

BLAST (Basic Local Alignment Search Tool)

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

Blastp using microbial proteins

**BLAST®**

Basic Local Alignment Search Tool

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## BLAST Assembled Genomes

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## Basic BLAST

Choose a BLAST program to run.

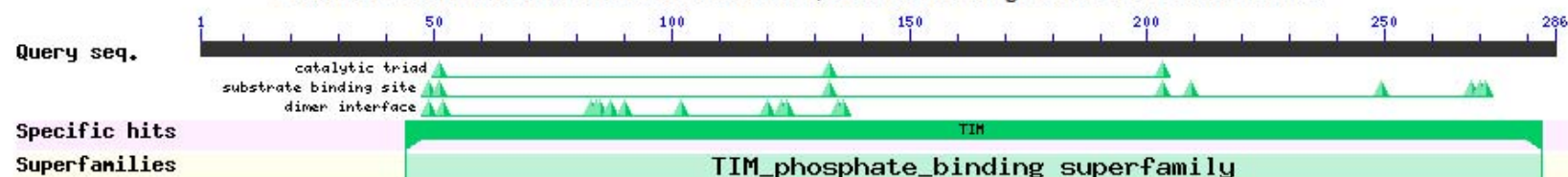
[nucleotide blast](#)Search a **nucleotide** database using a **nucleotide** query*Algorithms: blastn, megablast, discontinuous megablast*[protein blast](#)Search **protein** database using a **protein** query*Algorithms: blastp, psi-blast, phi-blast, delta-blast*

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Basic Local Alignment Search Tool

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Putative conserved domains have been detected, click on the image below for detailed results.

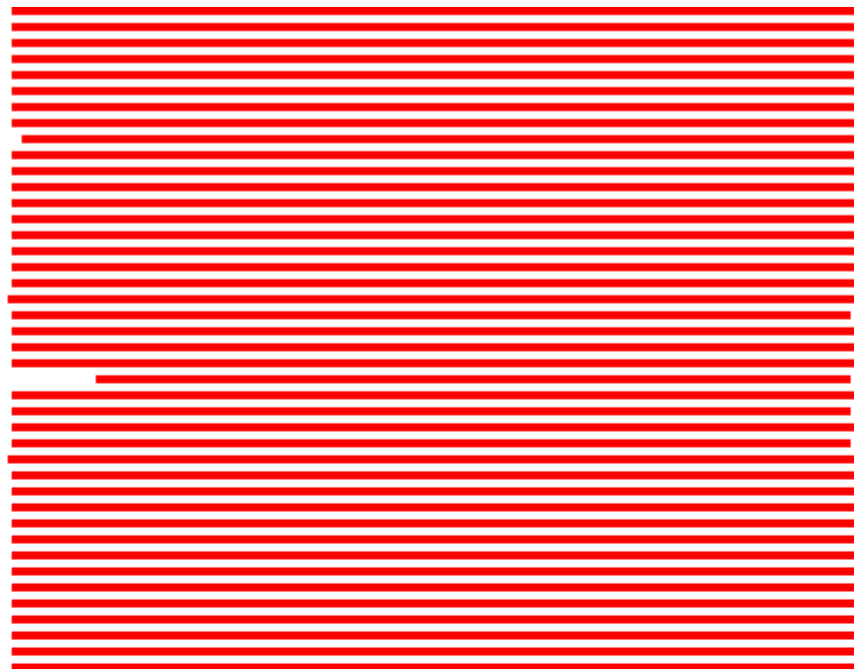


|                       |                          |
|-----------------------|--------------------------|
| Request ID            | H6TZY7BN016              |
| Status                | Searching                |
| Submitted at          | Wed Mar 25 21:59:26 2015 |
| Current time          | Wed Mar 25 22:07:29 2015 |
| Time since submission | 00:08:02                 |

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## Descriptions

### Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

|  Alignments  Download  GenPept  Graphics  Distance tree of results  Multiple alignment  |                                                                                 |           |             |             |         |       |                                |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|-----------|-------------|-------------|---------|-------|--------------------------------|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Description                                                                     | Max score | Total score | Query cover | E value | Ident | Accession                      |
| <input type="checkbox"/>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | <a href="#">hypothetical protein [Proteobacteria bacterium JGI 0000113-E04]</a> | 248       | 248         | 83%         | 1e-77   | 52%   | <a href="#">WP_028831033.1</a> |
| <input type="checkbox"/>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | <a href="#">triosephosphate isomerase [Neptuniibacter caesariensis]</a>         | 223       | 223         | 84%         | 4e-68   | 49%   | <a href="#">WP_007021185.1</a> |
| <input type="checkbox"/>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | <a href="#">triosephosphate isomerase [Krokinobacter sp. 4H-3-7-5]</a>          | 222       | 222         | 84%         | 1e-67   | 49%   | <a href="#">WP_013751574.1</a> |
| <input type="checkbox"/>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | <a href="#">triosephosphate isomerase [Krokinobacter sp. 4H-3-7-5]</a>          | 221       | 221         | 84%         | 1e-67   | 49%   | <a href="#">WP_013751574.1</a> |

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hypothetical protein [Proteobacteria bacterium JGI 0000113-E04]

Sequence ID: [ref|WP\\_028831033.1|](#) Length: 256 Number of Matches: 1

### Related Information

Range 1: 3 to 254  GenPept  Graphics

 Next Match  Previous Match

|       | Score         | Expect                                                        | Method                                  | Identities   | Positives    | Gaps       |  |
|-------|---------------|---------------------------------------------------------------|-----------------------------------------|--------------|--------------|------------|--|
|       | 248 bits(632) | 1e-77                                                         | Compositional matrix adjust.            | 131/252(52%) | 163/252(64%) | 12/252(4%) |  |
| Query | 45            | FVGGNWKMN-GRKQSLGE---                                         | LIGTLN-AAKVPADTEVVCAPPTAYIDFARQKLDPK-IA | 98           |              |            |  |
|       |               | VGGNWK+N G + G+ L+ LN A + +VVCAPP Y+D Q LD                    |                                         |              |              |            |  |
| Sbjct | 3             | IVGGNWKLNAGNGTTTGDVDTLVNGLNETASLAGKCQVVCAPPAIYLDRVNQALDSSTFQ  | 62                                      |              |              |            |  |
| Query | 99            | VAAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESEDELIGQKVAHALAEG | 158                                     |              |              |            |  |
|       |               | VAAQNC+ T+GA+TGE S M+KD G W ++GHSERR +FGE+D L+ +K+AHAL G      |                                         |              |              |            |  |
| Sbjct | 63            | VAAQNCFHETSGAYTGENSAAMLKDLGINWTLIGHSEERRDIFGETDGLLEKKIAHALETG | 122                                     |              |              |            |  |
| Query | 159           | LGVIACIGEKLDEREAGITEKVVFEQTKVIADNVK-----DWSKVVLAYEPVWAIGTGKT  | 213                                     |              |              |            |  |
|       |               | L VIAC GE ++RE G T V+ Q + + D V+ +W VV+AYEPVWAIGTG T          |                                         |              |              |            |  |
| Sbjct | 123           | LSVIACCGEHKEDRENGTTMDVLVPQLQAMVDGVEQGAGGNWDNVVIAIEPVWAIGTGTLT | 182                                     |              |              |            |  |
| Query | 214           | ATPQQAQEVHEKLRGWLKSNVSDAVAQSTRIIYGGSVTGATCKELASQPDVDGFLVGGAS  | 273                                     |              |              |            |  |
|       |               | ATPQQAQE H +RGWL +N VA S RI YGGSV A EL + PD+DGFLVGGAS         |                                         |              |              |            |  |
| Sbjct | 183           | ATPQQAQETHADIRGWLANNAPAGVADSVRIQYGGSVNDANAAELGAMPDIDGFLVGGAS  | 242                                     |              |              |            |  |
| Query | 274           | LKP-EFVDIINA                                                  | 284                                     |              |              |            |  |
|       |               | L +F I +A                                                     |                                         |              |              |            |  |
| Sbjct | 243           | LDAGKFSTIFHA                                                  | 254                                     |              |              |            |  |

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triosephosphate isomerase [Neptuniibacter caesariensis]

Sequence ID: [ref|WP\\_007021185.1|](#) Length: 250 Number of Matches: 1

[▶ See 1 more title\(s\)](#)

### Related Information

Range 1: 3 to 247 GenPept Graphics

 Next Match  Previous Match

## Assignment

1. 10 microbial protein sequences of divergent species
2. Perform Multiple alignment