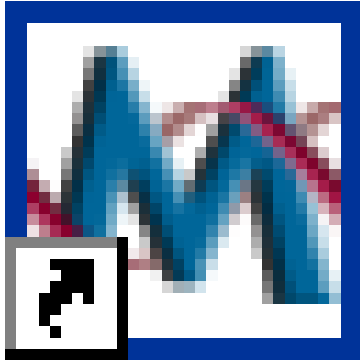




Mega3.Ink

MEGA on yksi aika monista ilmaisista ja erinomaisista DNA-sekvenssien käsittelyohjelmista

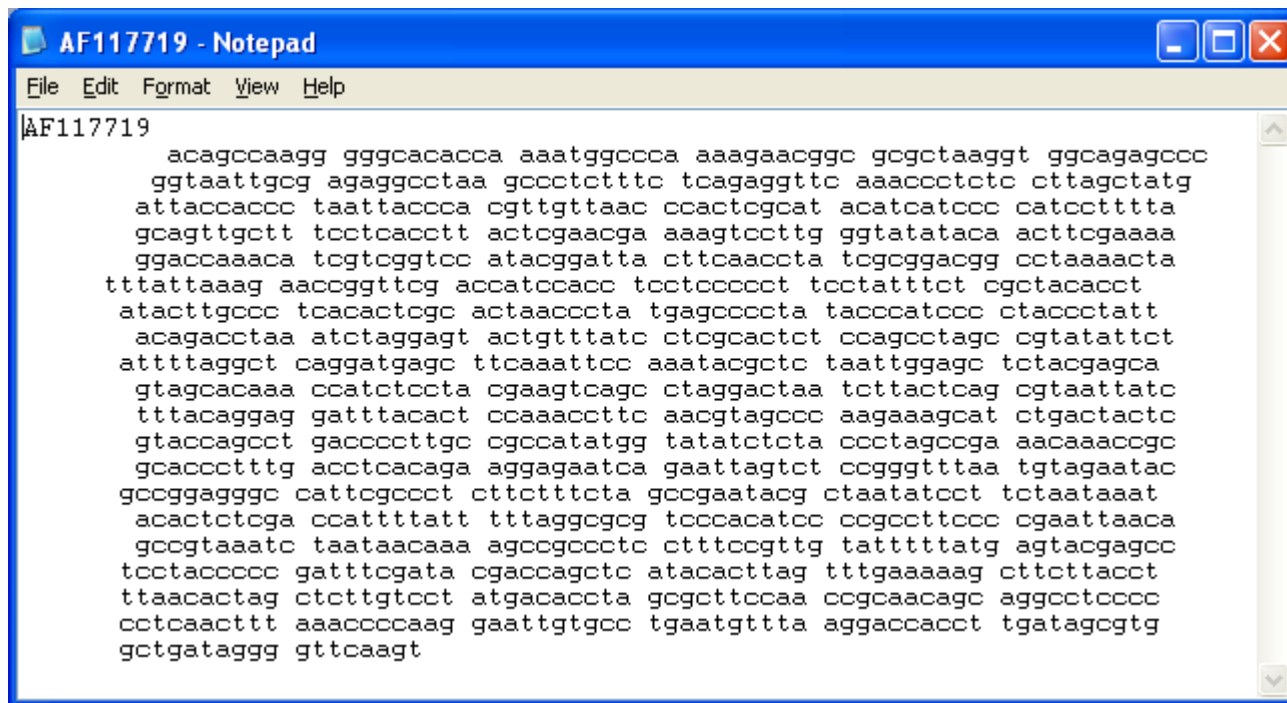
Sillä voi laskeskella erilaisia diversiteettistatistiikkoja ja konstruoida fylogeneettisia puita (hypoteeseja)

Se on helppokäyttöinen, vaikka onkin 'aikuisten' työkalu

Näytän tässä, miten MEGA3:lla aloitetaan homma

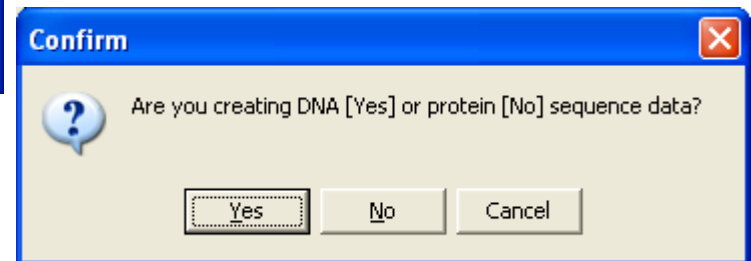
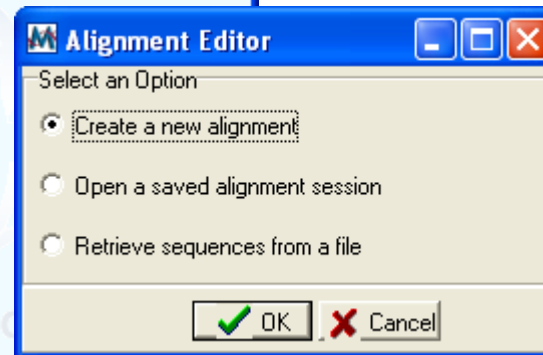
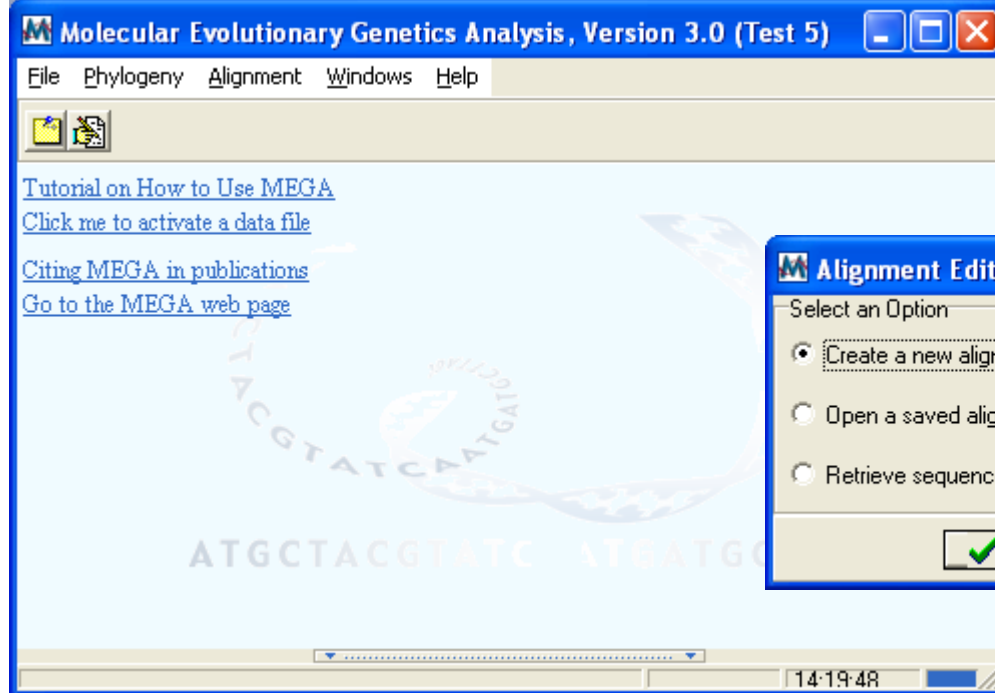
Esimerkkinä on lohen ND1 sekvenssi, jonka sijoitamme muiden lohikalojen sekvenssien joukkoon

MEGA3 on vasta toukokuussa 2004 julkistettu testiversio, joten se vaatii harjoitusta

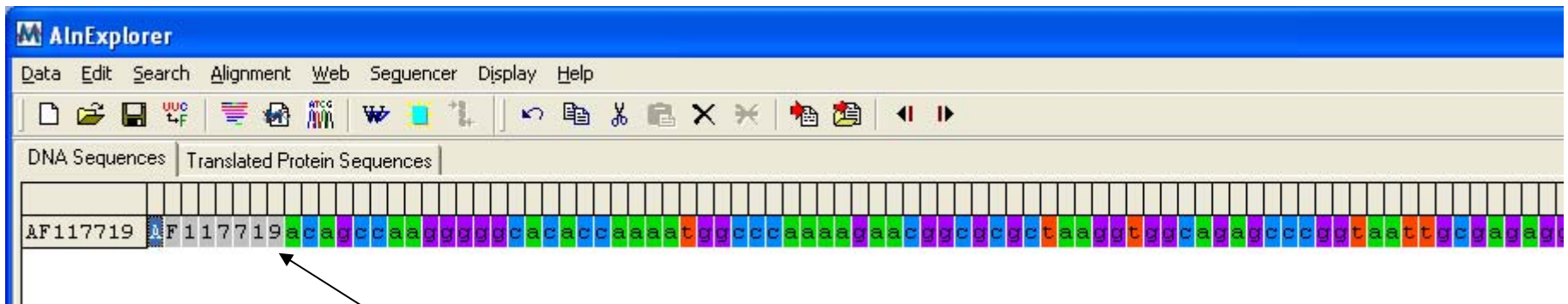


```
AF117719
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attaccacc taattacca cgttgtaac cactogcat acatcatcc catccttta
gcagttgctt tctcacctt actogaaga aaagtcttg ggtatataca acttcgaaaa
ggaccaaaca tctcggtcc atacggatta cttaacctc tcgggaagg cctaaaacta
tttattaaag aacgggttc accatccacc tctccccc tctatttct cgtacacct
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gcacctttg acctcacaga aggagaatca gaattagtct cgggtttta tgtagaatac
gcggagggc cattgcctt cttctttcta gcgaataag ctaatatct tctaataaat
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gcgtaaatc taataacaaa agccgcctc ctttcggtg ttttttatg agtacgagcc
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ttaacactag ctcttgctt atgacacctc gcgcttcaa ccgcaacagc aggcctcccc
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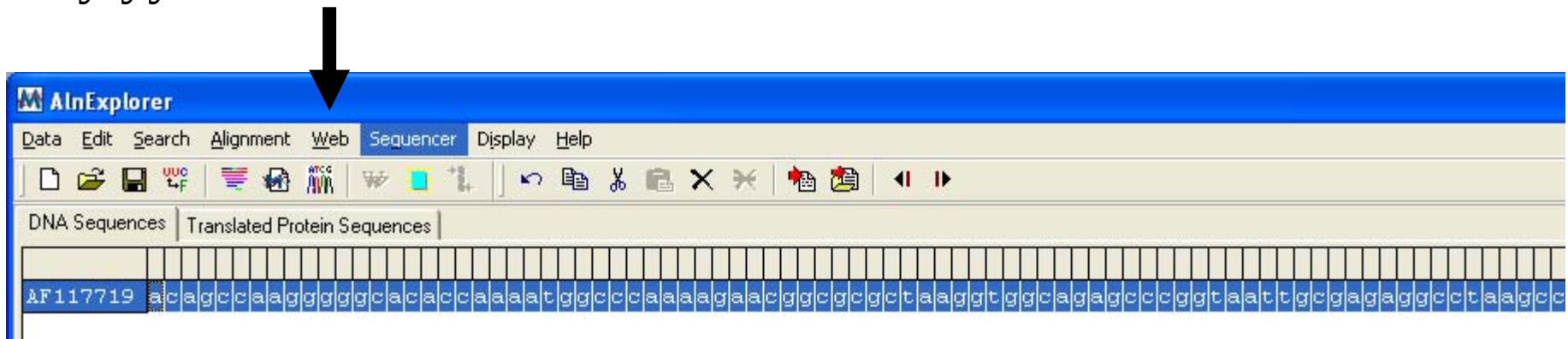
Otin lähtökohdaksi yhden taimenen ND1-sekvenssin geenipankista, poistin ensin numerot ja talletin sen notepadilla

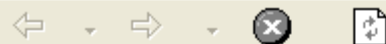


Avasin MEGAn ja ehdotin uuden linjauksen luomista nukleotidisekvenssien pohjalta



Poistelin sitten nuo ylimääräiset merkit tuolta alusta, merkkasin rivin ja suoritin sillä rivillä BLAST-haun. BLAST-komento löytyy tuolta web-toimien alta



Address http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?CMD=Web&LAYOUT=OneWindows&AUTO_FORMAT=Fullauto&PAGE=Nucleotides&NC

Links NCBI



Nucleotide

Protein

nucleotide-nucleotide **BLAST**

Translations

Retrieve results for an RID

[Search](#)

```
acagccaagggggcacacccaaaatggcccaaaagaacggcgcgctaaggtggcagagccc  
ggtaattgcgagaggcctaagccctctttctcagagggtcaaaccctctccttagctatg  
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gcagttgctttcttcaccttactcgaacgaaaagtccctgggtatatacaacttcgaaa  
ggaccaaacatcgtcgggtccatacggattacttcaacctatcgcggaaggcctaaaacta
```

[Set subsequence](#)

From:

To:

[Choose database](#)

nr

Now:

BLAST!

or

Reset query

Reset all

Options for advanced blasting[Limit by entrez query](#)

or select from:

All organisms

[Choose filter](#)

Low complexity



Human repeats



Mask for lookup table only



Mask lower case

[Expect](#)

10

[Word Size](#)

11

Other advanced



results of BLAST

BLASTN 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1086002643-18964-41465145165.BLASTQ3

Query=

(1158 letters)

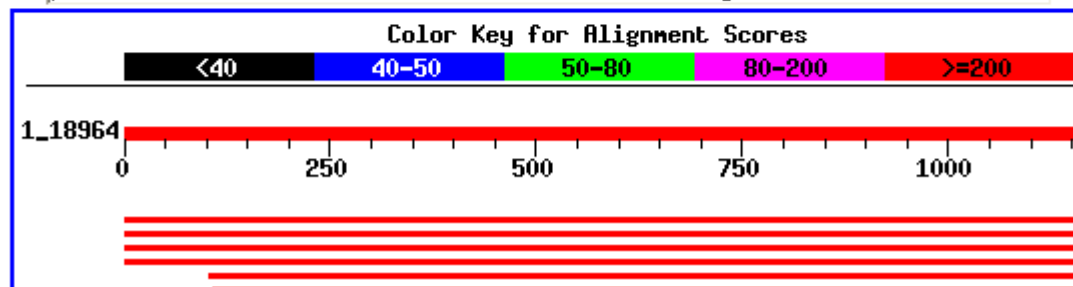
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
2,201,381 sequences; 10,665,298,906 total letters

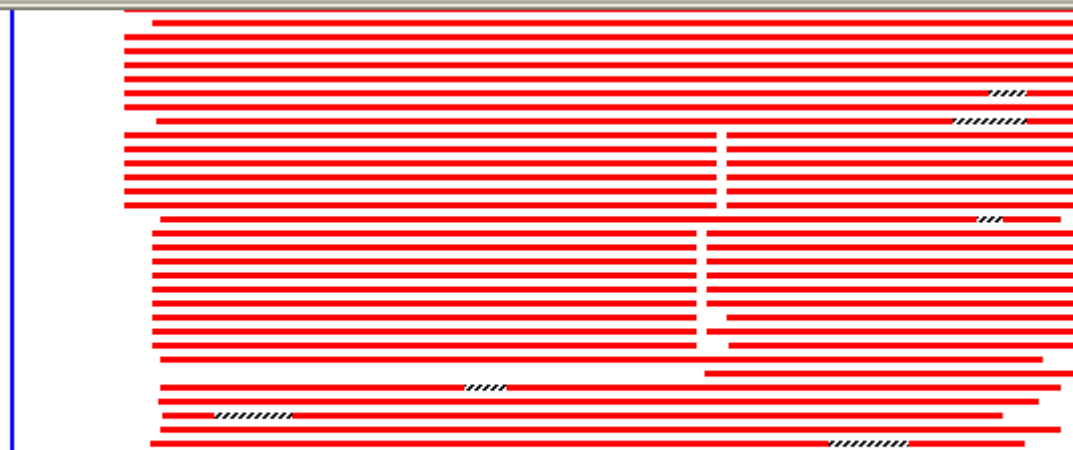
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

[Distribution of 159 Blast Hits on the Query Sequence](#)

Mouse-over to show define and scores. Click to show alignments





Sequences producing significant alignments:

	Score	E
	(bits)	Value

gi 4426924 gb AF117719.1 AF117719	Salmo trutta strain Guden...	2296	0.0
gi 4426918 gb AF117716.1 AF117716	Salmo trutta strain Guden...	2264	0.0
gi 4426922 gb AF117718.1 AF117718	Salmo trutta strain Guden...	2256	0.0
gi 4426920 gb AF117717.1 AF117717	Salmo trutta strain Guden...	2240	0.0
gi 4426926 gb AF117720.1 AF117720	Salmo trutta strain Roman...	1939	0.0
gi 4426928 gb AF117721.1 AF117721	Salmo trutta strain Roman...	1937	0.0
gi 5442055 gb AF115416.1 AF115416	Salmo salar 16S ribosomal...	1737	0.0
gi 5442063 gb AF115420.1 AF115420	Salmo salar 16S ribosomal...	1729	0.0
gi 5442051 gb AF115414.1 AF115414	Salmo salar 16S ribosomal...	1729	0.0
gi 5442059 gb AF115418.1 AF115418	Salmo salar 16S ribosomal...	1725	0.0
gi 5442057 gb AF115417.1 AF115417	Salmo salar 16S ribosomal...	1725	0.0
gi 3775976 gb U12143.1 	Salmo salar mitochondrion, complete...	1721	0.0
gi 5442061 gb AF115419.1 AF115419	Salmo salar 16S ribosomal...	1721	0.0
gi 5442053 gb AF115415.1 AF115415	Salmo salar 16S ribosomal...	1721	0.0
gi 7381061 gb AF133701.1 	Salmo salar mitochondrion, comple...	1713	0.0
gi 5442049 gb AF115413.1 AF115413	Salmo salar 16S ribosomal...	1713	0.0
gi 5442047 gb AF115412.1 AF115412	Salmo salar 16S ribosomal...	1713	0.0
gi 5257523 gb AF154851.1 	Salvelinus alpinus mitochondrion ...	1376	0.0
gi 5257509 gb AF154850.1 	Salvelinus fontinalis mitochondri...	1318	0.0
gi 14595671 gb AF392054.1 AF392054	Oncorhynchus tshawytscha...	1122	0.0
gi 1246865 gb L29771.1 ONHMTG	Oncorhynchus mykiss mitochon...	1118	0.0
gi 12082024 dbj AB034824.1 	Coregonus lavaretus mitochondri...	864	0.0

Data Edit View Links Go Help



Add to Alignment

Address http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=Nucleotide&list_uids=04426918&dopt=GenBank

Links NCBI



CGCTCAGGATAGGACTTCGCGGCTAGAGATCGGATCCCGGCGCGGATATTATATAGCTCGATCGATC1
 TTCTCTATATCCGCGCGGCTAGGATATATACACACACGCGCGGATAGCATGACTGATCTA
 CCCCACCTTCTCTATATCCGCGGCTAGGATATATACACACACGCGCGGATAGCATGACTGATCTA
 CACAGACTTACGCTTCTCTATATCCGCGGCTAGGATATATACACACACGCGCGGATAGCATGACTGATCTA

Entrez
 Nucleotide

Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Books
Search		Nucleotide	for		Go	Clear		
Limits		Preview/Index		History		Clipboard		Details
Display	GenBank	Show: 20	Send to	File	Get Subsequence		Features	

☐ 1: [AF117716](#). *Salmo trutta* stra...[gi:4426918]

Links

LOCUS AF117716 1177 bp DNA linear VRT 17-MAR-1999

DEFINITION *Salmo trutta* strain Gudena haplotype 2 16S ribosomal RNA gene, partial sequence; tRNA-Leu gene, complete sequence; NADH dehydrogenase subunit 1 (NADH 1) gene, complete cds; and tRNA-Ile gene, partial sequence, mitochondrial genes for mitochondrial products.

ACCESSION AF117716

VERSION AF117716.1 GI:4426918

KEYWORDS .

SOURCE mitochondrion *Salmo trutta* (brown trout)ORGANISM [Salmo trutta](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; *Salmo*.

REFERENCE 1 (bases 1 to 1177)

AUTHORS Loytynoja,A.P., Nielsen,E.E. and Hansen,M.M.

TITLE Variation of the mitochondrial ND1 gene in the brown trout (*Salmo trutta*)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1177)

AUTHORS Loytynoja,A.P., Nielsen,E.E. and Hansen,M.M.

TITLE Direct Submission

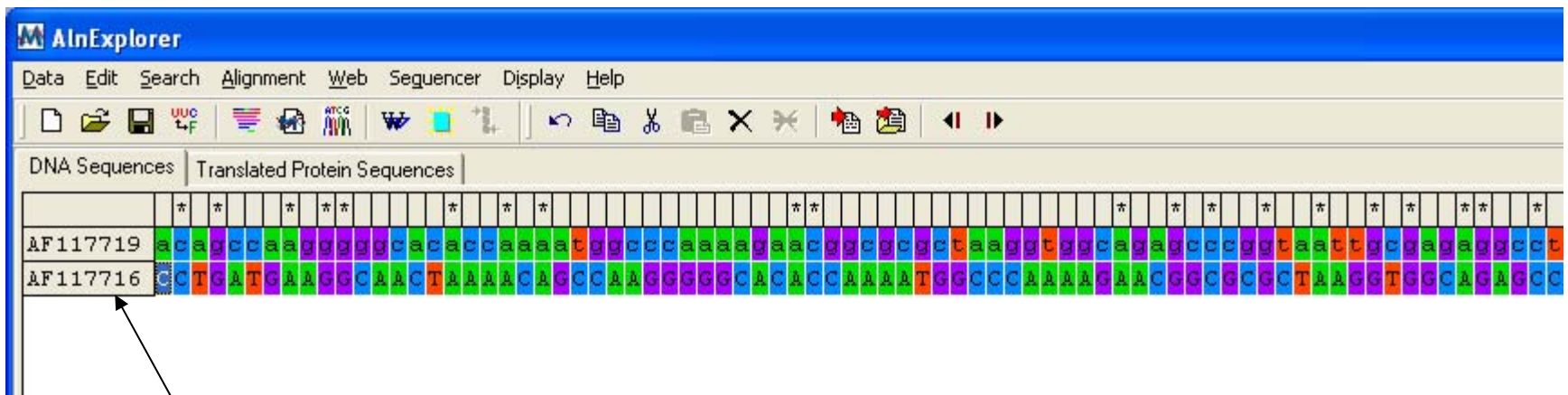
JOURNAL Submitted (22-DEC-1998) Inland Fisheries, Danish Institute of Fisheries Research, Vejlsøvej 39, Silkeborg DK-8600, Denmark

FEATURES Location/Qualifiers

source 1..1177

/organism="Salmo trutta"

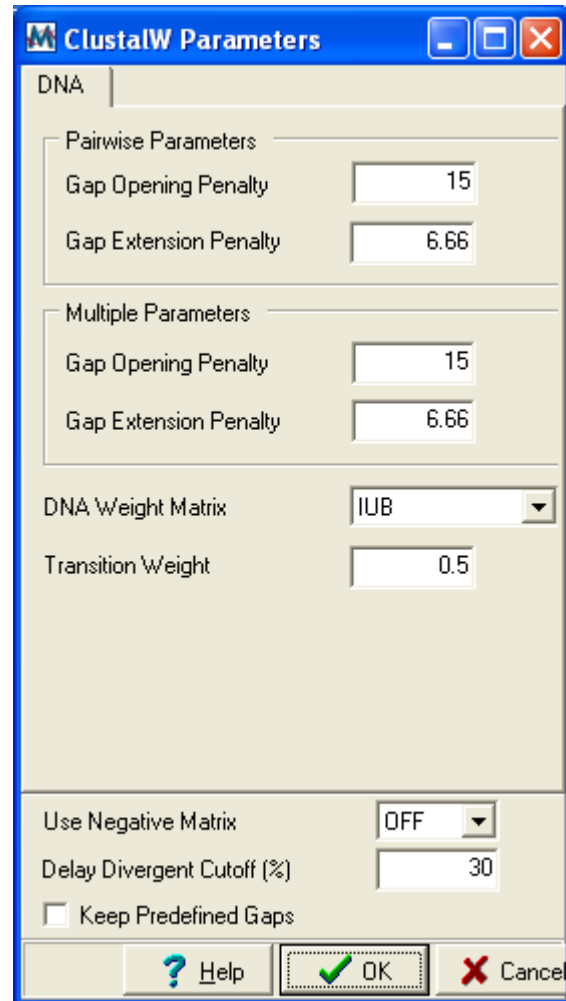
Sekvenssin voi lisätä linjaukseensa yhdellä napin painalluksella (eli klikkauksella)

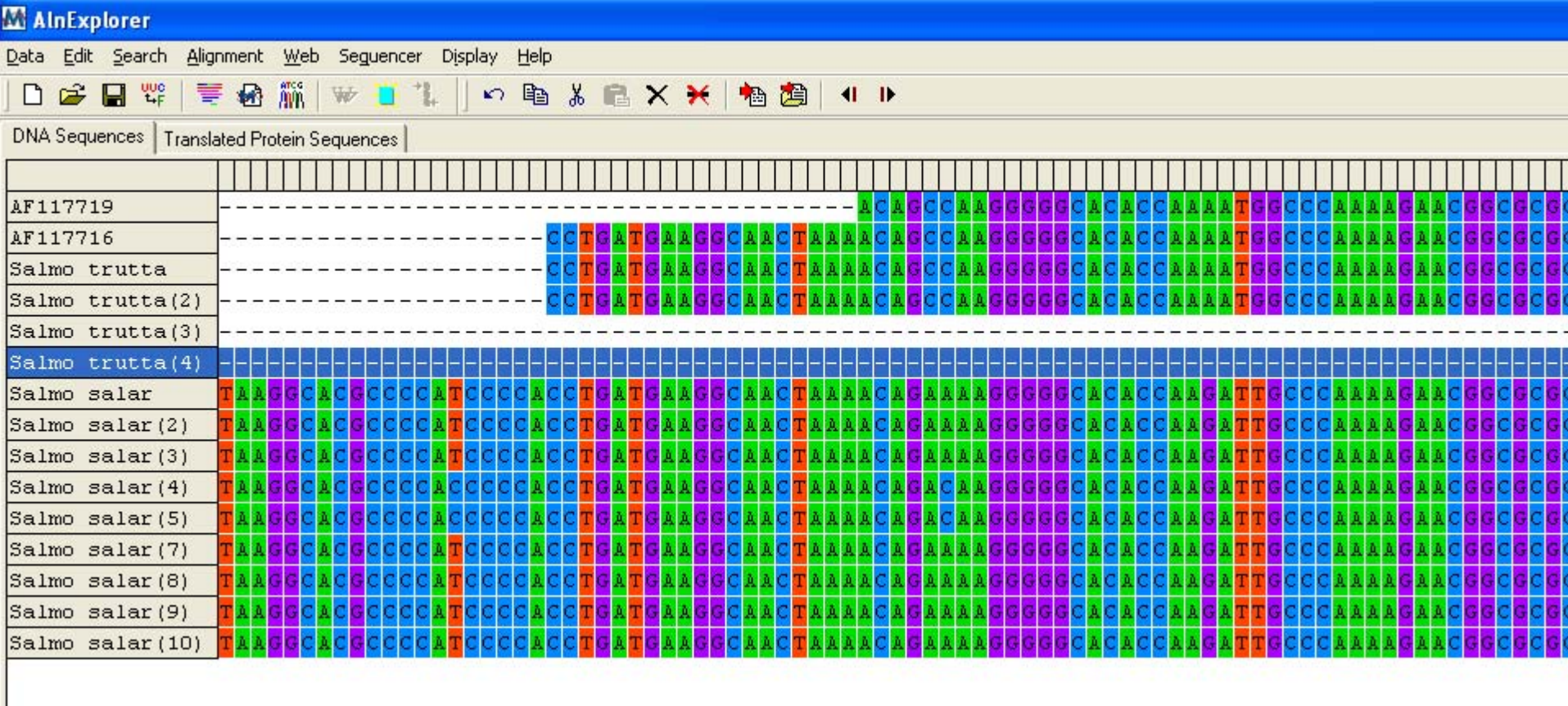


Sekenssin nimeä pääsee editoimaan merkkamalla sen ja klikkaamalla hiiren oikeanpuoleista kytöntä

ClustalW-linjausohjelma on istutettu tähän uuteen MEGAan.

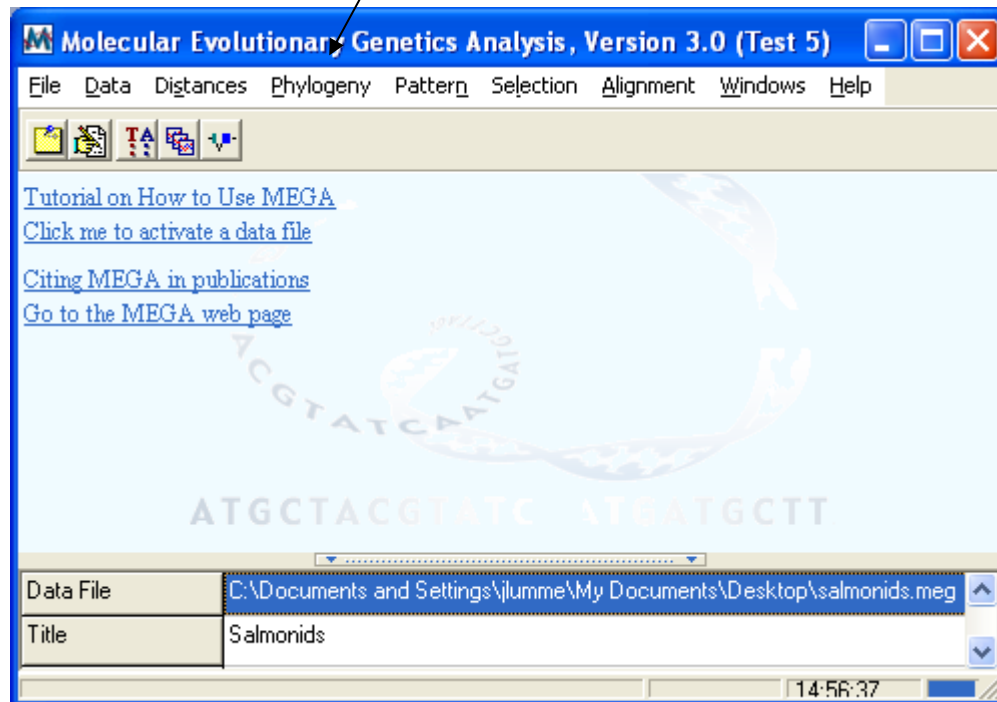
Valikossa on linjausparametrien asetuksen. Aukon teko on paljon kalliimpaa kuin aukon pidentäminen

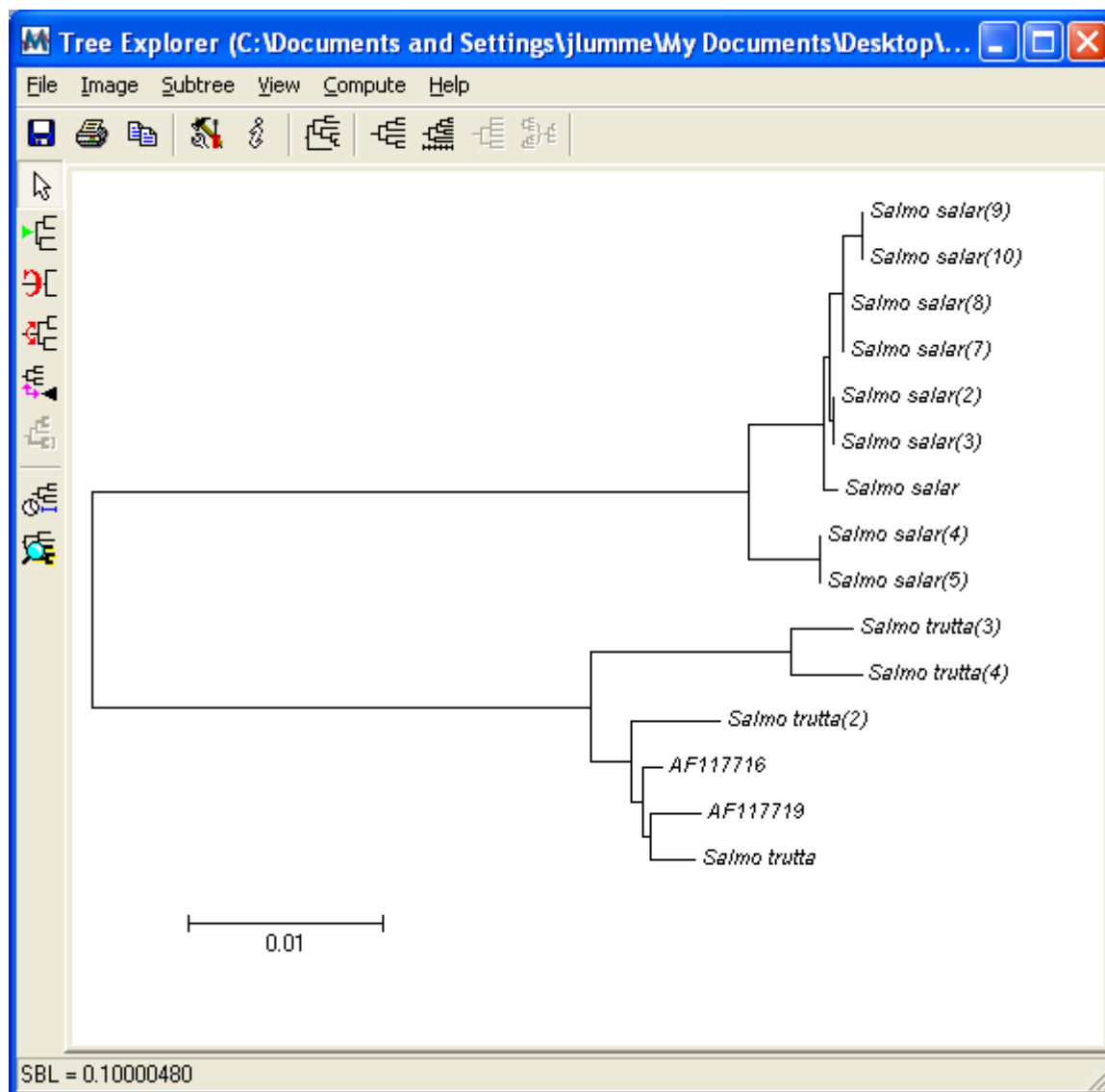


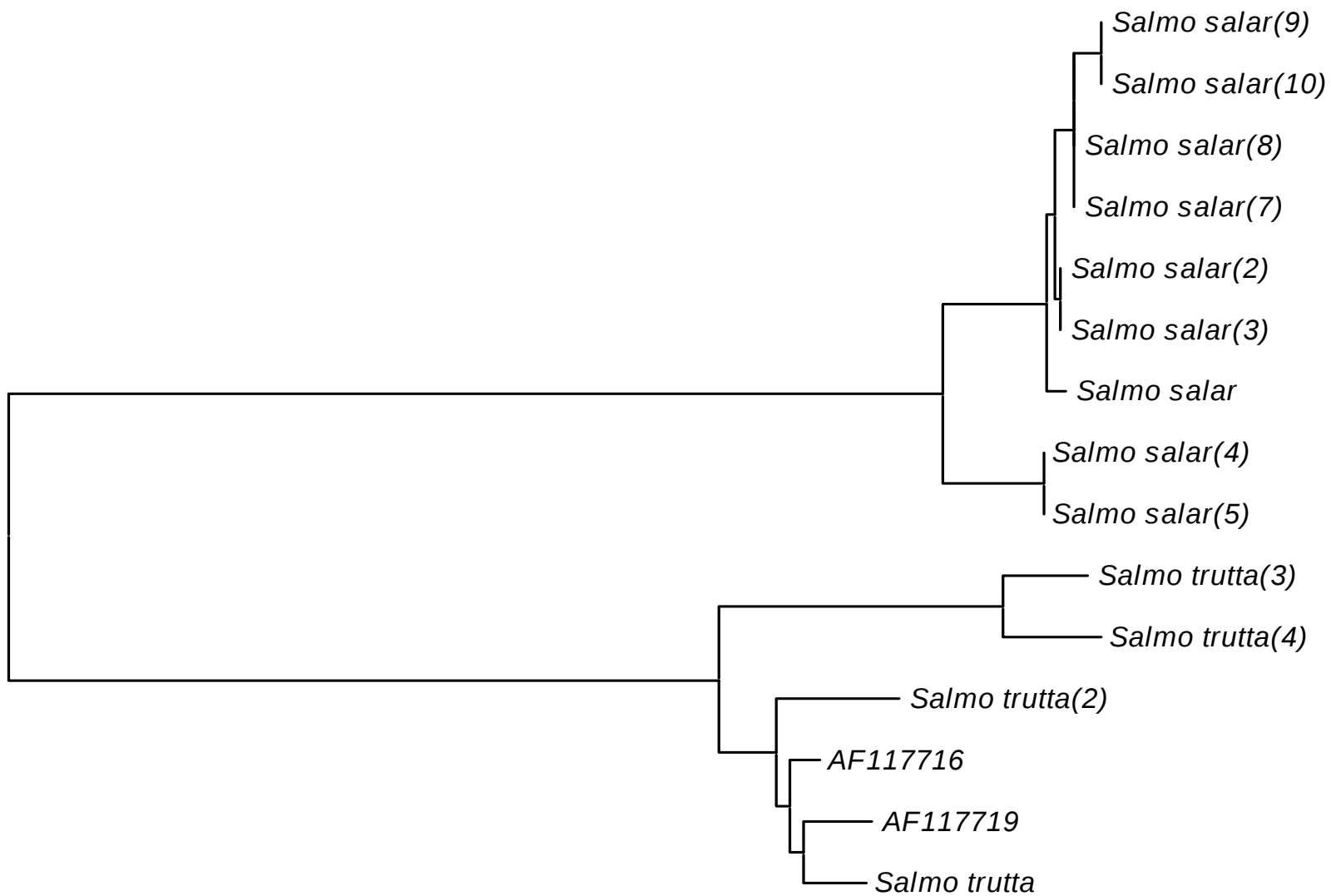


No tässä demo-tilanteessa jätin nämä sekvenssit linjattaviksi. Ne eivät näköjään ole yhtä pitkiä, vaan Ari Löytynoja on tallettanut Tanskassa ollessaan taimensekvenssien tynkiä.

[illegible]







0.01