

Top page

# Klebsormidium flaccidum genome project

HOME TEAM DOWNLOAD LINK

HOME

All Sequence data download

K. flaccidum V1.0

◦ [CGA2](#)

Genome viewer

(Under maintenance)

BLAST

(Under maintenance)

◦ [Alternate BLAST server](#)

BLAST

Project Information

• 140528 *Klebsormidium flaccidum* genome V1.0 released

Sequence data have been deposited in GenBank/EMBL/DBJ Accession number: DF236950-DF238763 (1814 entries)

BioProject ID: PRJDB718

Release Information

140528 *Klebsormidium flaccidum* genome

BLAST server

Click!  
BLAST query page

BLAST <*Klebsormidium flaccidum* v1.0>

Choose program to use and database to search:

Program

Database (K. flaccidum V1.0)

Enter sequence below in FASTA format (MAX 10,000 letters)

```
[KYQPD I I I SVHPLM OHVPLRVL RSKGLLKK I VF TTV I TDLSTCHPTWFHKL VTRCYCPST
EVAKRAQKAGLETSQIKVYGLPVRPSFVKVPRKVELRREL GMDENL PAVLL MGGGEGMG
P I E A T A R A L A D A L Y D K N L G E A V G O V L I I C G R N K K L Q S K L S S L D W K I P V Q V K G F I T K M E E C
M G A C D C I I T K A G P G T I A E A M I R G L P I I L N G Y I A G Q V S R E C T V R G G K R M M E I L K I T E R D I E
D C S G L V W T G I E R V G D N V T E C I E A G
```

Paste the query sequence

Click!

BLAST result page

Database: 131203\_kf1\_initial\_genesets\_v1.0\_AA.fasta  
16,215 sequences; 8,771,158 total letters

Query=  
Length=504

Sequences producing significant alignments:

[kf100047\\_0200](#)

Click!

> kf100047\_0200  
Length=547

Score = 455 bits (1170), Expect = 2e-15  
Identities = 203/320 (63%), Positives = 283/320 (88%)

Query 136 VEADRPKKVLILMSDTGGGHRASAEAI RAA  
VE PK VLILMSDTGGGHRASA+A+++AF  
Sbjct 148 VERGGPKTVLILMSDTGGGHRASAQALKSAF

Query 196 SYNFLVKHGTLWKMTYYGTSRPIVHQSNFA  
SY+F+VKH +WK+ + +SP+ +HQ +F A  
Sbjct 208 SYSFMVKHEWIWKLAFDFSSPKFIHQPHFA

Sequence data page

Score (Bits) E Value

[455](#) 2e-154

Gene name

CDS sequence

Protein sequence

kf100047\_0200 CDS monogalactosyl diacylglycerol synthase, MGDG synthase

```
>kf100047_0200
ATGGCGTCTCTCTCTCGCCCTTCCCATGCCCTCATCACCTTCCGAAGCCGCACTG
AGCAGGAGCAAAAAGCACTTCGCGCAAAGCACCGCTTTTAGAGCGAGTCTCCTGCAACCCC
CCCGTTGGCGAGTCAACCGTTTTTCGTGAGACCAAAAAGCCGTCGCCCTCCTCAAAAACCG
GGTTTGTGACAGAGGAAAATGACGGGCAACCCAAAAGGCAAGGTTCAAGCGACGAACC
CCCAACCCACATGGCCGTTCCGTGACCCGCTTACTCCAGCAGCTCCGCTCTCGACAAG
TTGCTCGAAAAGAAGCATGGCTTAAACCCGTTTTTCGTTTGGGGGGGGAGCAATGCACCG
ACGGACCGCGGGGGTGCDAADGGCTTGGATTTCGACCCCTTATTCGTGCGCTCGGGGGGA
GGGGGAAAGGAAAGGGGATGAGTGAAGCGGGAGGCCCTAAAACAGTGCCTCATTTTGATG
AGCGACAGCGGAGGGGGCCATCCGCGAAGGGCGCAAGGGCTGAAGTCAGCATCTTTCTGTG
GAGTTTTGGGACGAGTATGAGGTGATCATCGTATGATGTAAGGACGACACACCCCGCTGG
CCGTTCAACAGTTCCCGGACGCTACAGCTTCATGTTGTAAGCAAGGATGATGATGGAAG
CTCGGGTTGAGCTTCAGCAGCCCAAAATTTATCCACCCAGCCGCACTTTGTGCGCACCC
GCCCTTCGTGCGCAGGAGATGGCCAGGCGTTTCGTCAGTACAAGCTGACATCATGTT
AGCGTGCACCCGCTGATGACGACGTCGCCCTGGCGGCTCCGCTCGCGCGGCCCTCCTC
CACCGCATCCCTTACACACCGTCAATTACCGACCTGCACACCTGCCACCCACCTGGTTCC
CACAAAGCTGGTGACGAGCTGTTTTCGCCCCAGGACAGGGTGGGGAGCGGGCTCAAG
GCGGGCCCTCAACCGGGCCAGTCCGAGTGCAGGCTCGCCATTCGCCAGATTTGCGG
CGCAAGTTACCGCCCGGAAAGAGCTTCGGCAGCAGCTCGGGATGACCCGAGDCTGCCA
GCTGTCATCTCATCGCGGGGGGGAGGCCATGGGCCCGTAGAAGCGACGGCCGGGCA
CTTGGGAGCTCCTCGGGGGGACGAGCGGAACCGCCCTTGGGGCAGCTGATCATATT
TGGGGCGAAACAAAGAGCTGCAGTCCATCTAGAAGCGGTGGATTGGCCATGCGCGAGC
CAGGTGCAAGGGCTTCGTGAAGAATGACCGGAGTGGATGGCCGCTGGATTGGGTGATC
ACCAAGCAGGGCCGGGACGATCGCTGAGGGCTCATCGGGGACGCCCATGCTGCTG
AACGACTTCATCGCTGGACAGAGAGGGGAAACGTCGCTGCTGGTGGAGAAATGGCTGT
GGCAAGTACAGTGAGTACCCACCGGAGATCGCCACCATCTGTGGCCGAGTGGTTCGGGGAG
AAGAAAGGGGAGCTGACCGGATGAAGGAGCGGGCTCAAGCTGCCACGCGGGACCGCC
GTGTTCAACATGTTAGGGACCTAGACAAGCTAGTGAGGAAAGCCAAAGAGGGTACGGT
AGCAAGGGGTTGTTTATGTA
```

```
>kf100047_0200
MASLSLALSRASHLLFEAALSRSKSTSAKHSRSLRVSNPPVAGSPVLLRPKAVPLLQKP
GLL TEENDAAPKRRFRKRPRTMVAPEPVLTPSSALDKLLERSMLNPFSLGGGSNAP
TDAGANGLDLDFPLLASAGGAKGKAVVERGGPKTVLILMSDTGGGHRASAQALKSAFFL
EFGTQYEV I VDMKHEPTWPFNTFSDSYFMVKHEWIKWLAFFDFSSPKFIHQPHVAT I
AFVAREMAKAFVYKPD I I SVHPLM OHVPLRVL RSKGLLHR I PF TTV I TDLTCHPTWF
HKL V T T C P T D R V G E R A L K A G L P G O V R V H G L P I R P D F A R K L P P R K E L R O O L A M H P T L P
AV I L I G G G E G M P V E A T A R A L A D V L G G T S T A P L G O L I I I C G R N K K L Q S K L S S L D W K I L E A V D W P M P T
O V Q G F V K N M P E W M A A S D C V I T K A G P G T I A E A L I R G L P I V L N D F I A G D E T G N V P F V E N G C
G K Y S D V P T E I A T I V A E W F G E R K G E L T A M K E R A L K L A R P D A V F N I V R D L D K L V R K A G E A Y G
S K G Y V V Y
```