

Contribute to BRENDA! Your enzyme data is important for BRENDA. Send us your paper, and we will do all the work to include your data into our database. [More...](#)

Please enter a search term

Enzyme, Ligand contains

[add search field](#) [delete search field](#) [start search](#)

Text-based queries

- Full-text Search
- Advanced Search
- Enzyme & Disease

Structure-based queries

- Ligand Structure Search
- Metabolic Pathways
- Enzyme Structures

Explorer

- Enzyme Classification
- TaxTree
- Protein folding: CATH / SCOPe
- Ontologies

Visualization

- Word Maps
- Genomes
- Functional Parameter Statistics
- Metabolic Pathways

Prediction

- Membrane Helices
- Localization Prediction
- EnzymeDetector

Supporting & External

- BRENDA Tissue Ontology
- Biochemical Reactions
- MetaboMAPS

News

NEW Release online! - February 1, 2021
Release 2021.1 online including 76 new and 623 updated enzyme classes.

for Release 2021.1 

[evaluate BRENDA!](#)

[Information](#)

BRENDA Tutorial

EnzymeDetector

member of  de NBI

 **elixir**
Core Data Resource

Release 2021.1 (January 2021)
BRENDA professional

Contribute to BRENDa! Your enzyme data is important for BRENDa. Send us your paper, and we will do all the work to include your data into our database. [More...](#)

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Enzyme, Ligand contains

<p><u>Text-based queries</u></p> <ul style="list-style-type: none">Full-text SearchAdvanced SearchEnzyme & Disease	<p><u>Structure-based queries</u></p> <ul style="list-style-type: none">Ligand Structure SearchMetabolic PathwaysEnzyme Structures	<p><u>Explorer</u></p> <ul style="list-style-type: none">Enzyme ClassificationTaxTreeProtein folding: CATH / SCOPeOntologies
<p><u>Visualization</u></p> <ul style="list-style-type: none">Word MapsGenomesFunctional Parameter Statistics	<p><u>Prediction</u></p> <ul style="list-style-type: none">Membrane HelicesLocalization PredictionEnzymeDetector	<p><u>Supporting & External</u></p> <ul style="list-style-type: none">BRENDaTissue OntologyBiochemical Reactions

EnzymeDetector

- comparative and integrative approach for enzyme function annotations
- integration of manually annotated and text mining data from BRENDa, UniProt, KEGG, PATRIC and RefSeq
- completed with predictions from BLAST and BrEPS enzyme pattern recognitions

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add search field delete search field start search

- Text-based queries**
 - Full-text Search
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 - Ontologies
- Visualization**
 - Word Maps 4.2.3.108
 - Genomes
 - Functional Parameter Statistics
 - Metabolic Pathways
- Prediction**
 - Membrane Helices
 - Localization Prediction
 - EnzymeDetector
- Supporting & External**
 - BRENDA Tissue Ontology
 - Biochemical Reactions
 - MetaboMAPS
- News**

<https://ed.brenda-enzymes.org/>

- more than 15 million predictions for eukaryote genomes
- More than 20 million predictions for bacterial and archaeal genomes

Welcome to EnzymeDetector, the database for integrated enzyme annotations.

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Search for organisms:

[Show all organisms](#)

Search for enzymes:

[Show all enzymes](#)

News



November 2020

- New database release online
- Filter and download function revised

August 2020

You can either search an organism or an enzyme

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Search for organisms:

[Show all organisms](#)

- Arabidopsis lyrata subsp. lyrata (Arabidopsis lyrata subsp. lyrata)
- Arabidopsis salsuginea (Eutrema salsugineum)
- Arabidopsis salsuginea (Pall.) N.Busch (Eutrema salsugineum)
- Arabidopsis salsuginea (Pall.) N.Busch, 1913 (Eutrema salsugineum)
- Arabidopsis thaliana (Arabidopsis thaliana)
- Arabidopsis thaliana (L.) Heynh. (Arabidopsis thaliana)
- Arabidopsis thaliana (thale cress) (Arabidopsis thaliana)
- Arabidopsis_thaliana (Arabidopsis thaliana)

November 2020

- New database release online
- Filter and download function revised

August 2020

Enter a search term and select the organism of interest.

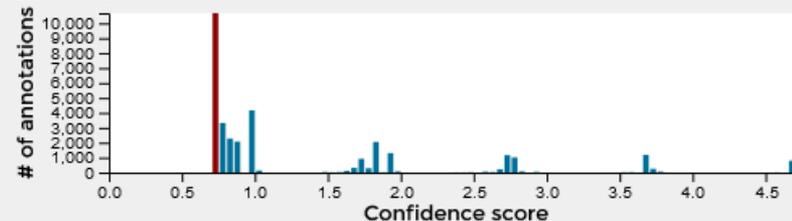
Organism: Arabidopsis thaliana
Domain: Eukaryota
Taxonomy ID: 3702
Proteins: 27500 (+14107 isoforms)

External Links: [BRENDA](#)

Clear filters

Distribution of confidence scores: cutoff:

32.4 % of proteins that have an enzymatic function due to this threshold



21,983 filtered predictions using cutoff
 10,754 rejected predictions using cutoff
 32,737 predictions in total

Enzymes

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On the result page you find

- taxonomic information, including the Tax ID linked to NCBI Taxonomy

	UniProt accession	locus tag	Other Names	EC number	Confidence	KEGG				Enzyme Name
>	O65201	MQN23.4	ACX2, At5g65110	1.3.3.6	4.66	✓	S	B	0.00e+0	✓ acyl-CoA oxidase
>	POCZ23	T2D23.1	ACX3, At1g06290, F9P14.15, F9P14_11	1.3.3.6	4.66	✓	S	B	0.00e+0	✓ acyl-CoA oxidase
>	Q8GWW7	T22D6.110	AIH, EMB1873, At5g08170	3.5.3.12	4.66	✓	S	B	0.00e+0	✓ agmatine deiminase

Help

Enzyme Name

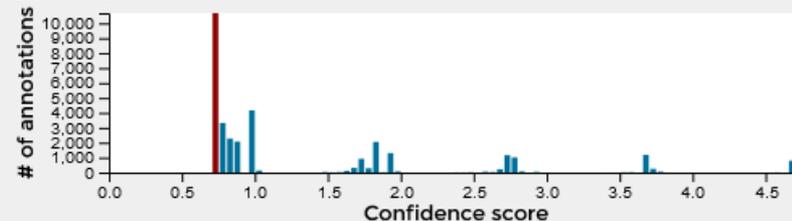
filter

Organism: Arabidopsis thaliana
Domain: Eukaryota
Taxonomy ID: 3702
Proteins: 27500 (+14107 isoforms)
External Links: [BRENDA](#)

Clear filters

Distribution of confidence scores: cutoff:

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Enzymes

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Compare

On the result page you find

- the number of predicted proteins (isoforms)
- Links to BRENDA

Help

Enzyme Name X

filter

	UniProt accession	locus tag	Other Names	EC number	Confidence	KEGG	S	B		Enzyme Name
>	O65201	MQN23.4	ACX2, At5g65110	1.3.3.6	4.66	✓	S	B	0.00e+0	✓ acyl-CoA oxidase
>	POCZ23	T2D23.1	ACX3, At1g06290, F9P14.15, F9P14_11	1.3.3.6	4.66	✓	S	B	0.00e+0	✓ acyl-CoA oxidase
>	Q8GWW7	T22D6.110	AIH, EMB1873, At5g08170	3.5.3.12	4.66	✓	S	B	0.00e+0	✓ agmatine deiminase

Organism: A
Domain: Eu
Taxonomy I
Proteins: 27

External Lin

Clear filters

Enzym

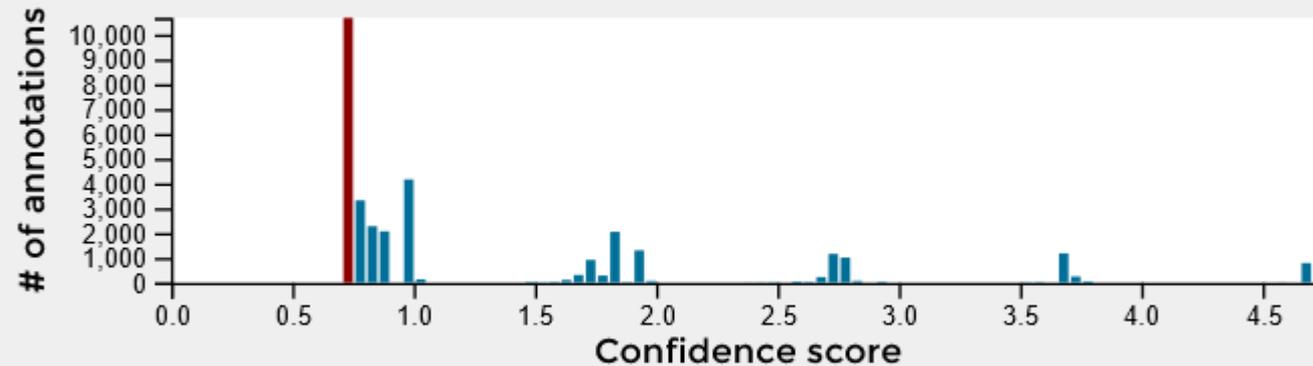
UniP
accessi

filter

Distribution of confidence scores: cutoff:

0.78

32.4 % of proteins that have an enzymatic function due to this threshold



21,983 filtered predictions using cutoff
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32,737 predictions in total

The confidence score is

- an indicator for the quality of an enzyme annotation
- calculated from the sum of the weighted domain-specific reliability of a source
- based on the comparison with manually annotated data
- the default score is above 0.78, but you can adapt the score to your needs

this



Help

Enzyme Name

filter

CoA oxilase

CoA oxilase

matine
minase

monoyl-
lino acid
12-
oxylase

jasmonoyl-

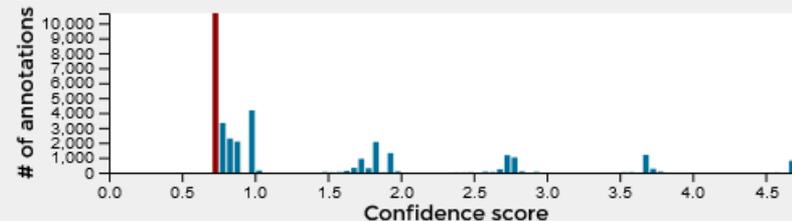
Organism: Arabidopsis thaliana
Domain: Eukaryota
Taxonomy ID: 3702
Proteins: 27500 (+14107 isoforms)

External Links: [BRENDA](#)

Clear filters

Distribution of confidence scores: cutoff:

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	UniProt accession	locus tag	Other Names	EC number	Confidence	KEGG	RefSeq	UniProt	BRENDA	BLAST	BrEPS	Enzyme Name
	<input type="text" value="filter"/>	<input type="text" value="filter"/>	<input type="text" value="filter"/>	<input type="text" value="filter"/>	≥ <input type="text" value="0.78"/>							<input type="text" value="filter"/>
>	O65201	MQN23.4	ACX2, At5g65110	1.3.3.6	4.66	✓						acyl-CoA oxidase
>	P0CZ23	T2D23.1	ACX3, At1g06290, F9P14.15, F9P14_11	1.3.3.6	4.66	✓						acyl-CoA oxidase
>	Q8GWW7	T22D6.110	AIH, EMB1873, At5g08170	3.5.3.12	4.66	✓		S	B	0.00e+0	✓	agmatine deiminase

On the result page you can
 click on „Customize confidence“
 to adapt the confidence scores to
 your need...

 Customize confidence

Customize confidence score weighting and download the resulting annotation table:

BRENDA	<input type="text" value="1"/>
TrEMBL	<input type="text" value="0.75"/>
Swiss-Prot	<input type="text" value="0.87"/>
KEGG	<input type="text" value="0.88"/>
PATRIC	<input type="text" value="0"/>
NCBI's RefSeq	<input type="text" value="0.89"/>
BLAST < 1e-80	<input type="text" value="0.86"/>
BLAST > 1e-20	<input type="text" value="0.72"/>
BLAST < 1e-120	<input type="text" value="0.95"/>
BLAST < 1e-20	<input type="text" value="0.78"/>
BLAST < 1e-50	<input type="text" value="0.82"/>
BrEPS	<input type="text" value="0.96"/>

Format: CSV JSON

[Download Information](#)

**Change the confidence scores
and download the resulting
annotation table**

32,737 predictions in total

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	UniProt accession	locus tag	Other Names	EC number	Confidence	KEGG	RefSeq	UniProt	BRENDA	BLAST	BrEPS	Enzyme Name
	<input type="text" value="filter"/>	<input type="text" value="filter"/>	<input type="text" value="filter"/>	<input type="text" value="filter"/>	≥ <input type="text" value="0.78"/>	<input type="checkbox"/> found	<input type="checkbox"/> found	<input type="checkbox"/> SwissProt <input type="checkbox"/> TrEMBL	<input type="checkbox"/> found	≤ <input type="text" value="filter"/>	<input type="checkbox"/> found	<input type="text" value="filter"/>
>	O65201	MQN23.4	ACX2, At5g65110	1.3.3.6	4.66	✓						
>	P0CZ23	T2D23.1	ACX3, At1g06290, F9P14.15, F9P14_11	1.3.3.6	4.66	✓						
>	Q8GWW7	T22D6.110	AIH, EMB1873, At5g08170	3.5.3.12	4.66	✓		S	B	0.00e+0	✓	agmatine deiminase
>	Q9FMV7 5	MLE2.8	CYP94B1, At5g63450	1.14.14.48	4.66	✓		S	B	0.00e+0	✓	jasmonoyl-L-amino acid 12-hydroxylase
>	Q9SMP5 4	T8P19.30	CYP94B3, At3g48520	1.14.14.48	4.66	✓		S	B	0.00e+0	✓	jasmonoyl-L-amino acid 12-hydroxylase
>	Q9ZUX1 5	F15K20.21	CYP94C1, At2g27690	1.14.14.49	4.66	✓		S	B	0.00e+0	✓	12-hydroxyjasmonoyl-L-amino acid 12-hydroxylase

On the result page you find

- a list of annotated enzymes

Number of filtered predictions: 21983 (13498 unique genes)

32,737 predictions in total

Enzymes

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	UniProt accession	locus tag	Other Names	EC number	Confidence	KEGG	RefSeq	UniProt	BRENDA	BLAST	BrEPS	Enzyme Name
	filter	filter	filter	filter	≥ 0.78	found	found	SwissProt TrEMBL	found	≤ filter	found	filter
>	O65201	MQN23.4	ACX2, At5g65110	1.3.3.6	4.66	✓						
>	P0CZ23	T2D23.1	ACX3, At1g06290, F9P14.15, F9P14_11	1.3.3.6	4.66	✓						
>	Q8GWW7	T22D6.110	AIH, EMB1873, At5g08170	3.5.3.12	4.66	✓						
>	Q9FMV7 5	MLE2.8	CYP94B1, At5g63450	1.14.14.48	4.66	✓		S	B	0.00e+0	✓	jasmonoyl-L-amino acid 12-hydroxylase
>	Q9SMP5 4	T8P19.30	CYP94B3, At3g48520	1.14.14.48	4.66	✓		S	B	0.00e+0	✓	jasmonoyl-L-amino acid 12-hydroxylase
>	Q9ZUX1 5	F15K20.21	CYP94C1, At2g27690	1.14.14.49	4.66	✓		S	B	0.00e+0	✓	12-hydrox-yjasmonoyl-L-amino acid 12-hydroxylase

On the result page you find

- the number of predictions
 - in total
 - filtered
 - unique genes

Number of filtered predictions: 21983 (13498 unique genes)

32,737 predictions in total

Enzymes

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	UniProt accession	locus tag	Other Names	EC number	Confidence		RefSeq	UniProt	BRENDA	BLAST	BrEPS	Enzyme Name
	filter	filter	filter	filter	≥ 0.78	KEGG	found	found	found	≤ filter	found	filter
>	O65201	MQN23.4	ACX2, At5g65110	1.3.3.6	4.66	✓						
>	P0CZ23	T2D23.1	ACX3, At1g06290, F9P14.15, F9P14_11	1.3.3.6	4.66	✓						
>	Q8GWW7	T22D6.110	AIH, EMB1873, At5g08170	3.5.3.12	4.66	✓						
>	Q9FMV7 5	MLE2.8	CYP94B1, At5g63450	1.14.14.48	4.66	✓						
>	Q9SMP5 4	T8P19.30	CYP94B3, At3g48520	1.14.14.48	4.66	✓						
>	Q9ZUX1 5	F15K20.21	CYP94C1, At2g27690	1.14.14.49	4.66	✓						

On the result page you find

- a list of annotated enzymes with
 - UniProt-ID
 - locus tags
 - synonyms
 - EC numbers
 - confidence score
 - KEGG
 - RefSeq
 - SwissProt / TrEMBL
 - BRENDA
 - BLAST e-values
 - BrEPS
 - enzyme names

Number of filtered predictions: 21983 (13498 unique genes)

On the result page you find

- Entries based on manually or text mining data, not based on sequences (NSB)

Enzymes

NSB

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* BRENDA and AMENDA ¹ ◦ only BRENDA (manually curated) ◦ only AMENDA (based on textmining) ¹

Search enzyme:

	EC Number 	Enzyme Name 	Source 	Reliability 	# of References
>	1.1.1.1	alcohol dehydrogenase	AMENDA	textmining (++)	15
>	1.1.1.1	alcohol dehydrogenase	AMENDA	textmining (++++)	6
>	1.1.1.1	alcohol dehydrogenase	AMENDA	textmining (++)	13
>	1.1.1.1	alcohol dehydrogenase	AMENDA	textmining (+)	19
>	1.1.1.1	alcohol dehydrogenase	AMENDA	textmining (+++)	5
>	1.1.1.1	alcohol dehydrogenase	BRENDA	manually curated	1
>	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase	AMENDA	textmining (++)	1
>	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase	AMENDA	textmining (+)	1
>	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase	BRENDA	manually curated	1
>	1.1.1.102	3-dehydrosphinganine reductase	BRENDA	manually curated	1

Overall number of genes with predicted enzyme function:

13498

with 1 EC-candidate

8387

with 2 or more EC-candidates

5111

with confidence group 0 [0-1]

5670

with confidence group 1 [1-2]

3229

with confidence group 2 [2-3]

2314

with relevance group 3 [>3]

2242

Number of distinct EC-numbers:

2133

with 1 gene position

474

with 2-4 gene positions

766

with 5-10 gene positions

510

with >10 gene positions

383

not sequence based

1423

Entries in:

21983

BRENDA

1520

SwissProt

6167

TrEMBL

794

BREPS

6035

BLAST-based annotation

20728

NCBI

0

KEGG Orthology

4947

On the result page you find

- **some statistics on**
 - **the number of genes with predicted enzyme functions**
 - **the number of distinct EC numbers**
 - **the number of entries of all used data resources**

* BRENDA Pathways ◦ MetaCyc Pathways

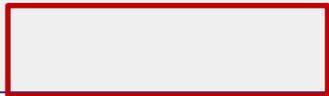
Search pathway or EC numbers:

Pathway	Coverage	Coverage [%]	Enzymes in this pathway (unpredicted in red)
> dolichyl-diphosphooligosaccharide biosynthesis	15/15	100	2.4.1.117 2.4.1.131 2.4.1.132 2.4.1.141 2.4.1.142 2.4.1.256 2.4.1.257 2.4.1.258 2.4.1.259 2.4.1.260
> cyanate degradation	2/2	100	4.2.1.1 4.2.1.104
> ppGpp biosynthesis	3/3	100	2.7.6.5 3.1.7.2 3.6.1.
> coenzyme A metabolism	5/5	100	2.7.1.24 2.7.1.33 2.7.
> sulfolipid biosynthesis	2/2	100	2.4.1.- 3.13.1.1
> photosynthesis	20/21	95.2	1.1.1.40 1.1.1.82 1.10 2.7.9.1 3.1.3.11 3.1.3 5.3.1.6 7.1.1.6 1.2.1.
> valine metabolism	12/13	92.3	1.1.1.1 1.1.1.31 1.1.1. 4.2.1.17 4.2.1.9 6.1.1
> vitamin K metabolism	8/9	88.9	2.1.1.163 2.2.1.9 3.1. 2.5.1.74
> allantoin degradation	7/8	87.5	1.7.3.3 3.5.1.116 3.5.2.17 3.5.2.5 3.5.3.26 3.5.3.9 4.1.1.97 1.1.1.350
> arachidonate biosynthesis	14/16	87.5	1.1.1.100 1.1.1.330 1.14.14.129 1.14.19.2 1.14.19.45 1.3.1.9 1.3.1.93 2.3.1.- 2.3.1.23 2.3.1.41 3.1.2.14 4.2.1.134 4.2.1.59 6.2.1.3 1.14.19.30 1.14.19.46

On the result page you find

- pathway information of the predicted enzyme functions
- You can choose between BRENDA and MetaCyc Pathways
- the predicted (grey) and unpredicted (red) enzymes are directly linked to the Enzyme Summary Pages in BRENDA

Found 146 pathways (27 with > 80 % coverage)



Arabidopsis thaliana	helia
Maximum confidence	Helianthus annua (Helianthus annuus)
EC number	Helianthus annus (Helianthus annuus)
1.-.-	Helianthus annuus (Helianthus annuus)
1.1.-	Helianthus annuus L. (Helianthus annuus)
1.1.1	Helianthus annuus8 (Helianthus annuus)
1.1.100	
1.1.102	
1.1.107	

er in the selected organisms:

Search EC numbers:

On the result page you can

- compare the number of predicted enzyme annotations with other organisms**

1.1.116	2.7
1.1.122	3.66
1.1.133	1.74
	1.74
	1.74
	2.82

Found 2008 enzymes

Arabidopsis thaliana

Helianthus annuus ×

Brassica napus ×

Add organism

Maximum confidence score for each EC number in the selected organisms:

Search EC numbers:

EC number	Arabidopsis thaliana	Helianthus annuus	Brassica napus
1.-.-.-	2.78	1.91	1.91
1.1.-.-	2.78	1.91	1.91
1.1.1.-	2.78	1.91	3.67
1.1.1	3.66	1.91	1.91
1.1.1.100	2.7	1.7	2.59
1.1.1.102	3.66	0.95	0.95
1.1.1.105		0.82	
1.1.1.107	1.74		
1.1.1.116	1.74		
1.1.1.122	1.74		

Found 2154 enzymes

On the result page you can

- compare the number of predicted enzyme annotations with other organisms

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Arabidopsis thaliana

Helianthus annuus ×

Brassica napus ×

Add organism

Maximum confidence score for each EC number in the selected organisms:

Search EC numbers:

EC number	Arabidopsis thaliana	Helianthus annuus	Brassica napus
1.-.-.-			1.91
1.1.-.-			1.91
1.1.1.-			3.67
1.1.1.1	3.66	1.91	1.91
1.1.1.100	2.7	1.7	2.59
1.1.1.102	3.66	0.95	0.95
1.1.1.105		0.82	
1.1.1.107	1.74		
1.1.1.116	1.74		
1.1.1.122	1.74		

At the bottom of the result pages you can download the entries as *.csv or *.json file

Found 2154 enzymes

« ‹ 1 2 3 4 5 › »

10 entries per page

Download as CSV

Download as JSON