

W3.5: Clustal Omega を用いた MSA と分子系統樹の作成

生物種の異なるトリオースリン酸異性化酵素の配列（ヒト TPIS_HUMAN, マウス TPIS_MOUSE

ニワトリ TPIS_CHICK

ショウジョウバエ TPIS_DROME

イネ TPIS_ORYSA

トウモロコシ TPIS_MAIZE

大腸菌 TPIS_ECOLI) のマルチ FASTA 形式のデータを以下に示す。

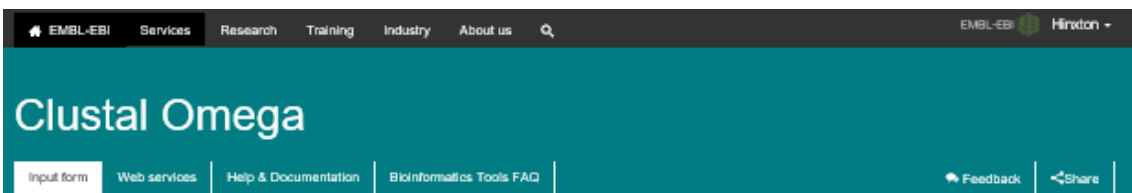
```
>P60174|TPIS_HUMAN Triosephosphate isomerase - Homo sapiens
(Human).
MAPSRKFFVGGNWKMNGRKQSLGELIGTLNAAKVPADTEVVCAPPTAYIDFARQKLDPKI
AVAAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESEDELIGQVAHALAE
GLGVIACIGEKLDEREAGITEKVVFEQTKVIADNVKDWKVVLAYEPVWAI GTGKTATPQ
QAQEVHEKLRGWLKSNVSDAVAQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE
FVDIINAKQ
>P17751|TPIS_MOUSE Triosephosphate isomerase - Mus musculus
(Mouse).
MAPTRKFFVGGNWKMNGRKKCLGELICTLNANVPAGTEVVCAPPTAYIDFARQKLDPKI
AVAAQNCYKVTNGAFTGEISPGMIKDLGATWVVLGHSERRHVFGESEDELIGQVSHALAE
GLGVIACIGEKLDEREAGITEKVVFEQTKVIADNVKDWKVVLAYEPVWAI GTGKTATPQ
QAQEVHEKLRGWLKSNVNDGVAQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE
FVDIINAKQ
>P00940|TPIS_CHICK Triosephosphate isomerase - Gallus gallus
(Chicken).
MAPRKFFVGGNWKMNKDQKSLGELIHTLNGAKLSADTEVVCAPPSIYLDFAHQKLDKIG
VAAQNCYKVPKGAFTGEISPAKIDIGAAWVILGHSERRHVFGESEDELIGQVAHALAEG
LGVIACIGEKLDEREAGITEKVVFEQTKAIADNVKDWKVVLAYEPVWAI GTGKTATPQQ
AQEVHEKLRGWLKSHVSDAVAQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPEF
VDIINAKH
>P29613|TPIS_DROME Triosephosphate isomerase - Drosophila
melanogaster (Fruit fly).
MSRKFCVGGNWKMNQDQKSI AEIAKTLSSAALDPNTEVVIGCPAIYLMYARNLLPCELGL
AGQNAYKVAKGAFTGEISPAKLDIGADWVILGHSERRAIFGESDALIAEKAHALAEG
KVIACIGETLEEREAGKTNEVVARQMCAYAQKIKDWKNVVVAYEPVWAI GTGQTATPDQA
QEVHAFRLQWLSDNISKEVSASLRIQYGGSVTAANAKELAKKPIDIDGFLVGGASLKPEFV
DIINARQ
>P48494|TPIS_ORYSA Triosephosphate isomerase, cytosolic - Oryza
sativa (Rice).
MGRKFFVGGNWKCNQTTDQVDKIVKILNEGQIASTDVVEVVVSPPYVFLPVVKSQLRPEI
QVAAQNCVWKKGAFTGEVSAEMLVNL SIPWVILGHSERRSLLGESNEFVGDKVAYALSQ
```

```

GLKVIACVGETLEQRESGSTMDVVAAQTKAISERIKDWTN VVVVAYEPVWAI GTGKVATPD
QAQEVHDGLRKWLAANVSAEVAESTRIIYGGSVTGANCKELAAKPDVDGFLVGGASLKPE
FIDIINSATVKSA
>P12863|TPIS_MAIZE Triosephosphate isomerase, cytosolic - Zea mays
(Maize) .
MGRKFFVGGNWKCNGTTDQVEKIVKTLNEGQVPPSDVVEVVVSPPYVFLPVVKSQLRQEF
HVAAQNCVWKKGGAFTGEVSAEMLVNLGVPWVILGHSEERRALLGESNEFVGDKVAYALSQ
GLKVIACVGETLEQREAGSTMDVVAAQTKAIAEKIKDWSNVVVVAYEPVWAI GTGKVATPA
QAQEVHASLRDWLKTNASPEVAESTRIIYGGSVTAANCKELAAQPDVDGFLVGGASLKPE
FIDIINAATVKSA
>P0A858|TPIS_ECOLI Triosephosphate isomerase - Escherichia coli.
MRHPLVMGNWKLNGSRHMVHELVSNLRKELAGVAGCAVAIAPPEMYIDMAKREAEGSHIM
LGAQNVLDLNLGSAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQG
LTPVLCIGETEAEENEAGKTEEV CARQIDAVLKTQGA AAFEGAVIAYEPVWAI GTGKSATP
AQAQAVHKFIRDHIAKVDANIAEQV I IQYGGSVNASNAELFAQPDIDGALVGGASLKAD
AFAVIVKAAEAAKQA

```

これを [Clustal Omega](https://www.ebi.ac.uk/Tools/psa/ClustalOmega) のサイトで入力する。



Tools > Multiple Sequence Alignment > Clustal Omega

Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments between **three or more** sequences. For the alignment of two sequences please instead use our [pairwise sequence alignment tools](#).

「PROTEIN」がデフォルト

Important note: This tool can align up to 4000 sequences or a maximum file size of 4 MB.

STEP 1 - Enter your input sequences

Enter or paste a set of

PROTEIN

sequences in any supported format:

```

FIDIINAATVKSA
>P0A858|TPIS_ECOLI Triosephosphate isomerase - Escherichia coli.
MRHPLVMGNWKLNGSRHMVHELVSNLRKELAGVAGCAVAIAPPEMYIDMAKREAEGSHIM
LGAQNVLDLNLGSAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQG
LTPVLCIGETEAEENEAGKTEEV CARQIDAVLKTQGA AAFEGAVIAYEPVWAI GTGKSATP
AQAQAVHKFIRDHIAKVDANIAEQV I IQYGGSVNASNAELFAQPDIDGALVGGASLKAD
AFAVIVKAAEAAKQA

```

入力する配列 (マルチ FASTA 形式)

Or, upload a file:

Use a [example sequence](#) | [Clear sequence](#) | [See more example inputs](#)

STEP 2 - Set your parameters

OUTPUT FORMAT

ClustalW with character counts

The default settings will fulfil the needs of most users.

More options... (Click here, if you want to view or change the default settings.)

デフォルトの設定を変えたいとき、ここでオプションを設定

STEP 3 - Submit your job

Be notified by email. (Click this box if you want to be notified by email when the results are available)

時間がかかるとき、メールで通知

「Submit」ボタンを押す

If you use this service, please consider citing the following publication: [The EMBL-EBI search and sequence analysis tools APIs in 2019](#)

MSA の結果

EMBL-EBI Services Research Training Industry About us

Clustal Omega

Input form | Web services | Help & Documentation | Bioinformatics Tools FAQ

Feedback | Share

Tools > Multiple Sequence Alignment > Clustal Omega

Results for job clustalo-E20211015-083905-0229-79202906-p2m

Alignments | **Result Summary** | Guide Tree | Phylogenetic Tree | Results Viewers | Submission Details

Download Alignment File | Show Colors

CLUSTAL O(1.2.4) multiple sequence alignment

```

P0A858|TPIS_ECOLI      --MRHPLVMSGNWKLNGSRHMVHELVSNLRYELAG-VAGCAVAIAPPEMYIDMAKREAE  56
P48494|TPIS_ORYSA     --MGRKFFVGSNWKNCNITDQVDKIVKILNEGQIASTDVEVWVSPVFLPVKSQL-R    57
P12863|TPIS_MAIZE     --MGRKFFVGSNWKNCNITDQVEIKVILNEGQVFPFSDVVEVWVSPVFLPVKSQL-R    57
P29613|TPIS_DROME     --MSRKFVGSNWKNGDQKSLAEIAKTLSSAALDPN--TEVVIQCPAIVLYMVARNLL-P  55
P00940|TPIS_CHICK     -MAPRKFVGSNWKNGDQKSLGELIHTLNGAKLSAD--TEVVCAPSTIYIDFARQKL-D   56
P60174|TPIS_HUMAN     MAPSRKFVGSNWKNGRQKSLGELIGTLNAKVPAD--TEVVCAPSTIYIDFARQKL-D   57
P17751|TPIS_MOUSE     MAPTRKFVGSNWKNGRQKSLGELIGTLNAANVPAD--TEVVCAPSTIYIDFARQKL-D   57
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

P0A858|TPIS_ECOLI      SHIMLGQNVDMLSGAFGETSAAMLKDIGAQVILIGHSERRTYHKESEDELIAGKFAVL  116
P48494|TPIS_ORYSA     PEIQVAAQNCWVKGGGAFTEVSAEMLVNLSPFWILGHSERRLLGESNEFVGDQKVAVA  117
P12863|TPIS_MAIZE     QEFHVAQNCWVKGGGAFTEVSAEMLVNLGVFVWILGHSERRLLGESNEFVGDQKVAVA  117
P29613|TPIS_DROME     CELGLASQAYKVAKGAFTEISFAMLKDIGADWVILGHSERRIFGESDALLAEKAEHA  115
P00940|TPIS_CHICK     AKISVAAQNCVYVNGAFTEISFAMIKDIGAANWVILGHSERRHVFGESEDLIGQKVAHA  116
P60174|TPIS_HUMAN     PKIATAAQCNCVYVNGAFTEISFGMIKDCGATWVWVILGHSERRHVFGESEDLIGQKVAHA  117
P17751|TPIS_MOUSE     PKIATAAQCNCVYVNGAFTEISFGMIKDLGATWVWVILGHSERRHVFGESEDLIGQKVAHA  117
      :  :  :  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
      :  :  :  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

P0A858|TPIS_ECOLI      KEQGLIFVLCIGETEAEENAGKTEEVCAQIDAVLKTQGAARAFEGAVIAYEFVWAIIGTK  176
P48494|TPIS_ORYSA     LSGSLKVIACVSEITLQREAGSTMDVVAQTKAIA--EKIKDWSNVVYAYEFVWAIIGTK  175
P12863|TPIS_MAIZE     LSGSLKVIACVSEITLQREAGSTMDVVAQTKAIA--EKIKDWSNVVYAYEFVWAIIGTK  175
P29613|TPIS_DROME     LAEGLVIACIGELDEREAGTEKVVFEQTKAIA--DNVKDWSKVVLAYEFVWAIIGTKG  173
P00940|TPIS_CHICK     LAEGLVIACIGELDEREAGTEKVVFEQTKAIA--DNVKDWSKVVLAYEFVWAIIGTK  174
P60174|TPIS_HUMAN     LAEGLVIACIGELDEREAGTEKVVFEQTKAIA--DNVKDWSKVVLAYEFVWAIIGTK  175
P17751|TPIS_MOUSE     LAEGLVIACIGELDEREAGTEKVVFEQTKAIA--DNVKDWSKVVLAYEFVWAIIGTK  175
      :  :  :  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
      :  :  :  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

P0A858|TPIS_ECOLI      SATPAQAQAVHKFIRDHIA-KVDANIAEQVILVGGSSVNASNAELFAQPDIDGALVGG  235
P48494|TPIS_ORYSA     VATPDQAQEVHDLRKLWLANVSAEVAESTRIIVGGSSVTGANCKELAAKPDVDGFLVGG  235
  
```

さらに分子系統樹を描くには、Phylogenetic Tree のタブを利用する。

EMBL-EBI Services Research Training Industry About us

Clustal Omega

Input form | Web services | Help & Documentation | Feedback | Share

Tools > Multiple Sequence Alignment > Clustal Omega

EMBL-EBI to be HTTPS by default from 1st October

On the 1st October the majority of services hosted on www.ebi.ac.uk will be served over HTTPS by default. Services that are becoming HTTPS by default will automatically redirect users accessing the site on insecure HTTP URLs to secure HTTPS URLs.

Users of EMBL-EBI services may wish to update links, bookmarks or API clients to use the HTTPS URLs.

Results for job clustalo-I20171006-093355-0181-84955476-oy

Alignments | Result Summary | **Phylogenetic Tree** | Submission Details

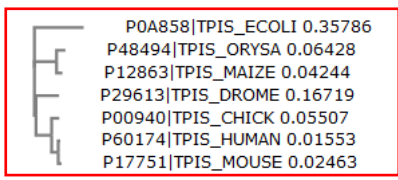
分子系統樹の表示

Phylogenetic Tree

This is a Neighbour-joining tree without distance corrections.

Download Phylogenetic Tree Data

Branch length: Cladogram Real



進化距離を枝長に反映した表示も可能

Tree Data

```

{
  P0A858|TPIS_ECOLI:0.35786,
  (
    P48494|TPIS_ORYSA:0.06428,
    P12863|TPIS_MAIZE:0.04244)
  :0.16079,
  (
    P29613|TPIS_DROME:0.16719,
    (
      P00940|TPIS_CHICK:0.05507,
      (
        P60174|TPIS_HUMAN:0.01553,
        P17751|TPIS_MOUSE:0.02463)
      :0.04783)
    :0.11343)
  :0.01156),
}
  
```