



The Taxonomy Reports View of BLAST Results

<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

A BLAST result display format for evaluating taxonomic distribution of matched sequences

National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

Introduction

NCBI BLAST web services offer additional result display options. The updated “Taxonomy reports” view (A) provides details of the taxonomic distribution of matches BLAST found. This display, particularly the **Organism Report**, directly addresses the question of “which organisms have matches to the input query?” This fact-sheet describes the structure of the Taxonomy Reports display to help facilitate the usage of this report format.

BLAST® >> blastp suite >> RID-H1YZ82ZB014

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BLAST Results

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rabbit Aspartate aminotransferase

RID [H1YZ82ZB014](#) (Expires on 04-16 22:34 pm) **A** [\[Taxonomy reports\]](#) [\[Distance tree\]](#)

Query ID lcl|Query_94001

Description rabbit Aspartate aminotransferase

Molecule type amino acid

Query Length 429

Database Name nr

Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program BLASTP 2.3.1+ > Citation

Other reports: > Search Summary [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#) [\[Multiple alignment\]](#)

See results arranged by taxonomy

Structure of the Taxonomy Reports

The Taxonomy Reports summarizes BLAST search results by grouping hits by their taxonomic assignment and presents grouped hits in three sections: the **Lineage Report**, the **Organism Report**, and the **Taxonomy Report**. These sections are open by default, but the example shown to the left has two of them closed (B).

Tax BLAST report

Tax BLAST report

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B

Lineage Report

Organism Report

Taxonomy Report

[Organism Report Taxonomy Report](#)

[Lineage Report Taxonomy Report](#)

[Organism Report Lineage Report](#)

Taxonomy	Number of hits	Number of Organisms	Description
[-] root	161	84	
[-] Theria	158	83	
[-] Eutheria	157	82	
[-] Boreoeutheria	149	76	
[-] Euarchontoglires	94	37	
[-] Glires	54	17	
[-] Primates	38	19	
[-] Tupaia chinensis	2	1	Tupaia chinensis hits
[-] Laurasiatheria	55	39	
[-] Chiroptera	9	7	
[-] Carnivora	9	7	
[-] Insectivora	2	2	
[-] Perissodactyla	6	4	
[-] Cetartiodactyla	29	19	
[-] Afrotheria	7	5	
[-] Orycteropus afer afer	2	1	Orycteropus afer afer hits
[-] Elephantulus edwardii	1	1	Elephantulus edwardii hits
[-] Trichechus manatus latirostris	1	1	Trichechus manatus latirostris hits
[-] Chrysochloris asiatica	2	1	Chrysochloris asiatica hits
[-] Loxodonta africana	1	1	Loxodonta africana hits
[-] Dasypus novemcinctus	1	1	Dasypus novemcinctus hits
[-] Monodelphis domestica	1	1	Monodelphis domestica hits
[-] synthetic construct	3	1	synthetic construct hits

The Lineage and Taxonomy Reports sum up the number of hits for a given taxonomic node and place them in a lineage structure. For non-terminal nodes, this is the sum of hits from all included terminal nodes. The Lineage Report provides the score from the top match for each terminal node, while the Taxonomy Report provides a more detailed and interactive display without the score.

The Organism Report collects hits from each organism together in separate subsections, along with the title, score, Expect value, and Accession.

The Lineage Report

The Lineage Report summarizes the BLAST hits by placing organisms with hits in a taxonomic lineage display along with the number of hits found and the bit score of the top matches for the terminal nodes.

This is the easiest display for seeing all species of organisms represented in the results. The taxonomic level is indicated by the indentation in the Organism column (A), with dots as visual aids to allow the level of indentation to be determined quickly. The Blast Name column (B) lists the alias used by BLAST for the group or organisms. Entries in these two columns link to relevant entries in the Taxonomy database. The Score column (C) lists the highest bit score for hits found from that group. The Number of Hits column (D) are the total number of hits found for that group, which is the sum of hits from all leaf nodes under that level. The hit numbers link to relevant entries in the source database, the Protein database in this case. The text descriptions in the Description column (E) are anchored to the relevant subsection in the Organism Report, which shows more details on these hits.

Close this report by clicking the "-" sign to bring other sections to the top

Use page anchors to jump to other sections

A	Organism	B	C	D	E
		Blast Name	Score	Number of Hits	Description
	root			665	
	cellular organisms			662	
	Eukaryota	eukaryotes		594	
	Opisthokonta	eukaryotes		531	
	Eumetazoa	animals		461	
	Bilateria	animals		460	
	Deuterostomia	animals		407	
	Chordata	chordates		406	
	Gnathostomata	vertebrates		405	
	Euteleostomi	vertebrates		404	
	Lutimera	vertebrates		199	
	Boreoeutheria	placentals		178	
	Euarchontoglires	placentals		110	
	Glires	placentals		61	
	Lagomorpha	rabbits & hares		4	
	Oryctolagus cuniculus	rabbits & hares	899	2	Oryctolagus cuniculus hits
	Ochotona princeps	rabbits & hares	875	2	Ochotona princeps hits
	Heterocephalus glaber	rodents	856	2	Heterocephalus glaber hits
	Microtus ochrogaster	rodents	848	1	Microtus ochrogaster hits
	Cricetulus griseus	rodents	848	4	Cricetulus griseus hits
	Peromyscus maniculatus bairdii	rodents	847	1	Peromyscus maniculatus bairdii hits
	Mus musculus	rodents	847	29	Mus musculus hits
	Nannospalax galili	rodents	847	1	Nannospalax galili hits
	Chinchilla lanigera	rodents	846	1	Chinchilla lanigera hits
	Cavia porcellus	rodents	846	1	
	Marmota marmota marmota	rodents	845	1	
	Fukomys damarensis	rodents	843	2	
	Rattus norvegicus	rodents	843	8	
	Mesocricetus auratus	rodents	842	1	Mesocricetus auratus hits
	Octodon degus	rodents	833	1	Octodon degus hits
	Dipodomys ordii	rodents	830	1	Dipodomys ordii hits
	Ictidomys tridecemlineatus	rodents	803	2	Ictidomys tridecemlineatus hits
	Jaculus jaculus	rodents	716	1	Jaculus jaculus hits
	Macaca fascicularis	primates	853	5	Macaca fascicularis hits
	Chlorocebus sabaeus	primates	853	1	Chlorocebus sabaeus hits
	Papio anubis				Papio anubis hits
	Xanthomonas cassavae				Xanthomonas cassavae hits
	synthetic construct	other sequences	840	3	synthetic construct hits

Click a name to get their taxonomic details from the Taxonomy database

The number of hits for a non-leaf node is the sum of hits from all leaf nodes below it: 61 for **Glires** = sum of hits for all leaf nodes within the box

Use links to see details of these hits from this organism in the Organism Report

Lineage level indicated by level of indentation with dots as a visual aid

Extra hits removed for brevity and clarity

Click the number to see these sequence records in the source database

Background highlight upon mouseover facilitates the visual examination

The Organism Report

The Organism Report resembles the Description table of the traditional BLAST results. This is the best report for examining all matches for a particular species.

- It organizes hits by their source organisms, each in their own subsections (A). The subsection titles are anchored and linked from Number of Hits column in the other two reports
- It shows details of the hits by providing their sequence titles (such as in B)
- It also provides a summary on alignment quality by listing the Score and Expect value (C)
- The title of each hit links back to the corresponding alignment in the traditional BLAST results page to allow re-examination of the alignment details (D)
- The accessions (E) are linked to the sequence record in the source database

Toggle close this report by clicking the “-” sign to bring other sections to the top

Use page anchors to jump to other sections

Organism Report Page Report Taxonomy Report

Description	Score	E value	Accession
Oryctolagus cuniculus (rabbit) [rabbits & hares] ▼ Next ▲ Previous ▲ First			
PREDICTED: aspartate aminotransferase, mitochondrial [Oryctolagus cuniculus]	899	0.0	XP_002711597
RecName: Full=Aspartate aminotransferase, mitochondrial; Short=mAspAT; AltName: Full=Fatty acid-binding protein; Short=FABP-1;	899	0.0	P12345
Ochotona princeps (American pika) [rabbits & hares] ▼ Next ▲ Previous ▲ First			
PREDICTED: aspartate aminotransferase, mitochondrial isoform X1 [Ochotona princeps]	875	0.0	XP_004583963
Heterocephalus glaber (naked mole-rat) [rodents] ▼ Next ▲ Previous ▲ First			
PREDICTED: aspartate aminotransferase, mitochondrial [Heterocephalus glaber]	856	0.0	XP_004843177
Aspartate aminotransferase, mitochondrial [Heterocephalus glaber]	856	0.0	EHB01268
Eptesicus fuscus (big brown bat) [bats] ▼ Next ▲ Previous ▲ First			
PREDICTED: aspartate aminotransferase, mitochondrial isoform X1 [Eptesicus fuscus]	855	0.0	XP_008138091
Macaca fascicularis (crab-eating macaque) [primates] ▼ Next ▲ Previous ▲ First			
aspartate aminotransferase, mitochondrial [Macaca fascicularis]	853	0.0	NP_001270119
RecName: Full=Aspartate aminotransferase, mitochondrial; Short=mAspAT; AltName: Full=Fatty acid-binding protein; Short=FABP-1;	853	0.0	Q4R559
unnamed protein product [Macaca fascicularis]	853	0.0	BAE01766
Aspartate aminotransferase, mitochondrial [Macaca fascicularis] Go to alignment for unnamed protein product [Macaca fascicularis]	837	0.0	EHH60442
Chlorocebus sabaeus (brown lemur) [primates] ▼ Next ▲ Previous ▲ First			
PREDICTED: aspartate aminotransferase, mitochondrial isoform X1 [Chlorocebus sabaeus]	853	0.0	XP_007991734
Papio anubis (olive backed guinea pig) [carnivores] ▼ Next ▲ Previous ▲ First			
PREDICTED: aspartate aminotransferase, mitochondrial [Papio anubis]	853	0.0	XP_009194835
Panthera tigris altaica (Amur tiger) [carnivores] ▼ Next ▲ Previous ▲ First			
PREDICTED: aspartate aminotransferase, mitochondrial [Panthera tigris altaica]	808	0.0	XP_007090444
Ictidomys tridecemlineatus (thirteen-lined ground squirrel) [rodents] ▼ Next ▲ Previous ▲ First			
PREDICTED: LOW QUALITY PROTEIN: aspartate aminotransferase, mitochondrial-like [Ictidomys tridecemlineatus]	803	0.0	XP_013214748
Mandrillus leucophaeus (drill) [primates] ▼ Next ▲ Previous ▲ First			
PREDICTED: aspartate aminotransferase, mitochondrial [Mandrillus leucophaeus]	802	0.0	XP_011849395
Sus scrofa domesticus (domestic pig) [even-toed ungulates] ▼ Next ▲ Previous ▲ First			
aspartate aminotransferase, Asp [Sus scrofa domesticus]	801	0.0	0308236A
Loxodonta africana (African savanna elephant) [placentals] ▼ Next ▲ Previous ▲ First			
PREDICTED: LOW QUALITY PROTEIN: aspartate aminotransferase, mitochondrial [Loxodonta africana]	800	0.0	XP_010594999

Click accession to see the sequence record in its source database

Mouseover title to see tooltip popup, and click the title to see alignment in the traditional BLAST result page

Use the arrows to navigate to different subsections within this report

The Taxonomy Report

The Taxonomy Report is very similar to the Lineage Report, but provides an easy way to focus on a particular group of organisms. The lineage display is more detailed and interactive, with collapsible, intervening, non-leaf node subsections making it easy to collapse hits from groups of organisms that are not of interest. It also reports the number of organisms with hits for all non-leaf nodes. In this report, the taxonomic level is indicated by the indentation in the Taxonomy column (A), with dots as a visual aid so the level of indentation can be determined quickly. Each subsection for a specific non-leaf node can be toggled off and on using the “-/+” sign (B) and the organism name links to actual records in the Taxonomy database to provide additional details. The Number of Hits column (C) sums the total number of hits found for that group, which is the sum of hits from all leaf nodes under that level, with the number links to the relevant entries in the source database, i.e., Protein or Nucleotide database. The text description in the Description column (D) is anchored to the relevant subsection in the Organism Report that shows these hits grouped together with additional details on the quality of matches.

Close this report by clicking the “-” sign to bring other sections to the top

Use page anchors to jump to other sections

Feedback

Organism Report Lineage Report

Taxonomy	Number of hits	Number of Organisms	Description
[-] root	158	84	
[-] Theria	155	83	
[-] [-] Eutheria	154	82	
[-] [-] [-] Boreoeutheria	146	76	
[-] [-] [-] [-] Euarchontoglires	91	37	
[-] [-] [-] [-] [-] Laurasiatheria	55	39	
[-] [-] [-] [-] [-] [-] Chiroptera	8	6	
[-] [-] [-] [-] [-] [-] Carnivora	10	8	
[-] [-] [-] [-] [-] [-] Insectivora	2	2	
[-] [-] [-] [-] [-] [-] Perissodactyla	6	4	
[-] [-] [-] [-] [-] [-] [-] Ceratotherium simum simum	1	1	Ceratotherium simum simum hits
[-] [-] [-] [-] [-] [-] [-] Equus	5	3	
[-] [-] [-] [-] [-] [-] [-] [-] Equus caballus	4	2	
[-] [-] [-] [-] [-] [-] [-] [-] Equus przewalskii	3	1	Equus caballus hits
[-] [-] [-] [-] [-] [-] [-] [-] Equus asinus	1	1	Equus przewalskii hits
[-] [-] [-] [-] [-] [-] [-] [-] Equus asinus	1	1	Equus asinus hits
[-] [-] [-] [-] [-] [-] [-] [-] [-] Vicuona pacos	29	19	
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Vicuona pacos	5	4	
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Vicuona pacos	1	1	Vicuona pacos hits
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Camelus	4	3	
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Camelus bactrianus	1	1	Camelus bactrianus hits
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Camelus ferus	2	1	Camelus ferus hits
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Camelus dromedarius	1	1	Camelus dromedarius hits
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Bovidae	14	8	
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Sus	4	2	
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Sus scrofa	2	2	Sus scrofa hits
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Sus scrofa	1	1	Sus scrofa domesticus hits
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Cetacea	5	5	
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Balaenoptera acutorostrata scammoni	1	1	Balaenoptera acutorostrata scammoni hits
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Odontoceti	5	4	
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Physeter catodon	2	1	Physeter catodon hits
[-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] [-] Lipotes vexillifer	1	1	Lipotes vexillifer hits
[-] Delphinidae	2	2	
[-] Orcinus orca	1	1	
[-] Tursiops truncatus	1	1	
[-] Afrotheria	7	5	
[-] Orycteropus afer afer	2	1	Orycteropus afer afer hits
[-] Elephantulus edwardii	1	1	Elephantulus edwardii hits
[-] Trichechus manatus latirostris	1	1	Trichechus manatus latirostris hits
[-] Chrysochloris asiatica	1	1	Chrysochloris asiatica hits
[-] Loxodonta africana	1	1	Loxodonta africana hits
[-] Dasyypus novemcinctus	1	1	Dasyypus novemcinctus hits
[-] Monodelphis domestica	1	1	Monodelphis domestica hits
[-] synthetic construct	3	1	synthetic construct hits

Click a name to get the taxonomic details from the Taxonomy database

Use these links to see details of these hits from this organism in the Organism Report

The number of hits for a non-terminal node (with “+/-” sign) is the sum of hits from all leaf nodes below it, and the number of organisms is the sum of leaf nodes (organisms) under that node

Lineage level is indicated by level of indentation with dots as a visual aid

Click the number to see these sequence records in the source database

Background highlight upon mouseover facilitates the visual examination

We welcome feedback from our users. Please address them to: blast-help@ncbi.nlm.nih.gov