975	3975	92%	0.0	84%	XM_008667350.2		
	Sorghum bicolor hypothetical protein, mRNA	3960	3960	92%	0.0	84%	XM_002463714.1		
	PREDICTED: Zea mays indole-3-acetaldehyde oxidase-like (LOC103644153), mRNA	3186	3186	84%	0.0	82%	XM_020546989.1		
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	PREDICTED: Oryza sativa Japonica Group probable aldehyde oxidase 3 (LOC4334381), mRNA	2401	2401	91%	0.0	78%	XM_015774952.1		
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	Zea mays PCO077114 mRNA sequence	2368	2368	49%	0.0	86%	AY106434.1		

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REFERENCE
           3 (bases 1 to 4382)
                                                                                                                               See the reference protein sequence for indole-3-
  AUTHORS
            Koshiba T, Saito E, Ono N, Yamamoto N and Sato M.
                                                                                                                               acetaldehyde oxidase (NP_001105308.1).
 TITLE
            Purification and Properties of Flavin- and Molybdenum-Containing
            Aldehyde Oxidase from Coleoptiles of Maize
           Plant Physiol. 110 (3), 781-789 (1996)
  JOURNAL
  PUBMED
           12226218
                                                                                                                              More about the gene cl1856_2(520)
COMMENT
           PROVISIONAL REFSEO: This record has not yet been subject to final
                                                                                                                               cl1856_2(520) gene
            NCBI review. The reference sequence was derived from D88451.1.
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                                                                                                                                  Zea mays uncharacterized LOC542228
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                                                                                                                                  (cl1856 2(520)), mRNA
                                                                                                                                                                  Nucleotide
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```

Links from Nucleotide

Showing Current items.

Summary

cl1856_2(520) uncharacterized LOC542228 [Zea mays]

Gene ID: 542228, updated on 4-Apr-2017

Gene symbol cl1856 2(520)

Gene description uncharacterized LOC542228
Locus tag ZEAMMB73_Zm00001d034387

Gene type protein coding
RefSeq status PROVISIONAL
Organism Zea mays

Lineage Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae;

Andropogonodae; Andropogoneae; Tripsacinae; Zea

Also known as AO1; zmAO-1; GRMZM2G141535

■ Genomic context

Location: chromosome: 1

See cl1856_2(520) in Genome Data Viewer Map Viewer

Exon count: 10

Annotation release	Status	Assembly	Chr	Location
<u>101</u>	current	B73 RefGen_v4 (GCF_000005005.2)	1	NC_024459.2 (291605312291613050, complement)
100	previous assembly	B73 RefGen_v3 (GCF_000005005.1)	1	NC_024459.1 (286519547286527285, complement)

▼ Genomic regions, transcripts, and products

■ Bibliography

Table of contents
Summary

Genomic context

Genomic regions, transcripts, and products

Bibliography

Variation

☆ ?

Pathways from BioSystems

General gene information Markers, Homology

General protein information

NCBI Reference Sequences (RefSeq)

Related sequences

Additional links

Genome Browsers

Genome Data Viewer

Map Viewer

Related information

BioProjects

BioSystems

Conserved Domains

Full text in PMC

Full text in PMC_nucleotide

Functional Class

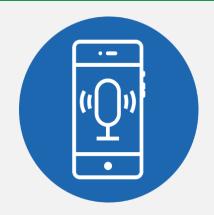
Gene neighbors

Genome

☆ ?

CEO Drofilos

Aspiration



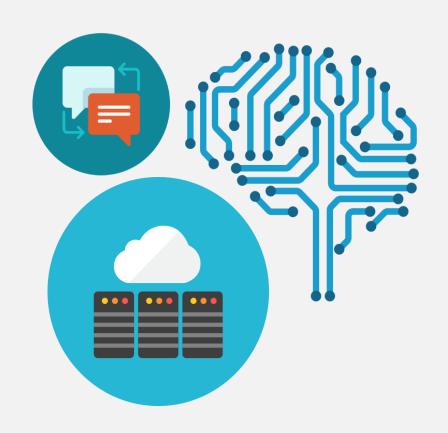
Hey Cigi, when should I plant my maize? How should I manage my crop?

Real-time decision support for farmers

Easy natural language as an interface

Smart artificial intelligence trained by CGIAR and partners

Leveraging multiple open, harmonized and interoperable databases





Thanks!



























