

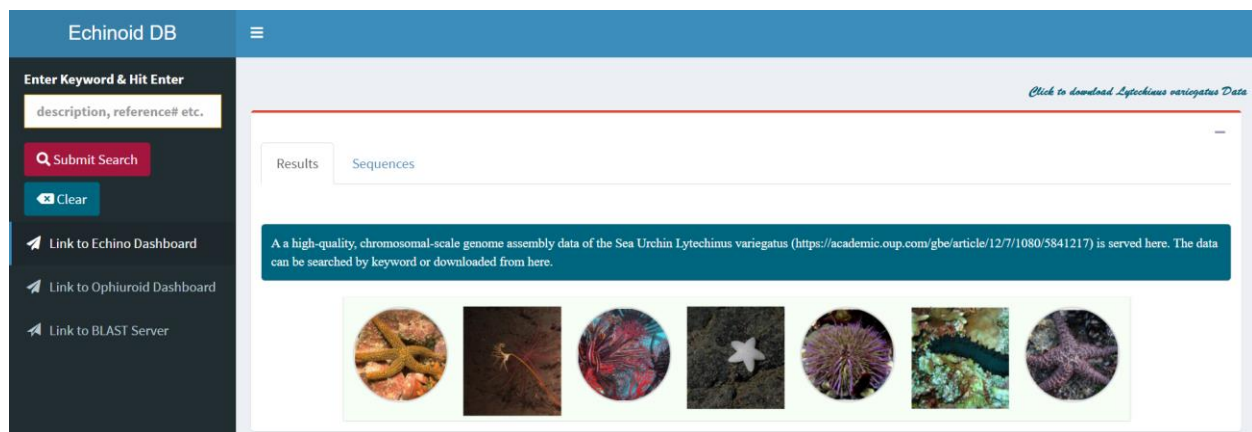
Echinoid Database (EchinoidDB) User Manual

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Date: Nov. 2, 2021

1. Access the EchinoidDB Application

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



The screenshot displays the EchinoidDB application interface. The top navigation bar is blue and contains the text "Echinoid DB" and a hamburger menu icon. Below the navigation bar, the main content area is divided into a left sidebar and a main panel. The sidebar is dark grey and contains a search input field with the placeholder text "Enter Keyword & Hit Enter" and "description, reference# etc.". Below the search field are two buttons: "Submit Search" (red) and "Clear" (blue). At the bottom of the sidebar are three links: "Link to Echino Dashboard", "Link to Ophiuroid Dashboard", and "Link to BLAST Server". The main panel has a light grey background and contains a search results area with tabs for "Results" and "Sequences". A blue banner at the top of the main panel reads "Click to download Lytechinus variegatus Data". Below the banner is a text box stating: "A high-quality, chromosomal-scale genome assembly data of the Sea Urchin *Lytechinus variegatus* (<https://academic.oup.com/gbe/article/12/7/1080/5841217>) is served here. The data can be searched by keyword or downloaded from here." Below the text box is a row of seven circular images showing different views of sea urchins and their internal structures.

2. Search Within the Genome of the Sea Urchin *Lytechinus variegatus*

The user can search data in the chromosome-level assembly of the sea urchin *Lytechinus variegatus* (Davidson et al. 2020). Use any keyword such as “zinc”, “chlor”, “iron” or an NCBI’s accession number such as XP_0220792. Hit the “Submit Search” button in the upper left side of the web page or press “Enter.”

The screenshot shows the Echinoid DB search interface. The search bar contains the keyword "XP_0220792". The search results page displays 21 results found. The search bar in the top right corner is empty. The table below shows the first four results:

Lytechinus variegatus ID	ChrLoc	Start-Stop	Best BLAST Hit Used in Annotation	Best BLAST Hit Used in Description
1 L_var_00103-RA	chr1	4346735-4371274	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]
2 L_var_00149-RA	chr1	6104939-6162104	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]
3 L_var_02236-RA	chr1	76169842-76177737	XP_022079278.1	uncharacterized protein LOC110973096 isoform X1 [Acanthaster planci]
4 L_var_02300-RA	chr1	78068027-78078270	XP_022079270.1	guanylate kinase-like isoform X3 [Acanthaster planci]

- In the example above we used the accession number XP_0220792 keyword and found 21 results. Note that the results may change as we update our databases.

- **Other Search Options**

You can search by description or NCBI’s accession number in the search box in top right corner.

The screenshot shows the Echinoid DB search interface with the search bar in the top right corner containing the keyword "heliq". The search results page displays 21 results found. The table below shows the first three results:

Lytechinus variegatus ID	ChrLoc	Start-Stop	Best BLAST Hit Used in Annotation	Best BLAST Hit Used in Description
1 L_var_00103-RA	chr1	4346735-4371274	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]
2 L_var_00149-RA	chr1	6104939-6162104	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]
7 L_var_02486-RA	chr1	83728648-83792237	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]

Showing 1 to 3 of 3 entries (filtered from 21 total entries)

- **Download Data**

The link “Click to Download *Lytechinus variegatus* Data” is provided in the top right corner to download *Lytechinus variegatus* transcriptome sequences.

The screenshot shows the Echinoid DB search interface. On the left, there is a search bar with the keyword 'XP_0220792' and buttons for 'Submit Search', 'Clear', and navigation links to the Echino Dashboard, Ophiroid Dashboard, and BLAST Server. The main content area shows search results for 'XP_0220792'. At the top right, there is a red box containing the text 'Downloads *Lytechinus variegatus* data in a text file' and a red arrow pointing to a link that says 'Click to download *Lytechinus variegatus* Data'. Below this, the search results are displayed in a table with 21 results found. The table has columns for 'Lytechinus variegatus ID', 'ChrLoc', 'Start-Stop', 'Best BLAST Hit Used in Annotation', and 'Best BLAST Hit Used in Description'. The first three results are shown, all with a 'Best BLAST Hit Used in Annotation' of 'XP_022079225.1' and a description of 'LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]'. The table is paginated, showing 'Showing 1 to 3 of 3 entries (filtered from 21 total entries)' and navigation buttons for 'Previous', '1', and 'Next'.

Lytechinus variegatus ID	ChrLoc	Start-Stop	Best BLAST Hit Used in Annotation	Best BLAST Hit Used in Description
1 L_var_00103-RA	chr1	4346735-4371274	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]
2 L_var_00149-RA	chr1	6104939-6162104	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]
7 L_var_02486-RA	chr1	83728648-83792237	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]

3. Visualize *Lytechinus variegatus* Sequences

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

Echinoid DB

Enter Keyword & Hit Enter
XP_0220792

Submit Search

Clear

Link to Echino Dashboard

Link to Ophiuroid Dashboard

Link to BLAST Server

Click to download *Lytechinus variegatus* Data

Results Sequences

21 result(s) found

Show 10 entries Search:

Lytechinus variegatus ID	ChrLoc	Start-Stop	Best BLAST Hit Used in Annotation	Best BLAST Hit Used in Description
1 L_var_00103-RA	chr1	4346735-4371274	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]
2 L_var_00149-RA	chr1	6104939-6162104	XP_022079225.1	LOW QUALITY PROTEIN: helicase with zinc finger domain 2-like [Acanthaster planci]
3 L_var_02236-RA	chr1	76169842-76177737	XP_022079278.1	uncharacterized protein LOC110973096 isoform X1 [Acanthaster planci]
4 L_var_02300-RA	chr1	78068027-78078270	XP_022079270.1	guanylate kinase-like isoform X3 [Acanthaster planci]
5 L_var_02398-RA	chr1	81054200-	XP_022079252.1	COP9 signalosome complex subunit 8-like [Acanthaster planci]

- **Sequences Tab**

After the record is selected, the user is redirected to the “Sequences” tab and display protein sequences from Ophiuroids repository. Furthermore, it allows downloading the search results in FASTA format.

Echinoid DB

Enter Keyword & Hit Enter
XP_0220792

Submit Search

Clear

Link to Echino Dashboard

Link to Ophiuroid Dashboard

Link to BLAST Server

Click to download *Lytechinus variegatus* Data

Results Sequences

BLAST Details-

- * guanylate kinase-like isoform X3 [Acanthaster planci]
- * Reference#: XP_022079270.1
- * chrLoc: chr1
- * sstart-stop: 78068027-78078270

Lytechinus variegatus ID: L_var_02300-RA

Downloads protein sequence in a FASTA file format [Download Protein Sequence](#)

MSIHSKRNGETDSLTIJMAEYIPRRCVFCPSGSGKSTLIKQLMDEHKDTFGFVSHSTTRNPRPGEQGVHYHYTTREKMLAISNGEFLHAQFSGNMYGTRCLMGNAISEERLGRKTDSEEAIQRLATAIK ELEYIDEETSANATFVVNDREVAYEKIKGILSDIVKLRDIRFKAK

Downloads nucleotide sequence in a FASTA file format [Download DNA Sequence](#)

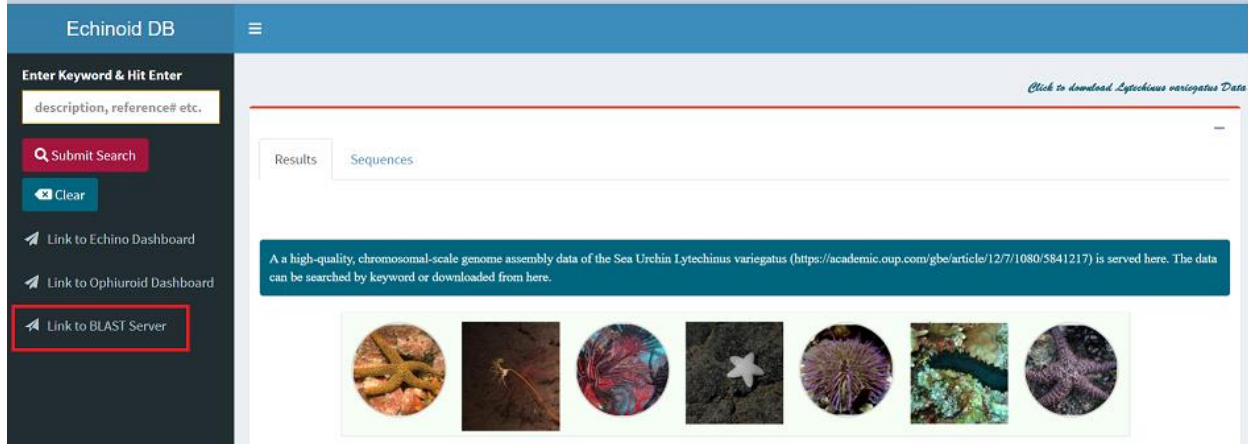
```

ATGAGCATCTGGTCAAAGAGGAATGGGACAGAGGACAGTCTGACTATAATGGCTGAATACATCCAAGACCGTGTGTTTCTGTGGACCTTCAGGGTCTGGTAAAAGCACATTGATTAACAGCTGATGGATGA
ACACAAGATACATTTGGGTTCTCTGTCACTACACGACGAGGAATCCAAGACCTGGGGAACAGGATGGAGTTCATTATCATTATACAACCTCGAGAGAAGATGGAATGGCCATTCAAATGGAGAATTCCTAG
AGCATGCACAGTTTTCAGGCAATATGTATGGTACAAGGTGTCTCATGGCAATGCAATATCTGAGGAGAGACTAGAGGCAGAAAAACAGATTCTGAAGAAAGCATTCAAAGAGATTAGCTACTGCAATAAAG
GAATGGAGTACATCGATGAAGAGACATCCGCAAAACGCAACCTTCGTTGTAAGTCAATGATGACAGAGAGGTAGCTATGAAAAGATCAAGGGAATCCTAAGTACCGATATCGTCAAACCTTAGGGATATCAGATT
CAAGGCAAGTGACCCCTTCATTGTGTATACCTCCAGATGAAATATCTTGAACAAATCTTAAACTATAGATGAATATTATGTATCTTAGTGTAAAGTACATGATGTTTATCGCTTAAAAAGATA
AAATTCGATATGATTATGACTTTAATGCATTACAATATATCACTGTCTTGAAATGATATTCATGAATATTTAATGATATCCATACTAATTCAAATGCTTTAATATATTTCTGTGCCAA
    
```

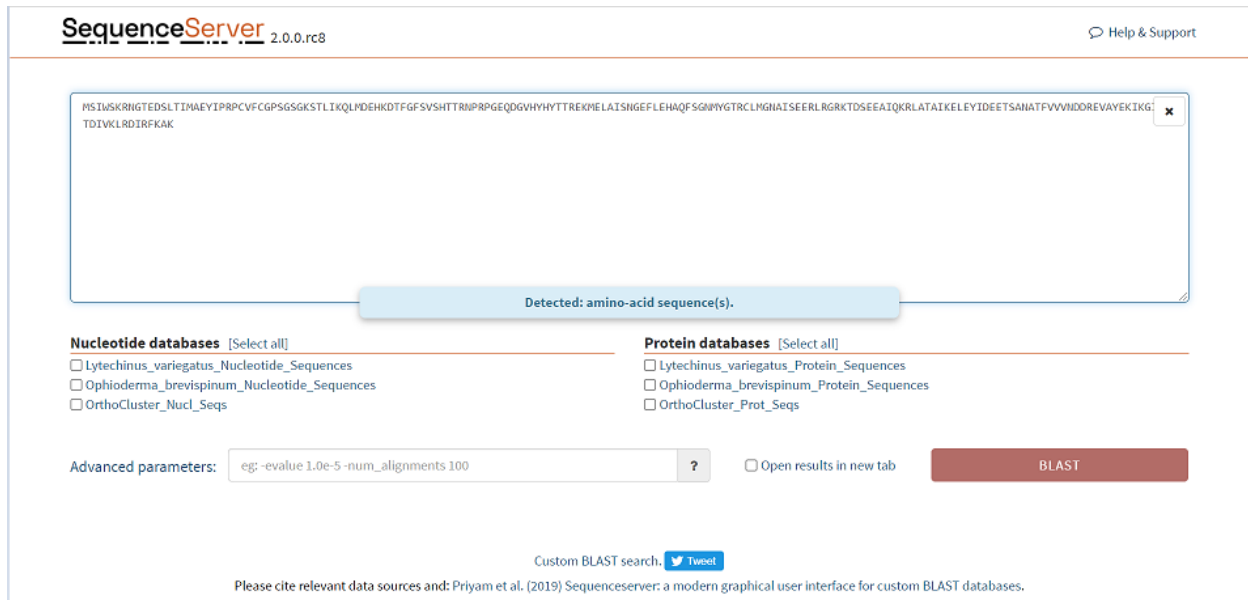
4. Using Sequenceserver

The user can access Sequenceserver (Priyam et al. 2019) to run BLAST by clicking the “Link to BLAST Server” in the left pane or by typing in the following URL:

<https://echinodb.uncc.edu/sequenceserver/>



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



- Select database(s) to perform a BLAST search against the query sequences.

SequenceServer 2.0.0.rc8 Help & Support

```
MSIWSKRNIGT EDSLTI MAEYI PRPCVF CGPSGSGKST LKQLNDEHKDT FGSVSHTRNRPGEQDGVHYHTT REKME LAISMG EFL EHAQFSGNMYGTRCLMGNAISEERLRGRKTDSEEA IQRLATAI KELEYIDEETSANAT FVVVNDREVAYEKIGG
TDIVKLRDIRFKAK
```

Nucleotide databases [Select all]

Lytechinus_variegatus_Nucleotide_Sequences

Ophioderma_brevispinum_Nucleotide_Sequences

OrthoCluster_Nucl_Seqs

Protein databases [Select all]

Lytechinus_variegatus_Protein_Sequences

Ophioderma_brevispinum_Protein_Sequences

OrthoCluster_Prot_Seqs

Advanced parameters: ? Open results in new tab BLASTP

Custom BLAST search. [Tweet](#)

Please cite relevant data sources and: Priyam et al. (2019) Sequenceserver: a modern graphical user interface for custom BLAST databases.

• Sequenceserver Results

SequenceServer 2.0.0.rc8 Help & Support

BLASTP: 1 query, 2 databases

[Edit search](#) | [New search](#)

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](#)

SequenceServer 2.0.0.rc8 using **BLASTP 2.9.0+**, query submitted on 2021-09-30 02:35:38 UTC

Databases: Lytechinus_variegatus_Protein_Sequences, OrthoCluster_Prot_Seqs (1225944 sequences, 304144365 characters)

Parameters: evaluate 1e-05, matrix BLOSUM62, gap-open 11, gap-extend 1, filter F

Please cite: <https://doi.org/10.1093/molbev/msz185>

Queries and their top hits: chord diagram

Query= Query_1 length: 182

Graphical overview of hits [SVG](#) | [PNG](#)

[View More](#) ⌵

Length distribution of hits

Summary table of hits

#	Similar sequences	Query coverage (%)	Total score	E value	Identity (%)
1.	L_var_02300-RA protein AED:0.23 eAED:0.23 Qi:0 0.33 0.71 0.71 0.33 0.57 7...	100	981	1.03×10 ⁻¹³⁶	100
2.	10:11273 OS=Pisaster ochraceus	99	564	1.21×10 ⁻⁷²	51
3.	22:19589 OS=Remaster gourdoni	91	542	4.38×10 ⁻⁶⁹	51
4.	21:67695 OS=Labidiaster annulatus	98	540	6.35×10 ⁻⁶⁹	48
5.	7:54800 OS=Pteraster tessellatus	91	512	6.98×10 ⁻⁶⁵	49
6.	7:54727 OS=Pteraster tessellatus	91	512	6.98×10 ⁻⁶⁵	49
7.	7:54758 OS=Pteraster tessellatus	91	512	6.98×10 ⁻⁶⁵	49

- **Download Sequenceserver Results**

The user can use the buttons “FASTA” and “Alignment” to download data corresponding to the results sequences or alignments, respectively.

22:19589 OS=Remaster gourdoni hit 3, length: 237

Select |
 Sequence |
 FASTA |
 Alignment

Graphical overview of aligning region(s)
 [SVG](#) | [PNG](#)

Score: 213.39 (542), E value: 4.38×10^{-69} , Identity: 106/204 (52%), Positives: 136/204 (66.7%), Gaps: 38/204 (18.6%)

```

Query    17 MAEYIPRPCVFCGSPSGSKSTLIKQLMDEHKDTFGFSVSHTRNRPGEQDGVVHYHTTREKME LAISNGEFL EHAQFSGNMYGTR-----C 103
        18 MA+Y PRPCV CGPSGSGKSTLIK+LMDE+KD FGFSVSHTR PR GEQDGVVHYHTTRE ME AI EF+E+A+FSGN+YGT C
Subject  17 MADYTPRPCVLCGSPSGSKSTLIKKLMDEYKDYFGFSVSHTRKPRSGEQDGVVHYHTTRESMEAAIKRKEFIENAEFSGNLYGTSKKAVQDVLKKNKIC 116
Query    104 LM-----GNAISEERLRGRKTDSEEAIQRLATAIKELEYIDEETSANATFVVVNDREVAYEKIKGILSTDIVKLRDIR 178
        105 ++
        106 + E+RLR R+TD+EEAIQ+RL TA +E+++I + + + V+VND +VAYEK+ GILS+ I +L+D++
Subject  117 ILDIDVQGVQIIQTKLKPVIYIFIKPPNMKVLDRKRKRETD EEAIQRRLETARREMDFIHQHESAVSHVIVNDVDVAYEKLHGILSSHISQLKDLK 216
Query    179 FKAK 182
        180 +K K
Subject  217 YKRK 220
  
```

5. Clear Search/Results in OphiuroiDB

Go to the results tab and hit “Clear” button to clear the search. Alternatively, the user can clear the search results by pressing “Delete.”

Echinoid DB

Enter Keyword & Hit Enter

XP_0220792

Submit Search

Clear

Link to Echino Dashboard

Link to Ophiuroi Dashboard

Link to BLAST Server

Click to download *Lytechinus variegatus* Data

Results Sequences

21 result(s) found

Show 10 entries Search:

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3 L_var_02236-RA	chr1	76169842-76177737	XP_022079278.1	uncharacterized protein LOC110973096 isoform X1 [Acanthaster planci]
4 L_var_02300-RA	chr1	78068027-78078270	XP_022079270.1	guanylate kinase-like isoform X3 [Acanthaster planci]

- The search will be cleared after the button is clicked or delete key is pressed.

Echinoid DB

Enter Keyword & Hit Enter
description, reference# etc.

Submit Search

Clear

Link to Echino Dashboard

Link to Ophiuroid Dashboard

Link to BLAST Server

Click to download *Lytechinus variegatus* Data

Results Sequences

A high-quality, chromosomal-scale genome assembly data of the Sea Urchin *Lytechinus variegatus* (<https://academic.oup.com/gbe/article/12/7/1080/5841217>) is served here. The data can be searched by keyword or downloaded from here.

6. Additional Links

Links in the left pane are provided to redirect users to “EchinoDB” or “OphiuroidDB” page.

Echinoid DB

Enter Keyword & Hit Enter
description, reference# etc.

Submit Search

Clear

Link to Echino Dashboard

Link to Ophiuroid Dashboard

Link to BLAST Server

Click to download *Lytechinus variegatus* Data

Results Sequences

A high-quality, chromosomal-scale genome assembly data of the Sea Urchin *Lytechinus variegatus* (<https://academic.oup.com/gbe/article/12/7/1080/5841217>) is served here. The data can be searched by keyword or downloaded from here.

7. References

Davidson PL, Guo H, Wang L, Berrio A, Zhang H, Chang Y, Soborowski AL, McClay DR, Fan G, Wray GA. Chromosomal-level genome assembly of the sea urchin *Lytechinus variegatus* substantially improves functional genomic analyses. *Genome Biology and Evolution* 2020; **12(7)**:1080-6; doi: 10.1093/gbe/evaa101.

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. doi: 10.1093/molbev/msz185.