

EchinoDB User Manual

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1. Access EchinoDB Application

Click on the following link to access the application: <https://echinodb.uncc.edu>

EchinoDB is a database consisting of amino acid sequence orthoclusters from 42 echinoderm transcriptomes. We sampled taxa to span the deepest divergences within each of the 5 extant echinoderm classes. Data can be searched by keywords such as annotation and database identifiers from the Strongylocentrotus purpuratus reference protein set at NCBI.

a. Echinaster spinulosus
d. Pteraster tessellatus
g. Pisaster ochraceus

b. Hyocrinus & Florometra
e. Strongylocentrotus purpuratus

c. Various Mariametrea
f. Stichopus chloronotus

2. Perform Search against Orthocluster Database

Type in any any keyword such as “zinc,” “chlor,” “iron” or NCBI’s accession numbers like “XP_78042.” Hit the “Submit Search” button in the upper left side of the web page or press the “Enter” key to execute search.

4 result(s) found

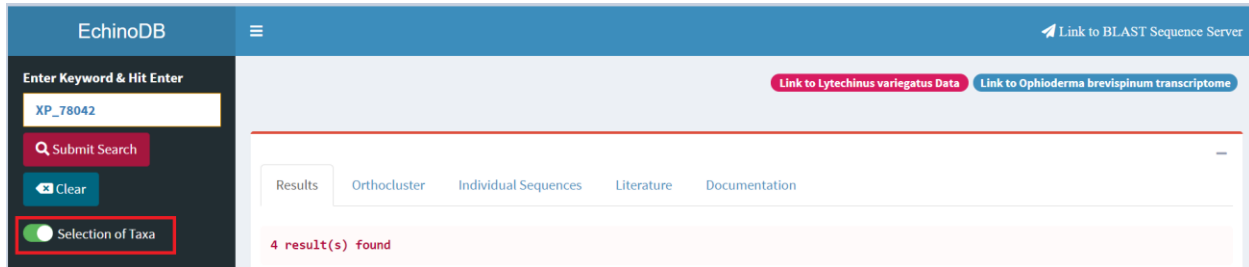
Show 10 entries

gi_num	rfname	otherids	Accession#	TotalHits
72004278	PREDICTED: tryptophan--tRNA ligase, cytoplasmic-like isoform 3 [Strongylocentrotus purpuratus]	"gi"=>"72004278", "ref"=>"XP_780428.1"	XP_780428.1	65
72009986	PREDICTED: dihydrofolate reductase-like isoform 1 [Strongylocentrotus purpuratus]	"gi"=>"72009986", "ref"=>"XP_780421.1"	XP_780421.1	68
72084113	PREDICTED: ribonucleoside-diphosphate reductase large subunit isoform 1 [Strongylocentrotus purpuratus]	"gi"=>"72084113", "ref"=>"XP_780425.1"	XP_780425.1	110
115892152	PREDICTED: synapse-associated protein 1-like [Strongylocentrotus purpuratus]	"gi"=>"115692152", "ref"=>"XP_780429.2"	XP_780429.2	85

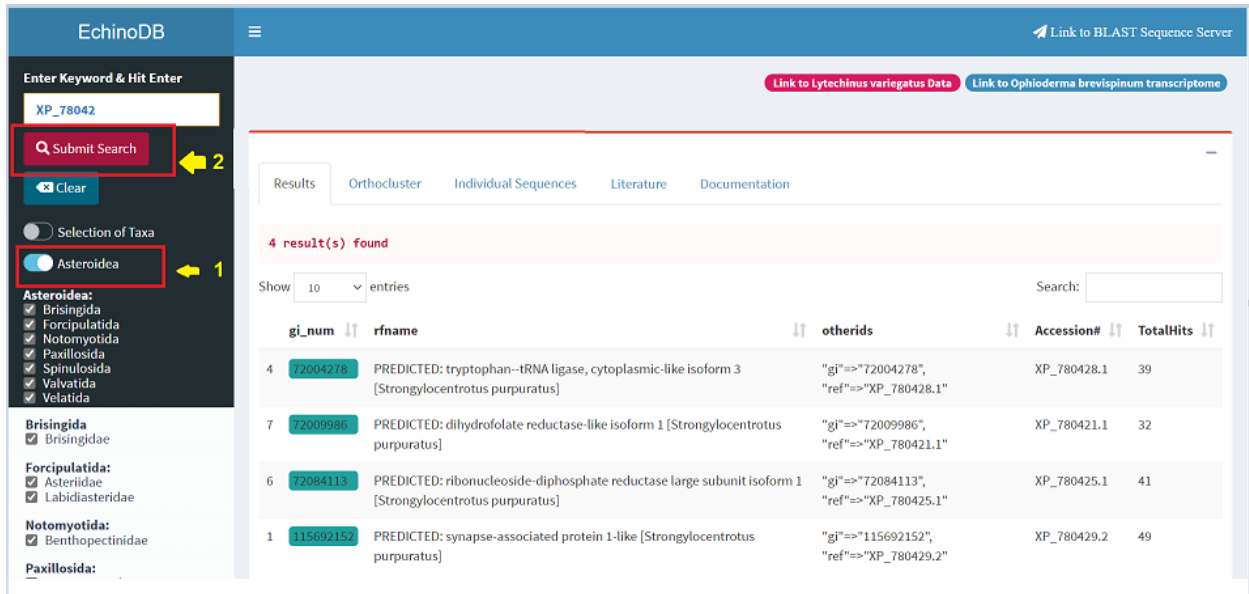
- Note that, using the accession number XP_78042, 4 results are found in this example. However, using the zinc keyword, 98 results are found. These numbers may change as we update the database.

- **Filter Results**

All the names extant Echinoderm classes, orders, and families for which we have data can be used as keywords to filter the search. If information to be retrieved for particular taxon, un-toggle “Selection of Taxa” in the left pane.



- Select Asteroidea and hit the submit button to conduct a search within this class of echinoderms.



- Unselect families to include only those which you would like to use in your search.

The image shows three sequential screenshots of a taxonomic filter interface. In the first, 'All' is selected. In the second, 'Asteroidea' is selected and 'Brisingida' is unselected, with an orange box around it and the text 'Unselecting here will hide the species family underneath'. In the third, 'Asteroidea' is selected, 'Brisingida' is unselected, and 'Labidiasteridae' is unselected, with a red box around it and the text 'Unselecting checkbox will not include that family in the search and will include all others (checked ones)'. Arrows indicate the progression from left to right.

- Hit the search button with all these filters applied to narrow down the results.

The screenshot shows a search interface with 'zinc' entered in the search bar. The filter sidebar on the left has 'Asteroidea' selected and 'Brisingida' unselected. The main results area shows '97 result(s) found' and a table of results. The table has columns for 'g_num', 'rfname', 'otherids', 'Refseq_id', and 'TotalHits'. The first row is: g_num: 47551285, rfname: zinc-finger transcription factor-Snail [Strongylocentrotus purpuratus], otherids: "g|"=>"47551285", "ref|"=>"NP_999825.1", Refseq_id: "g|"=>"47551285", "ref|"=>"NP_999825.1", TotalHits: 21.

g_num	rfname	otherids	Refseq_id	TotalHits
47551285	zinc-finger transcription factor-Snail [Strongylocentrotus purpuratus]	"g "=>"47551285", "ref "=>"NP_999825.1"	"g "=>"47551285", "ref "=>"NP_999825.1"	21
72006728	PREDICTED: zinc finger matrix-type protein 5-like [Strongylocentrotus purpuratus]	"g "=>"72006728", "ref "=>"XP_780288.1"	XP_780288.1	7
72011355	PREDICTED: zinc transporter ZIP1-like [Strongylocentrotus purpuratus]	"g "=>"72011355", "ref "=>"XP_782100.1"	XP_782100.1	7
72015911	PREDICTED: zinc finger protein-like 1 homolog isoform 2 [Strongylocentrotus purpuratus]	"g "=>"72015911", "ref "=>"XP_785452.1"	XP_785452.1	13
72019828	PREDICTED: zinc finger protein ZIC 1-like, partial [Strongylocentrotus purpuratus]	"g "=>"72019828", "ref "=>"XP_792929.1"	XP_792929.1	22
72025879	PREDICTED: zinc transporter 6-like [Strongylocentrotus purpuratus]	"g "=>"72025879", "ref "=>"XP_794610.1"	XP_794610.1	23
72062514	PREDICTED: zinc finger CCHC-type and RNA-binding motif-containing protein 1-like [Strongylocentrotus purpuratus]	"g "=>"72062514", "ref "=>"XP_796219.1"	XP_796219.1	17
72065517	PREDICTED: GATA zinc finger domain-containing protein 1-like [Strongylocentrotus purpuratus]	"g "=>"72065517", "ref "=>"XP_796303.1"	XP_796303.1	12
115631565	PREDICTED: zinc finger protein castor homolog 1-like [Strongylocentrotus purpuratus]	"g "=>"115631565", "ref "=>"XP_781684.2"	XP_781684.2	10
115644462	PREDICTED: NF1-type zinc finger-containing protein 1-like [Strongylocentrotus purpuratus]	"g "=>"115644462", "ref "=>"XP_001180883.1"	XP_001180883.1	11

- **Search Based on Taxonomic Group**

The user can narrow the search to, for example, only a single family of echinoderms. In the example below we are checking only the family Solasteridae within the order Valvatida of the class Asteroidea.

The screenshot shows the EchinoDB search interface. On the left sidebar, the search term 'zinc' is entered. The 'Selection of Taxa' section is expanded to 'Asteroidea', and within it, 'Valvatida' and 'Solasteridae' are selected. The main results area shows 60 results found. A table displays the following data:

gi_num	rfname	otherids	Accession#	TotalHits
15 72015911	PREDICTED: zinc finger protein-like 1 homolog isoform 2 [Strongylocentrotus purpuratus]	"gi"=>"72015911", "ref"=>"XP_785452.1"	XP_785452.1	1
217 72019828	PREDICTED: zinc finger protein ZIC 1-like, partial [Strongylocentrotus purpuratus]	"gi"=>"72019828", "ref"=>"XP_792929.1"	XP_792929.1	2
216 72025879	PREDICTED: zinc transporter 6-like [Strongylocentrotus purpuratus]	"gi"=>"72025879", "ref"=>"XP_794610.1"	XP_794610.1	2
214 72065517	PREDICTED: GATA zinc finger domain-containing protein 1-like [Strongylocentrotus purpuratus]	"gi"=>"72065517", "ref"=>"XP_796303.1"	XP_796303.1	1
208 115644913	PREDICTED: zinc finger SWIM domain-containing protein 6-like,	"gi"=>"115644913",	XP_001192148.1	1

- **Other Search Options**

You can search by name or gi number in the search box in top right corner.

The screenshot shows the EchinoDB search results for '7201'. A red box highlights the search box containing '7201'. A red arrow points from the text 'GI numbers started with 7201 are displayed below' to the search box. The results table is filtered to show only entries with GI numbers starting with 7201:

gi_num	rfname	otherids	Accession#	TotalHits
15 72015911	PREDICTED: zinc finger protein-like 1 homolog isoform 2 [Strongylocentrotus purpuratus]	"gi"=>"72015911", "ref"=>"XP_785452.1"	XP_785452.1	1
217 72019828	PREDICTED: zinc finger protein ZIC 1-like, partial [Strongylocentrotus purpuratus]	"gi"=>"72019828", "ref"=>"XP_792929.1"	XP_792929.1	2
177 115720173	PREDICTED: zinc finger protein 622-like [Strongylocentrotus purpuratus]	"gi"=>"115720173", "ref"=>"XP_001200563.1"	XP_001200563.1	3

3. View Orthocluster Sequences

Select a whole row and the record will be highlighted in blue (you can select only one row at a time).

EchinoDB Link to BLAST Sequence Server

Enter Keyword & Hit Enter
zinc
Submit Search
Clear

Selection of Taxa
Asteroidae

Asteroidae:
 Brisingida
 Forcipulatida
 Notomysotida
 Paxillosoida
 Spinulosida
 Valvatida
 Velatida

Brisingida
 Brisingidae

Forcipulatida:
 Asteriidae
 Labidiasteridae

Notomysotida:
 Benthoplectinidae

Paxillosoida:
 Astropectinidae
 Luidiidae

Spinulosida:
 Echinasteridae

Valvatida:
 Asteropeidae
 Poranidae
 Solasteridae

Results | Orthocluster | Individual Sequences | Literature | Documentation

60 result(s) found

Show 10 entries

Total Hits denote the total number of sequences having the same accession number

gl_num	rfname	otherids	Accession#	TotalHits
15	72019911 PREDICTED: zinc finger protein-like 1 homolog isoform 2 [Strongylocentrotus purpuratus]	"gi"=>"72019911", "ref"=>"XP_785452.1"	XP_785452.1	1
217	72019828 PREDICTED: zinc finger protein ZIC 1-like, partial [Strongylocentrotus purpuratus]	"gi"=>"72019828", "ref"=>"XP_792929.1"	XP_792929.1	2
216	72025679 PREDICTED: zinc transporter 6-like [Strongylocentrotus purpuratus]	"gi"=>"72025679", "ref"=>"XP_794610.1"	XP_794610.1	2
214	72065517 PREDICTED: GATA zinc finger domain-containing protein 1-like [Strongylocentrotus purpuratus]	"gi"=>"72065517", "ref"=>"XP_796303.1"	XP_796303.1	1
208	115644913 PREDICTED: zinc finger SWIM domain-containing protein 6-like, partial [Strongylocentrotus purpuratus]	"gi"=>"115644913", "ref"=>"XP_001192148.1"	XP_001192148.1	1
179	115670818 PREDICTED: NF-X1-type zinc finger protein NF-X1-like [Strongylocentrotus purpuratus]	"gi"=>"115670818", "ref"=>"XP_786259.2"	XP_786259.2	2
177	115720173 PREDICTED: zinc finger protein 622-like [Strongylocentrotus purpuratus]	"gi"=>"115720173", "ref"=>"XP_001200563.1"	XP_001200563.1	3
202	115758157 PREDICTED: NF-X1-type zinc finger-containing protein 1-like [Strongylocentrotus purpuratus]	"gi"=>"115758157", "ref"=>"XP_793224.2"	XP_793224.2	15
201	115767252 PREDICTED: zinc finger CCH domain-containing protein 10-like isoform 1 [Strongylocentrotus purpuratus]	"gi"=>"115767252", "ref"=>"XP_001177886.1"	XP_001177886.1	2
196	115905924 PREDICTED: zinc finger protein 28 homolog [Strongylocentrotus purpuratus]	"gi"=>"115905924", "ref"=>"XP_785795.2"	XP_785795.2	2

Showing 1 to 10 of 60 entries

Previous 1 2 3 4 5 6 Next

- Amino Acid Sequences**

Display amino acid sequences from the selected orthocluster.

EchinoDB Link to BLAST Sequence Server

Enter Keyword & Hit Enter
zinc
Submit Search
Clear

Selection of Taxa
Asteroidae

Asteroidae:
 Brisingida
 Forcipulatida
 Notomysotida
 Paxillosoida
 Spinulosida
 Valvatida
 Velatida

Brisingida
 Brisingidae

Forcipulatida:
 Asteriidae
 Labidiasteridae

Notomysotida:
 Benthoplectinidae

Paxillosoida:
 Astropectinidae
 Luidiidae

Spinulosida:
 Echinasteridae

Valvatida:
 Asteropeidae
 Poranidae
 Solasteridae

Results | **Orthocluster** | Individual Sequences | Literature | Documentation

Redirects to Orthocluster tab after selection is made on Results screen

Download amino sequences in fasta format

Orthocluster for XP_793224.2 (115758157)
 PREDICTED: NF-X1-type zinc finger-containing protein 1-like [Strongylocentrotus purpuratus]
 15 sequences in orthocluster

Show 10 entries

sp_name	bio_proj_accession	amino_sequence
1 Peribolaster BJ30 folliculatus	PRJNA299409	LGSIKRCQDLKSTPEAELRNPDSMTDHDARLVKDIWRLKEFDRWRRLYLWTKYIAYHQ EGLKELQHYDELSKVKHLIETQEDLEILRGAARVGMTTTGAARHSLQLGPRVWVVE EAAEVLAEHIITLAKQHLILGDHQQLKPNPTVYRLAKLNFMDLSLFRMINNGVPY KSLTHQHRMRPEI
2 Peribolaster BJ30 folliculatus	PRJNA299409	DHESVKVYPPVGGIDSNIFLHAFLEESVQDSTSKNHEAEFLVSLCKYIIQGGYRP TQITLTYVQFLNLRALMKKSVSGVRVSAVDNFGQGEENDVILLVRSWEEGNIGFL KVSNRMCVALSRARHGLFCIGNFSVMQDPLWHRIAEMDRKGLGQQTMLVCRNHPEQK TRVSRQDFLNISEGGCSKPEYRLNCGHSCSTLLCHPTDQEHKEFKLCKNQCQTLKCGHK CGQLCCRPCGKCFKVVY
3 Peribolaster BJ30 folliculatus	PRJNA299409	NVHFQNLHSTQRGECMGDKSARLLKVLGVDSEKLDQDDERLQKTESMPSQHVIVDD EAQRKQRQLDDTHLSDLEQQAELAEFLNQAAVGL
4 Peribolaster BJ30 folliculatus	PRJNA299409	TYDSVEHYLDVQFRLLREDVAPLREGVTEYLSNTRRLQDIRIQVHKVIRKMITQNGK ISYRLQFVDSGLKRVVWEAGKRLYVSVCLTKDFKHMHCATVEDRSVEGLRKGVF
5 Peribolaster BJ30 folliculatus	PRJNA299409	ALRLDESQKAVQAALTQELAVIQPPGTYGKTYIGLKVQALLHLNDKWTGAEDKRPILV VCYTNHALDQFLGIMAFNQIVIRVGRNSSEMTNKNLFLKREERRNRKRVAVHVRV GEILREMSYRQLMEMSQKK

- **Individual Sequences Tab**

Select a row in Orthocluster results which contain amino acids sequences to further view related nucleotide sequences.

Orthocluster for XP_793224.2 (115758157)
 PREDICTED: NFX1-type zinc finger-containing protein 1-like [Strongylocentrotus purpuratus]
 15 sequences in orthocluster

sp_name	bio_proj_accesion	amino_sequence
1 Peribolaster BJ30 folliculatus	PRJNA299409	LGSIKRCGQDLKSTPEALRNPDSMTDHDARLVKDIWRKKEFDRWRRLVWTKYIAYHQ EGLKELQHKYDELKSKVHLIETQEDLEILRGARVGMTTGAARHRLQLCLGPRVVVVE EAAEVLAAHIITLAKQQLHLIGDHQQLKPNPTVYRLAKLNMDSLFRMINNGVPPY KSLTHQHRMPEI
2 Peribolaster BJ30 folliculatus	PRJNA299409	DHESVKVYPMVGGIDSNIFLHAFLEESVQDSTSKSNKHEAEFLVSLCKYIIQQGQYRP TQITLTYVYVGLFNLRALMKKSVFSGVRVSAVDNFGQEENDVILLSVRSNEEGNIGFL KVSNRMCVALSRARHGLFCIGNFVIMQDPLWHRIAEMDRKGLGQMTLVCRNHPQK TRVSRADQLNISEGGCSKPCYRLNCGHSCTLLCHPTDQEHKFKCLLNKQQLTKCGHK CGQLCCRPCGCKFKVY
3 Peribolaster BJ30 folliculatus	PRJNA299409	NVHFQNLHSTRGECMGDKSARLLKWLGVVDSDEKLDQDDERLQKTESMPSQHVVD EAKRIKQERLDDOHELDSTLEQAEALEFLQNAAYGL
4 Peribolaster BJ30 folliculatus	PRJNA299409	TYDSVEHYLDVQFRLLREDFVAPLRGVTYELNSTRRLQDIRIQKVHVRKNITQNGK ISYRLQFDVSLKRVREAGKRLIYGSFVCLTKDDFKHMLCATVEDRSVEGLRKGIV
5 Peribolaster BJ30 folliculatus	PRJNA299409	ALRLDESQKAVQAALTQELAVIQGPPGTGKTYIGLKVQALLHNLKDKWTGAEDKRPILV VCYTNHLDQFLGEMAFNQIVNRVGRSNEEMTNKLNFLKREERRNRKVARAVHIRV GEILREMSYQRQLMEMSQKK

- **Amino Acid and DNA Sequences**

The user will find different buttons to download amino acid (protein) or DNA sequences.

Orthocluster for XP_793224.2 (115758157)
 PREDICTED: NFX1-type zinc finger-containing protein 1-like [Strongylocentrotus purpuratus]
 15 sequences in orthocluster

Download Amino Sequence → **Protein Sequence**

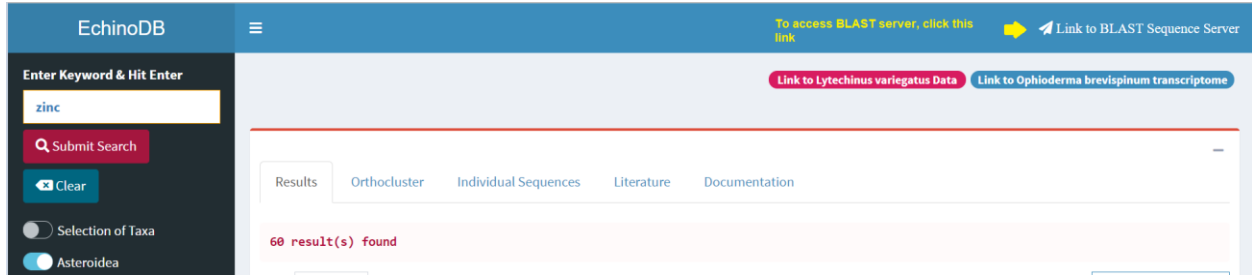
Protein Sequence: DHESVKVYPMVGGIDSNIFLHAFLEESVQDSTSKSNKHEAEFLVSLCKYIIQQGQYRPTQITLTYVYVGLFNLRALMKKSVFSGVRVSAVDNFGQEENDVILLSVRSNEEGNIGFLKVSNRMCVALSRARHGLFCIGNFVIMQDPLWHRIAEMDRKGLGQMTLVCRNHPQKTRVSRADQLNISEGGCSKPCYRLNCGHSCTLLCHPTDQEHKFKCLLNKQQLTKCGHKCGQLCCRPCGCKFKVY

Download Nucleotide Sequence → **DNA Sequence**

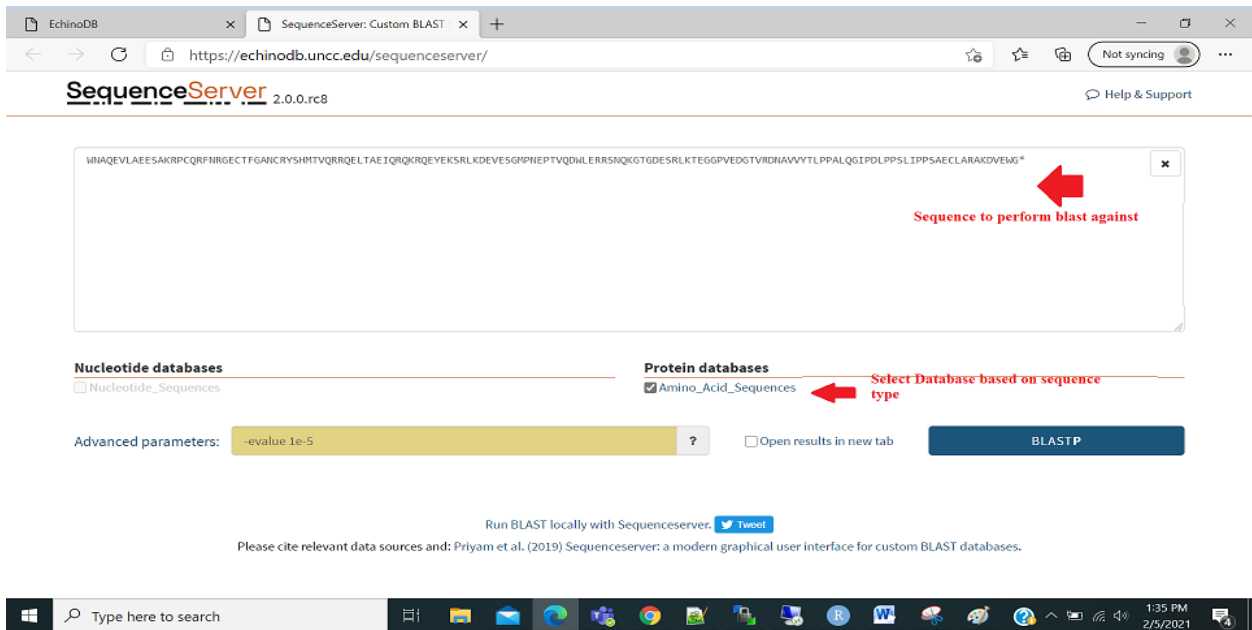
Nucleotide Sequence: GTACACCTCTTGAAACATTTACACATG6TCTACAGCATAACGACCACACTTATGACCACACTGAGTGTCTGTGGCAATCTCAAGCACCTAAACTCTTATGCTCTTGATCTGTAGGATGGCACAAGAGGTTGACGCTGTGACCGGATTAAGGCGGTATTCCGATGGCTTGCTGATCTCTCAGAAATTTAGGAAATCTGTGACACGGCTGACTGAGTTCTGTCTGTGATGATTACGACAGCAAGGTCAATTTGCTGACCAAGGCGCTTTCTATCCATCTCAGCAGCAATCTATGCCACAGGGATCTTGATATGACACTAAAGTTTCAATGCAAAAAAGACCATGAGTGGCCCTAGACATGCTACACACATCGGATTAGACACTTCAAGAATCCAGTGTACCTCTCTACTGGAACCAACGACAGCAAAATACGCTATTCTCTCTTGAAGATTATCCAGCGCCGAGACGAAACCACTGAAACCCGACTTCTCAT AAGTGCTCGGAGTTGAAAGCTGCTCCGACATAGCTGTTAGGATTGAACTGCGTGTGCTGTATTTGCCCTGCTGATGATGACTTGCATAATGATACAGAAACTCTGCTGTTGTTGCTGACTGCTGTTGAGTCTTGGACGCTCTCAAGAAACCGATGATTCAGG AAAAAGATGTTGATCAATCTCCACATTTGGATAAACCCTGACGGACTGTGGTCTT.

4. Sequenceserver for Basic Local Alignment Search Tool

Access Sequenceserver (Priyam *et al.* 2019) from EchinoDB by clicking the “Link to Sequenceserver” in the header line or by type in the following URL:
<https://echinodb.uncc.edu/sequenceserver>



- Paste your query string (amino acid or nucleotide sequences) in the text area to perform BLAST search.



- Sequenceserver Results

BLASTP: 1 query, 1 database

Download FASTA, XML, TSV

FASTA of all hits

FASTA of selected hit(s)

Alignment of all hits

Alignment of selected hit(s)

Standard tabular report

Full tabular report

Full XML report

Rank	Accession	Score	E value	Identity	Positives	Gaps
20.	sp 7:77021 PRJNA299398 OS=Pteraster tessellatus	99	277	2.08x10 ⁻³⁰	42	
21.	sp 36:828 PRJNA299411 OS=Isometra vivipara	97	260	1.33x10 ⁻²⁷	39	
22.	sp 37:9328 PRJNA299478 OS=Promachocrinus kerguelensis	88	240	8.39x10 ⁻²⁵	38	
23.	sp 23:13388 PRJNA300546 OS=Gephyrocinus messingi	97	231	1.47x10 ⁻²³	36	
24.	sp 23:13389 PRJNA300546 OS=Gephyrocinus messingi	97	232	2.15x10 ⁻²³	36	
25.	sp 13:60438 PRJNA299887 OS=Oligometra serripinna	97	230	3.57x10 ⁻²³	36	
26.	sp 11:14214 PRJNA299550 OS=Psolus BJ11 sp	98	216	4.85x10 ⁻²¹	35	
27.	sp 1:4754 PRJNA299480 OS=Psathryometra fragilis	84	197	5.80x10 ⁻¹⁹	33	
28.	sp 47:7311 PRJNA299886 OS=Astrophyton muricatum	60	152	2.02x10 ⁻¹²	32	

hit 1, length: 146

Score: 300.44 (768), E value: 1.52x10⁻¹⁸⁵, Identity: 146/146 (100%), Positives: 146/146 (100%), Gaps: 0/146 (0%)

Query 1 WNAQEVLAEEASAKRQCQRFNRGECTFGANCYSHHTVQRQELTAEIQKQKQYEKSRKDKVEVSGHPNEPTVDLERRSQKGTGDESRLKTEGGPV 100

Subject 1 WNAQEVLAEEASAKRQCQRFNRGECTFGANCYSHHTVQRQELTAEIQKQKQYEKSRKDKVEVSGHPNEPTVDLERRSQKGTGDESRLKTEGGPV 100

Query 101 EDGTVRDNAVVTLPALQGIPLDPPSLIPPSAECLARAKDVEWG* 146

Subject 101 EDGTVRDNAVVTLPALQGIPLDPPSLIPPSAECLARAKDVEWG* 146

hit 2, length: 187

- Download FASTA Sequence from a high scoring pair from Sequenceserver

Subject 181 GCNLACEFRLGCGHSCGMLCHPTDPEHOYKCLKKCEKTLKCGHRCKLLCFORCDNCRER 240

Query 256 V 256

Subject 241 V 241

sp|47:17258|PRJNA299886 OS=Astrophyton muricatum

Hit length: 502

Rank	Score	E value
1.	310.84 (795)	1.20 x 10 ⁻¹⁰²
2.	46.21 (108)	2.36 x 10 ⁻⁰⁴

Query 1 DHESVKVYPNVGGIDSDH+SVK + N+ G+ SN DHDSVKQFDNIMGVASH

Subject 102 TQITILLITYVQGFENLH +SQTILLITY QLEN + SQTILLITYTAQLFNFK

Query 61 TQITILLITYVQGFENLH +SQTILLITY QLEN + SQTILLITYTAQLFNFK

Subject 161 TQITILLITYVQGFENLH +SQTILLITY QLEN + SQTILLITYTAQLFNFK

Query 121 KVSNRMCVALSRARHGLKV+NR+CVALSRAR GL

Subject 221 KVANRVCVALSRARHGLKV+NR+CVALSRAR GL

Query 180 KTRVSRADFLNISEGGT VS +DFL + EGG

Subject 281 GTEVSIQKDFLKVPEGGT VS +DFL + EGG

Query 239 --HKCGQLCCRPCKG--C H+C LC + C K C

Subject 341 LKHRCKNLCKEYKVKMG

sp|47:17258|PRJNA299886 OS=Astrophyton muricatum

```

1 NMLQR IKPRI IVVEE AAEVL ESHII TTLTK ECQQL ILIGD
41 HQQLR PNPTV YELAK NFNLD ISLFE RMVKN GLPCQ RLAQQ
81 HRMRP EISQI MKLSH FYPHL IDHDS VKQFD NIMGV ASNVF
121 FLDHN KLEAY VDDTK SHSNK HEAEF LVSLR RYFLQ QGYAP
161 SQITI LTTYT AQLFN FKRVM EKKLF KGIRV CAVDN FQGEE
201 NDII LSLVR SNEEG SIGFL KVANR VCVAL SRARK GLFICI
241 GNFSL LASQS QLWGD IVTKM KKNISY FGTKL KLVCH NHPET
281 GTEVS IQKDF LKVPE GGCSK PCGTR LGCGH ACSMP CHPRD
321 PEHVE YRCLK QCTKS VLGCP LKHRC KNLCY KECVK MCKEK
361 VEKRL MCGHT TEVLC FKDVR LVVQC KSCSK SLLCG HSCNK
401 KCGEE CQSKC EELVK YSDLP CGHVV TMSCS AEAGD CPYPC
441 DVELL CGHKC TGTCG KCHRG RIHIP CKQKC GRTL V CGHEC
481 PEPCT KSCPP CQMPK QNRVC HS
  
```

Select | **FASTA**

5. Clear Search/Results

Go to the results tab and hit the “Clear” button underneath the search button to clear search.

The screenshot shows the EchinoDB search interface. The search bar contains the keyword 'zinc'. The 'Clear' button is highlighted with a yellow box. The search results show 60 results found. The first result is a predicted zinc finger protein-like 1 homolog isoform 2 from *Strongylocentrotus purpuratus*. The table below shows the details of this result.

gi_num	rfname	otherids	Accession#	TotalHits
72015911	PREDICTED: zinc finger protein-like 1 homolog isoform 2 [<i>Strongylocentrotus purpuratus</i>]	"gi"=>"72015911", "ref"=>"XP_785452.1"	XP_785452.1	1

- The search will be cleared after the button is clicked. The user can turn the switch “Selection of Taxa” on if further taxon selection is desired.

The screenshot shows the EchinoDB search interface with the search bar containing 'gene name, keywords, etc.'. The 'Selection of Taxa' switch is turned on. The search results show a list of images of echinoderms, labeled a through g. Below the images are the names of the species.

EchinoDB is a database consisting of amino acid sequence orthoclusters from 42 echinoderm transcriptomes. We sampled taxa to span the deepest divergences within each of the 5 extant echinoderm classes. Data can be searched by keywords such as annotation and database identifiers from the *Strongylocentrotus purpuratus* reference protein set at NCBI.

a. *Echinaster spinulosus*
b. *Hyocrinus* & *Florometra*
c. Various *Mariametrea*
d. *Pteraster tessellatus*
e. *Strongylocentrotus purpuratus*
f. *Stichopus chloronotus*
g. *Pisaster ochraceus*

6. Additional Links

Links in the top right are provided to redirect users to “OphiuroidDB” by clicking blue button (“Link to *Ophioderma brevispinum* transcriptome”) or “EchinoidDB” by clicking red button (“Link to *Lytechinus variegatus* Data”).

EchinoDB

Enter Keyword & Hit Enter
gene name, keywords, etc.
Submit Search
Clear
Selection of Taxa

Link to BLAST Sequence Server

Link to Echinoid DB web page → Link to Lytechinus variegatus Data → Link to Ophioderma brevispinum transcriptome
Link to Ophiuroid DB web page

Results Orthocluster Individual Sequences Literature Documentation

EchinoDB is a database consisting of amino acid sequence orthoclusters from 42 echinoderm transcriptomes. We sampled taxa to span the deepest divergences within each of the 5 extant echinoderm classes. Data can be searched by keywords such as annotation and database identifiers from the Strongylocentrotus purpuratus reference protein set at NCBI.

a. b. c. d. e. f. g.

a. Echinaster spinulosus
d. Pteraster tessellatus
g. Pisaster ochraceus

b. Hyocrinus & Fibrometra
e. Strongylocentrotus purpuratus

c. Various Marimastrea
f. Stichopus chloronotus

7. References

Priyam A, Woodcroft BJ, Rai V, Moghul I, Munagala A, Ter F, Chowdhary H, Pieniak I, Maynard LJ, Gibbins MA, Moon H. Sequenceserver: a modern graphical user interface for custom BLAST databases. *Molecular Biology and Evolution*. 2019; **36(12)**: 2922-4.