

# TP5 Entrepôt des données biologiques

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## Soumettre une séquence d'ADN :

Lancer une recherche BLAST pour la séquence Deinococcus, avec comme base de donnée nr/nt :

Standard Nucleotide BLAST

blastn blasto blastx tblastn tblastx

BLASTN programs search nucleotide databases using a nucleotide query. [more...](#) [Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#)

Deinococcus  
GACGAATGGTATTCTGACGGCGCACTAGCAGTTCAAGGAGGTGCGCTTTATCTCGCAGGA  
AATCTGGGCGGACGTGCTGGGTTACGTCGCAAAACATCTCGGAAGTGGAGTACCACAC  
CTGGTTTGCTCTCTGAAAAATCTGGGCTCCAGGACGGTT

Clear Query subrange [?](#)

From

To

Or, upload file  Aucun fichier choisi [?](#)

Job Title   
Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database ☒ Standard databases (nr etc.): ☐ rRNA/ITS databases ☐ Genomic + transcript databases ☐ Betacoronavirus

Nucleotide collection (nr/nt) [?](#)

Organism [Optional](#)   
Enter organism name or id--completions will be suggested ☐ exclude [+](#)  
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

Exclude [Optional](#) ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Limit to [Optional](#) ☐ Sequences from type material

Entrez Query [Optional](#)  [YouTube](#) [Create custom database](#)  
Enter an Entrez query to limit search [?](#)

Program Selection

Optimize for ☒ Highly similar sequences (megablast)  
☐ More dissimilar sequences (discontinuous megablast)

BLAST results will be displayed in a new format by default. You can always switch back to the Traditional Results page. [New](#)

## Le résultat de la recherche :

BLAST® » blastn suite » results for RID-DBZ4W0BH01R

HomeRecent ResultsSaved StrategiesHelp

< Edit Search

Save Search

Search Summary ▾

Job Title

Deinococcus

RID

DBZ4W0BH01R

Search expires on 06-03 15:15 pm

Download All ▾

Program

BLASTN ⓘ

Citation ▾

Database

nt

See details ▾

Query ID

lcl|Query\_57363

Description

Deinococcus

Molecule type

dna

Query Length

162

Other reports

Distance tree of results

MSA viewer ⓘ

How to read this report?

BLAST Help Videos

Back to Traditional Results Page

Filter Results

Organism

only top 20 will appear

☐ exclude

Type common name, binomial, taxid or group name

+ Add organism

Percent Identity

to

E value

to

Query Coverage

to

Filter

Reset

Feedback

Descriptions

Graphic Summary

Alignments

Taxonomy

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download ▾

Manage Columns ▾

Show 100 ▾ ⓘ

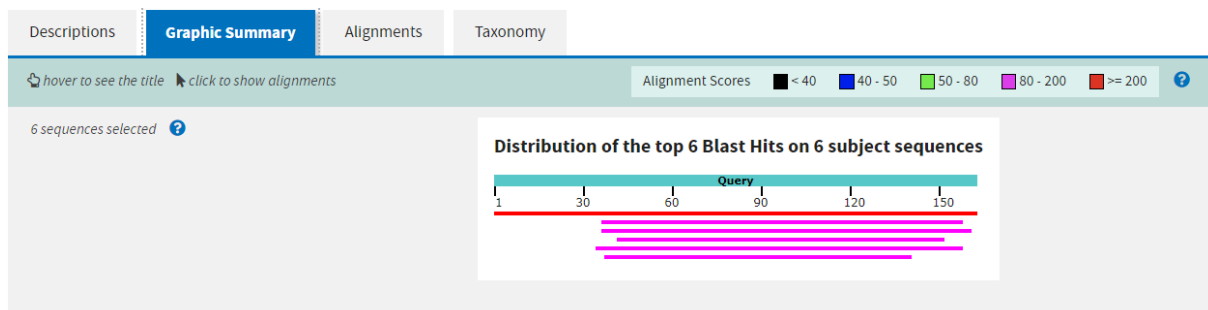
☒ select all 6 sequences selected

[GenBank](#)

[Graphics](#)

[Distance tree of results](#)

|                                     | Description   | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession                  |
|-------------------------------------|---|-----------|-------------|-------------|---------|------------|----------------------------|
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus deserti VCD115 .complete genome</a>           | 300       | 300         | 100%        | 1e-77   | 100.00%    | <a href="#">CP001114.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus ficus strain CC-FR2-10 .complete genome</a>   | 163       | 163         | 74%         | 2e-36   | 90.98%     | <a href="#">CP021081.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus geothermalis DSM 11300 .complete genome</a>   | 158       | 158         | 76%         | 1e-34   | 89.52%     | <a href="#">CP000359.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus sp. NW-56 chromosome .complete genome</a>     | 148       | 148         | 67%         | 6e-32   | 90.91%     | <a href="#">CP026516.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus puniceus strain DY1 .complete genome</a>      | 145       | 145         | 75%         | 7e-31   | 87.90%     | <a href="#">CP011387.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus maricopenensis DSM 21211 .complete genome</a> | 128       | 128         | 63%         | 7e-26   | 89.32%     | <a href="#">CP002454.1</a> |



Descriptions

Graphic Summary

Alignments

Taxonomy

Alignment view

Pairwise

☐ CDS feature

Restore defaults

Download

6 sequences selected

Download

GenBank

Graphics

NextPreviousDescriptions

Deinococcus deserti VCD115, complete genome

Sequence ID: CP001114.1Length: 2819842Number of Matches: 1

Range 1: 1 to 162

GenBank

Graphics

Next MatchPrevious Match

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 300 bits(162) | 1e-77  | 162/162(100%) | 0/162(0%) | Plus/Plus |
| Query 1       | GACGAATGGTATTCTGACGGCGCACTAGCAGTTCAAGGGAGGTGCGCTTTATCTCGCAGG | 60            |           |           |
| Sbjct 1       | GACGAATGGTATTCTGACGGCGCACTAGCAGTTCAAGGGAGGTGCGCTTTATCTCGCAGG | 60            |           |           |
| Query 61      | AAATCTGGGCGGACGTGCTGGGTACGTCCGCAAAACATCTCGGAAGTGGAGTACCACA   | 120           |           |           |
| Sbjct 61      | AAATCTGGGCGGACGTGCTGGGTACGTCCGCAAAACATCTCGGAAGTGGAGTACCACA   | 120           |           |           |
| Query 121     | CCTGGTTTGCTCCTCTGAAAAATCTTGGCGTCCAGGACGGTT                   | 162           |           |           |
| Sbjct 121     | CCTGGTTTGCTCCTCTGAAAAATCTTGGCGTCCAGGACGGTT                   | 162           |           |           |

Descriptions

Graphic Summary

Alignments

Taxonomy

Reports

Lineage

Organism

Taxonomy

6 sequences selected

| Organism                               | Blast Name | Score | Number of Hits | Description                               |
|--|------------|-------|----------------|---|
| Deinococcus                            | bacteria   |       | 6              |   |
| • Deinococcus deserti VCD115           | bacteria   | 300   | 1              | Deinococcus deserti VCD115 hits           |
| • Deinococcus ficus                    | bacteria   | 163   | 1              | Deinococcus ficus hits                    |
| • Deinococcus geothermalis DSM 11300   | bacteria   | 158   | 1              | Deinococcus geothermalis DSM 11300 hits   |
| • Deinococcus sp. NW-56                | bacteria   | 148   | 1              | Deinococcus sp. NW-56 hits                |
| • Deinococcus puniceus                 | bacteria   | 145   | 1              | Deinococcus puniceus hits                 |
| • Deinococcus maricopenensis DSM 21211 | bacteria   | 128   | 1              | Deinococcus maricopenensis DSM 21211 hits |

Descriptions

Graphic Summary

Alignments

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Reports

Lineage

Organism

Taxonomy

6 sequences selected

| Description   | Score | E value | Accession |
|---|-------|---------|-----------|
| Deinococcus deserti VCD115 [bacteria ]                |       |         |           |
| Deinococcus deserti VCD115, complete genome           | 300   | 1e-77   | CP001114  |
| Deinococcus ficus [bacteria ]                         |       |         |           |
| Deinococcus ficus strain CC-FR2-10, complete genome   | 163   | 2e-36   | CP021081  |
| Deinococcus geothermalis DSM 11300 [bacteria ]        |       |         |           |
| Deinococcus geothermalis DSM 11300, complete genome   | 158   | 1e-34   | CP000359  |
| Deinococcus sp. NW-56 [bacteria ]                     |       |         |           |
| Deinococcus sp. NW-56 chromosome, complete genome     | 148   | 6e-32   | CP026516  |
| Deinococcus puniceus [bacteria ]                      |       |         |           |
| Deinococcus puniceus strain DY1, complete genome      | 145   | 7e-31   | CP011387  |
| Deinococcus maricopenensis DSM 21211 [bacteria ]      |       |         |           |
| Deinococcus maricopenensis DSM 21211, complete genome | 128   | 7e-26   | CP002454  |

Descriptions

Graphic Summary

Alignments

Taxonomy

Reports

Lineage

Organism

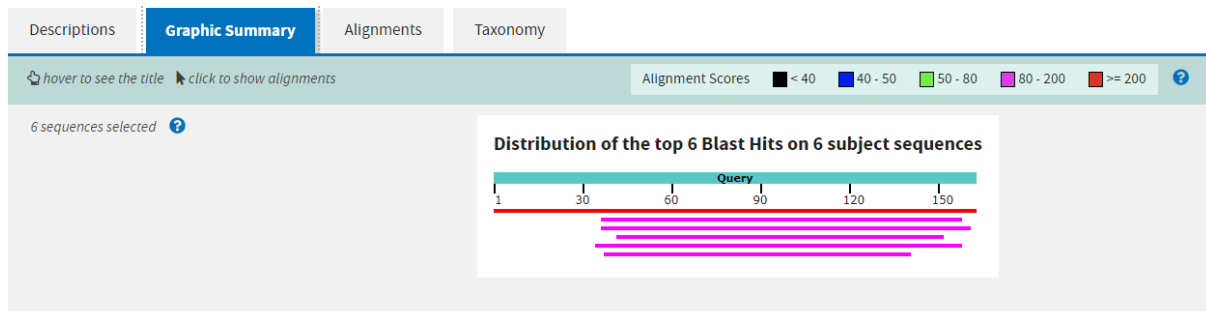
Taxonomy

6 sequences selected

| Taxonomy                               | Number of hits | Number of Organisms | Description                               |
|--|----------------|---------------------|---|
| Deinococcus                            | 6              | 6                   |   |
| • Deinococcus deserti VCD115           | 1              | 1                   | Deinococcus deserti VCD115 hits           |
| • Deinococcus ficus                    | 1              | 1                   | Deinococcus ficus hits                    |
| • Deinococcus geothermalis DSM 11300   | 1              | 1                   | Deinococcus geothermalis DSM 11300 hits   |
| • Deinococcus sp. NW-56                | 1              | 1                   | Deinococcus sp. NW-56 hits                |
| • Deinococcus puniceus                 | 1              | 1                   | Deinococcus puniceus hits                 |
| • Deinococcus maricopenensis DSM 21211 | 1              | 1                   | Deinococcus maricopenensis DSM 21211 hits |

# Comparer une séquence d'ADN avec celles des bases de données :

## 1) Vue graphique :



## 2) La liste des séquences avec leur score et leur E-value :

Sequences producing significant alignments Download Manage Columns Show 100 ?

☒ select all 6 sequences selected

GenBank Graphics Distance tree of results

|                                     | Description   | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession                  |
|-------------------------------------|---|-----------|-------------|-------------|---------|------------|----------------------------|
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus deserti VCD115, complete genome</a>         | 300       | 300         | 100%        | 1e-77   | 100.00%    | <a href="#">CP001114.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus ficus strain CC-FR2-10, complete genome</a> | 163       | 163         | 74%         | 2e-36   | 90.98%     | <a href="#">CP021081.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus geothermalis DSM 11300, complete genome</a> | 158       | 158         | 76%         | 1e-34   | 89.52%     | <a href="#">CP000359.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus sp. NW-56 chromosome, complete genome</a>   | 148       | 148         | 67%         | 6e-32   | 90.91%     | <a href="#">CP026516.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus puniceus strain DY1, complete genome</a>    | 145       | 145         | 75%         | 7e-31   | 87.90%     | <a href="#">CP011387.1</a> |
| <input checked="" type="checkbox"/> | <a href="#">Deinococcus maricopensis DSM 21211, complete genome</a> | 128       | 128         | 63%         | 7e-26   | 89.32%     | <a href="#">CP002454.1</a> |

## 3) L'alignement avec notre séquence requête

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise CDS feature ? Restore defaults Download

6 sequences selected ?

Download GenBank Graphics

▼ Next ▲ Previous ◀ Descriptions

**Deinococcus deserti VCD115, complete genome**

Sequence ID: [CP001114.1](#) Length: 2819842 Number of Matches: 1

Range 1: 1 to 162 GenBank Graphics ▼ Next Match ▲ Previous Match

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 300 bits(162) | 1e-77  | 162/162(100%) | 0/162(0%) | Plus/Plus |
| Query 1       | GACGAATGGTATTCTGACGGCGCACTAGCAGTTCAAGGGAGGTGCGCTTTATCTCGCAGG | 60            |           |           |
| Sbjct 1       | GACGAATGGTATTCTGACGGCGCACTAGCAGTTCAAGGGAGGTGCGCTTTATCTCGCAGG | 60            |           |           |
| Query 61      | AAATCTGGGCGGACGTGCTGGGTTACGTCCGCAAAACATCTCGGAAGTGGAGTACCACA  | 120           |           |           |
| Sbjct 61      | AAATCTGGGCGGACGTGCTGGGTTACGTCCGCAAAACATCTCGGAAGTGGAGTACCACA  | 120           |           |           |
| Query 121     | CCTGGTTTGCTCCTCTGAAAAATCTTGGCGTCCAGGACGGTT                   | 162           |           |           |
| Sbjct 121     | CCTGGTTTGCTCCTCTGAAAAATCTTGGCGTCCAGGACGGTT                   | 162           |           |           |

## Les 5 couleurs différents :

Alignment Scores

■ < 40

■ 40 - 50

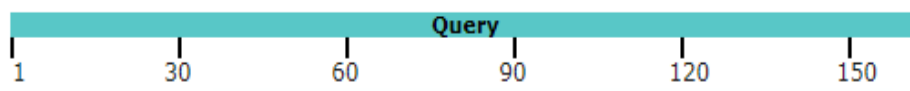
■ 50 - 80

■ 80 - 200

■ >= 200

## Déterminer l'identité des segments d'ADN :

### Distribution of the top 6 Blast Hits on 6 subject sequences



**Deinococcus ficus strain CC-FR2-10, complete genome**

Score:163 Eval:2e-36 Accession:CP021081.1

[Alignment](#)

### **Deinococcus deserti VCD115, complete genome**

Sequence ID: [CP001114.1](#) Length: 2819842 Number of Matches: 1

Range 1: 1 to 162 [GenBank](#) [Graphics](#)

▼ [Next Match](#) ▲ [Previous Match](#)

| Score         | Expect   | Identities    | Gaps      | Strand    |
|---------------|--|---------------|-----------|-----------|
| 300 bits(162) | 1e-77  | 162/162(100%) | 0/162(0%) | Plus/Plus |
| Query 1       | GACGAATGGTATTCTGACGGCGCACTAGCAGTTCAAGGGAGGTGCGCTTTATCTCGCAGG | 60            |           |           |
| Sbjct 1       | GACGAATGGTATTCTGACGGCGCACTAGCAGTTCAAGGGAGGTGCGCTTTATCTCGCAGG | 60            |           |           |
| Query 61      | AAATCTGGGCGGACGTGCTGGGTTACGTCCGCAAAAACATCTCGGAAGTGGAGTACCACA | 120           |           |           |
| Sbjct 61      | AAATCTGGGCGGACGTGCTGGGTTACGTCCGCAAAAACATCTCGGAAGTGGAGTACCACA | 120           |           |           |
| Query 121     | CCTGGTTTGCTCCTCTGAAAAATCTTGGCGTCCAGGACGGTT                   | 162           |           |           |
| Sbjct 121     | CCTGGTTTGCTCCTCTGAAAAATCTTGGCGTCCAGGACGGTT                   | 162           |           |           |

### **Obtenir plus d'information sur une séquence :**

Le numéro d'accès de cette séquence : CP001114.1

La longueur de la séquence : 2819842

La longueur du gène *Deinococcus* :

Quelques articles publiés pour cette bactérie :

- 1) TITLE :** Alliance of proteomics and genomics to unravel the specificities of Sahara bacterium *Deinococcus deserti*

**JOURNAL :** PLoS Genet. 5 (3), E1000434 (2009)

- 2) TITLE :** Proteomics-based refinement of *Deinococcus deserti* genome annotation reveals an unwanted use of non-canonical translation initiation codons

**JOURNAL :** Mol. Cell Proteomics 9 (2), 415-426 (2010)

- 3) TITLE :** RNA Sequencing and Proteogenomics Reveal the Importance of Leaderless mRNAs in the Radiation-Tolerant Bacterium *Deinococcus deserti*

**JOURNAL :** Genome Biol Evol 6 (4), 932-948 (2014)

Quelques protéines qui constituent le gène de cette bactérie :

**1)**

```
"MKANVTKKTLSEGLSLLERVIPGRSSNPLLTALKVETTEAGTL  
SGTNLEIDLSCFVPAEVQQPQNFVVPAPHLFAQIVRNLGGELEITGNELSVRSGGS  
DFKLQTDIEAYPPLSFPEHADVSLNAEELAKAFSSVRYAASNEAFQAVFRGIKLEHR  
PESARVVASDGYRVAIRDFPASGDGRNLIIPARSADELIRVLKDGARFTYGEGLLSV  
TTDRVRMNLKLLDGFDPDYERVIPKDIKLQVTLPATALKEAVNRVAVLADKNANNRVE  
FLVSEGLRLAAEGDYGRAQDTLDVVQGGSEPAMSLAFNARHVLDALGPIEGDAELLF  
SGSTSPAIFRAAGGGGYMAVMVTLRV"
```

2) "MNIEKVIAREVLDSRGNPTVEAEVHLD SGFVGRAIVPSGASTGT  
HEALELRDGGSSRYMGKGVQQAVRNVEEALGPAIVGLDASEQIAIDAALMAVDGTPNKG  
KMGGNAILAVSLATSRAAAEELGVPLYRYLGGSNAKTLVPMMNLINGGAHADNSVDF  
QEFMVMPIGAPTFREALRYGTETFHSLKKVLSSRGYNTNVGDEGGFAPDLKSNEEALQ  
VLEAIEKAGYEPGKDIAIALDPAVTELYKDGHYDLESEGRTLSTAEMVDFWADWADR  
YPIVSIEDGLAEDDWDGWQALTTKIGDRVQLVGDDLFVTNPERLQRGIDTGVGNAILV  
KVNQIGSLTESMDAIELAKRHHYGTIISHRSGESED SFIADLAVATNAGQIKTGSASR  
SDRIAKYNQLLRIEHALGDRAVYLGRKALR"

3)

"MKHSDRSTKIVATIGPASRDPEVLSRMIDAGLNVVRMNFSGHDH  
EDHRQTVMVRELAARKGVITIGILQDLQGP KIRVGRFAQGAVTLNAGDKFVITMDDVD  
GDESRTSTYKSLAEDVQPGMALLDDGNMALRVDHVRGADIHTTVVIGGVLKNNKGI  
NVPDADLSVPAMSEKDVSDMEFGAQIGVDWVALSFVRSRDDLLARHYLSRYGSRACL  
MAKIEKPQAVERFADILKEVDGIMVARGDLGVEMRPEQVPTIQKHIIRMCREAGKPVI  
TATQMLES MISLPRPTRAESDVANAIYDGTDAVMSAESAGQYPVEAVAMMDRIAR  
EAESSDHYLLLRHLMVDTELAQDAIAHSACSIGENLEASVIVTFTSTGGAAARVAKN  
RPPLAILALTPNEQTRNQLALSWGVPVLS EDPRTDDMVRIANDELKSGLADLGDR  
YVITAGVPFGVRGTTNMLRVERLR"

## Chercher dans une banque de données protéique :

blastn blastp blastx tblastn tblastx

BLASTP programs search protein databases using a protein query. [more](#)

**Enter Query Sequence**

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#)

Clear Query subrange [?](#)

From

To

Or, upload file  Aucun fichier choisi [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

**Choose Search Set**

Database [?](#) UniProtKB/Swiss-Prot([swissprot](#)) [?](#)

Organism [?](#) Optional

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?](#) ☐ exclude [+](#)

Exclude [?](#) Optional ☐ Models (XM/XP) ☐ Non-redundant RefSeq proteins (WP) ☐ Uncultured/environmental sample sequences

```

/product="putative chromosomal replication initiator
protein"
/protein_id="ACO44797.2"
/translation="MSQEIWADV LGYVRKNISEVEYHTWFAPLKNLGVQDGS LVLGVR
NSFAQEWLRKQYQGLLEDALRSLGAQHPQVSFQVLPASQDALLPSDPPPAPISPGR
APPPPADNRKTLNPKYTFENFVVGPNNNLAHAAALAVAESPGKAYNPLFIYGDVGLGK
THLMHAVGHYIAERFPEKRIEYVSTETFTNELINAIREDKTTQFRNRYRSVDLLLVD
IQFLAGKERTQEEFFHTFNALYENHKQIILSSDRPPKDIQTLEGRLSRFEWGLITDI
QSPEFETRVA I LKMNAEHNRI DIPQEVLELIARQVTTNIRELEGALMRV VAFSSLNNV
PFSRAVASKALSNVFAPQEVK VEMMDVL RQVASHFNMPD VIRGSGRVREV VVPRQVA
QYLIRDLTDHSLPEIGQFFGRDHS TVMHAISKVTEQLGKDSEL TAAVETLRRKMKGLE
DEDSRA"

```

|                                     | Description   | Max Score | Total Score | Query Cover | E value | Per. Ident | Accession                |
|-------------------------------------|---|-----------|-------------|-------------|---------|------------|--------------------------|
| <input checked="" type="checkbox"/> | RecName: Full=Chromosomal replication initiator protein DnaA [Deinococcus deserti VCD115] | 938       | 938         | 100%        | 0.0     | 100.00%    | <a href="#">C1CXJ1.2</a> |
| <input checked="" type="checkbox"/> | RecName: Full=Chromosomal replication initiator protein DnaA [Deinococcus radiodurans R1] | 733       | 733         | 99%         | 0.0     | 82.25%     | <a href="#">Q9RYE7.2</a> |
| <input checked="" type="checkbox"/> | RecName: Full=Chromosomal replication initiator protein DnaA [Thermus thermophilus HB8]   | 567       | 567         | 97%         | 0.0     | 64.49%     | <a href="#">Q9X9D5.1</a> |
| <input checked="" type="checkbox"/> | RecName: Full=Chromosomal replication initiator protein DnaA [Thermus thermophilus HB27]  | 566       | 566         | 97%         | 0.0     | 64.27%     | <a href="#">Q72H87.2</a> |

blastn

**blastp**

blastx

tblastn

tblastx

BLASTP programs search protein databases using a protein query. [more...](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) ?

> ACO44797.2

MSQEIWADV LGYVRKNISEVEYHTWFAPLKNLGVQDGS LVLGVR

NSFAQEWLRKQYQGLLEDALRSLGAQHPQVSFQVLPASQDALLPSDPPPAPISPGR

PAPPPPADNRKTLNPKYTFENFVVGPNNNLAHAAALAVAESPGKAYNPLFIYGDVGLGK

THLMHAVGHYIAERFPEKRIEYVSTETFTNELINAIREDKTTQFRNRYRSVDLLLVD

Clear

Query subrange ?

From

To

Or, upload file

Choisir un fichier

Aucun fichier choisi ?

Job Title

ACO44797.2

Enter a descriptive title for your BLAST search ?

☐ Align two or more sequences ?

Choose Search Set

Database

Protein Data Bank proteins(pdb)

Organism

Optional

Enter organism name or id--completions will be suggested

☐ exclude +

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. ?

Exclude

Optional

☐ Models (XM/XP)
☐ Non-redundant RefSeq proteins (WP)
☐ Uncultured/environmental sample sequences



## Chain A, Chromosomal Replication Initiator Protein Dnaa [Thermotoga maritima]

Sequence ID: [2Z4R\\_A](#) Length: 440 Number of Matches: 1

[See 3 more title\(s\)](#)

Range 1: 5 to 401 [GenPept](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

| Score         | Expect  | Method                       | Identities   | Positives    | Gaps       |
|---------------|---|------------------------------|--------------|--------------|------------|
| 266 bits(680) | 3e-84   | Compositional matrix adjust. | 141/413(34%) | 233/413(56%) | 22/413(5%) |
| Query 9       | VLGYVRKNISEVEYHTWFAPLKNLGVQDGSVLGVRNSFAQEWLRKQYQGLLEDALRSLG | 68                           |              |              |            |
|               | +L ++ ++ + WF+ ++ +V V N F +EWL K+Y +L A++ +                |                              |              |              |            |
| Sbjct 5       | ILQEIKTRVNRKSWELWFSSFDVKSIEGNKVVFSVGNLFKEWLEKKYYSVLSKAVKVVL | 64                           |              |              |            |
| Query 69      | AQHPQVSFQVLPASQDALLPSDPPPAPISPGRAPAPPADNRKTLNPKYTFENFVVGPN  | 128                          |              |              |            |
|               | +F++ ++ + P P+ RA P LNP YTFENFVVG                           |                              |              |              |            |
| Sbjct 65      | GN--DATFEITYEAFE----PHSSYSEPLVKKRAVLLTP-----LNPDYTFENFVVGPG | 112                          |              |              |            |

### Related Information

[Structure](#) - 3D structure displays

[Identical Proteins](#) - Identical proteins to 2Z4R\_A

## Visualisation en 3D

Biological Unit for 2Z4R: monomeric; determined by software (PISA) [?](#)

Molecular Graphic
?

3D view

full-featured 3D viewer

Interactions
?

Drag symbols to move  
Double click symbols to explore molecules

Download Structure Data
?

Download

Format: ASN.1 (Cn3D)

Data Set: Single 3D structure

Download Cn3D

Molecular Components in 2Z4R [?](#)