

TEMPLO

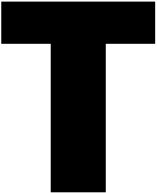
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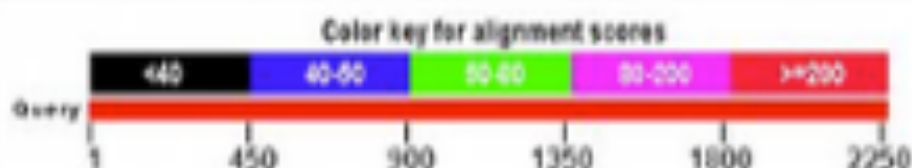
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Distribution of 27 Blast Hits on the Query Sequence

^aNO, 10% Me Homo sapiens glutathione S-transferase, pseudogene (GJ_016871) Ref.

- ☐ FASTA (complete sequence)
- ☒ FASTA (aligned sequences)
- ☐ GenBank (complete sequence)
- ☐ Hit Table (text)
- ☐ Hit Table (CSV)
- ☐ Text
- ☐ XML
- ☐ ASN.1

Continue Cancel

Available columns

- Description
- Max Score
- Total Score
- Coverage
- E-value
- Ident
- Accession

Restore Defaults Ok Cancel

ⓘ Descriptions

Sequences producing sig

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

Alignments Download ▾ GeneBank Graphics Distance tree of results

	Description	Max score	Total score	Query cover	E value	Max ident	Accession
<input checked="" type="checkbox"/>	Rattus norvegicus Ousl2 gene for L-glutino gamma lactone oxidase, complete cds	850	2870	99%	0.0	96%	Cc23542
<input checked="" type="checkbox"/>	Homo sapiens						

Download - GenBank Graphics Sort by: Query start position

▼ [Next](#) ▲ [Previous](#) 📖 [Descriptions](#)

FASTA (complete sequence)
FASTA (aligned sequences)
GenBank (complete sequence)
Continue Cancel

mus norvegicus GULO gene for L-gulon-gamma-lactone oxidase, complete cds

Accession ID: [G012754.2](#) Length: 6009 Number of Matches: 12

Page 1: 303 to 345 Contents Graphics

▼ Next Match: [J. Previous Match](#)

Age	Export	Identifies	Cape	Grand
10/14 (36%)	6/36	135/162 (83%)	9/162 (5%)	Plus/Plus

```

Query 7 CTTGGTACCTCTGGCTTAACCTTCACCTCCCGTCTTGGCTTGAGCTTAACCCAGAGCCGAGCT 66
Subject 393 CTTAGTATGGCTGGCTTAACACCCAGCTCTCTCTTCTGGCTTGAGCTTAACCCAGAGCTGAGCT 432
Query 47 TGCTGACCACTGCATCTGCTGCTGCGCCAGGGCTTTGTTTCATTCTCTGTGGAGAGGCTT 124
Subject 453 TGCTGACCACTGC-----TACCCAGGGCTTTGCTGACTTCTGTGGAGAGGCTT 503
Query 127 CAGGTCAGCTCTCTGACCTGTTGGTGGCTGGAGTCTGGT 144
Subject 144 CAGGTCAGCTCTCTGATCTCTGATCACTGGAGTCTGGT 145

```

Range 2: 844 to 948 [Confer](#), [Graphics](#)

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Gaps	Strand
156 bits(357)	9e-35	98/105(93%)	0/105(0%)	Plus/Plus

Query 148 GGTCATGGGTCAGAGGGGTCCAGTTCACAAACTGGGCCAAGACCTNCGCTGCAGTTC 270
|
Sbjct 944 GGTCATGGGTCAGAGGGGTCCAGTTCACAAACTGGGCCAAGACCTNCGCTGCAGTTC 968

Query 226 AGAGATTCTACCAACCACATCCTCTGGGGGAAGCTCAGAGAGGT 270
|||
Sbjct 904 AGAGATTCTACCAACCACATCCTCTGGGGGAAGCTCAGAGAGGT 948











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