SUPPLEMENTARY MATERIALS (**SM**)

RESULTS

rs2218404. Neither WM nor PO and PS domain scores (N = 19 patients for the T allele carriers for WM and PS) were significantly attenuated comparing to G/G carriers (N = 34 patients for WM and PS; $p = 0.12$ (F = 2.50) and $p = 0.11$ (F = 2.59) for the WM and PIQ, respectively, and $p = 0.14$ (F = 2.19) for the PS) (**Figure 1B-1**). None of the healthy human subjects IQ scores were affected by the presence of T allele (N = 62 for T and N = 81 for G/G) and were significantly higher than patients' scores (see **ST1** for the diagnosis effect statistics and interaction).

rs96501. No substantial difference in the IQ scores has been observed among the patients either C (N = 20) or T/T (N = 41) allele carriers despite a decline across the all scores comparing to healthy subjects (**ST1**).

rs1105684. Within SCZ patients cohort a cognitive endophenotype was not detectable (N = 33 and N = 67 for the A and T/T alleles carriers, respectively) with very close scores for both genotyping groups but substantially lower than for the healthy subjects (**ST1**).

rs2149171. WM contributing scores of letter number sequencing (LNS), digit span (DS) and arithmetic (AM) did not differ significantly among the genotypes (**Figure 1B-2**, lower panel) indicative of rather a distributive nature of the mutation allele effect on the final WM score. None of the healthy human subjects IQ scores were affected by the C allele presence and were repeatedly higher than for the SCZ patients' scores at the diagnosis level (**ST1**).

rs2274855. Similarly to the rs2149171 C-allele-produced phenotype, the attenuated PIQ was due to lower PO scores ($p = 0.012$ (F = 6.36)) while the PS stays unaffected by the A-allele presence, contrary to the rs2218404 endophenotype. None of the healthy subjects scores were affected by the A-allele presence but meanwhile diagnostically being higher than that of SCZ patients (**ST1**).

None of the other 3 ROIs of *NTNG1* (rs7851893, rs3824574 and rs2149171) display any significantly different evolutionary rate changes (**Figure 3C**) possibly due to the highly conservative nature of the embedding them DNA (**Figure 3B**). The ROI of rs2218404 is 100% conserved across all hominins (no other mutations are detectable in the ±50 nu regions as well, **SM**) but contains two point mutations in chimpansee, 6 in marmoset (due to «GCC» duplication) and 9 in mouse (**Figure 2D**, **SM:** rs2218404). Evolution of the other 3 ROIs non-affecting IQ SNPs (rs1373336, rs1444042 and rs4915045) shows much in common such as major allele fixation in primates (C, A and A, respectively), stronger conservation of the primates' ROIs and the following 100% conservation of ROIs across the hominin species. There is 1 mutation for chimpanzee and 3 for marmoset in rs1373336 ROI plus an extra marmoset-related mutation in rs1444042 ROI. Other primates ROIs are 100% identical to the human ones. Next on the gene is a non-affecting IQ ROI of rs628117 also characterised by 100% conservation in hominins and has only 1 mutation in chimpanzee comparing to human but 9 mutations in the marmoset ROI with 7 of them being asymmetrically nested in the preceding the allele 5'-sequence and resulting in the characteristic inflection point of brake on the percent identity plot on **Figure 2B**. It is also interesting to note the C/T alleles intermingled transition across the all analysed species. rs96501 ROI is 100% conserved starting from chimpanzee but dramatically different in the following the allele's positioning 3'-sequence shoulder of marmoset (contains 6 mutations). The T-allele of rs1105684 is strongly conserved across all primates and hominins however its ROI undergoes dramatic changes with 8 and 15 out of 20 nu mutated in marmoset and mice, respectively. Mice rs7851893 ROI is poorly conserved (5 mutations) and displays the third highest value for the evolutionary advancements rate (**Figure 3C**) from mice to marmoset after rs1105684 and rs2274855 (**Figure 3C**). Mice rs3824574 ROI ccontains 1 mutation. The T-allele of rs3824574 is not detectable in any of the analysed species but its analogue in rs7851893 is gradually substituted on G-allele starting from MezmayskayaNea and Mesolithic hominins. -50 nu DNA stretch preceeding the rs3824574 allele position contains a MezmayskayaNea-specific substitution however 30 nu away (**Figure 3B**, right panel). A Denisovan-specific mutation is found 46 nu downstream of the rs2149171 mutation allele position within the ROI. The ROI of rs2274855 is strongly conserved in primates with 1 mutation per chimpanzee and marmoset each but containing significant evolutionary changes in mice ROI (8 mutations). This is the another ROI (alongside with the rs2218404 ROI affecting the VC, **Figure 2C**) undergoing an AE from chimapanzee to human.

There are 5 point mutations in Eskimos Netrin-G1 relative to modern human reference genome (N363S, V385G, D405G, E461G, P506R) located in the middle and end of the protein with no other aa substitutions found across all other analysed hominins (due to poor genome coverage the protein information for both genes is not always complete, see **SM**). One mutation found for chimpanzee (A81S) is absent in all other analysed species; marmoset contains 4 mutations (L32V, D553G, P564R, A565T), and mouse – 20 mutations relative to the human ortholog (P24L, L25F, L32V, T35S, Q36L, M48T, T78S, D184H, T215S, V305S, V307L, N363T, H501Y, H523Q, L529A, A532D, D553E, H561R, T571M, S577G). Two mutations are shared among the mice and marmoset proteins (L32V and D553E/G) and one mice mutation is also found in the reconstructed Eskimos protein (N363T/S). As for Netrin-G2, there are 5 mutations in the Eskimos protein (T346A, K352R, A375G, D409G, E465G, P510R). Loschbour, Motala12, and AltaiNea each contains only one mutation - T346A. Motala3 – 2 mutations (S200L, R201C), VindijaNea – 3 mutations (H10Y, T346A, L573I), Denisovan – 2 mutations (R181Q, T346A), MezmayskayaNea – at least 1 mutation (T311I), chimpanzee – 2 mutations (T346A, S371A), marmoset – 12 mutations (A104V, M298V, A345S, T346A, S364G, A370V, S371V, A381T, Y389S, Q521L, R568H, R587H), and mouse – 49 mutations (H3R, A15V, K98R, E100D, I110V, T130S, M139V, S187P, L237M, L249F, S297T, M298V, K318R, S327A, T346A, K352S, W353Q, R355K, S357P, A359M, R365F, S367P, A370S, R372S, G377A, T378I, P379S, A380V, A382V, A384S, P385Q, G388D, Y389S, K390T, Q393E, K397R, M402I, A491V, L527Q, R536P, V541I, P550L, G555A, L557P, A565I, A566V, A570D, G586A, R587C). The mice protein is also 2 aa longer than human Netrin-G2 due to extra 3 aa present in {LE1(ex5)-Ukd} area: X350A; X364G; X365D (**Figure 3F**, as per mice coordinates) and one aa preceding the GPI-link (D554X) is absent (see **SM:** Netrin-G2). Similarly to Netrin-G1, Eskimos and mouse have the same aa residue affected – K352R/S (**Figure 4F**). Marmoset and mouse share four mutations not found in other species (M298V, A370V/S, Y389S, R587H/C), and the aforementioned T346A shared with other hosts. Interestingly that despite truly belonging anatomically to primates (as a “New World Monkey”) marmoset shares higher number of coding (**Figure 3F**) and non-coding (**Figure 3D**) mutations with mouse rather than with the “Old World Monkey” - chimpanzee though corroborating the reported conservation of the cortical area genetic markers with mice (**Mashiko et al., 2012**). It is also noted that if the mice-specific Netrin-G1 point mutations are predominantly located at the N- and C-termini of the protein (domains LE1 and GPI-link, respectively), 26 out of total 52 Netrin-G2 point mutations are middle part nested (exon5 + Ukd domain), another 12 are at the C-termini and the rest is spread across the other areas (**SM**).

DISCUSSION

The T-allele of rs1105684 is strongly conserved across all primates and hominins but not the ROI area which in turn undergoes dramatic changes with 8 and 15 out of 20 nu being mutated in marmoset and mice, respectively, demonstrating some potential evolutionary siginifcant events taking place and possibly linked to the T-allele emergence. The mutation alleles of rs11056893 (affecting VIQ and PIQ) and rs7851893 (non-affecting IQ) occupy strategically important locations at the beginning of the gene (intron (1-2) preceeds the coding exon 2, **Figure 3A**) but are separated from each other by 428 nu. Displaying distinct cognitive endophenotypes functionality (while both being associated with SCZ) they represent an example of a strong positive selection of an intron loci as opposite to a neutral drift (**Kimura, 1983**) of the non-coding area. The fact that rs1105684 A-allele substitution of a strongly conserved T allele (>40 mln yrs as per marmoset) affects healthy individuals may be indicative of its devastating impact on *NTNG2* function which does not require an interaction with the diagnosis of SCZ for an effect to take a place (a variation of a TATA-box embedding the allele is envisaged). In general, two distinct patterns emerge when the ROIs embedding all 11 analysed *NTNG* SNPs are compared. 1 pattern: a ROI either undergoes a sequence identity relaxation when moving away down from human across the evolutionary distant species (rs2218404, rs1373336, rs628117, rs96501, rs1105684), or opposite, 2 pattern: a ROI represents a high level of conservation (>95%) starting from marmoset (rs1444042, rs4915045, rs7851893, rs3824574, rs2149171, and rs2274855) and sometimes even including the mice ROI (rs3824574, rs2149171). Two ROIs belonging to group 1 pattern, rs2218404 and rs1105684, share substantial visual geometrical similarity represented as a funel-like plots where the low percent of sequence identity preceding and following the mutation allele (and embedded predominantly into the defined ROIs) is gradually removed upon moving both sides away from the allele position. Two other ROIs from this group, rs628117 and rs96501, display unique among others asymmetrically dramatic changes in the identity affecting either of the area sides (**Figure 3B**, low left and middle). Notably that rs628117 and rs96501 are both located in the centre of the identity plot inclination points possibly demarcating the boundaries of the following and preceding, respectively, non-coding conserved islands of the intron (9-10) (**Figure 3A**). Significance of such intron-specific location manifests itself in the PS score affected by the rs96501 (**Figure 1B-1**). Group 2 pattern can be further subdivided as: a) with the percent identity becoming stronger when moving away from the ROI (rs1444042); b) weaker (rs7851893 and rs2149171); and c) mixed (rs4915045, rs3824574, rs2274855). Interestingly, that 3 out of the group 1 pattern ROIs (rs2218404, rs96501, rs1105684) affect IQ scores in human with two of them being *NTNG1* borne (rs2218404, rs96501) and one - *NTNG2* (rs1105684). In the second group there are two out of six ROIs (rs2149171 and rs2274855) affecting IQ and both are *NTNG2*-nested (**Figure 3A**).

With all cares being taken to represent the extinct *NTNGs* composition as accurately as possible some potential technical faults cannot be excluded. C to T and G to A are known drastically elevated transitions in the ancient DNA strands breaks (**Briggs et al., 2007**). And C deamination at 5’-overhangs leads to greater C/T misincorporation rates and converts into a complementary increase in G/A (**Briggs et al., 2007**), e.g. 5′-TCC-3′→5′-TTC-3′ (potentially affecting rs96501), which is a common somatic mutation in melanoma skin cancers (**Harris, 2015**).

Eskimos is described as having had brown eyes, A+ blood type, not a light skin but having had dark and thick hair (for ref. see **Rasmussen et al., 2010**). Based on the prevailing number of SNPs (coinciding with our findings for *NTNG2* protein, **Figure 3F**) its genome does not show affinity to the modern-day Europeans but rather to the modern populations of northeast Siberia (**Sarkissian et al., 2015**). As for Neanderthals, some of them were probably red-haired and pale skinned, were able to taste bitter, have had a blood type *O* (for ref. see **Sanchez-Quinto and Lalueza-Fox, 2015**) and even were able to “enunciate as we do” (**Pollard, 2009;** interpreting **Krause et al., 2007**).

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SUPPLEMENTARY METHODS

Ancient hominins and primates genomes reconstruction

Aligned bam-files (IceMan, Hunters, VindijaNea, AltaiNea, MezmaiskayaNea) or vcf-files (Denisovan/pinky, Chimpanzee) were obtained from the corresponding open sources (**ST2**) and re-processed by using one of the following pipelines – depending on type of the source file available. In the case if bam-files were available – a “consensus DNA sequence” was generated by using “SAMtools” and “seqtk” [1] software:

```
$ samtools mpileup -uf genome.fa input.bam | bcftools view -cg - | vcfutils.pl vcf2fq > consencus.fq
$ seqtk seq -l 50 -A consencus.fq > consencus.fa
```

In the case when only vcf-files were available, - the consensus DNA sequence was generated by using Genome Analysis Toolkit (GATK) software [2]:

```
$ java -Xmx2g –jar GenomeAnalysisTK.jar -lw 50 -R genome.fa -T FastaAlternateReferenceMaker \
-L TARGET.intervals -o consencus.fa --variant input.vcf.gz
```

Having consensus DNA sequences and coordinates of regions of interest (ROI) around each SNPs position it was straightforward to extract ROI’s nucleotide sequences and/or exons/introns nucleotide sequences corresponding to a particular ancient DNA sample by using “fastahack” software [3] and custom Python scripts (available upon request).

Supplementary References

[1] Heng Li, “seqtk” - tool for processing sequences in the FASTA or FASTQ format.
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[2] DePristo MA, Banks E, Poplin RE, et al. A framework for variation discovery and genotyping using next-generation DNA sequencing data. Nature genetics. 2011;43(5):491-498. doi:10.1038/ng.806.

[3] Erik Garrison, “fastahack” - FASTA file indexing and sequence extraction tool.
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Supplementary Table 1 (ST1). Statistics for the effect of *NTNG1* SNPs (rs2218404 and rs96501) on cognitive domains and scores in human subjects as measured by WAIS-III. Related to **Fig. 1B-1** in the main text. # - working memory, processing speed and symbol search.

WAIS-III Variables	Schizophrenia (N = 61)				Control (N = 143)				ANCOVA (sex, education) p values (F values)				
	G/G (N = 36)		T carrier (N = 25)		G/G (N = 81)		T carrier (N = 62)		Diagnosis effect	Genotype effect	Interaction		
NETRIN G1; NTNG1 rs2218404	Mean	SD	Mean	SD	Mean	SD	Mean	SD				SZ	HC
Verbal IQ	96.1	14.3	83.6	16.3	108.9	13.2	108.6	13.8	**5.18×10^{-13} (59.81)**	**0.0033 (8.87)**	**0.0058 (7.78)**	**0.0059 (8.19)**	0.81 (0.06)
Performance IQ	84.5	16.5	77.0	13.5	109.0	10.3	109.5	12.5	**1.05×10^{-29} (180.76)**	0.11 (2.59)	0.061 (3.54)	0.089 (3.00)	0.77 (0.08)
Full-scale IQ	90.0	15.9	78.9	14.9	109.9	11.6	109.5	12.5	**1.05×10^{-23} (131.74)**	**0.0057 (7.80)**	**0.012 (6.48)**	**0.017 (6.01)**	0.76 (0.09)
Verbal Comprehension	97.5	13.2	84.4	16.6	106.6	13.2	107.1	12.9	**1.30×10^{-9} (40.58)**	**0.0050 (8.08)**	**0.0018 (9.99)**	**0.0037 (9.14)**	0.79 (0.07)
Perceptual Organization	86.6	16.8	81.5	14.2	108.0	10.0	107.7	14.6	**2.57×10^{-21} (114.05)**	0.19 (1.74)	0.28 (1.19)	0.22 (1.52)	0.82 (0.05)
Working Memory#	91.1	13.8	84.2	13.5	106.3	15.9	105.4	16.1	**7.14×10^{-10} (42.17)**	0.12 (2.50)	0.25 (1.33)	0.16 (2.06)	0.64 (0.21)
Processing Speed#	82.9	14.9	75.1	12.9	110.0	12.9	108.8	13.3	**1.02×10^{-26} (157.61)**	0.14 (2.19)	0.23 (1.44)	0.24 (1.41)	0.71 (0.14)
Vocabulary	9.7	2.8	7.1	3.2	11.4	3.0	11.7	3.1	**1.69×10^{-7} (29.42)**	**0.020 (5.49)**	**0.0041 (8.44)**	**0.0053 (8.39)**	0.65 (0.20)
Similarities	9.6	2.9	7.6	3.3	11.2	2.3	11.2	2.4	**4.75×10^{-7} (27.13)**	**0.041 (4.23)**	**0.022 (5.35)**	**0.044 (4.26)**	0.79 (0.07)
Information	9.3	2.6	7.1	3.0	10.9	3.0	10.9	2.4	**1.57×10^{-7} (29.58)**	**0.0067 (7.50)**	**0.014 (6.09)**	**0.0047 (8.39)**	0.78 (0.08)
	#N=34		#N=19										

WAIS-III Variables	Schizophrenia (N = 61)				Control (N = 143)				ANCOVA (sex, education) p values (F values)		
	C carrier (N = 20)		T/T (N = 41)		C carrier (N = 45)		T/T (N = 98)		Diagnosis effect	Genotype effect	Interaction
NETRIN G1; NTNG1 rs96501	Mean	SD	Mean	SD	Mean	SD	Mean	SD			
Verbal IQ	90.3	12.6	91.3	17.9	109.7	12.7	108.3	13.8	**3.97×10^{-11} (48.95)**	0.58 (0.31)	0.33 (0.95)
Performance IQ	79.7	13.5	82.2	16.7	108.5	10.1	109.6	11.8	**3.36×10^{-27} (159.45)**	0.53 (0.40)	0.57 (0.33)
Full-scale IQ	84.1	13.4	86.1	17.7	110.1	10.7	109.5	12.5	**4.87×10^{-21} (112.06)**	0.94 (0.01)	0.33 (0.96)
Verbal Comprehension	89.0	12.5	93.6	17.3	107.6	12.4	106.5	13.3	**1.15×10^{-8} (35.50)**	0.72 (0.13)	0.07 (3.31)
Perceptual Organization	83.2	14.3	85.1	16.7	108.5	12.1	107.6	12.3	**3.95×10^{-20} (105.62)**	>0.99 (<0.01)	0.39 (0.73)
Working Memory#	91.4	11.3	87.0	15.2	107.9	15.3	105.0	16.2	**7.39×10^{-9} (36.65)**	0.084 (3.01)	0.87 (0.03)
Processing Speed#	77.9	10.5	81.3	16.5	104.9	11.4	111.6	13.2	**3.65×10^{-25} (144.85)**	**0.028 (4.89)**	0.52 (0.42)
Digit Symbol	6.2	2.4	6.3	3.0	11.0	2.6	12.3	2.6	**2.16×10^{-24} (137.00)**	0.12 (2.40)	0.23 (1.48)
Symbol Search#	5.9	2.0	6.7	3.5	10.9	2.7	12.1	2.8	**2.98×10^{-19} (100.48)**	**0.053 (3.79)**	0.71 (0.14)
	#N=19		#N=34								

Supplementary Table 1 (ST1, cont.). Statistics for the effect of *NTNG2* SNPs (rs2274855 and rs1105684) on cognitive domains and scores in human subjects as measured by WAIS-III. Related to **Fig. 1B-2** in the main text. $^{\$}$ - working memory, letter number sequencing and processing speed.

WAIS-III	Schizophrenia (N = 59)				Control (N = 143)				ANCOVA (sex, education) *p* values (*F* values)				
Variables	A carrier		G/G		A carrier		G/G		Diagnosis	Genotype	Interaction		
NETRIN G2; NTNG2	(N = 33)		(N = 26)		(N = 91)		(N = 52)		effect	effect			
rs2274855	Mean	SD	Mean	SD	Mean	SD	Mean	SD				SZ	HC
Verbal IQ	86.1	16.2	96.5	15.0	108.8	14.2	108.6	12.2	**9.68×10^{-11} (46.83)**	**0.017 (5.83)**	**0.018 (5.70)**	**0.020 (5.70)**	0.98 (<0.01)
Performance IQ	78.3	15.8	86.0	15.1	108.9	11.1	109.8	11.6	**3.77×10^{-27} (159.57)**	**0.036 (4.46)**	0.11 (2.58)		
Full-scale IQ	81.1	16.2	90.9	15.6	109.6	12.2	109.9	11.6	**1.03×10^{-20} (110.02)**	**0.012 (6.44)**	**0.025 (5.07)**	**0.033 (4.80)**	0.77 (0.09)
Verbal Comprehension	88.8	17.0	95.5	14.1	106.8	13.4	106.7	12.5	**1.37×10^{-7} (29.91)**	0.14 (2.23)	0.16 (1.98)		
Perceptual Organization	80.9	15.9	90.0	14.7	107.5	11.8	108.6	12.8	**1.49×10^{-19} (101.86)**	**0.012 (6.36)**	0.056 (3.68)		
Working Memory$^{\$}$	84.0	11.8	95.0	14.3	106.0	16.7	105.8	14.6	**1.30×10^{-8} (35.36)**	**0.023 (5.28)**	**0.023 (5.23)**	**0.0031 (9.73)**	0.99 (<0.01)
Processing Speed$^{\$}$	77.0	16.9	84.0	10.6	109.2	11.8	109.9	15.0	**1.01×10^{-25} (149.62)**	0.12 (2.45)	0.20 (1.64)		
Comprehension	13.4	5.2	17.4	5.0	21.0	4.4	19.9	4.1	**1.99×10^{-9} (39.61)**	**0.035 (4.49)**	**2.27×10^{-4} (14.12)**	**0.0063 (8.06)**	0.12 (2.44)
Arithmetic	11.9	3.7	13.7	4.2	17.2	4.6	17.5	4.3	**2.06×10^{-8} (34.19)**	0.067 (3.39)	0.27 (1.24)		
Digit Span	16.1	3.2	18.2	4.2	19.0	4.3	19.3	4.5	**0.0040 (8.47)**	**0.026 (5.04)**	0.10 (2.70)		
Letter Number Sequen.$^{\$}$	10.0	3.1	11.4	2.4	13.9	2.8	13.3	2.3	**4.77×10^{-8} (32.39)**	0.27 (1.22)	**0.031 (4.73)**	0.053 (3.95)	0.32 (0.98)
Picture Completion	7.2	3.0	7.7	3.2	11.1	2.4	11.3	2.9	**3.98×10^{-15} (72.74)**	0.46 (0.56)	0.77 (0.09)		
Block Design	7.0	3.9	9.1	3.4	11.1	2.7	11.3	2.9	**2.07×10^{-8} (34.18)**	**0.010 (6.82)**	**0.041 (4.23)**	**0.028 (5.08)**	0.57 (0.32)
Matrix Reasoning	6.8	3.0	8.7	3.2	11.6	2.7	11.6	2.4	**2.11×10^{-14} (68.26)**	**0.024 (5.19)**	**0.038 (4.34)**	**0.038 (4.54)**	0.84 (0.04)
	$^{\$}$N=29		$^{\$}$N=23										

WAIS	Schizophrenia (N = 100)				Control (N = 145)				ANCOVA (sex, education) *p* values (*F* values)				
Variables	A carriers		T/T		A carriers		T/T		Diagnosis	Genotype	Interaction		
NETRIN G2; NTNG2	(N = 33)		(N = 67)		(N = 49)		(N = 96)		effect	effect			
rs1105684	Mean	SD	Mean	SD	Mean	SD	Mean	SD				SZ	HC
Verbal IQ	91.5	18.9	92.4	14.9	106.3	13.2	110.5	13.5	**2.59×10^{-11} (48.98)**	0.10 (2.72)	0.32 (1.01)	0.82 (0.05)	**0.029 (4.90)**
Performance IQ	84.4	18.7	82.6	15.4	107.2	12.1	110.6	10.8	**3.03×10^{-27} (151.16)**	0.58 (0.31)	0.11 (2.51)	0.52 (0.41)	**0.048 (3.99)**
Full-scale IQ	87.2	19.8	86.7	15.5	107.3	12.5	111.4	11.6	**6.24×10^{-21} (106.78)**	0.23 (1.45)	0.17 (1.92)	0.81 (0.06)	**0.018 (5.70)**

Supplementary Table 1 (ST1, cont.). Statistics for the effect of *NTNG2* SNPs (rs2149171) on cognitive domains and scores in human subjects as measured by WAIS-III. Related to **Fig. 1B-2** in the main text. $^{\$}$ - working memory, letter number sequencing and processing speed.

WAIS-III	Schizophrenia (N = 58)						Control (N = 142)						ANCOVA (sex, education) p values (F values)				
Variables	C/C		C/T		T/T		C/C		C/T		T/T		Diagnosis	Genotype	Interaction		
NETRIN G2; NTNG2	(N = 14)		(N = 29)		(N = 15)		(N = 39)		(N = 73)		(N = 30)		effect	effect			
rs2149171	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD				SZ	HC
Verbal IQ	88.3	18.9	88.2	14.2	99.4	15.7	109.8	11.4	107.8	15.1	109.5	11.9	**1.88×10^{-9} (39.82)**	**0.029 (3.60)**	0.083 (2.52)		
Performance IQ	77.9	17.8	79.1	13.9	88.9	16.8	109.1	11.1	108.9	11.1	110.5	12.2	**1.57×10^{-25} (147.32)**	**0.035 (3.42)**	0.15 (1.89)		
Full-scale IQ	82.3	18.7	82.6	14.3	94.1	17.2	110.4	10.7	108.9	12.8	110.8	11.8	**5.72×10^{-19} (98.28)**	**0.014 (4.35)**	0.066 (2.76)		
Verbal Comprehension	90.1	18.0	90.7	15.2	97.4	15.0	107.0	10.6	106.5	14.6	107.2	12.2	**1.62×10^{-6} (24.50)**	0.27 (1.31)	0.39 (0.95)		
Perceptual Organization	81.4	17.5	82.0	14.9	92.2	16.1	107.6	12.1	107.9	11.9	108.5	13.4	**4.71×10^{-18} (92.03)**	0.050 (3.04)	0.11 (2.20)		
Working Memory$^{\$}$	83.9	15.0	86.5	11.0	97.0	16.0	107.3	14.9	104.5	16.8	107.7	15.2	**1.21×10^{-8} (35.60)**	**0.040 (3.27)**	0.16 (1.85)		
Processing Speed$^{\$}$	76.3	18.2	79.3	14.7	84.3	11.4	106.6	12.1	110.6	12.5	110.7	15.0	**2.67×10^{-24} (139.08)**	0.19 (1.69)	0.71 (0.34)		
Comprehension	6.6	3.9	7.7	3.3	11.0	3.5	12.5	2.9	12.1	3.2	11.7	3.1	**1.15×10^{-8} (35.59)**	**0.012 (4.54)**	**3.56×10^{-4} (8.28)**	**0.0030 (6.48)**	0.61 (0.49)
Arithmetic	8.6	3.7	7.4	2.7	9.1	3.4	11.8	2.8	11.3	3.5	11.8	3.1	**2.83×10^{-7} (28.34)**	0.092 (2.42)	0.58 (0.54)		
Digit Span	8.9	2.2	9.0	2.9	10.7	3.2	11.1	3.6	10.6	3.0	11.5	3.6	**0.0043 (8.34)**	0.066 (2.75)	0.61 (0.50)		
Letter Number Sequen.$^{\$}$	5.9	2.5	7.1	2.8	8.5	3.6	11.1	3.6	10.7	3.4	10.8	2.7	**1.34×10^{-8} (35.37)**	0.27 (1.32)	0.18 (1.73)		
	$^{\$}$N=12		$^{\$}$N=25		$^{\$}$N=14												

Supplementary Table 2 (ST2)

Dataset Name	Link to the dataset	File name(s) used
Saqqaq-Eskimos (**Rasmussen et al., 2010**)	http://www.binf.ku.dk/saqqaq/	chr1.diff.annotation chr1.same.annotation.gz chr9.diff.annotation chr9.same.annotation.gz chr1.diff.highconfidence.PP chr1.same.highconfidence.PP chr9.diff.highconfidence.PP chr9.same.highconfidence.PP
IceMan (Ötzi, **Keller et al., 2012**)*	ftp://ftp.sra.ebi.ac.uk/vol1/ERA081/ERA081021/bam/	ellen1.bam
	ftp://ftp.sra.ebi.ac.uk/vol1/ERA081/ERA081149/bam/	ellen2.bam
	ftp://ftp.sra.ebi.ac.uk/vol1/ERA081/ERA081149/bam/	teresa.bam
Hunters (**Lazaradis et al., 2014**)**	http://www.ebi.ac.uk/ena/data/view/PRJEB6272	Loschbour.hg19_1000g.bam Motala1.bam Motala3.bam Motala12.bam
VindijaNea (**Geen et al., 2010**)*	ftp://hgdownload.cse.ucsc.edu/gbdb/hg18/neandertal/seqAlis/	all-hg18.bam
Denisovan/pinky (**Prüfer et al., 2013**)**	http://cdna.eva.mpg.de/neandertal/altai/Denisovan/	DenisovaPinky.hg19_1000g.1.mod.vcf.gz DenisovaPinky.hg19_1000g.9.mod.vcf.gz
AltaiNea (**Prüfer et al., 2013**)**	http://cdna.eva.mpg.de/neandertal/altai/AltaiNeandertal/bam/	AltaiNea.hg19_1000g.1.dq.bam AltaiNea.hg19_1000g.9.dq.bam
MezmaiskayaNea (**Prüfer et al., 2013**)**	http://cdna.eva.mpg.de/neandertal/Mezmaiskaya/bam/	E733.bam
Chimpanzee (**Prado-Martinez et al., 2013**)*	http://www.biologiaevolutiva.org/greatape/data.html https://eichlerlab.gs.washington.edu/greatape/data/VCFs/SNPs/	Pan_troglodytes.vcf.gz

*aligned against hg18: http://hgdownload.cse.ucsc.edu/goldenPath/hg18/bigZips/

**aligned against hg19 (iGenome by Illumina): http://support.illumina.com/sequencing/sequencing_software/igenome.html

rs2218404

Human vs Saqqaq-Eskimos

```
########################################
# Program: stretcher
# Rundate: Thu 25 Dec 2014 08:13:17
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141225-081316-0218-34995224-oy.asequence
#    -bsequence emboss_stretcher-I20141225-081316-0218-34995224-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
# 
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 GGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-elena1

```
########################################
# Program: stretcher
# Rundate: Thu 16 Oct 2014 08:26:46
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141016-082645-0369-18360949-es.asequence
#    -bsequence emboss_stretcher-I20141016-082645-0369-18360949-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-elena2

```
########################################
# Program: stretcher
# Rundate: Tue 28 Oct 2014 06:24:20
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141028-062419-0722-91680158-es.asequence
#    -bsequence emboss_stretcher-I20141028-062419-0722-91680158-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-teresa

```
########################################
# Program: stretcher
# Rundate: Thu 16 Oct 2014 08:29:25
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141016-082924-0515-99795881-oy.asequence
#    -bsequence emboss_stretcher-I20141016-082924-0515-99795881-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 GGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Loschbour

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:12:00
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-091159-0479-8403651-es.asequence
#    -bsequence emboss_stretcher-I20150103-091159-0479-8403651-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 GGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala12

```
########################################
# Program: stretcher
# Rundate: Thu 25 Dec 2014 12:05:56
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141225-120555-0779-82831793-es.asequence
#    -bsequence emboss_stretcher-I20141225-120555-0779-82831793-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala3

```
########################################
# Program: stretcher
# Rundate: Thu  8 Jan 2015 08:33:35
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150108-083334-0026-50789204-oy.asequence
#    -bsequence emboss_stretcher-I20150108-083334-0026-50789204-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Thu  8 Jan 2015 08:33:35
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150108-083334-0026-50789204-oy.asequence
#    -bsequence emboss_stretcher-I20150108-083334-0026-50789204-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs VindijaNea

```
########################################
# Program: stretcher
# Rundate: Thu 16 Oct 2014 08:34:32
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141016-083431-0426-76127058-pg.asequence
#    -bsequence emboss_stretcher-I20141016-083431-0426-76127058-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      94/101 (93.1%)
# Similarity:    94/101 (93.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 456
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||......
EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Denisovan

```
########################################
# Program: stretcher
# Rundate: Tue 28 Oct 2014 09:18:59
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141028-091858-0373-92108860-es.asequence
#    -bsequence emboss_stretcher-I20141028-091858-0373-92108860-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs AltaiNea

```
########################################
# Program: stretcher
# Rundate: Thu 16 Oct 2014 08:32:22
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141016-083220-0994-81694243-oy.asequence
#    -bsequence emboss_stretcher-I20141016-083220-0994-81694243-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs MezmayskayaNea

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 04:47:51
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-044750-0592-50107899-pg.asequence
#    -bsequence emboss_stretcher-I20141115-044750-0592-50107899-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs chimpanzee

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 05:09:35
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-050934-0543-88323379-es.asequence
#    -bsequence emboss_stretcher-I20150114-050934-0543-88323379-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      96/101 (95.0%)
# Similarity:    96/101 (95.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 460
# 
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                     |||||||||||.|||||||||||||||||||||||.||||.|||||||||
EMBOSS_001         1 GATTCCTTTCCTCTCCAAAGGGCAAGAATTCACACATAGATGACACTGCC     50

EMBOSS_001        51 TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100
                     |||||.|||||||||.||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGTTCTAGAGGGCACAGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
                      |||||||||||||||||||||||||||||||||||||||||||||||.||
7                1642 GATGGATGGAAAAGTAGTTCTTTGGCGTTGGGGTGTCTTTCTGTTTGAAG    1691

                 1686 TGTCAGTTGTATGTTGCATGGCCCCTCTAACTGTACTGCTCACTCGACAT    1735
                      ||||||||||||||||||||||||||||||||||.|||||||||||||||
7                1692 TGTCAGTTGTATGTTGCATGGCCCCTCTAACTGTTCTGCTCACTCGACAT    1741

                 1736 CCCATTCGGCCGCCTCCACCACATTCCCCATATCTGAGCATCAGCAGATG    1785
                      |||||||||||||||||||.||||.||||||.|.||||||||||||||||
7                1742 CCCATTCGGCCGCCTCCACTACATCCCCCATCTTTGAGCATCAGCAGATG    1791

                 1786 TTGACCTTTTACACATCAAATCAGGAAATTTCTGTTTTGTTTTGTTTTGT    1835
                      |||||||||||||||.||||||.|||.||||||||||||||||||||||
7                1792 TTGACCTTTTACACACCAAATCCGGACATTTCTGTTTTGTTTTGTTTTG-    1840

                 1836 TTTGTTTTGAAATCAGTGGTGACCTGAAAGGATGCTTCGTTGTGCCTTTG    1885
                               |||||||||||||||||||||||||||||.|||||||||||
7                1841 ---------AAATCAGTGGTGACCTGAAAGGATGCTTCATTGTGCCTTTG    1881

                 1886 AAAAAAATATATTAACCTTTATTATCGAGAACCTAGGAAAATTTACTCCT    1935
                      ||||||.. |||||||||||||||||.|||||||||||||||||||||||
7                1882 AAAAAACG-TATTAACCTTTATTATCAAGAACCTAGGAAAATTTACTCCT    1930

                 1936 AATAAAAACCCTCTGACTAAAAGTGATATTTTGGACTCTCCCTTCAATAT    1985
                      |||||||||||||||||||||||||||||||..|||.||.|||||.||||
7                1931 AATAAAAACCCTCTGACTAAAAGTGATATTTCAGACCCTGCCTTCGATAT    1980

                 1986 GCCTCTGGCTGTTCCGCTTAGAATGCAATGGGTATTTTCTCAGATTTCCA    2035
                      ||||||||||||||.|||||||||||||||||||||||||||||||||||
7                1981 GCCTCTGGCTGTTCTGCTTAGAATGCAATGGGTATTTTCTCAGATTTCCA    2030

                 2036 GCAAACAGGATGTAAGAGCTTCCAGAGGTCACCCAACATCACACATGACT    2085
                      ||||.|||||||||||||||||||||||||||||||||||||||||||||
7                2031 GCAAGCAGGATGTAAGAGCTTCCAGAGGTCACCCAACATCACACATGACT    2080

                 2086 AGCTTACCTGTTTCCTGGCTTTTAAGGTAAAGAG--TTACAGTAAAACCA    2133
                      |||||.||||||.|||||||||||||||||||||  ||||||||||||||
7                2081 AGCTTGCCTGTTGCCTGGCTTTTAAGGTAAAGAGATTTACAGTAAAACCA    2130

                 2134 TCAAACGTGATTGTATCTTCTAGGCTGCTTTAATGGCATTCGAAAGTTCC    2183
                      |||.||.|||||||||||||||||||||||||||||||||.|||||||||
7                2131 TCACACATGATTGTATCTTCTAGGCTGCTTTAATGGCATTTGAAAGTTCC    2180

                 2184 TTCTTTGTGGGCTTATAAGTTGCTTTTTGCGTGCACTCGTGGATTCCTTT    2233
                      |||||||||||||||||||.|||||..||.||||||||||||||||||||
7                2181 TTCTTTGTGGGCTTATAAGGTGCTTGCTGTGTGCACTCGTGGATTCCTTT    2230

                 2234 CCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC---TGTTCC    2280
                      ||.||.|||||||||||||||||||||||||.|||||||||   ||||.|
7                2231 CCTCTGCAAAGGGCAAGAATTCACACGTAGATGACACTGCCGCCTGTTTC    2280

                 2281 AGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGAAAAGGAAGC    2330
                      |||||||||.||||||||||||||||||||||||||||||.|.|||||||
7                2281 AGAGGGCACAGGAATGGGGTTTTCAAGGTGCAAGCCAGAGTAGAGGAAGC    2330

                 2331 TGTTTGGATATTTAGCTAAGTTATGGGTGTTTGCCAGTGCTTTTTGCATT    2380
                      |||||.|||||||||||||||||||||.|||||||||.|||||||.||||
7                2331 TGTTTAGATATTTAGCTAAGTTATGGGAGTTTGCCAGGGCTTTTTTCATT    2380

                 2381 ACCCCAAAGAAGGAATCAATGACTATAATTCCACTAACTATATAGAAAGA    2430
                      ||||||||||||||||.|||||.|||||||.||||||||.||||.|||||
7                2381 ACCCCAAAGAAGGAATAAATGAATATAATTTCACTAACTGTATATAAAGA    2430

                 2431 TACCATTATAGCAGATGTAACACCCCTGAGACCCCGATTATCACAGCATA    2480
                      ||||||||||.||||..|||||.||.||||||||.|||||||||||.|||
```

Human vs marmoset, 101 nu

```
########################################
# Program: stretcher
# Rundate: Thu  8 Jan 2015 08:57:54
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150108-085753-0362-85778851-pg.asequence
#    -bsequence emboss_stretcher-I20150108-085753-0362-85778851-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 104
# Identity:      91/104 (87.5%)
# Similarity:    91/104 (87.5%)
# Gaps:           6/104 ( 5.8%)
# Score: 379
# 
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACACTGCC     50
                        ||||||||.||.|||||||||||||||||||||||||.|||||||||
EMBOSS_001         1 ---TCCTTTCCTCTGCAAAGGGCAAGAATTCACACGTAGATGACACTGCC     47

EMBOSS_001        51 ---TGTTCCAGAGGGCACGGGAATGGGGTTTTCAAGGTGCAAGCCAGAGA     97
                        ||||.||||||||||.||||||||||||||||||||||||||||||.
EMBOSS_001        48 GCCTGTTTCAGAGGGCACAGGAATGGGGTTTTCAAGGTGCAAGCCAGAGT     97

EMBOSS_001        98 AAAG    101
                     |.||
EMBOSS_001        98 AGAG    101


#---------------------------------------
#---------------------------------------
```

Human int (5-6) vs mice int (5-6)

```
     .|||||||||||||||||.||||.|||||||.|||||||.|.|||..|||
1535 GAGTTTCAGAAATGGATGAATGGGAAAGTAGCTCTTTGGTGCTGGCATGT   1584

1672 CTTTCTGTTTGGAGTGTCAGTTGTATGTTGCATGGCCCCTCTAACTGTA-   1720
     .||||||.|..|||.|.|||.|||.||||||||||.|| |||.||||||
1585 GTTTCTGCTCTGAGAGGCAGATGTGTGTTGCATGGACC-TCTGACTGTAT   1633

1721 CTGCTCACTCGACATCCCATTCGGCCGCCTCCACCACATTCCCCATATCT   1770
     ||||||||||.|||||.|||..|||||||||||||.|||.||||||.|||
1634 CTGCTCACTCCACATCTCATCTGGCCGCCTCCACCCCATCCCCCATCTCT   1683

1771 GAGCATCAGCAGATGTTGACCTTTTACACATCAAATCAGGAAATTTCTGT   1820
     ||||||||||||||||||||||||||..|||..||||||||||||.|..|
1684 GAGCATCAGCAGATGTTGACCTTTTATGCATTGAATCAGGAAATTCCAAT   1733

1821 TTTGTTTTGTTTTGTTTTGTTTTGAAATCAGTGGTGACCTGAAAGGATGC   1870
     |||||||||....|||...|||||||||||||||||||||||||||||||
1734 TTTGTTTTGCACAGTTACCTTTTGAAATCAGTGGTGACCTGAAAGGATGC   1783

1871 TTCGTTGTGCCTTTGAAAAAAATATATTAACCTTTATTATCGAGAACCTA   1920
     |..||||||||.|||.||||  |.||.|||.|||.||||||..|||.||.
1784 TGTGTTGTGCCCTTGGAAAA--TGTACTAATCTTAATTATCAGGAATCTG   1831

1921 GGAAAATTT-ACTCCTAATA-----------AAAACCCTCTGACTAAAAG   1958
     .|||||||| ||..|||.||           ||||......|.|||..|.
1832 AGAAAATTTTACCACTAGTATCTGTGGGGGGAAAAAAAAAGGTCTACGAC   1881

1959 TGATATTTTGGACTCTCCCTTCAATATGCCTCTGGCTGTTCCGCTTAGAA   2008
     |.|.|.||.. |.|||....||...|||||.||||||.|||..||||.|.
1882 TCAGAATTAT-ATTCTATAGTCTGAATGCCCCTGGCTCTTCATCTTAAAG   1930

2009 TGCAATGGGT-------ATTTTCTCA---------------------GAT   2030
     ..||||||||       |||||.|.|                     |.|
1931 CACAATGGGTGTTTGGGATTTTTTTATTTTGGTTTGGTTTTGGTTTTGTT   1980

2031 TTCCAGCAAACAG---GATGTAAGAGCTTCCAGAGGTCACCCAACATCAC   2077
     ||.....||.|||   ||||.|||||..|.|.|.|.|||||||..|||||
1981 TTTTTCTAATCAGTAAGATGAAAGAGGATTCTGTGCTCACCCAGTATCAC   2030

2078 ACATGACTAGCTTACCTGTTTCCTGGCTTTTAAGGTAAAGAGTTACAGTA   2127
     |.|.|||||||||.||||||.|||||.||||||||||||.|||.|.|.||
2031 AAAGGACTAGCTTGCCTGTTGCCTGGTTTTTAAGGTAAATAGTCAAACTA   2080

2128 AAAC--CATCAAACGTGATTGTATCTTCTAGGCTGCTTTAATGGCATTCG   2175
     .|||  ||||.|...||||.||||.|||.|||....||||||||||||.|
2081 TAACATCATCGACTATGATGGTATGTTCCAGGTGTGTTTAATGGCATTAG   2130

2176 AAAGTTCCTTCTTTGTGGGCTTATAAGTTGCTTTTTGCGTGCACTCGTGG   2225
     .|||||||||||||||||.||||||.|.|||.|.|||.|||.|||.|||.
2131 CAAGTTCCTTCTTTGTGGCCTTATACGGTGCCTGTTGTGTGTACTGGTGA   2180

2226 ATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACAC--TGC   2273
     ||||||||||||||||.||.|||||||||||||.|||...|||.|  ||.
2181 ATTCCTTTCCCCTCCACAGAGCAAGAATTCACATGTATGTGACTCATTGA   2230

2274 CTGTTCCAGAGGG--CACGGGAATGGGGTT------TTCAAGGTGCAAGC   2315
     |.|..|.|||.||  ||..|||...||||.      |||.||||.||||.
2231 CAGGCCTAGAAGGTGCAAAGGATATGGGTACATAGCTTCCAGGTACAAGA   2280

2316 CAGAGAAAAGGAAGCTGTTTGGATATTTAGCTAAGTTATGGGTGTTTGCC   2365
     |||||..||||||||||.||.||||.||||||.|||. |||||.|||.||
2281 CAGAGGCAAGGAAGCTGCTTAGATACTTAGCTGAGTC-TGGGTATTTCCC   2329

2366 AGTGCTTTTTGCATTACCCCAAAGAAGGAATCAATGACTATAATTCCACT   2415
     ||.||||||..|.|.||...|||||||||||||||||.||.|||..||..
```

Human vs mouse, 101 nu

```
########################################
# Program: stretcher
# Rundate: Tue 10 Mar 2015 08:51:16
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150310-085115-0307-69651414-pg.asequence
#    -bsequence emboss_stretcher-I20150310-085115-0307-69651414-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 107
# Identity:      70/107 (65.4%)
# Similarity:    70/107 (65.4%)
# Gaps:          12/107 (11.2%)
# Score: 118
# 
#
#=======================================

EMBOSS_001         1 GATTCCTTTCCCCTCCAAAGGGCAAGAATTCACACGTAGACGACAC--TG     48
                       |||||||||||||||.||.|||||||||||||.|||...|||.|  ||
EMBOSS_001         1 --TTCCTTTCCCCTCCACAGAGCAAGAATTCACATGTATGTGACTCATTG     48

EMBOSS_001        49 CCTGTTCCAGAGGG--CACGGGA-ATGGGGTTTTCA-AGGTGCAAGCCAG     94
                     .|.|..|.|||.||  ||..||| |||||   |.|| ||.|.|.||..|.
EMBOSS_001        49 ACAGGCCTAGAAGGTGCAAAGGATATGGG---TACATAGCTTCCAGGTAC     95

EMBOSS_001        95 AGAAAAG    101
                     | |.|..
EMBOSS_001        96 A-AGACA    101


#---------------------------------------
#---------------------------------------
```

rs1373336

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 06:02:14
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-060213-0179-29738608-pg.asequence
#    -bsequence emboss_stretcher-I20150114-060213-0179-29738608-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      32/101 (31.7%)
# Similarity:    32/101 (31.7%)
# Gaps:          69/101 (68.3%)
# Score: -128
# 
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     ||||||||||||||||||||                              
EMBOSS_001         1 TTTATTGTCAACTTACACAC------------------------------     20

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                                                           |||||||||||
EMBOSS_001        21 ---------------------------------------AAACATTAAAA     31

EMBOSS_001       101 G    101
                     |
EMBOSS_001        32 G     32


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Fri 16 Jan 2015 02:14:41
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150116-021440-0185-36172471-es.asequence
#    -bsequence emboss_stretcher-I20150116-021440-0185-36172471-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      19/101 (18.8%)
# Similarity:    19/101 (18.8%)
# Gaps:           0/101 ( 0.0%)
# Score: -69
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     |||||||||||||||||||...............................
EMBOSS_001         1 TTTATTGTCAACTTACACANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Fri 16 Jan 2015 02:27:08
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150116-022707-0742-11109864-oy.asequence
#    -bsequence emboss_stretcher-I20150116-022707-0742-11109864-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       1/101 ( 1.0%)
# Similarity:     1/101 ( 1.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -195
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     |.................................................
EMBOSS_001         1 TNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Fri 16 Jan 2015 02:28:01
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150116-022759-0957-50775008-es.asequence
#    -bsequence emboss_stretcher-I20150116-022759-0957-50775008-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       6/101 ( 5.9%)
# Similarity:     6/101 ( 5.9%)
# Gaps:           0/101 ( 0.0%)
# Score: -160
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     ||||||............................................
EMBOSS_001         1 TTTATTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Loschbour

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:14:45
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-091444-0674-82049209-pg.asequence
#    -bsequence emboss_stretcher-I20150103-091444-0674-82049209-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 498
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 NGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Fri 26 Dec 2014 07:32:30
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141226-073229-0696-19006322-oy.asequence
#    -bsequence emboss_stretcher-I20141226-073229-0696-19006322-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      56/101 (55.4%)
# Similarity:    56/101 (55.4%)
# Gaps:           0/101 ( 0.0%)
# Score: 190
# 
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     |||||||||||||||||||||||||||||.....................
EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ........................||||||||||||||||||||||||||
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNTGCCTATGTACAGACAAACATTAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala3

```
########################################
# Program: stretcher
# Rundate: Fri 16 Jan 2015 02:40:18
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150116-024017-0167-99596366-es.asequence
#    -bsequence emboss_stretcher-I20150116-024017-0167-99596366-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Fri 16 Jan 2015 02:41:00
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150116-024059-0244-98812490-oy.asequence
#    -bsequence emboss_stretcher-I20150116-024059-0244-98812490-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAAATTACAGTTT     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs VindijaNea

```
########################################
# Program: stretcher
# Rundate: Fri 16 Jan 2015 03:29:44
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150116-032942-0926-2943424-oy.asequence
#    -bsequence emboss_stretcher-I20150116-032942-0926-2943424-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      10/101 ( 9.9%)
# Similarity:    10/101 ( 9.9%)
# Gaps:           0/101 ( 0.0%)
# Score: -132
# 
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     ||||||||||........................................
EMBOSS_001         1 TTTATTGTCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Tue 28 Oct 2014 09:38:07
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141028-093806-0554-89863933-es.asequence
#    -bsequence emboss_stretcher-I20141028-093806-0554-89863933-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs AltaiNea

```
########################################
# Program: stretcher
# Rundate: Fri 17 Oct 2014 09:02:30
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141017-090220-0474-58307313-pg.asequence
#    -bsequence emboss_stretcher-I20141017-090220-0474-58307313-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs MezmayskayaNea

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 04:50:49
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-045047-0948-55454092-oy.asequence
#    -bsequence emboss_stretcher-I20141115-045047-0948-55454092-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT      50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN      50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA     100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Chimpanzee

```
########################################
# Program: stretcher
# Rundate: Mon 12 Jan 2015 08:56:40
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150112-085639-0452-25072749-es.asequence
#    -bsequence emboss_stretcher-I20150112-085639-0452-25072749-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGTTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||.|||
EMBOSS_001         1 TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAATTT     50

EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAAAA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
EMBOSS_001      4076 GTTTAAATGTTTTACTGTTTTGTTTAATTTTGTTTACATTTTTT------     4119
                     ||||||.|.||.|||||||||||||||||||.||||||||||||
EMBOSS_001      4062 GTTTAACTATTCTACTGTTTTGTTTAATTTTCTTTACATTTTTTTTTTTT     4111

EMBOSS_001      4120 --GCCTCTAAAATCTTATATTAATTAATGGTCATGGGCTAATTGACTGGA     4167
                       ||||||||||.|||||||||||||||||||||||||||||||||||||
EMBOSS_001      4112 TTGCCTCTAAAACCTTATATTAATTAATGGTCATGGGCTAATTGACTGGA     4161

EMBOSS_001      4168 GGAGTATGTGAATTCACGTTGGCCAGATGTAACTCTGCTTACTGGCTTAC     4217
                     |.||||||||||||||||||||||||.|||||||||||||||||||||||
EMBOSS_001      4162 GAAGTATGTGAATTCACGTTGGCCAGCTGTAACTCTGCTTACTGGCTTAC     4211

EMBOSS_001      4218 AAAACATTGGTGATTTATTGTCAACTTACACACTTTAAACAGTAAAAAAA     4267
                     |..|...||||||||.|||||||||||||.|||||||||.|||....|||
EMBOSS_001      4212 AGTATGCTGGTGATTCATTGTCAACTTACTCACTTTAAATAGTTTTTAAA     4261

EMBOSS_001      4268 AAAATTACAGTTTCGATATAGGTACAAATTTATAATGTGCCTATGTACAG     4317
                     |  ||||||||||.|.||.|||||.|||||||||.||||.||.|||||||
EMBOSS_001      4262 A--ATTACAGTTTTGGTACAGGTAAAAATTTATAGTGTGTCTCTGTACAG     4309

EMBOSS_001      4318 ACAAACATTAAAAGCTTTCACAAAATTAGTATTTTAAAATATTTTTAATC     4367
                     ||||||||||||||||||||||||||||.|||||||||||||||||||||
EMBOSS_001      4310 ACAAACATTAAAAGCTTTCACAAAATTACTATTTTAAAATATTTTTAATC     4359

EMBOSS_001      4368 TGCTTCCATATACACATGCATATTAAAATAGAAAATGTTAATTTAAAATA     4417
                     .|.|||||||||.|||..|||..||||||||.||||||||||||||||.|
EMBOSS_001      4360 AGGTTCCATATATACACACATGCTAAAATAGGAAATGTTAATTTAAAAGA     4409

EMBOSS_001      4418 AAACTCTAGTTGTTAAGTACAAACTAAGCCAGGCAAGGAGAGAGCATTTT     4467
                     ||||.||||||||||||||||||||||||||||||||.||.|||||||||
EMBOSS_001      4410 AAACCCTAGTTGTTAAGTACAAACTAAGCCAGGCAAGAAGGGAGCATTTT     4459

EMBOSS_001      4468 AGAGTTTATTAAGTTTATTTTTACCTACATATATAACTATTCATCATAT     4517
                     ||||||||||.|||||||||||||||||||||||||||||||||||||||.
EMBOSS_001      4460 AGAGTTTATTGAGTTTATTTTTACCTACATATATAACTATTCATCATAG     4509

EMBOSS_001      4518 AAATGTTTGTTTTATAAGAATGCTGAACTCGAAACCTGACTTAATTAGCA     4567
                     ||||||||.||||.|||.|||||.||||||.||||..|||||||||||||
EMBOSS_001      4510 AAATGTTTATTTTCTAACAATGCGGAACTCAAAACTGGACTTAATTAGCA     4559

EMBOSS_001      4568 TAAAATAAATCATAATTCTAAGGTACTCCACATTTATTTGAAGAA-----     4612
                     ||||||||||||||.|||||||||.||||||.|||||||||||||
EMBOSS_001      4560 TAAAATAAATCATACTTCTAAGGTCCTCCACGTTTATTTGAAGAAATGAT     4609

EMBOSS_001      4613 -TAATTAGTGTCTGTGACATAAACTTAGAATCAAACCCCTAGACCCATCT     4661
                      ||||||||.||||.||||.|||.|||||.||||||||||.||.|||.|.
EMBOSS_001      4610 CTAATTAGTTTCTGAGACACAAATTTAGAGTCAAACCCCTGGATCCAACC     4659

EMBOSS_001      4662 ATAAGGCTAAACCCTGAATCCCCATAGCAAATCTAATATGCCAAACTTGA     4711
                     ||||.|.|||||||||||||||||||||||||||||.||||..|||||.|
EMBOSS_001      4660 ATAATGTTAAACCCTGAATCCCCATAGCAAATCTAAGATGCTCAACTTTA     4709

EMBOSS_001      4712 TTATATTAAACTAAATTTTCAAGACTTCTCTTGGTTAGTTGGATGGTATA     4761
                     ||||||||||||||.||||.|||||||||||||||..||||||||.||||
EMBOSS_001      4710 TTATATTAAACTAACTTTTTAAGACTTCTCTTGGTCGGTTGGATGATATA     4759

EMBOSS_001      4762 GTTTTATTTGGTTTTTCATGAGGGAACTGCTTAATGTACCCATTTTTAAA     4811
                     |||||.||||||||||..|.|||||||||||||||.||..||||||||||
EMBOSS_001      4760 GTTTTGTTTGGTTTTTAGTAAGGGAACTGCTTAATATATTCATTTTTAAA     4809

EMBOSS_001      4812 TAATGGAAACTGAGAGGCACAATAACTTCCTCAAAAGTATTAGAAGAGTA     4861
                     ||||||||||.|||||..|||.||||||||.|||||.|||||.|||||||
EMBOSS_001      4810 TAATGGAAACAGAGAGATACAGTAACTTCCCCAAAATTATTAAAAGAGTA     4859

EMBOSS_001      4862 ATGAGGAAAGAAACTTTAGCTCACAGTACCCAAAAGCTGCCAGCTACCTG     4911
```

Human vs marmoset

```
########################################
# Program: stretcher
# Rundate: Fri 16 Jan 2015 04:07:30
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150116-040729-0194-38913217-oy.asequence
#    -bsequence emboss_stretcher-I20150116-040729-0194-38913217-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 103
# Identity:      85/103 (82.5%)
# Similarity:    85/103 (82.5%)
# Gaps:           4/103 ( 3.9%)
# Score: 329
#
#
#=======================================

EMBOSS_001         1 --TTTATTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACAGT     48
                       ||.|||||||||||||.|||||||||.|||....||||  ||||||||
EMBOSS_001         1 GATTCATTGTCAACTTACTCACTTTAAATAGTTTTTAAAA--ATTACAGT     48

EMBOSS_001        49 TTCGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATTAA     98
                     ||.|.||.|||||.|||||||||.||||.||.||||||||||||||||||
EMBOSS_001        49 TTTGGTACAGGTAAAAATTTATAGTGTGTCTCTGTACAGACAAACATTAA     98

EMBOSS_001        99 AAG    101
                     |||
EMBOSS_001        99 AAG    101


#---------------------------------------
#---------------------------------------
```

```
4000 TTGTCCTTTATTTTCATGACTGCAAAACATTACACTTACCCACATTTTCC    4049
     |...|.||||||||.||.|||    ||.||||||.|..||..|  ||||.
3025 TACCCGTTTATTTTTATAACT----AAGATTACATTGTCCAGC--TTTCT    3068

4050 TATGACAATGACTGGGATATATTATGGTTTAAATGTTTTACTGTTTTGTT    4099
     ||..||||.||||||||..||.|||||.|||.|||||..||.||.|..||
3069 TACAACAAAGACTGGGACTTACTATGGATTAGATGTTGGACAGTATATTT    3118

4100 TAATTTTGTTTACATTTTTTGCCTCTAAAATCTTATATTAATTAATGGTC    4149
     |    |||     ||||||       ||||.|.|||.|.. ||.||....
3119 T----TTG-----ATTTTT-------AAAAACCTATCTCT-TTGATCACT    3151

4150 ATGGGCTAATTGACTGGAGGAGTATGTGAATTCACGTTGGCCAGATGTAA    4199
     .|||.|||.|    ||||..||.||||...||||...||.||||.|||||
3152 GTGGACTACT----TGGAACAGCATGTAGGTTCATACTGCCCAGGTGTAA    3197

4200 CTCTGCTTACTGGCTTACAAAACATTGGTGATTTATTGTCAACTTACACA    4249
     |..   ..||||||||||||||||......|.|..||.|||||.|.|.||
3198 CAA---AAACTGGCTTACAAAACACCAACAACTCTTTATCAACATGCCCA    3244

4250 CTTTAAACAGTAAAAAAAAAAATTACAGTTTCGATATAGGTACAAATTTA    4299
     |||||.|.|||.|.|...   |||.|||.. |||..||||.||||.|...
3245 CTTTATAAAGTGACACCC---ATTCCAGGG-CGACCTAGGCACAACTCAG    3290

4300 TAATGTGCCTATGTACAGACAAACATTAAAAGCTTTCACAAAATTAGTAT    4349
     |.|. |.|..|||||.|.|||||.||||||.|....|||||||.|..|.
3291 TGAA-TACAAATGTATAAACAAAAATTAAAAACCACAACAAAATAATGAC    3339

4350 TTTAAAATATTTTTAATCTGCTTCCATATACACATGCATATTAAAATAGA    4399
     |||.||.||||     .||.|...||.|||..||  ||.||||.||||.|
3340 TTTTAATTATT-----CCTACCCACACATAGGCA--CACATTAGAATAAA    3382

4400 AAATGTTA--ATTTAAAA-TAAAACTCTAGTTG---TTAAGTACAAACTA    4443
     |||||.|.  ||..|||| ||.||.|.|..|.|   ||.|.|..||..|.
3383 AAATGCTGCCATGGAAAAGTAGAAATGTTTTGGAATTTTATTTTAATTTT    3432

4444 AGCCAGGCAAGGAGAGAGCATTTTAGAGTTTATTAAGTTTTATTTTTACC    4493
     |..||..||...|.|.|.......|.|                   .||.
3433 ACACACACACACACACACACACACACA-------------------CACT    3463

4494 TACATATATAACTATTCATCATATAAATGTTTGTTTTATAAGAATGCTGA    4543
     ||||.|.  .|..|||..|..|||||.|||||||||.||.|||||.||.|
3464 TACACAC--CATCATTAGTTGTATAACTGTTTGTTTCATGAGAATTCTAA    3511

4544 ACTCGAAACCTGACTTAATTAGCATAAAATAAATCATAATTCTAAGGTAC    4593
     .|||.|||.   |||.|.|||.||.||.||||||||||||||.|||||..
3512 GCTCTAAAT---ACTGAGTTAACACAACATAAATCATAATTCAAAGGTCT    3558

4594 TCCACATTTATTTGAAGAA----TAATTAGTGTCTGTGACATAAACTTAG    4639
     |.|||||.. ||.||||||    |.|||.||.||..||.||  ||.||.|
3559 TTCACATCG-TTGGAAGAAATTTTCATTTGTCTCAATGTCA--AAATTTG    3605

4640 AATCAAACCCCTAGACCCATCTATAAGGCTAAACCCTGAATCCCCATAGC    4689
     |.|.|||||.|.||..|.||..|.||.|.|||..||. |||||.|||.||
3606 AGTAAAACCTCCAGGTCTATTCACAATGATAATTCCA-AATCCTCATCGC    3654

4690 AAATCTAATATGCCAAACTTGATTATATTAAACTAAATTTTCAAGACTTC    4739
     .|||.  |.|...|..||||.   |.|||||.||.||.|..|.|||..|
3655 TAATG--ACACAACTCACTTA---AAATTAAGCTGAACTCCCCAGAGCT-    3698

4740 TCTTGGTTAGTTGGATGGTATAGTTTTATTTGGTTTTTCATGAGG-GAAC    4788
       |||||...||.|.|.. ||..|||||||.....|||.||..|| ||.|
3699 --TTGGTCCATTTGCTAC-ATGATTTTATTCCAACTTTTATTGGGAGATC    3745

4789 TGCTTAATGTACCCATTTTTAAATAA--------TG-GAAACTGAGAGGC    4829
```

```
########################################
# Program: stretcher
# Rundate: Fri 17 Oct 2014 09:29:04
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141017-092903-0675-16087434-es.asequence
#    -bsequence emboss_stretcher-I20141017-092903-0675-16087434-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 106
# Identity:      63/106 (59.4%)
# Similarity:    63/106 (59.4%)
# Gaps:          10/106 ( 9.4%)
# Score: 83
#
#
#=======================================

EMBOSS_001         1 TTTA----TTGTCAACTTACACACTTTAAACAGTAAAAAAAAAAATTACA     46
                     ...|    ||.|||||.|.|.|||||||.|.|||.|.|...   |||.||
EMBOSS_001         1 ACAACTCTTTATCAACATGCCCACTTTATAAAGTGACACCC---ATTCCA     47

EMBOSS_001        47 GTTTCGATATAGGTACAAATTTATAATGTGCCTATGTACAGACAAACATT     96
                     |.. |||..||||.||||.|...|.|. |.|..|||||.|.|||||.|||
EMBOSS_001        48 GGG-CGACCTAGGCACAACTCAGTGAA-TACAAATGTATAAACAAAAATT     95

EMBOSS_001        97 AAAAG-    101
                     ||||.
EMBOSS_001        96 AAAAAC    101


#---------------------------------------
#---------------------------------------
```

rs1444042

Human vs Saqqaq-Eskimos

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 06:06:04
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-060603-0575-23860271-es.asequence
#    -bsequence emboss_stretcher-I20150114-060603-0575-23860271-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      42/101 (41.6%)
# Similarity:    42/101 (41.6%)
# Gaps:          59/101 (58.4%)
# Score: -38
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     |||||||||||||
EMBOSS_001         1 CCAATGGACTTAG-------------------------------------     13

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                                           ||||||||||||||||||||||||||||
EMBOSS_001        14 ----------------------TCCCACAGATGTTGAATGCAAAAAGACA     41

EMBOSS_001       101 A    101
                     |
EMBOSS_001        42 A     42


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-elena1

```
########################################
# Program: stretcher
# Rundate: Wed 11 Mar 2015 08:53:46
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150311-085345-0867-81190011-pg.asequence
#    -bsequence emboss_stretcher-I20150311-085345-0867-81190011-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      62/101 (61.4%)
# Similarity:    62/101 (61.4%)
# Gaps:           0/101 ( 0.0%)
# Score: 232
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     .......................................|||||||||||
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCATGAAAATCA     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Wed 11 Mar 2015 08:55:19
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150311-085517-0977-25266201-es.asequence
#    -bsequence emboss_stretcher-I20150311-085517-0977-25266201-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      89/101 (88.1%)
# Similarity:    89/101 (88.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 421
# 
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     |||||||||||||||||||||||||||||............|||||||||
EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCANNNNNNNNNNNNTGAAAATCA     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Wed 11 Mar 2015 08:56:18
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150311-085617-0501-62574028-pg.asequence
#    -bsequence emboss_stretcher-I20150311-085617-0501-62574028-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      41/101 (40.6%)
# Similarity:    41/101 (40.6%)
# Gaps:           0/101 ( 0.0%)
# Score: 85
# 
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ..........||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 NNNNNNNNNNCAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:17:54
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-091753-0004-8695705-oy.asequence
#    -bsequence emboss_stretcher-I20150103-091753-0004-8695705-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala12

```
########################################
# Program: stretcher
# Rundate: Fri 26 Dec 2014 07:38:12
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141226-073811-0564-53257594-oy.asequence
#    -bsequence emboss_stretcher-I20141226-073811-0564-53257594-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala3

```
########################################
# Program: stretcher
# Rundate: Wed 11 Mar 2015 08:58:29
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150311-085828-0180-35124358-oy.asequence
#    -bsequence emboss_stretcher-I20150311-085828-0180-35124358-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      30/101 (29.7%)
# Similarity:    30/101 (29.7%)
# Gaps:           0/101 ( 0.0%)
# Score: 8
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ||||||||||||||||||||||||||||||....................
EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 A    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Wed 11 Mar 2015 08:59:10
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150311-085909-0290-65179367-oy.asequence
#    -bsequence emboss_stretcher-I20150311-085909-0290-65179367-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 A    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs VindijaNea

```
########################################
# Program: stretcher
# Rundate: Mon 20 Oct 2014 10:31:45
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141020-103144-0650-61963349-es.asequence
#    -bsequence emboss_stretcher-I20141020-103144-0650-61963349-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      32/101 (31.7%)
# Similarity:    32/101 (31.7%)
# Gaps:           0/101 ( 0.0%)
# Score: 22
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ...................|||||||||||||||||||||||||||||||
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNTGTTCCCACAGATGTTGAATGCAAAAAGACA    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs Denisovan

```
########################################
# Program: stretcher
# Rundate: Tue 28 Oct 2014 09:45:34
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141028-094533-0961-67636483-pg.asequence
#    -bsequence emboss_stretcher-I20141028-094533-0961-67636483-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs AltaiNea

```
########################################
# Program: stretcher
# Rundate: Mon 20 Oct 2014 10:29:27
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141020-102926-0333-49917316-es.asequence
#    -bsequence emboss_stretcher-I20141020-102926-0333-49917316-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs MezmayskayaNea

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 04:53:11
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-045310-0781-30123857-es.asequence
#    -bsequence emboss_stretcher-I20141115-045310-0781-30123857-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 A    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Chimpanzee

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 04:50:51
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-045050-0887-44018081-oy.asequence
#    -bsequence emboss_stretcher-I20150113-045050-0887-44018081-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      99/101 (98.0%)
# Similarity:    99/101 (98.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 487
# 
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     ||.|||||||||||||||||||||||||||||||.|||||||||||||||
EMBOSS_001         1 CCTATGGACTTAGCCTATGTGTTAACCCATATTCCTTATCATGAAAATCA     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
EMBOSS_001     10120 TGCTCTGCCTCCG-CCTTAATCTTTGACTG---------GTTAGCAGTCA  10159
                     |||||||.|||.. |||||.|.|||||||.         |||||||||||
EMBOSS_001     10264 TGCTCTGTCTCTAACCTTATTGTTTGACTCATCCTCATAGTTAGCAGTCA  10313

EMBOSS_001     10160 AGATCATCCAGACACTGCTGGATGCTCATTTTTAAACAGAAACAATTGCT  10209
                     ||||||||||||||.|..||||||||||||||  ||.||||||||.||||
EMBOSS_001     10314 AGATCATCCAGACATTTTTGGATGCTCATTTT--AATAGAAACAACTGCT  10361

EMBOSS_001     10210 AAGATATATTTTTAACAATATTCTTTCCCTTATTCTGCAAAAGCATAGGA  10259
                     ||||||||||||||||||||||||||||||||||||||||||.|||||||
EMBOSS_001     10362 AAGATATATTTTTAACAATATTCTTTCCCTTATTCTGCAAAAGTATAGGA  10411

EMBOSS_001     10260 TTAACATTACATATTACAGATATTTTTTTCTAAACTACAACTCTTTTGGG  10309
                     ||      |.|||||||||||||||||| |||||||||||.||||.||||
EMBOSS_001     10412 TT------ATATATTACAGATATTTTTT-CTAAACTACAATTCTTATGGG  10454

EMBOSS_001     10310 GAAATGGGCATATGTCTCAGAGATAAAACACTATAAAAATGATGAAATAT  10359
                     |||||||||||||||||||||||||||||||.|.||||||||||||||||
EMBOSS_001     10455 GAAATGGGCATATGTCTCAGAGATAAAACACAACAAAAATGATGAAATAT  10504

EMBOSS_001     10360 TGATTTTATTTTTAAGACATACATTTAGGCCTCTTTTTAATTAGTATTGT  10409
                     ||||||||||||||||||||||||||||||.|||||||||||||||||||
EMBOSS_001     10505 TGATTTTATTTTTAAGACATACATTTAGGCATCTTTTTAATTAGTATTGT  10554

EMBOSS_001     10410 TGACCCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAA  10459
                     |||||||.||.||.||||||.|||||||||||||||||.|||||||||||
EMBOSS_001     10555 TGACCCATTGAACATAGCCTGTGTGTTAACCCATATTCCTTATCATGAAA  10604

EMBOSS_001     10460 ATCAATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAA  10509
                     ||||||.||||||||||||||...|||||||...||.||||||||||||.
EMBOSS_001     10605 ATCAATGATATGGACAACTACATGGTTCCCATGTATTTTGAATGCAAAAT  10654

EMBOSS_001     10510 GACAAAGTTAGGGAGTTTACAGAAGAGCTTGTTATCAGGATAACTTGACA  10559
                     |||.|||||.|.|..||||||||||||.|.||||||.||||||||||.||
EMBOSS_001     10655 GACGAAGTTTGAGCATTTACAGAAGAGTTGGTTATCGGGATAACTTGGCA  10704

EMBOSS_001     10560 ATTTATTAGTGATGCAATGTCAGAGGCCACCATCACTGCATTCTCTATGG  10609
                     |||||||||||||..||||||.||||||||.||||||.|.||||||||||
EMBOSS_001     10705 ATTTATTAGTGATATAATGTCGGAGGCCACAATCACTCCCTTCTCTATGG  10754

EMBOSS_001     10610 TGTTGCTGGTTCACCAGATGGAAGTTATTTGGGCGTACTAGTAAGTCTTT  10659
                     |||||||||.||||||||||||||||||||||||.|||||.|||||..||
EMBOSS_001     10755 TGTTGCTGGCTCACCAGATGGAAGTTATTTGGGCATACTATTAAGTTGTT  10804

EMBOSS_001     10660 CCTGAAATATTACACCCTTGTTCTTTCTAATTAAATGAAAAATTAAAGTT  10709
                     |||||.|||||||||||.|||||||||||||.||.||||||||||||.||
EMBOSS_001     10805 CCTGAGATATTACACCCCTGTTCTTTCTAATCAAGTGAAAAATTAAACTT  10854

EMBOSS_001     10710 GCTGATTTTGCAACAAGGATGCTAAACTACATACAGACATGATGTATGAA  10759
                     |||||||| |||||||||||||||||||||||.|||||||.||||.||||
EMBOSS_001     10855 GCTGATTT-GCAACAAGGATGCTAAACTACATGCAGACATAATGTGTGAA  10903

EMBOSS_001     10760 TTCCATATAGTTAAATCAGGCCTCGAAATTTCTGAAGTAACAATTTTAAT  10809
                     ||||||.||.||||||.||.||||.|||||||||||||||||||||||||
EMBOSS_001     10904 TTCCATCTACTTAAATTAGACCTCAAAATTTCTGAAGTAACAATTTTAAT  10953

EMBOSS_001     10810 AAAGACTGTCCAGGGTCTAGGCATGGAGGAGTTTGTGCTTCACTTGATAG  10859
                     ||||||||||||.|||||.||.||.|||||||||||||||||.|||||||
EMBOSS_001     10954 AAAGACTGTCCAAGGTCTTGGGATAGAGGAGTTTGTGCTTCATTTGATAG  11003

EMBOSS_001     10860 AAACATCTAATAAAACATGGTTCAATCAACTATGTTCAATACGTCCTTTC  10909
                     |||||||||||||||||||.|||.||||||||||||||||||.||||||.
EMBOSS_001     11004 AAACATCTAATAAAACATGATTCCATCAACTATGTTCAATACATCCTTTT  11053

EMBOSS_001     10910 AAATACAGCAAATGAGATGAGATCATACTCTACTCTACAGAAAACTATGC  10959
```

```
########################################
# Program: stretcher
# Rundate: Wed 18 Mar 2015 08:30:16
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150318-083015-0612-47599624-oy.asequence
#    -bsequence emboss_stretcher-I20150318-083015-0612-47599624-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      86/101 (85.1%)
# Similarity:    86/101 (85.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 370
#
#
#=======================================

EMBOSS_001         1 CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAAAATCA     50
                     |||.||.||.||||||.|||||||||||||||||.|||||||||||||||
EMBOSS_001         1 CCATTGAACATAGCCTGTGTGTTAACCCATATTCCTTATCATGAAAATCA     50

EMBOSS_001        51 ATAATATGGACAACTACTATGTTCCCACAGATGTTGAATGCAAAAAGACA    100
                     ||.||||||||||||||...|||||||...||.||||||||||||.|||.
EMBOSS_001        51 ATGATATGGACAACTACATGGTTCCCATGTATTTTGAATGCAAAATGACG    100

EMBOSS_001       101 A     101
                     |
EMBOSS_001       101 A     101


#---------------------------------------
#---------------------------------------
```

```
                         ||||..||||..|||.|   |||
EMBOSS_001     10076 GACTCAACATTTTTCAGGACAACATGGAAAATATTTCTTAAAATATTACA  10125

EMBOSS_001     10317 -----------GCAT-------------------------ATGTCT----  10326
                                |||                         ||||||
EMBOSS_001     10126 CTTACAGAAGTGCATTTTCTAACTAAAATAAAAATTAGAAATGTCTAATG  10175

EMBOSS_001     10327 ------CAGAG----------ATAAAACA---------------------  10339
                           ||||.          ||||||.|
EMBOSS_001     10176 GATCCTCAGATGTGTTTGTATATAAAATAAGAGTTCTATTTAATTATATT  10225

EMBOSS_001     10340 ---CTATAAAA----------------------ATGATGAAA--------  10356
                        ||.|||||                      ||..|||||
EMBOSS_001     10226 AAGCTTTAAAAGTTTTAATATACTGTAAATTCATTTTGAAAACTTTATG  10275

EMBOSS_001     10357 ----------TATTGATTT-TATTTTTA-----------AGACA------  10378
                               ||||.||.| |||.|.||           |||||
EMBOSS_001     10276 TATATACATATATTCATATATATATATATATGCATATAGAGACAGTTTAG  10325

EMBOSS_001     10379 -------TACATTT----AGGCCTC-------------------------  10392
                            |||||.|    ||.||||
EMBOSS_001     10326 TCATATTTACATCTTCCAAGTCCTCCCAGAACCCCAATGAACCCTTCCCA  10375

EMBOSS_001     10393 -------------TTTTT---------------AATTAGTATT-------  10407
                                  |||||               |||||||.||
EMBOSS_001     10376 ACTTCATATCTTATTTTTTAAAGATTATTGTCCAATTAGTGTTTTCTATA  10425

EMBOSS_001     10408 --------GTTG--------ACCCAATGGA-------CTTAGCCTATGTG  10434
                             ||||        |.|||.||||       ||||.|..|....
EMBOSS_001     10426 TATACATGGTTGTGGGGGTCATCCACTGGAGAGTCAACTTACCAGAGACC  10475

EMBOSS_001     10435 TTAACCCA---------------------TATTCTTTATCATGAAAA-TC  10462
                     .||.||||                     ||.|.||.|||||.||.. ||
EMBOSS_001     10476 ATACCCCAAAAGAAAACTGACTCTCTCTTTACTATTCATCATCAACTGTC  10525

EMBOSS_001     10463 AATA--------------ATATGGA--CAA----CTACTATGTTCC----  10488
                     |||.              ||.||||  |.|    ||.||||.||..
EMBOSS_001     10526 AATTGCTCCTCATTTGAGATTTGGATCCCATATGCTTCTATTTTTATTTC  10575

EMBOSS_001     10489 ---CACAGATGTTGAATGCAAAAAGACAA--------------AGTTAGG  10521
                        |..|.|||||||.|...|||...|||              ||||..|
EMBOSS_001     10576 ATGCTGAAATGTTGACTCTCAAAGTGCAACCACAGCTGCTGTGAGTTCAG  10625

EMBOSS_001     10522 GAGT-----------------TTA------------------CAGAAGAG  10536
                     .|||                 |||                  ||.|..|.
EMBOSS_001     10626 CAGTACAATGATCCTGTCGCATTAGAACTCTCCTCTCCTGTTCATATAAA  10675

EMBOSS_001     10537 CTTGTTATC-----------AGGATAACTTGACA----------------  10559
                     |||..||||           |||.|..|||...|
EMBOSS_001     10676 CTTTCTATCTCTCTTCCACTAGGTTCTCTTACTAGGGGGTTAGGGTATAA  10725

EMBOSS_001     10560 ------------ATTTATTAGTGA----TGCA------------------  10575
                                 ||||.||..|||    |.||
EMBOSS_001     10726 TATATATGTCTCATTTGTTTCTGAGCACTCCATATATATATATATATATA  10775

EMBOSS_001     10576 -ATGT--------CAGA-GGCCACCA---------------------TCA  10594
                      ||||        ||.| ||.||..|                     |||
EMBOSS_001     10776 TATGTGCTCTCTACACATGGACAGTAATGAGTAAGTGTCTTTATTACTCA  10825

EMBOSS_001     10595 CTGCATTCT---CTATGGTGTTGCTG-------------GTT-CACCA--  10625
                     |||...|||   |.|..||.||.|||             ||| |||.|
EMBOSS_001     10826 CTGTCCTCTACACAAATGTTTTTCTGATAAGGACTGATAGTTGCACAAAT  10875

EMBOSS_001     10626 ------------------------GATGGAAG-------------TTATT  10638
                                             ||||||||             |||||
```

Human vs mouse

```
########################################
# Program: stretcher
# Rundate: Fri 13 Mar 2015 08:11:32
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150313-081131-0802-13800900-oy.asequence
#    -bsequence emboss_stretcher-I20150313-081131-0802-13800900-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 107
# Identity:      47/107 (43.9%)
# Similarity:    47/107 (43.9%)
# Gaps:          12/107 (11.2%)
# Score: -65
#
#
#=======================================

EMBOSS_001         1 -----CCAATGGACTTAGCCTATGTGTTAACCCATATTCTTTATCATGAA     45
                          |.||.|.|....|.||.|.|.||.||   |||||.|.||||  |.
EMBOSS_001         1 TACCCCAAAAGAAAACTGACTCTCTCTTTAC---TATTCATCATCA--AC     45

EMBOSS_001        46 AATCAATAATATGGACAACTACTATGTTCC-CACAGATGTTGAATGCAAA     94
                     ..|||||... |..||..|...||.|... |.||.|||.|.........
EMBOSS_001        46 TGTCAATTGC-TCCTCATTTGAGATTTGGATCCCATATGCTTCTATTTTT     94

EMBOSS_001        95 AAGACAA    101
                     |...||.
EMBOSS_001        95 ATTTCAT    101


#---------------------------------------
#---------------------------------------
```

rs628117

Human vs Saqqaq-Eskimos

```
########################################
# Program: stretcher
# Rundate: Thu 25 Dec 2014 08:35:46
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141225-083545-0301-47998518-es.asequence
#    -bsequence emboss_stretcher-I20141225-083545-0301-47998518-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ||||||||||||.|||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 AGACATAGTCCCCACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Mon 16 Mar 2015 08:18:12
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150316-081811-0576-70744458-pg.asequence
#    -bsequence emboss_stretcher-I20150316-081811-0576-70744458-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      93/101 (92.1%)
# Similarity:    94/101 (93.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 452
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     .......|||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 NNNNNNNGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     :|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 YGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman elena2

```
########################################
# Program: stretcher
# Rundate: Mon 16 Mar 2015 08:19:51
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150316-081949-0642-17674448-es.asequence
#    -bsequence emboss_stretcher-I20150316-081949-0642-17674448-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      99/101 (98.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 497
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ||||||||||||:|||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 AGACATAGTCCCYACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     :|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 YGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Mon 16 Mar 2015 08:20:37
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150316-082036-0610-10234809-es.asequence
#    -bsequence emboss_stretcher-I20150316-082036-0610-10234809-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      71/101 (70.3%)
# Similarity:    71/101 (70.3%)
# Gaps:           0/101 ( 0.0%)
# Score: 293
# 
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ||||||||||||.||||||||||||.........................
EMBOSS_001         1 AGACATAGTCCCCACCCATTCTCATNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     ....||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 NNNNCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Loschbour

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:19:58
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-091957-0147-18680353-oy.asequence
#    -bsequence emboss_stretcher-I20150103-091957-0147-18680353-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      99/101 (98.0%)
# Similarity:    99/101 (98.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 489
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ||||||||||||.|||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 AGACATAGTCCCCACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 NGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Fri 26 Dec 2014 07:56:23
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141226-075622-0575-52359990-pg.asequence
#    -bsequence emboss_stretcher-I20141226-075622-0575-52359990-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      96/101 (95.0%)
# Similarity:    96/101 (95.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 468
# 
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ....||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 NNNNATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala3

```
########################################
# Program: stretcher
# Rundate: Mon 16 Mar 2015 08:25:34
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150316-082533-0664-77764032-es.asequence
#    -bsequence emboss_stretcher-I20150316-082533-0664-77764032-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Mon 16 Mar 2015 08:26:35
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150316-082633-0624-37442786-es.asequence
#    -bsequence emboss_stretcher-I20150316-082633-0624-37442786-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs VindijaNea

```
########################################
# Program: stretcher
# Rundate: Tue 21 Oct 2014 08:07:35
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141021-080735-0030-39139332-es.asequence
#    -bsequence emboss_stretcher-I20141021-080735-0030-39139332-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Denisovan

```
########################################
# Program: stretcher
# Rundate: Tue 28 Oct 2014 09:48:57
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141028-094856-0037-85165641-es.asequence
#    -bsequence emboss_stretcher-I20141028-094856-0037-85165641-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs AltaiNea

```
########################################
# Program: stretcher
# Rundate: Tue 21 Oct 2014 08:05:27
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141021-080526-0552-48136437-pg.asequence
#    -bsequence emboss_stretcher-I20141021-080526-0552-48136437-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs MezmayskayaNea

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 04:54:22
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-045421-0480-55903460-oy.asequence
#    -bsequence emboss_stretcher-I20141115-045421-0480-55903460-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      85/101 (84.2%)
# Similarity:    85/101 (84.2%)
# Gaps:           0/101 ( 0.0%)
# Score: 393
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ...|||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 NNNCATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     ||||||||||||||||||||||||||||||||||||||............
EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAANNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Chimpanzee

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 05:34:02
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-053401-0963-16778101-oy.asequence
#    -bsequence emboss_stretcher-I20150113-053401-0963-16778101-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      97/101 (96.0%)
# Similarity:    97/101 (96.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 469
#
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAA     50
                     ||||||||||||||||||||.||.|||||||||||||||||||||||.||
EMBOSS_001         1 AGACATAGTCCCTACCCATTTTCGTAGGCCTAAGATGTTAACGGAAAGAA     50

EMBOSS_001        51 CGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100
                     ||||||||||||.|||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGGGCTTTCATTTCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
                         |||||||||||||||||||||..|.|||||||||||||||||||||||||
7                  17487 AAATTATTTCAGTAATAAACATGCGTTGTGCCATCAGTATGCTTGGACAT  17536

                   16998 TTCACACATGTTACTTTATTTATTCTTCCAATAACCCTGCAAAGGAGTGC  17047
                         |||..|||.||||.||||||||||||.|||||||||| |||||||.|||||
7                  17537 TTCGTACACGTTATTTTATTTATTCTACCAATAACC-TGCAAAGAAGTGC  17585

                   17048 TAATATACTCATTTTAGAGATGAGGAAACTGAGTCTCAGAGAACTTAATA  17097
                         ||.||||.||||||||.|||.|||||||||||||||||||||..||||||
7                  17586 TAGTATATTCATTTTATAGAGGAGGAAACTGAGTCTCAGAGAGTTTAATA  17635

                   17098 TGCTCAAAGCAAACAACTAGTAGCTGATAGAGCTATTATAAAATCAAAAT  17147
                         ||||||||||||||||||||||||||||||||||||||||||||||.|||
7                  17636 TGCTCAAAGCAAACAACTAGTAGCTGATAGAGCTATTATAAAATCAGAAT  17685

                   17148 ACAGATTTGACTCCTTGCCCCACATGCCACACCAACTCACTGTGATAGGT  17197
                         |||||.||||||.|||||.|||||||||||||||||||||||||||||||
7                  17686 ACAGACTTGACTTCTTGCACCACATGCCACACCAACTCACTGTGATAGGT  17735

                   17198 CCAAAATAAACCCACCTCAAGCCCAACCCTCCTTTAGAACCAGGAGGGTA  17247
                         ||.||||||||||||||.||||..||||.|||||.|||||||||||||||
7                  17736 CCCAAATAAACCCACCTTAAGCTAAACCGTCCTTGAGAACCAGGAGGGTA  17785

                   17248 ATAGGAACTTGCAGTGTTCTAATATTGGACCACAGCCCAGCTACAGGATC  17297
                         |||.|||||..||.|||||||.|.|||||||||||||.||||..||||||
7                  17786 ATATGAACTCACACTGTTCTATTCTTGGACCACAGCCTAGCTGTAGGATC  17835

                   17298 AGTTTGCTTTCAGTGAAATGAAAACAGCCCTCAGTACTCATTAATGGGAG  17347
                         |||||.||||.|.|||||||||||||||||||||||.|||||||||||||
7                  17836 AGTTTTCTTTTAATGAAATGAAAACAGCCCTCAGTATTCATTAATGGGAG  17885

                   17348 TGTTGGTAAACACAAACAATACCACACAACAGAGAAAGAGACTTTAGGAT  17397
                         .|||||||||||||||||||||||||||||||||||||||||||...|||
7                  17886 GGTTGGTAAACACAAACAATACCACACAACAGAGAAAGAGACTTCTTGAT  17935

                   17398 AAAAGCAAGCAGTGACTGACAAGGCTTACCAATTCTCTCTCACTATCTGT  17447
                         ||||||||||||||||||||||.||||||..||.||||||||||||.|.|
7                  17936 AAAAGCAAGCAGTGACTGACAAAGCTTACAGATCCTCTCTCACTATGTCT  17985

                   17448 TTATCATTT---ATCAGGAACAAATGTTTGTTCACTGCCCTCTGTGTGCA  17494
                         |||||||.|   |.||||||||||||||||||||||||||||||||||||
7                  17986 TTATCATCTCCTAACAGGAACAAATGTTTGTTCACTGCCCTCTGTGTGCA  18035

                   17495 GTGAATTTATTTCTCAGAATCAACAACTATTGCACCCATGCATACTTTGC  17544
                         ||||||||||||||||||||||||||||||||||||||||.|||||||||
7                  18036 GTGAATTTATTTCTCAGAATCAACAACTATTGCACCCATGGATACTTTGC  18085

                   17545 ACAAGCAAGTTATACTCAGATTACCAGCTCACAAGGACAGTGTTTACTTG  17594
                         .|.||||||||||||||.||||.|||||||.|||||.|||||||.||.||
7                  18086 TCTAGCAAGTTATACTCCGATTCCCAGCTCTCAAGGCCAGTGTTGACATG  18135

                   17595 CATGCAGAGGAGAGACCCTGCCGTAAAGTA--GACACTGCTGAGACATAG  17642
                         |||||||||||||||||||.|.||||||.|  ||||||||||||||||||
7                  18136 CATGCAGAGGAGAGACCCTACAGTAAAGCACAGACACTGCTGAGACATAG  18185

                   17643 TCCCTACCCATTCTCATAGGCCTAAGATGTTAACGGAAACAACGGGCTTT  17692
                          ||||||.|.|||.|||.||||||||||              |.||||.|
7                  18186 -CCCTACACCTTCACATGGGCCTAAGAT--------------CAGGCTAT  18220

                   17693 CATTCCAAGGATGCAAATGATGCAATTCAAGCCAAATATCCTGTGTCTTT  17742
                         |||||||||||||||||||||||.||||||||||||.||||||||||.||
7                  18221 CATTCCAAGGATGCAAATGATGCGATTCAAGCCAAAAATCCTGTGTCCTT  18270

                   17743 TTACCAA-AAAAAAAAAATCACTCTGACCAATTCCTCAAACCTGTCAAAA  17791
                         |.||||| ||||||||||.|||||||||||||||||||||||..|.|||.
```

```
########################################
# Program: stretcher
# Rundate: Wed 18 Mar 2015 08:14:16
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150318-081415-0178-10397653-es.asequence
#    -bsequence emboss_stretcher-I20150318-081415-0178-10397653-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 116
# Identity:      78/116 (67.2%)
# Similarity:    78/116 (67.2%)
# Gaps:          30/116 (25.9%)
# Score: 202
#
#
#=======================================

EMBOSS_001         1 ---------------AGACATAGTCCCTACCCATTCTCATAGGCCTAAGA     35
                                    |||||||| ||||||.|.|||.|||.|||||||||
EMBOSS_001         1 GCACAGACACTGCTGAGACATAG-CCCTACACCTTCACATGGGCCTAAGA     49

EMBOSS_001        36 TGTTAACGGAAACAACGGGCTTTCATTCCAAGGATGCAAATGATGCAATT     85
                     |              |.||||.||||||||||||||||||||||||.|||
EMBOSS_001        50 T--------------CAGGCTATCATTCCAAGGATGCAAATGATGCGATT     85

EMBOSS_001        86 CAAGCCAAATATCCTG    101
                     |||||||||.||||||
EMBOSS_001        86 CAAGCCAAAAATCCTG    101


#---------------------------------------
#---------------------------------------
```

```
17526 GCACCCATGCATACTTTGCACAAGCAAGTTATACTCAGATTACCAGCTCA  17575
      ||||||.||...||||.|.|||..||..||||.|||||||..|||||||.
18724 GCACCCTTGTCCACTTGGAACACACACCTTATGCTCAGATGGCCAGCTCT  18773

17576 CAAGGACAGTGTTTACTTGCATGCAGAGGAGAGACCCTGCCGTAAAGTAG  17625
      |||.|.|     |.|..||..|||||||.|||||.|.||...|...|.|.
18774 CAAAGGC-----TCAGGTGTGTGCAGAGAAGAGATCTTGTGATGCTGCAT  18818

17626 ACACTGCTGAGACATAGTCCCTACCCATT-CTCATAGGCCTAAGATGTTA  17674
      .|.|  ||.|||...||.|  ||....|| |..|.||||||| |.|||..
18819 GCCC--CTAAGAAGCAGGC--TATGAGTTGCGTACAGGCCTA-GCTGTCC  18863

17675 ACGGAAACAACGGGCTTTCATTCCAAGGATGCAAATGATGCAATTCA-AG  17723
          ||||.|.|.|...||||||..|||||    |||  .||..||| ||
18864 ----AAACCATGAGGCGTCATTCTGAGGAT----ATG--TCAGGTCACAG  18903

17724 CCAAATATCCTGTGTCTTTTTACCAAAAAAAAAAAATCACT--------C  17765
      |  ||.||||   |....|.||||.|.|..||||.||||||        |
18904 C--AAGATCC---GCACATCTACCCACATGAAAACATCACTGAGATTTTC  18948

17766 TGACCAATTCCTCAAACCTGTCAAAAATTTAGATAAATAAACATCAAACT  17815
      ||||||.||.||||.|.||||||||||||.|.||||||.|||..|.|||.
18949 TGACCAGTTACTCACATCTGTCAAAAATTCAAATAAATTAACGCCGAACA  18998

17816 GTGGCCCAATAAGCAGACCCCATGTCA--CTTCACTAATTAATA-CCCAA  17862
      ||.|||||.|..||||||.|.|....|  |||||..||..||.| |||||
18999 GTAGCCCATTTGGCAGACTCTACAATAACCTTCATAAACCAACATCCCAA  19048

17863 AGGAGGA-AATAGCATGCAT--AAATAGCTATCATCTATTTAGTCACTGG  17909
      ||||..| ||.||..|||||  ||.|||.|| |||.||.|||.||||.|.
19049 AGGAAAAGAAAAGAGTGCATGTAAGTAGTTA-CATATAGTTAATCACAGA  19097

17910 ATCATATAT--GAAAAAGAGGTAACCTTATTCCAACATCATCATCATGGC  17957
      .|||.||.|  |.||.|.||..|.|||||| |||....|||..|.|||||
19098 CTCAGATGTAGGGAACAAAGACACCCTTAT-CCACTGGCATTGTTATGGC  19146

17958 AGGCTCTTCGCATC-ATTTTATCTGATCTTTGCAATATCCCTATAATAGA  18006
      ||.||.||..|..| ||.|||..|.||.||..|.||.||||||||||||
19147 AGACTTTTTTCTGCCATCTTACTTAATTTTCACTATGTCCCTATAATAG-  19195

18007 AGATACCATTTTTTGCTTCTTACAGATAAGGAAACCAAGCTTACAGAGGT  18056
       ||||...|.||..||.|.|||..|.|||.||||..||    |.|.|
19196 -GATATTGTGTTCAGCATTTTAAGGCTAAAGAAAAAAA----AAAAA---  19237

18057 GAAGCACATTTGAGGTCAGGAATTTAGAAGAGAAATGAATGAGGCTCAAA  18106
       ||.|.    |.|||.|.|||.                   |||..||||
19238 -AACCC----TAAGGCCTGGAT-------------------AGGGACAAA  19263

18107 CCCAGCTCTCTTCCTCTCCACCCCACACCAACATACATTCATCGTTCAGG  18156
                                   |||.|
19264 -----------------------------AACTT----------------  19268

18157 TGCTACGTGTGAGCACAGTGCTGTGCCAACTCTGTGGTAAGCCTTGTAGG  18206
                            ||||.||.||      |||      ||.
19269 ----------------------GTGCAAAGTC------AAG------AGA  19284

18207 GAAGCAGAGGCAAGAATGAGGAAGACTCTTGAACATTAGTCACTCACATG  18256
      .|..|||||..||||.|.||.|     .|||.|.||..||. |||.|.|
19285 CATCCAGAGCAAAGAGTAAGTA-----TTTGGAAATCGGTT-CTCTCCT-  19327

18257 GTGACTATTTTTTTTTTTTTTTTCTGAGACTGAGATTTGCTTTTGTCGCC  18306
           |.||.|||||||||||||||.....|....|||..||||.|.||.
19328 -----TTTTCTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTGCA  19372

18307 CAGGCTGGAGTGCAATGGGGCGATCTCAGCTCATTACAACCTCCACCTCC  18356
```

Human vs mouse

```
########################################
# Program: stretcher
# Rundate: Wed 18 Mar 2015 06:33:51
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150318-063350-0091-96680538-pg.asequence
#    -bsequence emboss_stretcher-I20150318-063350-0091-96680538-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 109
# Identity:      55/109 (50.5%)
# Similarity:    55/109 (50.5%)
# Gaps:          16/109 (14.7%)
# Score: -25
# 
#
#=======================================

EMBOSS_001         1 AGACATAGTCCCTACCCATT-----CTCATAGGCCTAAGATGTTAACGGA     45
                     ...|..||...|...|.||.     |..|.||||||| |.|||.    .|
EMBOSS_001         1 CCCCTAAGAAGCAGGCTATGAGTTGCGTACAGGCCTA-GCTGTC----CA     45

EMBOSS_001        46 AACAACGGGCTTTCATTCCAAGGATGCAAATGATG-CAATTCAAG--CCA     92
                     |||.|.|.|...||||||..|||||  |..|.|.| ||...||||  ||.
EMBOSS_001        46 AACCATGAGGCGTCATTCTGAGGAT--ATGTCAGGTCACAGCAAGATCCG     93

EMBOSS_001        93 AATATCCTG    101
                     .|.||| |.
EMBOSS_001        94 CACATC-TA    101


#---------------------------------------
#---------------------------------------
```

rs96501

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 06:25:40
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-062539-0041-9519764-oy.asequence
#    -bsequence emboss_stretcher-I20150114-062539-0041-9519764-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-elena1

```
########################################
# Program: stretcher
# Rundate: Tue 17 Mar 2015 07:53:24
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150317-075323-0166-70269818-es.asequence
#    -bsequence emboss_stretcher-I20150317-075323-0166-70269818-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      64/101 (63.4%)
# Similarity:    64/101 (63.4%)
# Gaps:           0/101 ( 0.0%)
# Score: 246
# 
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||....................................||||||
EMBOSS_001         1 TACCTTCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||.|
EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGNT    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-elena2

```
########################################
# Program: stretcher
# Rundate: Tue 17 Mar 2015 07:54:46
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150317-075444-0437-69932425-es.asequence
#    -bsequence emboss_stretcher-I20150317-075444-0437-69932425-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      84/101 (83.2%)
# Similarity:    84/101 (83.2%)
# Gaps:           0/101 ( 0.0%)
# Score: 384
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     .|||||||||||||||||||||||||||||||||................
EMBOSS_001        51 TCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Tue 17 Mar 2015 07:56:11
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150317-075610-0454-35318161-pg.asequence
#    -bsequence emboss_stretcher-I20150317-075610-0454-35318161-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      57/101 (56.4%)
# Similarity:    57/101 (56.4%)
# Gaps:           0/101 ( 0.0%)
# Score: 197
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||||||||..................
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACANNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     .|||||||||||||||||||||||||........................
EMBOSS_001        51 NCTTTATGGTCTTTCTCTTCCAATGGNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 T    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Loschbour

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:21:56
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-092155-0609-66954141-es.asequence
#    -bsequence emboss_stretcher-I20150103-092155-0609-66954141-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala12

```
########################################
# Program: stretcher
# Rundate: Fri 26 Dec 2014 08:01:57
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141226-080155-0954-77383607-pg.asequence
#    -bsequence emboss_stretcher-I20141226-080155-0954-77383607-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
# 
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala3

```
########################################
# Program: stretcher
# Rundate: Tue 17 Mar 2015 08:44:57
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150317-084455-0962-80333789-pg.asequence
#    -bsequence emboss_stretcher-I20150317-084455-0962-80333789-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 T    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Tue 17 Mar 2015 08:45:50
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150317-084549-0619-49003383-oy.asequence
#    -bsequence emboss_stretcher-I20150317-084549-0619-49003383-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 T    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Tue 21 Oct 2014 11:47:09
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141021-114708-0868-27115376-es.asequence
#    -bsequence emboss_stretcher-I20141021-114708-0868-27115376-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Tue 28 Oct 2014 09:50:42
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141028-095041-0047-96009693-es.asequence
#    -bsequence emboss_stretcher-I20141028-095041-0047-96009693-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

Human vs AltaiNea

```
########################################
# Program: stretcher
# Rundate: Tue 21 Oct 2014 11:44:11
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141021-114410-0364-67491574-pg.asequence
#    -bsequence emboss_stretcher-I20141021-114410-0364-67491574-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 04:57:22
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-045721-0284-86194665-es.asequence
#    -bsequence emboss_stretcher-I20141115-045721-0284-86194665-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      28/101 (27.7%)
# Similarity:    28/101 (27.7%)
# Gaps:           0/101 ( 0.0%)
# Score: -6
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||||......................
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 T    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs chimpanzee

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 05:51:37
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-055137-0015-7542218-oy.asequence
#    -bsequence emboss_stretcher-I20150113-055137-0015-7542218-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      98/101 (97.0%)
# Similarity:    98/101 (97.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 478
#
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||||||||||||||||||.||||.||||||||||||||||||
EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTTTGACGTTGTTTTCTTCTCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

```
                  .|..||||||||||.||||||||     |||||||||||.||||||||||
7           39108 TACTGTTGAGAACCTCTACTTTA-----ACATCCAAAGAAATCCATTAAA  39152

            39178 TGTTAATTCTTCAAAATTTTCAATCCTTTTTCCAATTATTCAAGAACCC  39227
                  ||||.||||||||||||..||||||||||||.|||||||||.||||||||
7           39153 TGTTCATTCTTCAAAATGCTTCAATCCTTTTTTCAATTATTCCAGAACCC  39202

            39228 CTTATGACAGAGTCAATCAAGAACATGCAATGTTTATTTTGCATATTTCA  39277
                  |||||||||||.||||||||||.||.|||.||||||||||||.||||||.
7           39203 CTTATGACAGATTCAATCAAGAGCACGCAGTGTTTATTTTGCCTATTTCG  39252

            39278 TTTGTCCAACTCAAAGTGCCCTTACTGTCACACTTTTCCAGTTTGTCGAT  39327
                  ||||.|||||||||||||||.||.||.|||.||..||||||||||||..|
7           39253 TTTGCCCAACTCAAAGTGCCTTTCCTCTCATACCCTTCCAGTTTGTCATT  39302

            39328 TCATAGATACAGTCATTCACATCAGGAAGACTTCTGCGGTTAATTTCATA  39377
                  |||||||||  ||||||||||.||..|||.|||||..||.|||.||||||
7           39303 TCATAGATA--GTCATTCACAGCACAAAGCCTTCTATGGGTAACTTCATA  39350

            39378 CCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCATC-  39426
                  ||||||||.||||||||||||||..|||||.|||||||||||||||||. 
7           39351 CCTTCATACGATCACTGCATTTTGTTGACACTGTTTTCTTCTCAGCATTT  39400

            39427 -CTTTATGGTCTTT----------------------------CTCTTC--  39445
                   ||||.|..|.|||                            |||||.  
7           39401 TCTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTTTCACTCTTGTT  39450

            39446 ---------------CAATGGC----------------------------  39452
                                 |||||||
7           39451 ACCCAGGCTGGAATGCAATGGCGCGATCTCGGCTCACCGCCACCCTCCGC  39500

            39453 --------------------------------------------------  39452

7           39501 CTCCTGGGTTCAGGCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  39550

            39453 --------------------------------------------------  39452

7           39551 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  39600

            39453 --------------------------------------------------  39452

7           39601 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  39650

            39453 --------------------------------------------------  39452

7           39651 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  39700

            39453 --------------------------------------------------  39452

7           39701 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  39750

            39453 --------------------------------------------------  39452

7           39751 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  39800

            39453 --------------------------------------------------  39452

7           39801 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  39850

            39453 --------------------------------------------------  39452

7           39851 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  39900

            39453 --------------------------------------------------  39452
```

```
########################################
# Program: stretcher
# Rundate: Wed 22 Oct 2014 05:47:45
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141022-054744-0110-76703527-pg.asequence
#    -bsequence emboss_stretcher-I20141022-054744-0110-76703527-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      67/101 (66.3%)
# Similarity:    67/101 (66.3%)
# Gaps:           0/101 ( 0.0%)
# Score: 199
# 
#
#=======================================

EMBOSS_001         1 TACCTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGCAT     50
                     ||||||||||.||||||||||||||..|||||.|||||||||||||||||
EMBOSS_001         1 TACCTTCATACGATCACTGCATTTTGTTGACACTGTTTTCTTCTCAGCAT     50

EMBOSS_001        51 CCTTTATGGTCTTTCTCTTCCAATGGCCTAAATGCTGATGTTCTTCAGTT    100
                     ..|.|.|..|.|||.|.||....|....|..|..|.||..|||.....|.
EMBOSS_001        51 TTTCTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTTTCACTCTTG    100

EMBOSS_001       101 T    101
                     |
EMBOSS_001       101 T    101


#---------------------------------------
#---------------------------------------
```

```
      |.|.||||||. ||.|...||.|..|||||.||.|..|.||  |.|.|.|
39799 ACCCTTTACAC-AACTTTTAATTTTTTCTTGGTAGAAGAGGAAGCTATCC  39847

38989 TGTATACTGCAGGATGTTAGCAACATTCCTGGCCTCGCTATACACATCAG  39038
      ...|.|.|..||||..||...|.|||.|.||.||||    |||.||.|..
39848 CAGACAATTTAGGACATTTTGAGCATCCATGACCTC----TACCCACCCA  39893

39039 TGGCCAGTAGTGTGCCCTCCCTACCCACTTGTGACAACCAAAAA------  39082
      ||||.       |||..|.|.||||||.||||||||...|.|||
39894 TGGCA-------TGCTATACTTACCCAGTTGTGACATAAATAAATAAATA  39936

39083 -----------AAATGTC-TCCAGACATTGTCAAATACCCA-TGGGAG-C  39118
                 |||||.. ||.||..||||.|.||||.||. ||.|.| |
39937 AATAAATAAATAAATGCAATCTAGTAATTGCCTAATATCCTCTGAGGGTC  39986

39119 AAAATCATCCAGCGT---TGAGAACCACTACTTTAGACTGACATCCAAAG  39165
      ..|||| ||||...|   ||.||.|.|||.||.|...||||..||.|..|
39987 TTAATC-TCCAAAATAATTGGGACCAACTCCTATCAGCTGATGTCTAGGG  40035

39166 ACATCCATTAAATGTTAATTCTTCAAAATTTTTCAATCCTTTTTCC-AAT  39214
      ||.|||||.||.|||.|...|.||||..|||..||.|..|||||.| |||
40036 ACTTCCATAAATTGTGATAACCTCAATCTTTCCCAGTGTTTTTTTCTAAT  40085

39215 TATTCAAGAACCCCTTATGACAGAGTCAATCAAGAACATGCAATGTTTAT  39264
      .||||.|.|||||.||.||.|.||.|||.|||      |.||....|||.
40086 CATTCCATAACCCTTTCTGGCTGATTCAGTCA------TTCAGGACTTAC  40129

39265 TTTGCATATTTCATTTGTCCAACTCAAAGTGCCCTTACTGTCACACTTTT  39314
      .||.||.||||..|..|.||||.||||| |||||||....||.| ||..|
40130 ATTACACATTTTGTCAGCCCAATTCAAA-TGCCCTTCTCCTCTC-CTACT  40177

39315 CCAGTTTGTCGATTCATAGATACAGTCATTCACATCAGGAAGAC--TTCT  39362
      .|| |.|||..||||||.|||.  |||.|.||.|.||||||..|  ||.|
40178 TCA-TATGTTAATTCATGGATG--GTCTTCCATAACAGGAAAGCATTTTT  40224

39363 GCGGTTAATTTCATACCTTCATAGGATCACTGCATTTTTCTGACATTGTT  39412
      ..|.|||.||||||..|.||||..||.|||||||||||..||||||  ||
40225 ATGATTAGTTTCATGGCATCATGTGACCACTGCATTTTGTTGACAT--TT  40272

39413 TTCTTCTCAGCATCCTTTA---TGGT-CTTTCTCTTCCAATGGCCTAAAT  39458
      .|||||....|||.|||.|   ||.| ||||||||.|..|||||..|.
40273 CTCTTCCAGCCATTCTTCACCCTGTTGCTTTCTCTGCATATGGCTGAG--  40320

39459 GCTGATGTTCTTCAGTTTTCTATCTGTAGTCCTCATTTTTACTTGGTCTA  39508
      ||||.|..|||||||....|||.....|||.||||.||..||.||....|
40321 GCTGGTACTCTTCAGGGCCCTAGACTCAGTTCTCACTTCGACATGACTGA  40370

39509 TATTCTTCTAGGATGAAGTCTTCTACTCTTTTTGATTCATCTTTTGCAAC  39558
      ||.|||.||...||||  .|.|.|...||||.||     |||..||  ||
40371 TACTCTCCTGCCATGA--GCGTGTGTACTTTGTG-----TCTGATG--AC  40411

39559 AACGACCACCACCACCCCAGCTCCAAATTTGTGTCTCCAGGATGACCTAT  39608
      ||||||...||||||....|.||||..|.|...||||||..||||.||..
40412 AACGACTTTCACCACTGGTGTTCCACGTCTCCATCTCCATAATGAACTGA  40461

39609 CTCCTGTTCCATTAAATAGTTTT-CCAACTAATAACAAAACAGCTGCAGA  39657
      ||.||...||.|.|.|||||||| ||||.||||.||||||||. |..|||
40462 CTTCTAAACCTTGATATAGTTTTACCAAATAATTACAAAACAT-TCAAGA  40510

39658 AGAACCTTGACAGTTCTAAAAGTCAATAGGTCCAAAAAACATTTCTCTCT  39707
      |||||.|  ||||..   |..|||||||.|||||||.|......||..||
40511 AGAACTT--ACAGAC---AGGGTCAATACGTCCAAACATAGCCACTGCCT  40555

39708 CTCCTGACCAAACTCTTCCTCTTATCTTCTTTTCTCAATAAATTTCTTTA  39757
      ...||.||..||.||.||.|||..| |..|.||||.|||||||.|||.|.
```

Human vs mouse

```
########################################
# Program: stretcher
# Rundate: Wed 22 Oct 2014 06:54:21
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141022-065420-0357-84219511-es.asequence
#    -bsequence emboss_stretcher-I20141022-065420-0357-84219511-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 107
# Identity:      69/107 (64.5%)
# Similarity:    69/107 (64.5%)
# Gaps:          12/107 (11.2%)
# Score: 121
#
#
#=======================================

EMBOSS_001         1 TAC--CTTCATAGGATCACTGCATTTTTCTGACATTGTTTTCTTCTCAGC     48
                     .|.  |.||||..||.|||||||||||..|||||||  |.|||||....|
EMBOSS_001         1 CATGGCATCATGTGACCACTGCATTTTGTTGACATT--TCTCTTCCAGCC     48

EMBOSS_001        49 ATCCTTTA---TGGT-CTTTCTCTTCCAATGGCCTAAATGCTGATGTTCT     94
                     ||.|||.|   ||.| ||||||||.|..|||||..|.  ||||.|..|||
EMBOSS_001        49 ATTCTTCACCCTGTTGCTTTCTCTGCATATGGCTGAG--GCTGGTACTCT     96

EMBOSS_001        95 TCAGTTT    101
                     ||||.
EMBOSS_001        97 TCAGG--    101


#---------------------------------------
#---------------------------------------
```

rs4915045

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 06:27:41
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-062740-0700-22351675-es.asequence
#    -bsequence emboss_stretcher-I20150114-062740-0700-22351675-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
# 
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-elena1

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 06:42:42
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-064241-0831-61995903-es.asequence
#    -bsequence emboss_stretcher-I20150319-064241-0831-61995903-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      88/101 (87.1%)
# Similarity:    88/101 (87.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 414
# 
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ||||||||||||||||||||||||||||||.............|||||||
EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCNNNNNNNNNNNNNACTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 06:43:47
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-064346-0204-34702429-pg.asequence
#    -bsequence emboss_stretcher-I20150319-064346-0204-34702429-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-teresa

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 06:44:32
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-064431-0578-74886253-oy.asequence
#    -bsequence emboss_stretcher-I20150319-064431-0578-74886253-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 501
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ||||||||||||||||||||||||||||||||||||||||||||:|||||
EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAAYTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:24:40
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-092439-0092-39846964-es.asequence
#    -bsequence emboss_stretcher-I20150103-092439-0092-39846964-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala12

```
########################################
# Program: stretcher
# Rundate: Fri 26 Dec 2014 08:06:03
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141226-080602-0807-27071606-pg.asequence
#    -bsequence emboss_stretcher-I20141226-080602-0807-27071606-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      54/101 (53.5%)
# Similarity:    54/101 (53.5%)
# Gaps:           0/101 ( 0.0%)
# Score: 176
# 
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ...............................................|||
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 07:20:02
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-072001-0120-19068707-pg.asequence
#    -bsequence emboss_stretcher-I20150319-072001-0120-19068707-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      32/101 (31.7%)
# Similarity:    32/101 (31.7%)
# Gaps:           0/101 ( 0.0%)
# Score: 22
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     |||||||...........................................
EMBOSS_001         1 GGAAACANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ..........................||||||||||||||||||||||||
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 07:20:55
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-072054-0219-70478208-pg.asequence
#    -bsequence emboss_stretcher-I20150319-072054-0219-70478208-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: 108023539-108023639_101bp_rs4915045
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       9/101 ( 8.9%)
# Similarity:     9/101 ( 8.9%)
# Gaps:           0/101 ( 0.0%)
# Score: -139
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ..................................................
108023539-108      1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ..........................................||||||||
108023539-108     51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACATCCGA    100

EMBOSS_001       101 G    101
                     |
108023539-108    101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Wed 22 Oct 2014 08:38:34
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141022-083833-0058-5470335-es.asequence
#    -bsequence emboss_stretcher-I20141022-083833-0058-5470335-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      86/101 (85.1%)
# Similarity:    86/101 (85.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 400
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ...............|||||||||||||||||||||||||||||||||||
EMBOSS_001         1 NNNNNNNNNNNNNNNCAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Denisovan

```
########################################
# Program: stretcher
# Rundate: Tue 28 Oct 2014 09:52:51
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141028-095250-0652-15592520-pg.asequence
#    -bsequence emboss_stretcher-I20141028-095250-0652-15592520-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Wed 22 Oct 2014 08:36:08
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141022-083607-0131-66153080-es.asequence
#    -bsequence emboss_stretcher-I20141022-083607-0131-66153080-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 05:00:06
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-050005-0307-42079061-pg.asequence
#    -bsequence emboss_stretcher-I20141115-050005-0307-42079061-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      19/101 (18.8%)
# Similarity:    19/101 (18.8%)
# Gaps:           0/101 ( 0.0%)
# Score: -69
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ................................||||||||||||||||||
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs chimpanzee

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 06:07:39
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-060738-0795-29403393-es.asequence
#    -bsequence emboss_stretcher-I20150113-060738-0795-29403393-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     |||||||.||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GGAAACAGACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
  51 CACAACAACGTGCGCTGCCTGTGCCCGGCCGCATACACGGGCATCCTCTG     100
     ||||||||||||||||||||||||||.|||||||||||||||||||||||
  51 CACAACAACGTGCGCTGCCTGTGCCCAGCCGCATACACGGGCATCCTCTG     100

 101 CGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGCGGCTCCGACTCTGGCC     150
     |||||||||||||||||||||||||||||||||.|||||||.|||.||||
 101 CGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGTGGCTCCGGCTCCGGCC     150

 151 AGGGCGCGCCCCCGCACGGCTCCCCAGCGCTGCTGCTGCTGACCACGCTG     200
     |||||||.||||||||||||||||...|||||||||||||||||||||||
 151 AGGGCGCACCCCCGCACGGCTCCCGCACGCTGCTGCTGCTGACCACGCTG     200

 201 CTGGGAACCGCCAGCCCCCTGGTGTTCTAGGTGTCACCTCCAGCCACACC     250
     |||||.||.||||||||||||||||||||||||.|.||.||.||||||||
 201 CTGGGGACGGCCAGCCCCCTGGTGTTCTAGGTGGCGCCACCGGCCACACC     250

 251 GGACGGGCCTGTGCCGTGGGGAAGCAGACACAACCCAAACATTTGCTACT     300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 251 GGACGGGCCTGTGCCGTGGGGAAGCAGACACAACCCAAACATTTGCTACT     300

 301 AACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAA     350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 301 AACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAA     350

 351 CTAAGAAGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCAC     400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 351 CTAAGAAGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCAC     400

 401 ATCCGAGTCAAGACTGTTAATTTCTGACTCCAGAGGAGTTGGCAGCTGTT     450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 401 ATCCGAGTCAAGACTGTTAATTTCTGACTCCAGAGGAGTTGGCAGCTGTT     450

 451 GATATTATCACTGCAAATCACATTGCCAGCTGCAGAGCATATTGTGGATT     500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 451 GATATTATCACTGCAAATCACATTGCCAGCTGCAGAGCATATTGTGGATT     500

 501 GGAAAGGCTGCGACAGCCCCCCAAACAGGAAAGACAAAAAACAAACAAA-     549
     ||||||||||||||||||||.||||||||||||||.||||..|||.||| 
 501 GGAAAGGCTGCGACAGCCCCACAAACAGGAAAGACGAAAACAAAAAAAAC     550

 550 --TCAACCGACCTAAAAACATTGGCTACTCTAGCGTGGTGCGCCCTAGTA     597
       ||||||||||||||||||||||||||||||||||||||||||||||||
 551 AATCAACCGACCTAAAAACATTGGCTACTCTAGCGTGGTGCGCCCTAGTA     600

 598 CGACTCCGCCCAGTGTGTGGACCAACCAAATAGCATTCTTTGCTGTCAGG     647
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 601 CGACTCCGCCCAGTGTGTGGACCAACCAAATAGCATTCTTTGCTGTCAGG     650

 648 TGCATTGTGGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCCTGCT     697
     |||||||.|||||||||||||||.||||||||||||||||||||||||||
 651 TGCATTGCGGGCATAAGGAAATCAGTTACAAGCTGCCATATTGGCCTGCT     700

 698 TCCGTCCCTGAATCCCTTCCAACCTGTGCTTTAGTGAACGTTGCTCTGTA     747
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 701 TCCGTCCCTGAATCCCTTCCAACCTGTGCTTTAGTGAACGTTGCTCTGTA     750

 748 ACCCTTGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACATGT     797
     |||||||||||||||||||||||||||||.||||||||||||||||||||
 751 ACCCTTGTTGGTTGAAAGATTTCTTTGTCCGATGTTAGTGATGCACATGT     800

 798 GTAACAGCCCCCTCTAAAAGCGCAAGCCAGTCATACCCCTGTATATCTTA     847
     ||||||||||||||.|||||||||||||||||||||||||||||||||||
 801 GTAACAGCCCCCTCCAAAAGCGCAAGCCAGTCATACCCCTGTATATCTTA     850
```

Human vs marmoset

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 07:50:02
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-075001-0633-18964825-pg.asequence
#    -bsequence emboss_stretcher-I20150319-075001-0633-18964825-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGA     50

EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 AGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGA    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
 51 CACAACAACGTGCGCTGCCTGTGCCCGGCCGCATACACGGGCATCCTCTG    100
    ||.|||||.|||||||||..||||||.|.|||.|||||.|||||||||||
 51 CAGAACAATGTGCGCTGCGCGTGCCCAGACGCCTACACCGGCATCCTCTG    100

101 CGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGCGGCTCCGACTCTGGCC    150
    .||||||||.||||||||.|||||.||||||||.||||||||.||.||||
101 TGAGAAGCTACGGTGCGAAGAGGCGGGCAGCTGTGGCTCCGAATCCGGCC    150

151 AGGGCGCGCCCCCGCACGGCTCCCCAGCGCTGCTGCTGCTGACCACGCTG    200
    ||||.||.|||||||..|||||||||||.||||||||||||||||.||||
151 AGGGAGCACCCCCGCGGGGCTCCCCAGCACTGCTGCTGCTGACCATGCTG    200

201 CTGGGAACCGCCAGCCCCCTGGTGTTCTAGGTGTCACCTCCAGCCACACC    250
    |||||.||.|||.|.||||||||||||||||.|||||..|||||| |.||
201 CTGGGGACTGCCGGTCCCCTGGTGTTCTAGGGGTCACACCCAGCC-CTCC    249

251 GGACGGGCCTGTGCCGTGGGGAAGCAGACACAACCCAAACATTTGCTACT    300
    | ||.|||||||||.|||||||||||.|||||||||||.|..||||.|||
250 G-ACAGGCCTGTGCTGTGGGGAAGCAAACACAACCCAAGCGATTGCCACT    298

301 AACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAA    350
    .||||||.||||||.||||        |||.|.|..|.||||||||.|||
299 GACATAGAAAACACGCACA--------CCCACTCCAACACAGTGTATAAA    340

351 CTAAGAAGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCAC    400
    ..||||.|||||||||||||||||||||||.|.|||.....|||||||||
341 AGAAGAGGGCCTAACTGAACTAAGCCATATCTCTCAGAACCGGACAGCAC    390

401 ATCC-------GAGTCAAGACTGTTAATTTCTGACTCCAGAGGAGTTGGC    443
    |||.       ||||..||||||||.||...|||||||||||||.|||||
391 ATCGCACATCGGAGTTGAGACTGTTCATCATTGACTCCAGAGGAATTGGC    440

444 AGCTGTTGATATTATCACTGCAAATCACATTGCCAGCTGCAGAGCATATT    493
    ||||||||.||||.||||||||||||.||||||||||||||||||..|||
441 AGCTGTTGCTATTCTCACTGCAAATCTCATTGCCAGCTGCAGAGCTGATT    490

494 GTGGATTGGAAAGGCTGCGACAGCCCCCCAAACAGGAAAGACAAAAAACA    543
    |.|||||||||||||||.||.|||.||||.||.|||||||||..||||||
491 GCGGATTGGAAAGGCTGTGAGAGCGCCCCCAAGAGGAAAGACGGAAAACA    540

544 AACAAATCAACCGACCTAAAAACATTGGCTACTCTAGCGTGGTGCGCCCT    593
    |||..|||||||.|||||||||||||.|||||||||.||||||||.||||
541 AACTGATCAACCAACCTAAAAACATTCGCTACTCTACCGTGGTGCACCCT    590

594 AGTACGACTCCGCCCAGTGTGTGGACCAACCAAATA---GCATTCTTTGC    640
    |||||..|||.||.||||||||||.|||||||||||   ||||||||.||
591 AGTACCGCTCTGCTCAGTGTGTGGGCCAACCAAATAAAAGCATTCTTCGC    640

641 TGTCAGGTGCATTGTGGGCATAAGGAAATCTGTTACAAGCTGCCATATTG    690
    ||||||||||||||||||.|||||||||||||||||||||||||||||||
641 TGTCAGGTGCATTGTGGGTATAAGGAAATCTGTTACAAGCTGCCATATTG    690

691 GCCTGCTTCCGTCCCTG---------AATCCCTTCCAACCTGTGCTTTAG    731
    |||||||||.|||||..         ||||||||||||||||||||||||
691 GCCTGCTTCAGTCCCCCGACCCCCAAATCCCTTCCAACCTGTGCTTTAG    740

732 TGAACGTTGCTCTGTAACCCTTGTTGGTTGAAAGATTTCTTTGTCTGATG    781
    ||||||||||||||||||||||||||||||||||||||||||||||||||
741 TGAACGTTGCTCTGTAACCCTTGTTGGTTGAAAGATTTCTTTGTCTGATG    790

782 TTAGTGATGCACATGTGTAACAGCCCCCTCTAAAAGCGCAAGCCAGTCAT    831
    ||||||||.||||.||||||||||||||||.||| |||||||||||||||
791 TTAGTGATACACACGTGTAACAGCCCCCTCCAAA-GCGCAAGCCAGTCAT    839
```

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 08:43:39
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-084338-0451-20007450-pg.asequence
#    -bsequence emboss_stretcher-I20150319-084338-0451-20007450-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 103
# Identity:      75/103 (72.8%)
# Similarity:    75/103 (72.8%)
# Gaps:           4/103 ( 3.9%)
# Score: 227
#
#
#=======================================

EMBOSS_001         1 GGAAACACACACATACAGACACCCCCACTC--AGACAGTGTACAAACTAA     48
                     ...| ||.|.| |.|||..|||.|||||||  |.||||||||.|||..||
EMBOSS_001         1 CTGA-CATAGA-AAACACGCACACCCACTCCAACACAGTGTATAAAAGAA     48

EMBOSS_001        49 GAAGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCC     98
                     ||.|||||||||||||||||||||||.|.|||.....||||||||||||.
EMBOSS_001        49 GAGGGCCTAACTGAACTAAGCCATATCTCTCAGAACCGGACAGCACATCG     98

EMBOSS_001        99 GAG    101
                     .|.
EMBOSS_001        99 CAC    101


#---------------------------------------
#---------------------------------------
```

rs1105684

Human vs Saqqaq-Eskimos

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 06:31:39
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-063138-0457-77792412-oy.asequence
#    -bsequence emboss_stretcher-I20150114-063138-0457-77792412-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 09:14:29
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-091428-0205-78380387-oy.asequence
#    -bsequence emboss_stretcher-I20150319-091428-0205-78380387-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      89/101 (88.1%)
# Similarity:    89/101 (88.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 421
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     |||||||||||||||||||||||||||||||||||||||||.........
EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTNNNNNNNNN     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ...|||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 NNNATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 09:15:26
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-091525-0046-76679205-pg.asequence
#    -bsequence emboss_stretcher-I20150319-091525-0046-76679205-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      97/101 (96.0%)
# Similarity:    97/101 (96.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 477
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     |||||||||||||||||||||||||||||||||||||||||||||||||.
EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTN     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ..||||||||||||||||||||||||||.|||||||||||||||||||||
EMBOSS_001        51 NNAATTTATTTATTTTCCAGGGAATGCGNGGCATTTAAACCAACAGGACT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-teresa

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 09:16:18
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-091617-0544-4275952-pg.asequence
#    -bsequence emboss_stretcher-I20150319-091617-0544-4275952-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      39/101 (38.6%)
# Similarity:    39/101 (38.6%)
# Gaps:           0/101 ( 0.0%)
# Score: 71
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     |||||||||||||||||||||||||||||||||||||||...........
EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGNNNNNNNNNNN     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:28:07
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-092806-0234-19525660-pg.asequence
#    -bsequence emboss_stretcher-I20150103-092806-0234-19525660-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
# 
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Fri 26 Dec 2014 08:13:18
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141226-081316-0927-90647123-oy.asequence
#    -bsequence emboss_stretcher-I20141226-081316-0927-90647123-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      98/101 (97.0%)
# Similarity:    98/101 (97.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 484
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     |||||||||||||||||.|||.||.|||||||||||||||||||||||||
EMBOSS_001        51 TAAATTTATTTATTTTCNAGGNAANGCGTGGCATTTAAACCAACAGGACT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala3

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 07:58:17
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-075816-0386-39500532-oy.asequence
#    -bsequence emboss_stretcher-I20150104-075816-0386-39500532-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      48/101 (47.5%)
# Similarity:    48/101 (47.5%)
# Gaps:           0/101 ( 0.0%)
# Score: 134
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     ............||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 NNNNNNNNNNNNTTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ||||||||||........................................
EMBOSS_001        51 TAAATTTATTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 09:23:14
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-092313-0347-81101365-oy.asequence
#    -bsequence emboss_stretcher-I20150319-092313-0347-81101365-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       3/101 ( 3.0%)
# Similarity:     3/101 ( 3.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -181
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ................................................||
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 23 Oct 2014 05:44:16
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141023-054415-0199-71688953-pg.asequence
#    -bsequence emboss_stretcher-I20141023-054415-0199-71688953-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      62/101 (61.4%)
# Similarity:    62/101 (61.4%)
# Gaps:           0/101 ( 0.0%)
# Score: 232
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     .......................................|||||||||||
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTAGGGTTTTT     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Denisovan

```
########################################
# Program: stretcher
# Rundate: Wed 29 Oct 2014 04:05:21
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141029-040520-0352-93320313-pg.asequence
#    -bsequence emboss_stretcher-I20141029-040520-0352-93320313-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs AltaiNea

```
########################################
# Program: stretcher
# Rundate: Thu 23 Oct 2014 05:33:24
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141023-053323-0154-3899619-es.asequence
#    -bsequence emboss_stretcher-I20141023-053323-0154-3899619-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 05:04:20
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-050419-0115-58853989-pg.asequence
#    -bsequence emboss_stretcher-I20141115-050419-0115-58853989-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs chimpanzee

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 07:07:06
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-070705-0375-30400762-es.asequence
#    -bsequence emboss_stretcher-I20150113-070705-0375-30400762-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      99/101 (98.0%)
# Similarity:    99/101 (98.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 487
# 
#
#=======================================

EMBOSS_001         1 GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTT     50
                     |||||||||||||||||.|||||||||||||||||||.||||||||||||||
EMBOSS_001         1 GTTGTAAACACATTTTTACCCTGGCAGATTTTGTTGCTGTTAGGGTTTTT     50

EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACT    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
                                  |||||||||||||||||||||||.||||||||||||||||||||.|||||
1                            1589 GGACTCTTAAAAGAAAATAAAGCGCATTGATTCTATTTGTTTCTTGGAGC   1638

                             1685 TGCAGTTTCTTAATAATATCAGGTGAAGATAAATTTTCCACGGAGAAAAC   1734
                                  ||||||||||||||||.||||||||||||||||||||..|||||||||||
1                            1639 TGCAGTTTCTTAATAACATCAGGTGAAGATAAATTTTTTACGGAGAAAAC   1688

                             1735 GATCCTCCGGGATGCAGCTTCTTACTCTGAAAATTTCCCTGCCGACTCCT   1784
                                  |||||.||||||||||||.|||||||||||||||||||||||||||||||
1                            1689 GATCCGCCGGGATGCAGCCTCTTACTCTGAAAATTTCCCTGCCGACTCCT   1738

                             1785 CACTCTCTGCGCTCCTCCTCGTTATCC-GGGGACTCCTGCCTCTCTTCCC   1833
                                  ||||||||||||||||||||||||.|| |||||.||||||.|||||.|||
1                            1739 CACTCTCTGCGCTCCTCCTCGTTACCCCGGGGAGTCCTGCGTCTCTCCCC   1788

                             1834 CCTTCTCTTTTTTCTTTTTGGCAGAACCCGCCTGCAATATTCGTGTGCTG   1883
                                  |||||||||||||||||||||||||||.|.||||.||||||||||..|||
1                            1789 CCTTCTCTTTTTTCTTTTTGGCAGAACTCTCCTGTAATATTCGTGCACTG   1838

                             1884 AGCTCGTAATTCCCCCTGCGATGCCAGCAACGCCCAATTGATTGACTAGT   1933
                                  |||||.||||||||||||||||||||||||||||||||||||||||||||
1                            1839 AGCTCATAATTCCCCCTGCGATGCCAGCAACGCCCAATTGATTGACTAGT   1888

                             1934 TGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTTTA   1983
                                  ||||||||||||||||||||||||||||||||||.||.|  ||||||||.
1                            1889 TGTAAACACATTTTTCCCCTGGCAGATTTTGTTGGTGGT--GGTTTTTTT   1936

                             1984 AATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACTGC   2033
                                  ..|||.||.|||||||||||||||||||||||||||.|||||||.|||||
1                            1937 CTTTTTTTAATTTTCCAGGGAATGCGTGGCATTTAAGCCAACAGAACTGC   1986

                             2034 AATTAATAGATTTGCGAGTTGCGCCGCGCGCGCCGCTCGCCCCAGCCTCC   2083
                                  ||||.||||||||||||||||||||.|||||||||||.||||||||||||
1                            1987 AATTCATAGATTTGCGAGTTGCGCCCCGCGCGCCGCTAGCCCCAGCCTCC   2036

                             2084 CGGCCTCCGGGCCTCGCTGCCTCCCCGCGCCCGGCGGCGTCCAGCGCCCT   2133
                                  ||||||||||.||||||||||||||.|||||.||.|||||||||||||.|
1                            2037 CGGCCTCCGGCCCTCGCTGCCTCCCTGCGCCTGGAGGCGTCCAGCGCCTT   2086

                             2134 GCAAGCCCCGAGCAGCC-GCGGGTCCTGCAGCTGAAGGAAGGTTGCAGCT   2182
                                  ||||||.|||||||||| ||.|||||||||||||||||||||..||||||
1                            2087 GCAAGCACCGAGCAGCCCGCAGGTCCTGCAGCTGAAGGAAGGCGGCAGCT   2136

                             2183 GCGCCCTCCTTGCAAGCCGCAGCCCGGCGTCCTGGTTGTCCCAGCAGCCA   2232
                                  |||.||||||||||||||||||||||||||||||||||||||||||||||
1                            2137 GCGTCCTCCTTGCAAGCCGCAGCCCGGCGTCCTGGTTGTCCCAGCAGCCA   2186

                             2233 GGAGATCCCTACCTGTTAGTGAACAGTTAGGAGTCGACTGCTGGAAGAAT   2282
                                  ||||..||||||||||||||||||||.|.||||||||||||||||||.||
1                            2187 GGAGCGCCCTACCTGTTAGTGAACAGCTGGGAGTCGACTGCTGGAAGGAT   2236

                             2283 TAATTAGGAACGTGCTGTGCTCTGGGCAGCGCGAGCTCGGGTAGAGGCAT   2332
                                  ||||||||||||||||||||||.|||||||||||||||||||||||||||
1                            2237 TAATTAGGAACGTGCTGTGCTCCGGGCAGCGCGAGCTCGGGTAGAGGCAT   2286

                             2333 CCAAACCTTTGCCGGCGGCGCTATTTTATTTTTACTACATTTTCTCAGGT   2382
                                  |||||.||||||||||.|||||||||||||||||||||||||||||||||
1                            2287 CCAAATCTTTGCCGGCCGCGCTATTTTATTTTTACTACATTTTCTCAGGT   2336

                             2383 TGCAAAAATAGACACCGGGCACGTTCTGTCTTAGAGTTTTCTAGCAAGGA   2432
                                  |||||||||||||||||||||||||||.|||.||||||||||||||||||
1                            2337 TGCAAAAATAGACACCGGGCACGTTCTTTCTGAGAGTTTTCTAGCAAGGA   2386

                             2433 GCGCCTTCAAGGCCAGGCAGGCTCTGTAACAGGTTCCCCTTTAAACAGCC   2482
                                  ||||||||||||||.||||||||||..||||||||||.||||||.|||||
```

Human vs marmoset

```
########################################
# Program: stretcher
# Rundate: Thu 23 Oct 2014 08:26:01
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141023-082559-0977-10064285-pg.asequence
#    -bsequence emboss_stretcher-I20141023-082559-0977-10064285-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 103
# Identity:      90/103 (87.4%)
# Similarity:    90/103 (87.4%)
# Gaps:           4/103 ( 3.9%)
# Score: 374
# 
#
#=======================================

EMBOSS_001         1 --GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTT     48
                       ||||||||||||||||||||||||||||||||||||.||.|  |||||
EMBOSS_001         1 TAGTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGGTGGT--GGTTT     48

EMBOSS_001        49 TTTAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGA     98
                     |||...|||.||.|||||||||||||||||||||||||||.|||||||.|
EMBOSS_001        49 TTTTCTTTTTTTAATTTTCCAGGGAATGCGTGGCATTTAAGCCAACAGAA     98

EMBOSS_001        99 CTG    101
                     |||
EMBOSS_001        99 CTG    101


#---------------------------------------
#---------------------------------------
```

```
     |||  |.|||.|||| |||.||| |||.|.|....|.||||.||||||.|
1633 GGG--GTGGAGGGGA-GGTAACCGCCGGCCGTGGGGTTCCCCTTCCCTTC    1679

1299 CGGCAACCGCCACTCTCCCCTGAAAGCAGATTTCACCCCCC-----TCTG    1343
     |.| |.||..|...|..||...||||||..|||||.|....     |||.
1680 CCG-ATCCTTCCTACGGCCTCCAAAGCAAGTTTCAGCTTGGGTAATTCTT    1728

1344 CCGCC------CCTGCCGAGGAGGGAGAGGGAACCCCGGGGTGGGCTGAG    1387
     |..||      ||.|||..||..|.|||...||||.|.|| |||.|||  
1729 CTACCTTTTGTCCAGCCTGGGTAGAAGAATTAACCTCCGG-TGGACTG--    1775

1388 TATCCCCCCTAGCCCCGGGAGCCCCCAGCGCCCTCCCTCCCGTGCCCCCA    1437
        ||||||             ||||.||   |||||...|.|  |||||
1776 ---CCCCCC-------------CCCCCGC---CTCCCCATCAT--CCCCA    1804

1438 GGGGCCCCGCGCCC-GCCGCGGCAAGTTTCCCACACGGCGAGGGCGCAGC    1486
     |||.|||.|||||| ||.|.|||||||||||||||.||.|||.||.||||
1805 GGGACCCTGCGCCCCGCAGAGGCAAGTTTCCCACAAGGAGAGCGCACAGC    1854

1487 AGGCAACTCCAAGAGGAACCTGCTGGCGAGCCCAGCCAGCTCGGGA-GGC    1535
     ..|..|||||. |..||.||||.|||| ||.||.|||||||.||.| |||
1855 CCGAGACTCCG-GCAGAGCCTGTTGGC-AGTCCGGCCAGCTTGGAAAGGC    1902

1536 GCTAATTCAATAAGACAGAGAAATCTGAGTTCAGAAATCCTGATAAAATC    1585
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1903 GCTAATTCAATAAGACAGAGAAATCTGAGTTCAGAAATCCTGATAAAATC    1952

1586 TAATTTTCGAGTTTTAATACCCTGGCTATCAGCCCCCC-----TTGGTTC    1630
     |||||||||.||||||||||||.|||||||||.|||||     |.|||||
1953 TAATTTTCGGGTTTTAATACCCAGGCTATCAGACCCCCCCGCCTCGGTTC    2002

1631 CTGAGGACTCTTAAAAGAAAATAAAGCACATTGATTCTATTTGTTTCTGG    1680
     |||||||||||||||||||||||||||.|||||||||.|||||||||.|.
2003 CTGAGGACTCTTAAAAGAAAATAAAGCGCATTGATTCCATTTGTTTCAGA    2052

1681 GAGCTGCAGTTTCTTAATAATATCAGGTGAAGATAAATTTTCCACGGAGA    1730
     ||||||||||||||||||||||||||||||||||..||||||||.|||||
2053 GAGCTGCAGTTTCTTAATAATATCAGGTGAAGATTTATTTTCCAAGGAGA    2102

1731 AAACGATCCTCCGGGATGCAGCTTCTTACTCTGAAAATTTCCC-TGCCGA    1779
     |||||||||.|..|||||||.|.||||||||.|||..|.|||| |||||.
2103 AAACGATCCGCGAGGATGCAACCTCTTACTCGGAATCTCTCCCCTGCCGG    2152

1780 CTCCTCACTCTCTGCGCTCCTCCTCGTTAT--CCGGGGACTCCTGCCTCT    1827
     .|||||.|||.||||..|||.||||||||.|  |||.||||||.||||...
2153 TTCCTCGCTCCCTGCTATCCACCTCGTTTTTTCCGCGGACTCTTGCCCGA    2202

1828 CTTCCCCCTTCTCTTTTTTCTTTTTGGCAGAACC-CGCCTGCAATATTCG    1876
     .|.||||...||.|.||||||||||||||.||.. |..|||.|||.||||
2203 GTCCCCCGCCCTTTATTTTCTTTTTGGCAAAAAATCTACTGTAATTTTCG    2252

1877 TGTGCTGAGCTCGTAATTCCCCCTGCGATGCCAGCAACGCCCAATTGATT    1926
     .||||.||||||..|.|.|||||| |||||||||||||||||||.|||||
2253 AGTGCCGAGCTCACAGTGCCCCCT-CGATGCCAGCAACGCCCAACTGATT    2301

1927 GACTAGTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGG    1976
     |||..|||||||||||||||| |||||||||||||||||||||       
2302 GACGGGTTGTAAACACATTTT-CCCCTGGCAGATTTTGTTGTT-------    2343

1977 TTTTTTAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACA    2026
        |............||||||.|||||.||.||||...|||||||||||
2344 ---TCCCCCACCCCCCATTTTCTAGGGATTGTGTGGTGCTTAAACCAACA    2390

2027 GGACTGCAA-----TTAATAGATTTGCGAGTTGCGCCGCGCGC-GC-CGC    2069
     ..|.|||||     |||||||||||||.|||||||||||..|| || |||
```

Human vs mouse

```
########################################
# Program: stretcher
# Rundate: Thu 23 Oct 2014 09:39:20
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141023-093919-0117-64930026-es.asequence
#    -bsequence emboss_stretcher-I20141023-093919-0117-64930026-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 112
# Identity:      69/112 (61.6%)
# Similarity:    69/112 (61.6%)
# Gaps:          22/112 (19.6%)
# Score: 137
# 
#
#=======================================

EMBOSS_001         1 -----------GTTGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTG     39
                                |||||||||||||||| |||||||||||||||||||||
EMBOSS_001         1 CTGATTGACGGGTTGTAAACACATTTT-CCCCTGGCAGATTTTGTTGTT-     48

EMBOSS_001        40 TTAGGGTTTTTTAAATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAA     89
                              |............||||||.|||||.||.||||...|||||
EMBOSS_001        49 ---------TCCCCCACCCCCCATTTTCTAGGGATTGTGTGGTGCTTAAA     89

EMBOSS_001        90 CCAACAGGACTG    101
                     ||||||..|.||
EMBOSS_001        90 CCAACAAAATTG    101


#---------------------------------------
#---------------------------------------
```

rs7851893

Human vs Saqqaq-Eskimos

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 06:34:09
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-063408-0697-53926784-pg.asequence
#    -bsequence emboss_stretcher-I20150114-063408-0697-53926784-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 22:40:35
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-224034-0837-49339237-oy.asequence
#    -bsequence emboss_stretcher-I20150319-224034-0837-49339237-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      43/101 (42.6%)
# Similarity:    43/101 (42.6%)
# Gaps:           0/101 ( 0.0%)
# Score: 99
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||||||........................
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ..................................||||||||||||||||
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 22:43:02
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-224300-0848-31715737-es.asequence
#    -bsequence emboss_stretcher-I20150319-224300-0848-31715737-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      98/101 (97.0%)
# Similarity:    98/101 (97.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 484
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||...|||||||||||||||||||||||||
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGNNNCAAAAATAGACACCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 22:43:47
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-224345-0917-61170008-pg.asequence
#    -bsequence emboss_stretcher-I20150319-224345-0917-61170008-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      64/101 (63.4%)
# Similarity:    64/101 (63.4%)
# Gaps:           0/101 ( 0.0%)
# Score: 246
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||.............................|||||||||||||
EMBOSS_001         1 ATTTTTACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ||||||||||||||||||........||||||||||||||||||||||||
EMBOSS_001        51 GTCTTAGAGTTTTCTAGCNNNNNNNNCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs Loschbour

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:29:08
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-092907-0267-68991030-oy.asequence
#    -bsequence emboss_stretcher-I20150103-092907-0267-68991030-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala12

```
########################################
# Program: stretcher
# Rundate: Fri 26 Dec 2014 08:17:50
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141226-081749-0514-98004358-oy.asequence
#    -bsequence emboss_stretcher-I20141226-081749-0514-98004358-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
# 
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 08:00:03
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-080002-0458-60844687-oy.asequence
#    -bsequence emboss_stretcher-I20150104-080002-0458-60844687-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      62/101 (61.4%)
# Similarity:    62/101 (61.4%)
# Gaps:           0/101 ( 0.0%)
# Score: 232
# 
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     |||||||.|.|.||.|||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATTTTTANTNCNTTNTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ||||||||||||||||..................................
EMBOSS_001        51 GTCTTAGAGTTTTCTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 A    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 22:46:20
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-224619-0372-4817525-pg.asequence
#    -bsequence emboss_stretcher-I20150319-224619-0372-4817525-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 A    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs VindijaNea

```
########################################
# Program: stretcher
# Rundate: Thu 19 Mar 2015 22:51:23
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150319-225122-0072-53731828-oy.asequence
#    -bsequence emboss_stretcher-I20150319-225122-0072-53731828-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      25/101 (24.8%)
# Similarity:    25/101 (24.8%)
# Gaps:           0/101 ( 0.0%)
# Score: -27
# 
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ..........................||||||||||||||||||||||||
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs Denisovan

```
########################################
# Program: stretcher
# Rundate: Wed 29 Oct 2014 04:10:08
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141029-041007-0214-53801550-pg.asequence
#    -bsequence emboss_stretcher-I20141029-041007-0214-53801550-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 23 Oct 2014 10:43:33
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141023-104332-0665-8875996-es.asequence
#    -bsequence emboss_stretcher-I20141023-104332-0665-8875996-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs MezmayskayaNea

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 05:06:09
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-050608-0843-49755397-oy.asequence
#    -bsequence emboss_stretcher-I20141115-050608-0843-49755397-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      94/101 (93.1%)
# Similarity:    94/101 (93.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 456
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||||||||||||||||||||||.......|
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGNNNNNNNT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs chimpanzee

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 07:28:49
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-072848-0436-90667373-es.asequence
#    -bsequence emboss_stretcher-I20150113-072848-0436-90667373-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
# 
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     .|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 TTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
                  |||||||||||||||||||||||.||||||||||||||||||||.|||||
1            1589 GGACTCTTAAAAGAAAATAAAGCGCATTGATTCTATTTGTTTCTTGGAGC    1638

             1685 TGCAGTTTCTTAATAATATCAGGTGAAGATAAATTTTCCACGGAGAAAAC    1734
                  ||||||||||||||||.||||||||||||||||||||..|||||||||||
1            1639 TGCAGTTTCTTAATAACATCAGGTGAAGATAAATTTTTTACGGAGAAAAC    1688

             1735 GATCCTCCGGGATGCAGCTTCTTACTCTGAAAATTTCCCTGCCGACTCCT    1784
                  |||||.||||||||||||.|||||||||||||||||||||||||||||||
1            1689 GATCCGCCGGGATGCAGCCTCTTACTCTGAAAATTTCCCTGCCGACTCCT    1738

             1785 CACTCTCTGCGCTCCTCCTCGTTATCC-GGGGACTCCTGCCTCTCTTCCC    1833
                  ||||||||||||||||||||||||.|| |||||.||||||.|||||.|||
1            1739 CACTCTCTGCGCTCCTCCTCGTTACCCCGGGGAGTCCTGCGTCTCTCCCC    1788

             1834 CCTTCTCTTTTTTCTTTTTGGCAGAACCCGCCTGCAATATTCGTGTGCTG    1883
                  |||||||||||||||||||||||||||.|.||||.||||||||||..|||
1            1789 CCTTCTCTTTTTTCTTTTTGGCAGAACTCTCCTGTAATATTCGTGCACTG    1838

             1884 AGCTCGTAATTCCCCCTGCGATGCCAGCAACGCCCAATTGATTGACTAGT    1933
                  |||||.||||||||||||||||||||||||||||||||||||||||||||
1            1839 AGCTCATAATTCCCCCTGCGATGCCAGCAACGCCCAATTGATTGACTAGT    1888

             1934 TGTAAACACATTTTTCCCCTGGCAGATTTTGTTGTTGTTAGGGTTTTTTA    1983
                  ||||||||||||||||||||||||||||||||||.||.|  ||||||||.
1            1889 TGTAAACACATTTTTCCCCTGGCAGATTTTGTTGGTGGT--GGTTTTTTT    1936

             1984 AATTTATTTATTTTCCAGGGAATGCGTGGCATTTAAACCAACAGGACTGC    2033
                  ..|||.||.|||||||||||||||||||||||||||.|||||||.|||||
1            1937 CTTTTTTTAATTTTCCAGGGAATGCGTGGCATTTAAGCCAACAGAACTGC    1986

             2034 AATTAATAGATTTGCGAGTTGCGCCGCGCGCGCCGCTCGCCCCAGCCTCC    2083
                  ||||.||||||||||||||||||||.|||||||||||.||||||||||||
1            1987 AATTCATAGATTTGCGAGTTGCGCCCCGCGCGCCGCTAGCCCCAGCCTCC    2036

             2084 CGGCCTCCGGGCCTCGCTGCCTCCCCGCGCCCGGCGGCGTCCAGCGCCCT    2133
                  ||||||||||.||||||||||||||.|||||.||.|||||||||||||.|
1            2037 CGGCCTCCGGCCCTCGCTGCCTCCCTGCGCCTGGAGGCGTCCAGCGCCTT    2086

             2134 GCAAGCCCCGAGCAGCC-GCGGGTCCTGCAGCTGAAGGAAGGTTGCAGCT    2182
                  ||||||.|||||||||| ||.|||||||||||||||||||||..||||||
1            2087 GCAAGCACCGAGCAGCCCGCAGGTCCTGCAGCTGAAGGAAGGCGGCAGCT    2136

             2183 GCGCCCTCCTTGCAAGCCGCAGCCCGGCGTCCTGGTTGTCCCAGCAGCCA    2232
                  |||.||||||||||||||||||||||||||||||||||||||||||||||
1            2137 GCGTCCTCCTTGCAAGCCGCAGCCCGGCGTCCTGGTTGTCCCAGCAGCCA    2186

             2233 GGAGATCCCTACCTGTTAGTGAACAGTTAGGAGTCGACTGCTGGAAGAAT    2282
                  ||||..||||||||||||||||||||.|.||||||||||||||||||.||
1            2187 GGAGCGCCCTACCTGTTAGTGAACAGCTGGGAGTCGACTGCTGGAAGGAT    2236

             2283 TAATTAGGAACGTGCTGTGCTCTGGGCAGCGCGAGCTCGGGTAGAGGCAT    2332
                  ||||||||||||||||||||||.|||||||||||||||||||||||||||
1            2237 TAATTAGGAACGTGCTGTGCTCCGGGCAGCGCGAGCTCGGGTAGAGGCAT    2286

             2333 CCAAACCTTTGCCGGCGGCGCTATTTTATTTTTACTACATTTTCTCAGGT    2382
                  |||||.||||||||||.|||||||||||||||||||||||||||||||||
1            2287 CCAAATCTTTGCCGGCCGCGCTATTTTATTTTTACTACATTTTCTCAGGT    2336

             2383 TGCAAAAATAGACACCGGGCACGTTCTGTCTTAGAGTTTTCTAGCAAGGA    2432
                  |||||||||||||||||||||||||||.|||.||||||||||||||||||
1            2337 TGCAAAAATAGACACCGGGCACGTTCTTTCTGAGAGTTTTCTAGCAAGGA    2386

             2433 GCGCCTTCAAGGCCAGGCAGGCTCTGTAACAGGTTCCCCTTTAAACAGCC    2482
                  ||||||||||||||.||||||||||..||||||||||.||||||.|||||
```

```
########################################
# Program: stretcher
# Rundate: Thu 23 Oct 2014 11:05:49
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141023-110548-0289-11194942-es.asequence
#    -bsequence emboss_stretcher-I20141023-110548-0289-11194942-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      96/101 (95.0%)
# Similarity:    96/101 (95.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 460
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAATAGACACCGGGCACGTTCT     50

EMBOSS_001        51 GTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCAGGCTCTGT    100
                     .|||.||||||||||||||||||||||||||||||||.||||||||||..
EMBOSS_001        51 TTCTGAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCGGGCAGGCTCTAC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
2391 AAATTGCAAAGCAATTAATAGATTTGCAAGTTGCGCCGCTTGCTGCTCGC   2440

2070 TCG--CCCCAGCCTCCCGGCCTCCGGGCCTCGCTGCCTCCCCGCGCCCGG   2117
     |.|  |.||.|||||..||||||.||||||||.|||||||||.|.|..|.
2441 TGGGGCTCCGGCCTCAGGGCCTCGGGGCCTCGTTGCCTCCCCACCCGAGC   2490

2118 CGGCGTCCAGCGCCCTGCAAGCCCCGAGCAGCCGCGGGTCCTGCAGCTGA   2167
     |||..||||||||..|.|.||||..||||||||||.||.|||||||.|||
2491 CGGAATCCAGCGCTGTCCCAGCCAGGAGCAGCCGCCGGCCCTGCAGATGA   2540

2168 AGGAAGGTTGCAGCTGCGCCCTCCTTGCAAGCCGCAGCCCGGCGTCCTGG   2217
     ||.    ..||.||||.||||.|||||..||||||||||.||||..|.||
2541 AGC----CGGCTGCTGGGCCCGCCTTGAGAGCCGCAGCCTGGCGCTCAGG   2586

2218 TTGTCCC-AGCAGCCAGGAGATCCCTACCTGTTAGTGAACAGTTAGGAGT   2266
     |.||||| |||.|.||||||..||||||||||||||||||||||..||||.
2587 TCGTCCCCAGCCGTCAGGAGCGCCCTACCTGTTAGTGAACAGTCGGGAGC   2636

2267 CGACTGCTGGAAGAATTAATTAGGAACGTGCTGTGCTCTGGGCAGCGC-G   2315
     ||.|||||||||||||||||||||..|.|||||...||||||||||.| |
2637 CGGCTGCTGGAAGAATTAATTAGGGGCATGCTGCTTTCTGGGCAGCTCAG   2686

2316 AGCTCGGGTAGAGGCATCCAAACCTTTGCCGG--CGGCGCTATTTTATTT   2363
     ||||.||.|.||..|.||||||||.||||||.  |.|.|.||.|||||||
2687 AGCTTGGTTGGAAACGTCCAAACCATTGCCGCGCCCGAGTTACTTTATTT   2736

2364 TTACTACATTTTCTCAGGTTGCAAAAA--------TAGACACCGGG-CAC   2404
     .||||||||||||||.|||||.|||||        |||||.|..|| |||
2737 GTACTACATTTTCTCTGGTTGGAAAAAAAAAAAAATAGACGCTTGGTCAC   2786

2405 GTTCTGTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGGCA-GG   2453
     |||||..|...|||||||||||||||.||.|      ||.||.|||. ||
2787 GTTCTTCCAGGGAGTTTTCTAGCAAGAAGTG------AGCCCGGGCCCGG   2830

2454 CTCTGTAACAGGTTCCCCTTTAAACAGCCAGAGGTGAGACGGGGAAAATG   2503
     .|||..|.||||||.|..|||.|.|.||||||.|||..|.|.|...||
2831 GTCTAGAGCAGGTTTCTGTTTAAGCCGTCAGAGGAGAGGTGTGAAGTGTG   2880

2504 GTCCTGGCTGGGTTCTCGTTCATCTCCATCAGCAGTCCTTCACCCAGAGA   2553
     ||| |||||||||||||.|.|||||..||.||.||||.||||.||..|||
2881 GTC-TGGCTGGGTTCTCATCCATCTGTATTAGGAGTCTTTCATCCCAAGA   2929

2554 GAGGGGCAGGGGTCGCCCTAACTCAGATGAATGAGTCCCA-TGCCTGGAG   2602
     | |||||||||.. |.|.||||..|||||.|||||.|||| |||.....|
2930 G-GGGGCAGGGCG-GTCTTAACCTAGATGGATGAGGCCCACTGCAGCCTG   2977

2603 CCCTGGGGCCCTGGCTGGGGGCTGCTCCGAGCCTGAGGTGCTCAGGGCGC   2652
     |....|..|.|||||||||||||...||..|....|||.||||.....||
2978 CAACAGAACACTGGCTGGGGGCTTACCCCTGAGCAAGGAGCTCTCTCAGC   3027

2653 TCAGG--GCAGCAAG-TGTCCGCCACTTCGGTTTGTCATTTTTGG-CAGG   2698
      ||||  |.|.|||. |||||....||.|.|..||||||.|..|| ||||
3028 -CAGGTTGGACCAAAATGTCCCATCCTCCTGCCTGTCATCTGAGGGCAGG   3076

2699 AGCGTTTTTCTGTCTGGGTGGAGAATGGAGTTTCACGGAAACACAGTTAA   2748
     |..||..|. ||||||.||||    ..|.||||||...|||||||.||||
3077 AATGTGCTG-TGTCTGTGTGG----CAGTGTTTCATATAAACACAATTAA   3121

2749 CTCTTCAGGGGCCTTGCAAGTACAGGAGGTGA-AGAGGATG---TCAGGG   2794
     |||.||.|||.|.||.....||.|...|.|.| ||.||.|.   |||||.
3122 CTCCTCTGGGACTTTTGGTATATAATGGCTAACAGGGGCTTCCTTCAGGT   3171

2795 GAGAGCCAGGTCCAGACTGGACATTTGGGGTGGTTTGGGAAATCAAATGC   2844
     |||||.||||.|       |.|||.||.|. ||||.|||||.|.|||.||
3172 GAGAGTCAGGCC-------GCCATATGTGA-GGTTAGGGAATTTAAAGGC   3213
```

```
########################################
# Program: stretcher
# Rundate: Thu 23 Oct 2014 11:36:27
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141023-113625-0978-22295800-pg.asequence
#    -bsequence emboss_stretcher-I20141023-113625-0978-22295800-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 111
# Identity:      65/111 (58.6%)
# Similarity:    65/111 (58.6%)
# Gaps:          20/111 (18.0%)
# Score: 81
#
#
#=======================================

EMBOSS_001         1 ATTTTTACTACATTTTCTCAGGTTGCAAAAA--------TAGACACCGGG     42
                     |         |||||||||.|||||.|||||        |||||.|..||
EMBOSS_001         1 A---------CATTTTCTCTGGTTGGAAAAAAAAAAAAATAGACGCTTGG     41

EMBOSS_001        43 -CACGTTCTGTCTTAGAGTTTTCTAGCAAGGAGCGCCTTCAAGGCCAGG-     90
                      ||||||||..|...||||||||||||||.||.|....|..|.||.||
EMBOSS_001        42 TCACGTTCTTCCAGGGAGTTTTCTAGCAAGAAGTGAGCCCGGGCCCGGGT     91

EMBOSS_001        91 CAGGCTCTGTA    101
                     |..|..|.|.
EMBOSS_001        92 CTAGAGCAGG-    101


#---------------------------------------
#---------------------------------------
```

rs3824574

Human vs Saqqaq-Eskimos

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 06:36:43
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-063642-0463-57816352-es.asequence
#    -bsequence emboss_stretcher-I20150114-063642-0463-57816352-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Fri 20 Mar 2015 09:05:52
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150320-090551-0256-38253185-pg.asequence
#    -bsequence emboss_stretcher-I20150320-090551-0256-38253185-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      76/101 (75.2%)
# Similarity:    76/101 (75.2%)
# Gaps:           0/101 ( 0.0%)
# Score: 330
# 
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     |||||||||||||||||||||||.........................||
EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCANNNNNNNNNNNNNNNNNNNNNNNNNCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Fri 20 Mar 2015 09:09:09
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150320-090908-0826-82602335-oy.asequence
#    -bsequence emboss_stretcher-I20150320-090908-0826-82602335-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      86/101 (85.1%)
# Similarity:    86/101 (85.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 400
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ||||||||||||||||||||||||||||...............|||||||
EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGNNNNNNNNNNNNNNNCTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-teresa

```
########################################
# Program: stretcher
# Rundate: Fri 20 Mar 2015 09:10:05
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150320-091004-0398-32864747-oy.asequence
#    -bsequence emboss_stretcher-I20150320-091004-0398-32864747-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      85/101 (84.2%)
# Similarity:    85/101 (84.2%)
# Gaps:           0/101 ( 0.0%)
# Score: 393
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||..
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGNN     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ..............||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 NNNNNNNNNNNNNNACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:30:33
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-093031-0773-78503093-pg.asequence
#    -bsequence emboss_stretcher-I20150103-093031-0773-78503093-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala12

```
########################################
# Program: stretcher
# Rundate: Fri 26 Dec 2014 08:20:40
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141226-082039-0665-58309950-es.asequence
#    -bsequence emboss_stretcher-I20141226-082039-0665-58309950-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      97/101 (96.0%)
# Similarity:    97/101 (96.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 477
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||.|||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCNCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     |||||...||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CTTCANNNTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala3

```
########################################
# Program: stretcher
# Rundate: Fri 20 Mar 2015 09:16:53
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150320-091652-0902-43209809-oy.asequence
#    -bsequence emboss_stretcher-I20150320-091652-0902-43209809-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       8/101 ( 7.9%)
# Similarity:     8/101 ( 7.9%)
# Gaps:           0/101 ( 0.0%)
# Score: -146
# 
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||..........................................
EMBOSS_001         1 ATGGACAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Fri 20 Mar 2015 09:18:50
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150320-091849-0769-71403594-oy.asequence
#    -bsequence emboss_stretcher-I20150320-091849-0769-71403594-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      14/101 (13.9%)
# Similarity:    14/101 (13.9%)
# Gaps:           0/101 ( 0.0%)
# Score: -104
# 
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||....................................
EMBOSS_001         1 ATGGACAACCTCTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs VindijaNea

```
########################################
# Program: stretcher
# Rundate: Fri 20 Mar 2015 09:20:16
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150320-092015-0282-17413842-es.asequence
#    -bsequence emboss_stretcher-I20150320-092015-0282-17413842-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ..................................................
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 G    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Denisovan

```
########################################
# Program: stretcher
# Rundate: Wed 29 Oct 2014 04:18:53
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141029-041852-0013-5792487-pg.asequence
#    -bsequence emboss_stretcher-I20141029-041852-0013-5792487-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human vs AltaiNea

```
########################################
# Program: stretcher
# Rundate: Fri 24 Oct 2014 06:13:23
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141024-061322-0938-64397329-pg.asequence
#    -bsequence emboss_stretcher-I20141024-061322-0938-64397329-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 05:10:08
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-051003-0169-23535321-oy.asequence
#    -bsequence emboss_stretcher-I20141115-051003-0169-23535321-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      98/101 (97.0%)
# Similarity:    99/101 (98.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 485
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     |||||||||||||||||||||||||||||.||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGTGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ||||||||||||||||||||||||.|:|||||||||||||||||||||||
EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATNCRGCTGCTGCGCCCGGCGCTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 07:31:48
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-073147-0851-40870416-oy.asequence
#    -bsequence emboss_stretcher-I20150113-073147-0851-40870416-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      99/101 (98.0%)
# Similarity:    99/101 (98.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 487
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     ||||||||||||.||||||||||||||||||||||||||||||.||||||
EMBOSS_001        51 CTTCACCCTCACTGACCTGCGCATGCGGCTGCTGCGCCCGGCGTTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human exon 3 vs marmoset exon 3

```
     |||||||||||||||||||||||||||||||||||||||||||||||.||
  51 GGCCCACCCGCCCAGGCTCATGTTCGACAAGGAGGAGGAGGGCCTGGTCA     100

 101 CCTACTGGCAGAGCATCACCTGGAGCCGCTACCCCAGCCCGCTGGAAGCC     150
     |||||||||||||||||||.||||||||||||||.|||||||||||||||
 101 CCTACTGGCAGAGCATCACATGGAGCCGCTACCCTAGCCCGCTGGAAGCC     150

 151 AACATCACCCTTTCGTGGAACAAGACCGTGGAGCTGACCGACGACGTGGT     200
     ||||||||||||||||||||||||||||||||||||||.|||||||||||
 151 AACATCACCCTTTCGTGGAACAAGACCGTGGAGCTGACGGACGACGTGGT     200

 201 GATGACCTTCGAGTACGGCCGGCCCACGGTCATGGTCCTGGAGAAGTCCC     250
     |||||||||||||||.||||||||||||||||||||||||||||||||||
 201 GATGACCTTCGAGTATGGCCGGCCCACGGTCATGGTCCTGGAGAAGTCCC     250

 251 TGGACAACGGGCGCACCTGGCAGCCCTACCAGTTCTACGCCGAGGACTGC     300
     ||||||||||||||||.|||||||||||||||||||||||||||||||||
 251 TGGACAACGGGCGCACGTGGCAGCCCTACCAGTTCTACGCCGAGGACTGC     300

 301 ATGGAGGCCTTCGGTATGTCCGCCCGCCGGGCCCGCGACATGTCATCCTC     350
     ||||||||||||||.|||||||||||||||||||||||||||||.|||||
 301 ATGGAGGCCTTCGGCATGTCCGCCCGCCGGGCCCGCGACATGTCGTCCTC     350

 351 CAGCGCGCACCGCGTGCTCTGCACCGAGGAGTACTCGCGCTGGGCAGGCT     400
     ||||||.|||||||||||||||||||||||||||||.||||||||.||||
 351 CAGCGCCCACCGCGTGCTCTGCACCGAGGAGTACTCACGCTGGGCGGGCT     400

 401 CCAAGAAGGAGAAGCACGTGCGCTTCGAGGTGCGGACCGCTTCGCCATC     450
     |||||||||||||.||||||||||||||||||||||||||||.|||||||
 401 CCAAGAAGGAGAAACACGTGCGCTTCGAGGTGCGGACCGCTTTGCCATC     450

 451 TTTGCCGGCCCCGACCTGCGCAACATGGACAACCTCTACACGCGGCTGGA     500
     |||||||||||.||||||||||||||||||||||||||||||||||||||
 451 TTTGCCGGCCCGGACCTGCGCAACATGGACAACCTCTACACGCGGCTGGA     500

 501 GAGCGCCAAGGGCCTCAAGGAGTTCTTCACCCTCACCGACCTGCGCATGC     550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 501 GAGCGCCAAGGGCCTCAAGGAGTTCTTCACCCTCACCGACCTGCGCATGC     550

 551 GGCTGCTGCGCCCGGCGCTGGGCGGCACCTATGTGCAGCGGGAGAACCTC     600
     |||||||||||||.||||||||||||||||||||||||||||||||||||
 551 GGCTGCTGCGCCCCGCGCTGGGCGGCACCTATGTGCAGCGGGAGAACCTC     600

 601 TACAAGTACTTCTACGCCATCTCCAACATCGAGGTCATCGGCAG     644
     ||||||||||||||.||||||||||||||.||||||||.|||||
 601 TACAAGTACTTCTATGCCATCTCCAACATTGAGGTCATTGGCAG     644


#---------------------------------------
#---------------------------------------
```

Human vs marmoset

```
########################################
# Program: stretcher
# Rundate: Wed 25 Mar 2015 10:46:45
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150325-104644-0505-23882772-oy.asequence
#    -bsequence emboss_stretcher-I20150325-104644-0505-23882772-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     |||||||||||||||||||||||||||||||||||||||.||||||||||
EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCCGCGCTGGGCG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

Human exon 3 vs mice exon 3

```
          |||||||||||||.||||.|||||.||||.|||.||.|||||.|||||.|
      51 GGCCCACCCGCCCCGGCTTATGTTTGACAGGGAAGATGAGGGACTGGCTA     100

     101 CCTACTGGCAGAGCATCACCTGGAGCCGCTACCCCAGCCCGCTGGAAGCC     150
         ||||||||||.|||.||||.|||||.|||||||||||.||.||.||.|||
     101 CCTACTGGCAAAGCGTCACGTGGAGTCGCTACCCCAGTCCACTAGAGGCC     150

     151 AACATCACCCTTTCGTGGAACAAGACCGTGGAGCTGACCGACGACGTGGT     200
         |||||||||||.||.||||||||||.|||||||.||||.|||||||||||
     151 AACATCACCCTCTCATGGAACAAGAGCGTGGAGTTGACAGACGACGTGGT     200

     201 GATGACCTTCGAGTACGGCCGGCCCACGGTCATGGTCCTGGAGAAGTCCC     250
         |.||||.||.|||||.|||||||||||||||||||||||.||||||||||
     201 GGTGACTTTTGAGTATGGCCGGCCCACGGTCATGGTCCTCGAGAAGTCCC     250

     251 TGGACAACGGGCGCACCTGGCAGCCCTACCAGTTCTACGCCGAGGACTGC     300
         |||||||.||.||||||||||||||||||||||||||.||.|||||||||
     251 TGGACAATGGCCGCACCTGGCAGCCCTACCAGTTCTATGCAGAGGACTGC     300

     301 ATGGAGGCCTTCGGTATGTCCGCCCGCCGGGCCCGCGACATGTCATCCTC     350
         ||||||||||||||.|||||.|||||.||.|||||.|||||||||.||||
     301 ATGGAGGCCTTCGGCATGTCTGCCCGACGTGCCCGAGACATGTCACCCTC     350

     351 CAGCGCGCACCGCGTGCTCTGCACCGAGGAGTACTCGCGCTGGGCAGGCT     400
         ||||||.|||||.|||||||||||||||||||||||.|||||||||||.|
     351 CAGCGCCCACCGGGTGCTCTGCACCGAGGAGTACTCACGCTGGGCAGGGT     400

     401 CCAAGAAGGAGAAGCACGTGCGCTTCGAGGTGCGGGACCGCTTCGCCATC     450
         |||||||.||||||||.||||||||.|||||..||||||||||.||||||
     401 CCAAGAAAGAGAAGCATGTGCGCTTTGAGGTAAGGGACCGCTTTGCCATC     450

     451 TTTGCCGGCCCCGACCTGCGCAACATGGACAACCTCTACACGCGGCTGGA     500
         |||||||||||.||||||||.||||||||||||||.||||||.||.||||
     451 TTTGCCGGCCCTGACCTGCGTAACATGGACAACCTGTACACGAGGATGGA     500

     501 GAGCGCCAAGGGCCTCAAGGAGTTCTTCACCCTCACCGACCTGCGCATGC     550
         ||||||||||||||||||||||||||||||||.||||.||||||||||||
     501 GAGCGCCAAGGGCCTCAAGGAGTTCTTCACCTTCACTGACCTGCGCATGC     550

     551 GGCTGCTGCGCCCGGCGCTGGGCGGCACCTATGTGCAGCGGGAGAACCTC     600
         |.||||||||.||.|||||||||.|||||||.||||||||.|||||||||
     551 GCCTGCTGCGTCCTGCGCTGGGTGGCACCTACGTGCAGCGAGAGAACCTC     600

     601 TACAAGTACTTCTACGCCATCTCCAACATCGAGGTCATCGGCAG     644
         ||||||||||||||.|||||||||||.|||||.|||||.|||||
     601 TACAAGTACTTCTATGCCATCTCCAATATCGAAGTCATTGGCAG     644


#---------------------------------------
#---------------------------------------
```

Human vs mouse

```
########################################
# Program: stretcher
# Rundate: Wed 25 Mar 2015 06:01:50
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150325-060148-0985-52181883-oy.asequence
#    -bsequence emboss_stretcher-I20150325-060148-0985-52181883-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      92/101 (91.1%)
# Similarity:    92/101 (91.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 424
#
#
#=======================================

EMBOSS_001         1 ATGGACAACCTCTACACGCGGCTGGAGAGCGCCAAGGGCCTCAAGGAGTT     50
                     |||||||||||.||||||.||.||||||||||||||||||||||||||||
EMBOSS_001         1 ATGGACAACCTGTACACGAGGATGGAGAGCGCCAAGGGCCTCAAGGAGTT     50

EMBOSS_001        51 CTTCACCCTCACCGACCTGCGCATGCGGCTGCTGCGCCCGGCGCTGGGCG    100
                     |||||||.||||.||||||||||||||.||||||||.||.||||||||.|
EMBOSS_001        51 CTTCACCTTCACTGACCTGCGCATGCGCCTGCTGCGTCCTGCGCTGGGTG    100

EMBOSS_001       101 G    101
                     |
EMBOSS_001       101 G    101


#---------------------------------------
#---------------------------------------
```

rs2149171

Human vs Saqqaq-Eskimos

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 06:39:50
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-063949-0867-45766045-es.asequence
#    -bsequence emboss_stretcher-I20150114-063949-0867-45766045-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 501
# 
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     :|||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 YGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Wed 25 Mar 2015 07:21:55
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150325-072149-0454-99236667-es.asequence
#    -bsequence emboss_stretcher-I20150325-072149-0454-99236667-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      90/101 (89.1%)
# Similarity:    90/101 (89.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 428
#
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||....
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCNNNN     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     .....||||||||||||||||||||||||||||||||||||||||||||.
EMBOSS_001        51 NNNNNACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGN    100

EMBOSS_001       101 A    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-elena2

```
########################################
# Program: stretcher
# Rundate: Wed 25 Mar 2015 07:23:18
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150325-072317-0001-77930394-pg.asequence
#    -bsequence emboss_stretcher-I20150325-072317-0001-77930394-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      76/101 (75.2%)
# Similarity:    76/101 (75.2%)
# Gaps:           0/101 ( 0.0%)
# Score: 328
# 
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     .||||||||||||||||||||||||||.......................
EMBOSS_001        51 TGCCAACCTGTGCTCCATGCGCGAGGGNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 A    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Wed 25 Mar 2015 07:24:15
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150325-072414-0073-27490661-pg.asequence
#    -bsequence emboss_stretcher-I20150325-072414-0073-27490661-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      44/101 (43.6%)
# Similarity:    44/101 (43.6%)
# Gaps:           0/101 ( 0.0%)
# Score: 106
#
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||......
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAANNNNNN     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     ..................................................
EMBOSS_001        51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 A    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:32:46
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-093245-0206-80445990-pg.asequence
#    -bsequence emboss_stretcher-I20150103-093245-0206-80445990-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
#
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala12

```
########################################
# Program: stretcher
# Rundate: Fri 26 Dec 2014 08:34:20
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141226-083419-0706-28313104-pg.asequence
#    -bsequence emboss_stretcher-I20141226-083419-0706-28313104-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 498
#
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100

EMBOSS_001       101 A    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 08:02:49
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-080248-0571-20592358-pg.asequence
#    -bsequence emboss_stretcher-I20150104-080248-0571-20592358-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      95/101 (94.1%)
# Similarity:    95/101 (94.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 463
# 
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||......
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAANNNNNN     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala1

```
########################################
# Program: stretcher
# Rundate: Wed 25 Mar 2015 07:30:08
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150325-073007-0135-99140164-pg.asequence
#    -bsequence emboss_stretcher-I20150325-073007-0135-99140164-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: 135102204-135102304_101bp_rs2149171
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:       0/101 ( 0.0%)
# Similarity:     0/101 ( 0.0%)
# Gaps:           0/101 ( 0.0%)
# Score: -202
#
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ..................................................
135102204-135      1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     ..................................................
135102204-135     51 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 A    101
                     .
135102204-135    101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs VindijaNea

```
########################################
# Program: stretcher
# Rundate: Fri 24 Oct 2014 09:53:29
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141024-095328-0831-57883541-es.asequence
#    -bsequence emboss_stretcher-I20141024-095328-0831-57883541-es.bsequence
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 101
# Identity:      98/101 (97.0%)
# Similarity:    98/101 (97.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 643
#
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     |||||||||||||||||||||||...||||||||||||||||||||||||
EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGNNNGCAGCCTGCAGTGCGAGTGCGAGC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs Denisovan

```
########################################
# Program: stretcher
# Rundate: Wed 29 Oct 2014 04:28:46
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141029-042845-0705-35192998-pg.asequence
#    -bsequence emboss_stretcher-I20141029-042845-0705-35192998-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     |||||||||||||||||||||||||||||||||||||||||||||.||||
EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGTGAGC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs AltaiNea

```
########################################
# Program: stretcher
# Rundate: Fri 24 Oct 2014 09:43:45
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141024-094344-0344-96567581-pg.asequence
#    -bsequence emboss_stretcher-I20141024-094344-0344-96567581-pg.bsequence
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 661
#
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human vs MezmayskayaNea

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 05:21:47
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-052146-0249-92205062-pg.asequence
#    -bsequence emboss_stretcher-I20141115-052146-0249-92205062-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      48/101 (47.5%)
# Similarity:    48/101 (47.5%)
# Gaps:           0/101 ( 0.0%)
# Score: 134
#
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ........................||||||||||||||||||||||||||
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     |||||||||.............................||||||||||||
EMBOSS_001        51 CGCCAACCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCGAGTGCGAGC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 08:03:18
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-080316-0967-16633028-pg.asequence
#    -bsequence emboss_stretcher-I20150113-080316-0967-16633028-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     101/101 (100.0%)
# Similarity:   101/101 (100.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 505
# 
#
#=======================================

EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

```
EMBOSS_001     27869 ----CCATCAACCCACATCAG-----------------------------  27885
                         |.||.|.||.|.|||||
EMBOSS_001     28880 GTTGCAATAAGCCGAGATCAGCCCATTGCACTCCGGCCCGGATGACAGTG  28929

EMBOSS_001     27886 ------------TCAAA--------GG---------------CTAGGGTG  27900
                                 |||||        ||               ||||||||
EMBOSS_001     28930 TGAGACTGTGTCTCAAAAAAAAGTTGGGTGAGGGGTGTGGTCCTAGGGTG  28979

EMBOSS_001     27901 ATCAGAAGCTGCATTACTAAGAATCTAGCATCTGGGACAAGGCAGTATCA  27950
                     |||.|||||||||||||||||||||||.|||||.||||||||.|||||||
EMBOSS_001     28980 ATCTGAAGCTGCATTACTAAGAATCTAACATCTAGGACAAGGGAGTATCA  29029

EMBOSS_001     27951 TCACTCTCCCCAACTGAGATGTGAGGAATCCTTGAAACCAGCATCAGAGC  28000
                     |||||||||||||||||||||||.||||||..|||||||||||||||||.
EMBOSS_001     29030 TCACTCTCCCCAACTGAGATGTGGGGAATCACTGAAACCAGCATCAGAGT  29079

EMBOSS_001     28001 AGAGAGGAGAGCCGCGCAGTGACTGCAGGTGTGGCCTTTGGAACAC--GG  28048
                     .|||||   ||||.|.||||||.||.|||.|..|||||.|||||||  ||
EMBOSS_001     29080 GGAGAG---AGCCACACAGTGAGTGTAGGGGCAGCCTTCGGAACACACGG  29126

EMBOSS_001     28049 CGTTGATCTCTCTGCAGGAAGGGGAATCAAGGAGTTTCTGGCCTAAAGGT  28098
                     |||||||||||||||||||.|||||||||||||.||||||||||||||.|
EMBOSS_001     29127 CGTTGATCTCTCTGCAGGAGGGGGAATCAAGGATTTTCTGGCCTAAAGCT  29176

EMBOSS_001     28099 TGGGCTGGTGGCCTCCAGGGTTTCTTCCTGGGCAGCCCAACACCCTCCTG  28148
                     ||||||||||||||||||||||||||||||||||.|||||||||
EMBOSS_001     29177 TGGGCTGGTGGCCTCCAGGGTTTCTTCCTGGGCATCCCAACACC------  29220

EMBOSS_001     28149 GGCCCCTCCTGGGAGGCGCTCCTTTCCCCAGAGGCCAGGCCAGGCTGCCC  28198
                           |||||||||||.||||||||||||.||.||||||||||||||||
EMBOSS_001     29221 ------TCCTGGGAGGCACTCCTTTCCCCAAAGTCCAGGCCAGGCTGCCC  29264
                                                     int (3-4)/exon 4
EMBOSS_001     28199 ACAAGCTCTCTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTG  28248
                     |..|||||||||||||||||||||.||.|.||||||||||||||||||||
EMBOSS_001     29265 ATGAGCTCTCTGACATCTCTGCCCCCTTGCTGTCTCCCCAGGTGCAAGTG  29314

EMBOSS_001     28249 CAACCTGCACGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCG  28298
                     ||||||||||||||||||||||||..|.||.|||||||||||||||||.|
EMBOSS_001     29315 CAACCTGCACGCCAACCTGTGCTCTGTCCGGGAGGGCAGCCTGCAGTGTG  29364

EMBOSS_001     28299 AGTGCGAGCACAACACCACCGGCCCCGACTGCGGCAAGTGCAAGAAGAAT  28348
                     ||||.||||||||||||||||||||.|||||||||||||||||||||||.
EMBOSS_001     29365 AGTGTGAGCACAACACCACCGGCCCTGACTGCGGCAAGTGCAAGAAGAAC  29414

EMBOSS_001     28349 TTCCGCACCCGGTCCTGGCGGGCCGGCTCCTACCTGCCGCTGCCCCATGG  28398
                     ||||||||||||||||||||||||||||||||||||||||||||||.||
EMBOSS_001     29415 TTCCGCACCCGGTCCTGGCGGGCCGGCTCCTACCTGCCGCTGCCCCACGG  29464

EMBOSS_001     28399 CTCTCCCAACGCCT  28412
                     ||||||||||||||
EMBOSS_001     29465 CTCTCCCAACGCCT  29478


#---------------------------------------
#---------------------------------------
```

Human vs marmoset

```
########################################
# Program: stretcher
# Rundate: Wed 25 Mar 2015 07:57:53
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150325-075752-0265-13064726-pg.asequence
#    -bsequence emboss_stretcher-I20150325-075752-0265-13064726-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      92/101 (91.1%)
# Similarity:    92/101 (91.1%)
# Gaps:           0/101 ( 0.0%)
# Score: 424
#
#
#=======================================
                                                  int (3-4)/exon 4
EMBOSS_001         1 CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50
                     |||||||||||||||.||.|.|||||||||||||||||||||||||||||
EMBOSS_001         1 CTGACATCTCTGCCCCCTTGCTGTCTCCCCAGGTGCAAGTGCAACCTGCA     50

EMBOSS_001        51 CGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGAGC    100
                     |||||||||||||||..|.||.|||||||||||||||||.|||||.||||
EMBOSS_001        51 CGCCAACCTGTGCTCTGTCCGGGAGGGCAGCCTGCAGTGTGAGTGTGAGC    100

EMBOSS_001       101 A    101
                     |
EMBOSS_001       101 A    101


#---------------------------------------
#---------------------------------------
```

Human int (3-4)/ex4 vs mice int (3-4)/ex 4

int (3-4)/exon 4

```
EMBOSS_001     28205 TCTCTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCT  28254
                     |..|||||..|||. |..||||.| ||||||.||||||.|||||||||||
EMBOSS_001     19955 TTGCTGACTCCTCC-CATTCTCTG-GTCTCCTCAGGTGTAAGTGCAACCT  20002

EMBOSS_001     28255 GCACGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCG  28304
                     |||.||||||||||||.|..||||.|||||||||||||||||.|||||.|
EMBOSS_001     20003 GCATGCCAACCTGTGCACAGTGCGAGAGGGCAGCCTGCAGTGTGAGTGTG  20052

EMBOSS_001     28305 AGCACAACACCACCGGCCCCGACTGCGGCAAGTGCAAGAAGAATTTCCGC  28354
                     |.|||||||||||.|||||||||||.||||.||||||||||||.||||||
EMBOSS_001     20053 AACACAACACCACGGGCCCCGACTGTGGCAGGTGCAAGAAGAACTTCCGC  20102

EMBOSS_001     28355 ACCCGGTCCTGGCGGGCCGGCTCCTACCTGCCGCTGCCCCATGGCTCTCC  28404
                     ||.||..|||||||.||.|||||||||||||||||||||||.||||||||
EMBOSS_001     20103 ACACGCGCCTGGCGAGCTGGCTCCTACCTGCCGCTGCCCCACGGCTCTCC  20152

EMBOSS_001     28405 CAACGCCT  28412
                     |||.||||
EMBOSS_001     20153 CAATGCCT  20160


#---------------------------------------
#---------------------------------------
```

Human vs mouse

```
########################################
# Program: stretcher
# Rundate: Wed 25 Mar 2015 08:46:02
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150325-084601-0791-34512226-oy.asequence
#    -bsequence emboss_stretcher-I20150325-084601-0791-34512226-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 103
# Identity:      83/103 (80.6%)
# Similarity:    83/103 (80.6%)
# Gaps:           4/103 ( 3.9%)
# Score: 299
#
#
#=======================================
```

int (3-4)/exon 4

```
EMBOSS_001         1 --CTGACATCTCTGCCCTCTCGGTGTCTCCCCAGGTGCAAGTGCAACCTG     48
                       |||||..|||. |..||||.| ||||||.||||||.||||||||||||
EMBOSS_001         1 TGCTGACTCCTCC-CATTCTCTG-GTCTCCTCAGGTGTAAGTGCAACCTG     48

EMBOSS_001        49 CACGCCAACCTGTGCTCCATGCGCGAGGGCAGCCTGCAGTGCGAGTGCGA     98
                     ||.||||||||||||.|..||||.||||||||||||||||.|||||.||
EMBOSS_001        49 CATGCCAACCTGTGCACAGTGCGAGAGGGCAGCCTGCAGTGTGAGTGTGA     98

EMBOSS_001        99 GCA    101
                     .||
EMBOSS_001        99 ACA    101


#---------------------------------------
#---------------------------------------
```

rs2274855

Human vs Saqqaq-Eskimos

```
########################################
# Program: stretcher
# Rundate: Wed 14 Jan 2015 06:43:04
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150114-064303-0487-50576403-oy.asequence
#    -bsequence emboss_stretcher-I20150114-064303-0487-50576403-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      99/101 (98.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 492
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     :|||||||||||||||||||.|||||||||||||||||||||||||||||
EMBOSS_001        51 RTCTCTCTCCCACAGGTGCCGCTGCAGGTTCCTTTGGCAGTAAGTACACG    100

EMBOSS_001       101 C    101
                     |
EMBOSS_001       101 C    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-elena1

```
########################################
# Program: stretcher
# Rundate: Thu 26 Mar 2015 07:35:36
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150326-073535-0465-62224922-oy.asequence
#    -bsequence emboss_stretcher-I20150326-073535-0465-62224922-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      93/101 (92.1%)
# Similarity:    93/101 (92.1%)
# Gaps:           1/101 ( 1.0%)
# Score: 435
# 
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     |||||||||||||||||||||||||||||.......||||||||||||||
EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCNNNNNNNGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100

EMBOSS_001       101 C    101

EMBOSS_001       101 -    100


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-elena2

```
########################################
# Program: stretcher
# Rundate: Thu 26 Mar 2015 07:57:16
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150326-075714-0934-39788948-pg.asequence
#    -bsequence emboss_stretcher-I20150326-075714-0934-39788948-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      32/101 (31.7%)
# Similarity:    32/101 (31.7%)
# Gaps:           0/101 ( 0.0%)
# Score: 22
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ....................................||||||||||||||
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     ||||||||||||||||||................................
EMBOSS_001        51 GTCTCTCTCCCACAGGTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 C    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Iceman-teresa

```
########################################
# Program: stretcher
# Rundate: Thu 26 Mar 2015 07:58:11
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150326-075809-0766-84999412-es.asequence
#    -bsequence emboss_stretcher-I20150326-075809-0766-84999412-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      45/101 (44.6%)
# Similarity:    45/101 (44.6%)
# Gaps:           0/101 ( 0.0%)
# Score: 113
# 
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ....................||||||||||||||||||||||||||||||
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     |||||||||||||||...................................
EMBOSS_001        51 GTCTCTCTCCCACAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 C    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 09:34:52
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-093451-0373-1833134-es.asequence
#    -bsequence emboss_stretcher-I20150103-093451-0373-1833134-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      99/101 (98.0%)
# Similarity:    99/101 (98.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 487
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     .|||||||||||||||||||.|||||||||||||||||||||||||||||
EMBOSS_001        51 ATCTCTCTCCCACAGGTGCCGCTGCAGGTTCCTTTGGCAGTAAGTACACG    100

EMBOSS_001       101 C    101
                     |
EMBOSS_001       101 C    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Thu 26 Mar 2015 08:01:35
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150326-080134-0766-72462402-oy.asequence
#    -bsequence emboss_stretcher-I20150326-080134-0766-72462402-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      79/101 (78.2%)
# Similarity:    79/101 (78.2%)
# Gaps:           0/101 ( 0.0%)
# Score: 347
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     .|||||||||||||||||||.||||||||||...................
EMBOSS_001        51 ATCTCTCTCCCACAGGTGCCGCTGCAGGTTCNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 C    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Motala3

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 08:04:40
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-080439-0888-96191266-es.asequence
#    -bsequence emboss_stretcher-I20150104-080439-0888-96191266-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      38/101 (37.6%)
# Similarity:    38/101 (37.6%)
# Gaps:           0/101 ( 0.0%)
# Score: 62
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ..........................||||||||||||||||||||||||
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNNCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     ||||||||||||.||...................................
EMBOSS_001        51 GTCTCTCTCCCATAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    100

EMBOSS_001       101 C    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat  3 Jan 2015 11:57:34
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150103-115733-0433-33962685-oy.asequence
#    -bsequence emboss_stretcher-I20150103-115733-0433-33962685-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      71/101 (70.3%)
# Similarity:    71/101 (70.3%)
# Gaps:           0/101 ( 0.0%)
# Score: 293
# 
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     ||||||||..............................||||||||||||
EMBOSS_001        51 GTCTCTCTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNAGTAAGTACACG    100

EMBOSS_001       101 C    101
                     |
EMBOSS_001       101 C    101


#---------------------------------------
#---------------------------------------
```

Human vs VindijaNea

```
########################################
# Program: stretcher
# Rundate: Thu 26 Mar 2015 08:04:58
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150326-080457-0200-69787751-oy.asequence
#    -bsequence emboss_stretcher-I20150326-080457-0200-69787751-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      85/101 (84.2%)
# Similarity:    85/101 (84.2%)
# Gaps:           0/101 ( 0.0%)
# Score: 391
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ..........||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 NNNNNNNNNNACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     ||||||||||||||||||||.|||||||||||||||||||||||||....
EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCGCTGCAGGTTCCTTTGGCAGTAAGTANNNN    100

EMBOSS_001       101 C    101
                     .
EMBOSS_001       101 N    101


#---------------------------------------
#---------------------------------------
```

Human vs Denisovan

```
########################################
# Program: stretcher
# Rundate: Wed 29 Oct 2014 04:39:18
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141029-043917-0031-85897828-es.asequence
#    -bsequence emboss_stretcher-I20141029-043917-0031-85897828-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
# 
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     ||||||||||||||||||||.|||||||||||||||||||||||||||||
EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCGCTGCAGGTTCCTTTGGCAGTAAGTACACG    100

EMBOSS_001       101 C    101
                     |
EMBOSS_001       101 C    101


#---------------------------------------
#---------------------------------------
```

Human vs AltaiNea

```
########################################
# Program: stretcher
# Rundate: Sat 25 Oct 2014 08:14:25
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141025-081421-0467-61647112-es.asequence
#    -bsequence emboss_stretcher-I20141025-081421-0467-61647112-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:     100/101 (99.0%)
# Similarity:   100/101 (99.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 496
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     ||||||||||||||||||||.|||||||||||||||||||||||||||||
EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCGCTGCAGGTTCCTTTGGCAGTAAGTACACG    100

EMBOSS_001       101 C    101
                     |
EMBOSS_001       101 C    101


#---------------------------------------
#---------------------------------------
```

```
########################################
# Program: stretcher
# Rundate: Sat 15 Nov 2014 05:27:00
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141115-052659-0557-78423949-pg.asequence
#    -bsequence emboss_stretcher-I20141115-052659-0557-78423949-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      41/101 (40.6%)
# Similarity:    41/101 (40.6%)
# Gaps:           0/101 ( 0.0%)
# Score: 85
# 
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     .........................|||||||||||||||||||||||||
EMBOSS_001         1 NNNNNNNNNNNNNNNNNNNNNNNNNCCCCTGGGGCAGCCAGCTCACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     ||||||||||||...................................|||
EMBOSS_001        51 GTCTCTCTCCCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACG    100

EMBOSS_001       101 C    101
                     |
EMBOSS_001       101 C    101


#---------------------------------------
#---------------------------------------
```

Human vs chimpanzee

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 08:05:46
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-080545-0086-4807703-pg.asequence
#    -bsequence emboss_stretcher-I20150113-080545-0086-4807703-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      99/101 (98.0%)
# Similarity:    99/101 (98.0%)
# Gaps:           0/101 ( 0.0%)
# Score: 487
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     |||||||||||||||||||||||||||||||||||||||||||.||||||
EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTTACGCCC     50

EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     ||||||||||||||||||||.|||||||||||||||||||||||||||||
EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCGCTGCAGGTTCCTTTGGCAGTAAGTACACG    100

EMBOSS_001       101 C    101
                     |
EMBOSS_001       101 C    101


#---------------------------------------
#---------------------------------------
```

Human int (4-5)/ex5/int (5-6) vs marmoset int (4-5)/ex5/int (5-6)

```
########################################
# Program: stretcher
# Rundate: Thu 26 Mar 2015 08:21:38
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150326-082137-0400-55844718-oy.asequence
#    -bsequence emboss_stretcher-I20150326-082137-0400-55844718-oy.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 225
# Identity:     193/225 (85.8%)
# Similarity:   193/225 (85.8%)
# Gaps:           2/225 ( 0.9%)
# Score: 813
#
#
#=======================================

EMBOSS_001         1 CCTCCAGGTGCTCCCCTGCCCTGCTGGCCCCTCTGCAGGGAGGTGACACC     50
                     ||.|.||....||.||||||||||||||.|||||||.|||.||..|||.|
EMBOSS_001         1 CCCCAAGTGTTTCTCCTGCCCTGCTGGCTCCTCTGCTGGGGGGACACAAC     50
                                                               int (4-5)/
EMBOSS_001        51 CAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCCGTCTCTCTCCCACAG    100
                     |||||||||.||||...|||||||||||||.||||.||||||||||.|||
EMBOSS_001        51 CAGGCCCCTCCCCCACAGGCAGCCAGCTCATGCCCCTCTCTCTCCCGCAG    100
                     exon 5             exon 5/int (5-6)
EMBOSS_001       101 GTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACGCCTGGGGAGGGTGGC    150
                     ||.||.|||||||||||||||||||||||||.|.|||||.||||||.|||
EMBOSS_001       101 GTTCCGCTGCAGGTTCCTTTGGCAGTAAGTAAAGGCCTGTGGAGGGCGGC    150

EMBOSS_001       151 CAGGGCCCCCACTGCACGAGCCTCTTTGCATGTCCTGGAAAAAGCTGGAG    200
                     | |||.|||||||||||.|||||||||||||||||||||||||||.||||
EMBOSS_001       151 C-GGGGCCCCACTGCACCAGCCTCTTTGCATGTCCTGGAAAAAGCAGGAG    199

EMBOSS_001       201 AGAAAAAAGGGGCTTCAGTGTC-CC    224
                     ||||||||||||||||.||||| ||
EMBOSS_001       200 AGAAAAAAGGGGCTTCGGTGTCACC    224


#---------------------------------------
#---------------------------------------
```

Human vs marmoset

```
########################################
# Program: stretcher
# Rundate: Mon 27 Oct 2014 07:16:17
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141027-071616-0156-66135972-pg.asequence
#    -bsequence emboss_stretcher-I20141027-071616-0156-66135972-pg.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 101
# Identity:      85/101 (84.2%)
# Similarity:    85/101 (84.2%)
# Gaps:           0/101 ( 0.0%)
# Score: 361
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCCCCTTCCCCTGGGGCAGCCAGCTCACGCCC     50
                     |.|||.||..|||.||||||||||.||||...|||||||||||||.||||
EMBOSS_001         1 CTGGGGGGACACAACCAGGCCCCTCCCCCACAGGCAGCCAGCTCATGCCC     50
                              int (4-5)/exon 5        exon 5/int (5-6)
EMBOSS_001        51 GTCTCTCTCCCACAGGTGCCACTGCAGGTTCCTTTGGCAGTAAGTACACG    100
                     .||||||||||.|||||.||.|||||||||||||||||||||||||.|.|
EMBOSS_001        51 CTCTCTCTCCCGCAGGTTCCGCTGCAGGTTCCTTTGGCAGTAAGTAAAGG    100

EMBOSS_001       101 C    101
                     |
EMBOSS_001       101 C    101


#---------------------------------------
#---------------------------------------
```

```
                     ..||.|.|      |.||||||| ||.||||||||||||.|.||.||..|
EMBOSS_001      2242 AAACAGTT------TACAGTGTC-CCATCTGCAAAATGGACTAAAAGCAG     2284

EMBOSS_001      3328 TTCCTCCCTCCCAGGGCTGAAGTGAGGATGAA-ATGGG-ATAATCCA---     3372
                       |||.|...|  .|.|.|.||.|||..|..| ||.|| ||.||||.
EMBOSS_001      2285 --CCTTCAGGC--AGTCAGTAGCGAGAGTCCACATAGGTATGATCCCACT     2330

EMBOSS_001      3373 -------CCCCCGTCCCCACACCCTG-CAGGTCATC-ATGATTGCTAGCA     3413
                            ||||.||..|||.||..|. ||||.|.|| |.|..|.||..|.
EMBOSS_001      2331 GAGGATGCCCCTGTGACCAGACAGTCTCAGGCCCTCTAAGTCTCCTTCCC     2380

EMBOSS_001      3414 GTTGTGTGGTGGAGCAGGTGCTCTTGAGGGAGCGACACCTCCAGGTGCTC     3463
                     .|    |.||||.||.||..             |||||.||...| ||||
EMBOSS_001      2381 TT----TAGTGGGGCTGGAA-------------GACACTTCTGTG-GCTC     2412

EMBOSS_001      3464 CCCTGCCCTGCTGGCC--CCTCTGCAGGGAGGTGACACCCAGGCCCCTTC     3511
                     |||...|||..|.|.|  |||.|||...|.||.|....|||||||
EMBOSS_001      2413 CCCATTCCTTGTAGACTTCCTGTGCCAAGTGGAGGTGGCCAGGCC-----     2457
                                                    int (4-5)/exon 5
EMBOSS_001      3512 CCCTGGGGCAGCCAGCTCACGCCCGTCTCTCTCCC-ACAGGTGCCACTGC     3560
                       .||.|.|...|| ||....||| |||.|..||| ||||||||..|.||
EMBOSS_001      2458 --TTGTGTCTAACA-CTGTAACCC-TCTGTGCCCCTACAGGTGCGGCCGC     2503
                                 exon 5/int (5-6)
EMBOSS_001      3561 AGGTTCC---TTTGGCAGTAAGTACACGCCTGGGGAGGGTGGCCAGGGCC     3607
                     .||.|||   |||||||||||||||    ||.|
EMBOSS_001      2504 GGGCTCCGCCTTTGGCAGTAAGTAC----CTTG-----------------     2532

EMBOSS_001      3608 CCCACTGCACGAGCCTCTTTGCATGTCCTGGAAAAAGCTGGAGAGAAAAA     3657
                       |.|||.|| |..|||  ||||  .||.||.     |||||||
EMBOSS_001      2533 --CTCTGTAC-ATACTC--TGCA--GCCAGGC-----CTGGAGA------     2564

EMBOSS_001      3658 AGGGGCTTCAGTGTCCCCTCTGGGACTTGGGCCTATTCACTCCCTCCTCT     3707
                     .|||||.|.||.|.|..||||                  |||.||
EMBOSS_001      2565 TGGGGCATGAGGGGCTGCTCT------------------CTCTCT-----     2591

EMBOSS_001      3708 AATTACACCCCATCTGCTTCTCCACCTCTCCCCCCTCCACCTCCCCCCCT     3757
                                |||| ||.|||  |||||||.||.|..|||
EMBOSS_001      2592 -----------ATCT-CTGCTC--CCTCTCCTCCGTGTACC---------     2618

EMBOSS_001      3758 CCACCCATCCCCACTTCACATCATATGCCATGTGTCATGTGTCATTTTGC     3807
                               |.|||.|||.|.||.         .|||.||||.
EMBOSS_001      2619 ----------CTACTGCACCTAATC---------GCATCTGTCC------     2643

EMBOSS_001      3808 TGTGGCCTGTGGCCCAGCAACTCTCAGGCTCTCCCAGGAGCTCCATCAGT     3857
                         ||||    ||||.|..|.|||||| |||||.|||||||...|.| |
EMBOSS_001      2644 ----GCCT----CCCACCCTCCCTCAGG-TCTCCTAGGAGCTTTCTTA-T     2683

EMBOSS_001      3858 GCTGCTTTGGAAAACGGGACAGGACTTTT------TGCAGGTCTCTTGGC     3901
                     ||||||||| |||...||||.||.|||||      |...||||.|.||.|
EMBOSS_001      2684 GCTGCTTTG-AAAGAAGGACGGGGCTTTTGTGTGATTGGGGTCCCCTGAC     2732

EMBOSS_001      3902 CCCTGGGTGGGCTCCCTGCTCCTCCTGCCACCCACGCCACTTCTC-TCAC     3950
                     |||||.||||.|              |..||||   ||...|||| ||||
EMBOSS_001      2733 CCCTGAGTGGAC--------------GGAACCC---CCTTGTCTCCTCAC     2765

EMBOSS_001      3951 CTGGATCTGGGAGAGCAGTCTCTCCTGCCAGTCAAGAGTGGGGTGACCTT     4000
                     |  |.||||    .||..|.|...|.|||||   |.|..||||   ||||
EMBOSS_001      2766 C--GTTCTG----TGCTTTGTGCACAGCCAG---ATACAGGGG---CCTT     2803

EMBOSS_001      4001 CCCCCACCAGGGGCAGAATCCA-CCCCCT-AGCCTAACCATGGGGGCAGC     4048
                     |.|..  |..|..||...||.. |||||| ||..|.|||.    ||.| |
EMBOSS_001      2804 CTCTG--CTAGATCAATGTCTGTCCCCCTGAGTTTGACCT----GGTA-C     2846

EMBOSS_001      4049 CTCCCTCTGGGCAGCCTCTGCAGCCAGCTTGTCCCAGGGCTCTGCTCGTC     4098
                     |||| ||..|||||||||||.|||..||.||..|.|..|....|||.|..
```

Human vs mouse

```
########################################
# Program: stretcher
# Rundate: Mon 27 Oct 2014 08:21:21
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141027-082120-0258-93813620-es.asequence
#    -bsequence emboss_stretcher-I20141027-082120-0258-93813620-es.bsequence
#    -datafile EDNAFULL
#    -gapopen 16
#    -gapextend 4
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 16
# Extend_penalty: 4
#
# Length: 106
# Identity:      58/106 (54.7%)
# Similarity:    58/106 (54.7%)
# Gaps:          11/106 (10.4%)
# Score: 26
#
#
#=======================================

EMBOSS_001         1 CAGGGAGGTGACACCCAGGCC-CCTTCCCCTGGGGCAGCCAGCTCACGCC     49
                     .......|..|.....|||.. ||...||.||.|.|...|| ||....||
EMBOSS_001         1 TTCCTGTGCCAAGTGGAGGTGGCCAGGCCTTGTGTCTAACA-CTGTAACC     49
                               int (4-5)/exon 5              exon 5/int (5-6)
EMBOSS_001        50 CGTCTCTCTCCC-ACAGGTGCCACTGCAGGTTCC---TTTGGCAGTAAGT     95
                     | |||.|..||| ||||||||..|.||.||.|||   |||||||||||||
EMBOSS_001        50 C-TCTGTGCCCCTACAGGTGCGGCCGCGGGCTCCGCCTTTGGCAGTAAGT     98

EMBOSS_001        96 ACACGC    101
                     ||
EMBOSS_001        99 AC----    100


#---------------------------------------
#---------------------------------------
```

Netrin-G1

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141224-074231-0080-6402773-oy

```
########################################
# Program: stretcher
# Rundate: Wed 24 Dec 2014 07:42:32
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141224-074231-0080-6402773-oy.aupfile
#    -bsequence emboss_stretcher-I20141224-074231-0080-6402773-oy.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     576/581 (99.1%)
# Similarity:   577/581 (99.3%)
# Gaps:           0/581 ( 0.0%)
# Score: 3218
#
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
```

```
     51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100

    101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150

    151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200

    201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250

    251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300

    301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350

    351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400
        ||||||||||||:|||||||||||||||||||||.|||||||||||||||
    351 ANTCIPSISSIGSPPKFNRIWPNISSLEVSNPKQGAPKLALSTVSSVQVA    400

    401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450
        ||||.|||||||||||||||||||||||||||||||||||||||||||||
    401 NHKRGCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450

    451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500
        ||||||||||.|||||||||||||||||||||||||||||||||||||||
    451 AQLDDENVCIGCYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500

    501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550
        |||||.||||||||||||||||||||||||||||||||||||||||||||
    501 HYGCQRNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550

    551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
        |||||||||||||||||||||||||||||||
    551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141114-081823-0327-28698407-pg

```
########################################
# Program: stretcher
# Rundate: Fri 14 Nov 2014 08:18:24
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141114-081823-0327-28698407-pg.aupfile
#    -bsequence emboss_stretcher-I20141114-081823-0327-28698407-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: 
# 2: 
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     556/581 (95.7%)
# Similarity:   556/581 (95.7%)
# Gaps:           0/581 ( 0.0%)
# Score: 3097
# 
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
```

```
      51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100

     101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150

     151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200

     201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250

     251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300

     301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350

     351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400
         |||..........|||||||||||||||||||||||||||||||||||||
     351 ANTXXXXXXXXXXPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400

     401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450

     451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500

     501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550
         |||||||||||||||||||||||||||||||||||||||||||.......
     501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRXXXXXXX    550

     551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
         ........|||||||||||||||||||||||
     551 XXXXXXXXPPHGSPALLLLTTLLGTASPLVF    581


#---------------------------------------
#---------------------------------------
```

Human vs Loschbour

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20150104-082500-0254-33035958-es

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 08:25:01
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-082500-0254-33035958-es.aupfile
#    -bsequence emboss_stretcher-I20150104-082500-0254-33035958-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: 
# 2: 
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     581/581 (100.0%)
# Similarity:   581/581 (100.0%)
# Gaps:           0/581 ( 0.0%)
# Score: 3253
# 
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
```

```
     51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100

    101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150

    151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200

    201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250

    251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300

    301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350

    351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400

    401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450

    451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500

    501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550

    551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
        |||||||||||||||||||||||||||||||
    551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581


#---------------------------------------
#---------------------------------------
```

Human vs Motala12

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141228-081355-0938-85822166-pg

```
########################################
# Program: stretcher
# Rundate: Sun 28 Dec 2014 08:13:57
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141228-081355-0938-85822166-pg.aupfile
#    -bsequence emboss_stretcher-I20141228-081355-0938-85822166-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     528/581 (90.9%)
# Similarity:   528/581 (90.9%)
# Gaps:           0/581 ( 0.0%)
# Score: 2903
#
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC      50
                     |||||||||||||||||||||||||||||||||||||||||.........
                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEXXXXXXXXX      50
```

```
  51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA     100
     .............|||||||||||||||||||||||||||||||||||||
  51 XXXXXXXXXXXXXKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA     100

 101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI     150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI     150

 151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT     200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT     200

 201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT     250
     |||||||||||||||||||||||||..............|||||||||||
 201 VLEIICTEEYSTGYTTNSKIIHFEIXXXXXXXXXXXXXXMASLYGQLDTT     250

 251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN     300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN     300

 301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT     350
     .|||||||||||||||||||||||||||||||||||||||||||||||||
 301 XHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT     350

 351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA     400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA     400

 401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS     450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS     450

 451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW     500
     ||||||||||||||||||||||................||||||||||||
 451 AQLDDENVCIECYCNPLGSIHDXXXXXXXXXXXXXXXXPKCDECLPGNSW     500

 501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC     550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC     550

 551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
     |||||||||||||||||||||||||||||||
 551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20150104-090503-0441-51962716-es

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 09:05:04
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-090503-0441-51962716-es.aupfile
#    -bsequence emboss_stretcher-I20150104-090503-0441-51962716-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 605
# Identity:     269/605 (44.5%)
# Similarity:   271/605 (44.8%)
# Gaps:          24/605 ( 4.0%)
# Score: 1199
#
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                     ||||||||||||||||||||||.........................|||
                   1 MYLSRFLSIHALWVTVSSVMQPXXXXXXXXXXXXXXXXXXXXXXXXXMAC     50
```

```
  51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA     100
     ||||||||||||||||||||.||.||||||||.|||||||||||||||||
  51 QPESTDMTKYLKVKLDPPDIXCGXPPETFCAMXNPYMCNNECDASTPELA     100

 101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI     150
     |||||.............................................
 101 HPPELXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     150

 151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT     200
     ..................................................
 151 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     200

 201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT     250
     ..........|||||||||||||||.........................
 201 XXXXXXXXXXSTGYTTNSKIIHFEIXXXXXXXXXXXXXXXXXXXXXXXXX     250

 251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN     300
     ..............................................|.||
 251 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXCN     300

 301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT     350
     ||||||..................||||||||||||||||||||||||||
 301 LHATVCXXXXXXXXXXXXXXXXXXDCGKCKKNYQGRPWSPGSYLPIPKGT     350

 351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA     400
     ||||||||.....|||||||||||||||||||||.......|||||||||
 351 ANTCIPSIXXXXXPPKFNRIWPNISSLEVSNPKQXXXXXXXSTVSSVQVA     400

 401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS     450
     ||||...........||||||||||||||||...................
 401 NHKRXXXXXXXXXXXSYIDLLNTVICVSCKHXXXXXXXXXXXXXXXXXXX     450

 451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW     500
     ...........|||||||||||................||||||||||||
 451 XXXXXXXXXXXCYCNPLGSIHDXXXXXXXXXXXXXXXXPKCDECLPGNSW     500

 501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC     550
     ||.|||||||||||||||||||||||||||||||||||||||||||||||
 501 HYXCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC     550

 551 GSDSGQGAPPHGSPALLLLTTLLGTASP----------------------     578
     ||||......||||||||..........
 551 GSDSXXXXXXHGSPALLLXXXXXXXXXXXXXXXXXXXXXXXXXXWGSRHN     600

 579 --LVF    581
       :.:
 601 PNICY    605


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20150104-094928-0383-66289948-pg

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 09:49:29
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-094928-0383-66289948-pg.aupfile
#    -bsequence emboss_stretcher-I20150104-094928-0383-66289948-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     146/581 (25.1%)
# Similarity:   146/581 (25.1%)
# Gaps:           0/581 ( 0.0%)
# Score: 397
#
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                     ...............................................|||
                   1 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXMAC     50
```

```
 51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100
    ||||||||||||||....................................
 51 QPESTDMTKYLKVKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    100

101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150
    ..................................................
101 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    150

151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200
    ||||||||||||||||||................................
151 TFESGRPDQMILEKSLDYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    200

201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250
    ..................................................
201 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    250

251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300
    ..................................................
251 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    300

301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350
    ..................................................
301 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    350

351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400
    .............................................|||||
351 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSVQVA    400

401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450
    ||||.................|||||||||||||||||||||||||||||
401 NHKRXXXXXXXXXXXXXXXXXNTVICVSCKHNTRGQHCELCRLGYFRNAS    450

451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500
    ||||||||||....||||||||||||||||||||||||||||||......
451 AQLDDENVCIXXXXNPLGSIHDRCNGSGFCECKTGTTGPKCDECXXXXXX    500

501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550
    .....................||||||||||||||||||||||||.....
501 XXXXXXXXXXXXXXXXXXXXXCHNNVRCLCPAAYTGILCEKLRCEXXXXX    550

551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
    ............|||||||||..........
551 XXXXXXXXXXXXSPALLLLTTXXXXXXXXXX    581


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141030-073844-0608-52390525-es

```
########################################
# Program: stretcher
# Rundate: Thu 30 Oct 2014 07:38:45
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141030-073844-0608-52390525-es.aupfile
#    -bsequence emboss_stretcher-I20141030-073844-0608-52390525-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     310/581 (53.4%)
# Similarity:   310/581 (53.4%)
# Gaps:           0/581 ( 0.0%)
# Score: 1492
#
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                     ..................................................
                   1 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     50
```

```
    51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA     100
       ..............................||||||||||||||||||||
    51 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAMGNPYMCNNECDASTPELA     100

   101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI     150
       ||||||||||.....||||||||||||||||||||||............|
   101 HPPELMFDFEXXXXXTFWQSATWKEYPKPLQVNITLSXXXXXXXXXXXXI     150

   151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT     200
       |||||||||||||||...................................
   151 TFESGRPDQMILEKSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     200

   201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT     250
       .......||||||||||||...........||||||||||||||||||||
   201 XXXXXXXEEYSTGYTTNSKXXXXXXXXXXXFFAGPRLRNMASLYGQLDTT     250

   251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN     300
       ||||||||||||||||||||||||||||||....................
   251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHXXXXXXXXXXXXXXXXXXXX     300

   301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT     350
       ....|||||||||||||||||||||||||||||||||||||||......|
   301 XXXXVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYXXXXXXT     350

   351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA     400
       ||||||||||||||||||||||||||||||||||................
   351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQXXXXXXXXXXXXXXXX     400

   401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS     450
       .....|||................||||||||||||||||||||......
   401 XXXXXCECXXXXXXXXXXXXXXXXICVSCKHNTRGQHCELCRLGXXXXXX     450

   451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW     500
       .....|||||........|||||||||||||||||||||||.........
   451 XXXXXENVCIXXXXXXXXSIHDRCNGSGFCECKTGTTGPKCXXXXXXXXX     500

   501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC     550
       ...||||||||||||||||||||||||||||......|||||||||||..
   501 XXXCQPNVCDNELLHCQNGGTCHNNVRCLCPXXXXXXLCEKLRCEEAGXX     550

   551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
       ...............||||||||||||||||
   551 XXXXXXXXXXXXXXXLLLLTTLLGTASPLVF    581


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141030-092317-0489-8765533-pg

```
########################################
# Program: stretcher
# Rundate: Thu 30 Oct 2014 09:23:18
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141030-092317-0489-8765533-pg.aupfile
#    -bsequence emboss_stretcher-I20141030-092317-0489-8765533-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     581/581 (100.0%)
# Similarity:   581/581 (100.0%)
# Gaps:           0/581 ( 0.0%)
# Score: 3253
#
#
#=======================================

                     1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
                     1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
```

```
 51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100

101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150

151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200

201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250

251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300

301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350

351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400

401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450

451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500

501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550

551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
    |||||||||||||||||||||||||||||||
551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141030-091833-0819-59941084-pg

```
########################################
# Program: stretcher
# Rundate: Thu 30 Oct 2014 09:18:34
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141030-091833-0819-59941084-pg.aupfile
#    -bsequence emboss_stretcher-I20141030-091833-0819-59941084-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     581/581 (100.0%)
# Similarity:   581/581 (100.0%)
# Gaps:           0/581 ( 0.0%)
# Score: 3253
#
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
```

```
                 51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                 51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100

                101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150

                151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200

                201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250

                251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300

                301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350

                351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400

                401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450

                451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500

                501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550

                551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
                    |||||||||||||||||||||||||||||||
                551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141113-055119-0555-27248971-es

```
########################################
# Program: stretcher
# Rundate: Thu 13 Nov 2014 05:51:20
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141113-055119-0555-27248971-es.aupfile
#    -bsequence emboss_stretcher-I20141113-055119-0555-27248971-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     328/581 (56.5%)
# Similarity:   328/581 (56.5%)
# Gaps:           0/581 ( 0.0%)
# Score: 1603
#
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                     .....||||||||||||||||||||||||||||||...||||||||||||
                   1 XXXXXFLSIHALWVTVSSVMQPYPLVWGHYDLCKTXXXTEEGKVWDYMAC     50
```

```
              51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA     100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
              51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA     100

             101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI     150
                 |||||||||||||||||||....|||||||||||||||||||......||
             101 HPPELMFDFEGRHPSTFWQXXXXKEYPKPLQVNITLSWSKTIXXXXXXVI     150

             151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT     200
                 ||||||||||||||||||||||............................
             151 TFESGRPDQMILEKSLDYGRTWXXXXXXXXXXXXXXXXXXXXXXXXXXXX     200

             201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT     250
                 ..................|||||||||||||...........||||||||
             201 XXXXXXXXXXXXXXXXXXKIIHFEIKDRFAFXXXXXXXXXXXLYGQLDTT     250

             251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN     300
                 ||||||||||||||||||||||||||||||||||||||||||||......
             251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRXXXXXX     300

             301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT     350
                 ........||||||||||||||.........|||||||||||||||||||
             301 XXXXXXXXDNSKLTCECEHNTTXXXXXXXXXNYQGRPWSPGSYLPIPKGT     350

             351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA     400
                 .............||||||...............................
             351 XXXXXXXXXXXXXPPKFNRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     400

             401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS     450
                 .....|||||||||||||||..............................
             401 XXXXXCECFGHSNRCSYIDLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     450

             451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW     500
                 .||||||||||||||||||||||||||.......................
             451 XQLDDENVCIECYCNPLGSIHDRCNGSXXXXXXXXXXXXXXXXXXXXXXX     500

             501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC     550
                 .......||||||||||||...............................
             501 XXXXXXXVCDNELLHCQNGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     550

             551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
                 .........||||||||||||||||.....|
             551 XXXXXXXXXPHGSPALLLLTTLLGTXXXXXF    581


#---------------------------------------
#---------------------------------------
```

Human vs Chimpanzee

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20150113-102302-0252-16718505-pg

```
########################################
# Program: stretcher
# Rundate: Tue 13 Jan 2015 10:23:04
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150113-102302-0252-16718505-pg.aupfile
#    -bsequence emboss_stretcher-I20150113-102302-0252-16718505-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     580/581 (99.8%)
# Similarity:   581/581 (100.0%)
# Gaps:           0/581 ( 0.0%)
# Score: 3250
#
#
#=======================================

                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC      50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
                   1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC      50
```

```
 51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA    100
    ||||||||||||||||||||||||||||||:|||||||||||||||||||
 51 QPESTDMTKYLKVKLDPPDITCGDPPETFCSMGNPYMCNNECDASTPELA    100

101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI    150

151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT    200

201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT    250

251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN    300

301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT    350

351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA    400

401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS    450

451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW    500

501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC    550

551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
    |||||||||||||||||||||||||||||||
551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141030-044349-0086-52277612-es

```
########################################
# Program: stretcher
# Rundate: Thu 30 Oct 2014 04:43:50
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141030-044349-0086-52277612-es.aupfile
#    -bsequence emboss_stretcher-I20141030-044349-0086-52277612-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     577/581 (99.3%)
# Similarity:   578/581 (99.5%)
# Gaps:           0/581 ( 0.0%)
# Score: 3230
#
#
#=======================================

                    1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                      |||||||||||||||||||||||||||||||:||||||||||||||||||
                    1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDVCKTQIYTEEGKVWDYMAC     50
```

```
  51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA     100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA     100

 101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI     150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI     150

 151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT     200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT     200

 201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT     250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT     250

 251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN     300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN     300

 301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT     350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT     350

 351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA     400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA     400

 401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS     450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS     450

 451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW     500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW     500

 501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC     550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC     550

 551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
     ||.||||||||||..||||||||||||||||
 551 GSGSGQGAPPHGSRTLLLLTTLLGTASPLVF    581


#---------------------------------------
#---------------------------------------
```

Human vs mouse

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141029-100408-0544-53291024-es

```
########################################
# Program: stretcher
# Rundate: Wed 29 Oct 2014 10:04:09
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141029-100408-0544-53291024-es.asequence
#    -bsequence emboss_stretcher-I20141029-100408-0544-53291024-es.bsequence
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 581
# Identity:     561/581 (96.6%)
# Similarity:   568/581 (97.8%)
# Gaps:           0/581 ( 0.0%)
# Score: 3142
#
#
#=======================================

EMBOSS_001         1 MYLSRFLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMAC     50
                     |||||||||||||||||||||||..||||||:||:.|||||||||||.||
EMBOSS_001         1 MYLSRFLSIHALWVTVSSVMQPYLFVWGHYDVCKSLIYTEEGKVWDYTAC     50
```

```
EMBOSS_001         51 QPESTDMTKYLKVKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELA     100
                      |||||||||||||||||||||||||||:||||||||||||||||||||||
EMBOSS_001         51 QPESTDMTKYLKVKLDPPDITCGDPPESFCAMGNPYMCNNECDASTPELA     100

EMBOSS_001        101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI     150
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        101 HPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI     150

EMBOSS_001        151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDLSQHT     200
                      |||||||||||||||||||||||||||||||||.||||||||||||||||
EMBOSS_001        151 TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLHAFHMDPKSVKDLSQHT     200

EMBOSS_001        201 VLEIICTEEYSTGYTTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT     250
                      ||||||||||||||:|||||||||||||||||||||||||||||||||||
EMBOSS_001        201 VLEIICTEEYSTGYSTNSKIIHFEIKDRFAFFAGPRLRNMASLYGQLDTT     250

EMBOSS_001        251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN     300
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        251 KKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN     300

EMBOSS_001        301 LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT     350
                      ||||.|:|||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        301 LHATSCLYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGT     350

EMBOSS_001        351 ANTCIPSISSIGNPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA     400
                      ||||||||||||.|||||||||||||||||||||||||||||||||||||
EMBOSS_001        351 ANTCIPSISSIGTPPKFNRIWPNISSLEVSNPKQVAPKLALSTVSSVQVA     400

EMBOSS_001        401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS     450
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        401 NHKRDCECFGHSNRCSYIDLLNTVICVSCKHNTRGQHCELCRLGYFRNAS     450

EMBOSS_001        451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW     500
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001        451 AQLDDENVCIECYCNPLGSIHDRCNGSGFCECKTGTTGPKCDECLPGNSW     500

EMBOSS_001        501 HYGCQPNVCDNELLHCQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSC     550
                      :|||||||||||||||||||||.|||||.||.||||||||||||||||||
EMBOSS_001        501 YYGCQPNVCDNELLHCQNGGTCQNNVRCACPDAYTGILCEKLRCEEAGSC     550

EMBOSS_001        551 GSDSGQGAPPHGSPALLLLTTLLGTASPLVF    581
                      ||:|||||||.|||||||||.|||||.||||
EMBOSS_001        551 GSESGQGAPPRGSPALLLLTMLLGTAGPLVF    581


#---------------------------------------
#---------------------------------------
```

Netrin-G2

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141228-072756-0547-67091880-es

```
########################################
# Program: stretcher
# Rundate: Sun 28 Dec 2014 07:27:57
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141228-072756-0547-67091880-es.aupfile
#    -bsequence emboss_stretcher-I20141228-072756-0547-67091880-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     580/587 (98.8%)
# Similarity:   581/587 (99.0%)
# Gaps:           0/587 ( 0.0%)
# Score: 3243
#
#
#=======================================

                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
```

```
  51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE     100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE     100

 101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV     150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV     150

 151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS     200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS     200

 201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT     250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT     250

 251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE     300
     |||||||||||||||||||||||||||||||||||||||||.||||||||
 251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLXANLCSMRE     300

 301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF     350
     ||||||||||||||||||||||||||||||||||||||||||||.|||||
 301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACAAAGSF     350

 351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ     400
     |:|||||||||||||||||||||.||||||||||||||||||||||||||
 351 GRWTRPSTAAPLSSRWSQVASRAEGVGTPAAAPAPAKGYKLFQLKPKSPQ     400

 401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY     450
     ||||||||.|||||||||||||||||||||||||||||||||||||||||
 401 VMPIEEFQGCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY     450

 451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP     500
     ||||||||||||||.|||||||||||||||||||||||||||||||||||
 451 RNGSAELDDENVCIGCNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP     500

 501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP     550
     |||||||||.||||||||||||||||||||||||||||||||||||||||
 501 THYWRQGCYRNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP     550

 551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
     |||||||||||||||||||||||||||||||||||||
 551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141114-081943-0424-67914677-oy

```
########################################
# Program: stretcher
# Rundate: Fri 14 Nov 2014 08:19:44
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141114-081943-0424-67914677-oy.aupfile
#    -bsequence emboss_stretcher-I20141114-081943-0424-67914677-oy.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     521/587 (88.8%)
# Similarity:   521/587 (88.8%)
# Gaps:           0/587 ( 0.0%)
# Score: 2873
#
#
#=======================================

                  1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                  1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
```

```
                 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100

                101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150

                151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS    200
                    |||||....||||||||||||||..........|||||||||||||||||
                151 LEKSLXXXXTWQPYQFYAEDCMEXXXXXXXXXXDMSSSSAHRVLCTEEYS    200

                201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250

                251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300

                301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF    350
                    ||||||||..||||||||||||||||||||||||||||||||||||||||
                301 GSLQCECEXXTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF    350

                351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ    400
                    |||...........||||||||||||||||.|||||||||||||||||||
                351 GKWXXXXXXXXXXXRWSQVASRAEAVGTPAXAPAPAKGYKLFQLKPKSPQ    400

                401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450
                    ||||||||||||||||||||||||||||||||||||||||...|||||||
                401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQXXXHCRLGYY    450

                451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500

                501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550
                    |||..|||||||||||||||||||||||||..|||||||||||||....|
                501 THYXXQGCYPNVCDDDQLLCQNGGTCLQNQXXACPRGYTGVRCEQXXXXP    550

                551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
                    ||||||||||...........................
                551 ADDDGGLDCDXXXXXXXXXXXXXXXXXXXXXXXXXXX    587


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20150104-084150-0835-90231466-pg

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 08:41:51
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-084150-0835-90231466-pg.aupfile
#    -bsequence emboss_stretcher-I20150104-084150-0835-90231466-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     563/587 (95.9%)
# Similarity:   563/587 (95.9%)
# Gaps:           0/587 ( 0.0%)
# Score: 3129
#
#
#=======================================

                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
```

```
                 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100

                101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150

                151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS    200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS    200

                201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250

                251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300

                301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF    350
                    |||||||||||||||||||||||||||||||||||||||||||||.||||
                301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACAAAGSF    350

                351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ    400
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ    400

                401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450

                451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500

                501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
                501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550

                551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
                    |.|......................||||||||||||
                551 AXDXXXXXXXXXXXXXXXXXXXXXXLLLLGLAARLGR    587


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141228-084603-0980-30825109-oy

```
########################################
# Program: stretcher
# Rundate: Sun 28 Dec 2014 08:46:05
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141228-084603-0980-30825109-oy.aupfile
#    -bsequence emboss_stretcher-I20141228-084603-0980-30825109-oy.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     456/587 (77.7%)
# Similarity:   456/587 (77.7%)
# Gaps:           0/587 ( 0.0%)
# Score: 2427
#
#
#=======================================

                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                     |||||||||||||||||||||||||........|||||||||||||||||
                   1 MLHLLALFLHCLPLASGDYDICKSWXXXXXXXXWEFYACQPKVMRLKDYV     50
```

```
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100
    .....................||||||||||||||||.|.||....||||
 51 XXXXXXXXXXXXXXXXXXXXXENPYLCSNECDASNPDXAXPPXXXXDKEE    100

101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150
    |.......................|||||||||||||||||||||.....
101 EXXXXXXXXXXXXXXXXXXXXXXXLSWNKTVELTDDVVMTFEYGRXXXXX    150

151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS    200
    ............||||||||||||||||||||||||||||||.|||||||
151 XXXXXXXXXXXXPYQFYAEDCMEAFGMSARRARDMSSSSAHRXLCTEEYS    200

201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250
    ||||||||||||||||||||||||||||||||||||||||||.||||..|
201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGXKEFFXXT    250

251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300

301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF    350
    ||||||||.....||||||||||||||||||||||||||||||||.||..
301 GSLQCECEXXXXXPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACAAAGXX    350

351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ    400
    ..||||||||||||||||||||||||||||||||||||||||||||.||.
351 XXWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPXSPX    400

401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450
    ||||||||....||||||||||||||||||||||||||||||||||||||
401 VMPIEEFQXXXXYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450

451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500

501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550
    |||||||||.............|||||||||||...........||||||
501 THYWRQGCYXXXXXXXXXXXXXGGTCLQNQRCAXXXXXXXXXXXQPRCDP    550

551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
    |||||||||||||...........|||||||||||.|
551 ADDDGGLDCDRAPXXXXXXXXXXXCLLLLGLAARLXR    587


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20150104-092015-0583-38914998-pg

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 09:20:16
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-092015-0583-38914998-pg.aupfile
#    -bsequence emboss_stretcher-I20150104-092015-0583-38914998-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     200/587 (34.1%)
# Similarity:   200/587 (34.1%)
# Gaps:           1/587 ( 0.2%)
# Score: 730
#
#
#=======================================

                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                     .......|||||||||||||||||..........................
                   1 XXXXXXXFLHCLPLASGDYDICKSXXXXXXXXXXXXXXXXXXXXXXXXXX     50
```

```
  51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE     100
     .................................|.||.|.||....||||
  51 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXPDXAXPPXXXXDKEE     100

 101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV     150
     |.................................................
 101 EXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     150

 151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS     200
     ..........................|||||||||||||||||||||||.
 151 XXXXXXXXXXXXXXXXXXXXXXXXXXMSARRARDMSSSSAHRVLCTEEYL     200

 201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT     250
     .|||||||.|||||||||||||||||.|.||...................
 201 CWAGSKKEXHVRFEVRDRFAIFAGPDXRXMDXXXXXXXXXXXXXXXXXXX     250

 251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE     300
     .....................||||||||||||||||||...||||||||
 251 XXXXXXXXXXXXXXXXXXXXXYKYFYAISNIEVIGRCKCXXXANLCSMRE     300

 301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF     350
     |||||||||................||||||||||||||||||.......
 301 GSLQCECEHXXXXXXXXXXXXXXXXRSWRAGSYLPLPHGSPNAXXXXXXX     350

 351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ     400
     .........................|||...................|||
 351 XXXXXXXXXXXXXXXXXXXXXXXXXVGTXXXXXXXXXXXXXXXXXXXSPQ     400

 401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY     450
     ||||||||..........................................
 401 VMPIEEFQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     450

 451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP     500
     |||||||||||||||||||||||||...||||||||||||||||||||||
 451 RNGSAELDDENVCIECNCNQIGSVHXXXNETGFCECREGAAGPKCDDCLP     500

 501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP     550
     |||.....................||..|..............||.. ..
 501 THYXXXXXXXXXXXXXXXXXXXXXTCXXNXXXXXXXXXXXXXXEQXX-XX     549

 551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
     .....................................
 550 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    586


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20150104-100207-0478-58526928-pg

```
########################################
# Program: stretcher
# Rundate: Sun  4 Jan 2015 10:02:08
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20150104-100207-0478-58526928-pg.aupfile
#    -bsequence emboss_stretcher-I20150104-100207-0478-58526928-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     124/587 (21.1%)
# Similarity:   124/587 (21.1%)
# Gaps:           0/587 ( 0.0%)
# Score: 270
#
#
#=======================================

                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                     ..................................................
                   1 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     50
```

```
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100
    ..................................................
 51 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    100

101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150
    ..................................................
101 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    150

151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS    200
    ...............................|||||||||||||||||||
151 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXARDMSSSSAHRVLCTEEYS    200

201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250
    |||||||||||||||||||||||||||||||||.................
201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLXXXXXXXXXXXXXXXXX    250

251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300
    ..................................................
251 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    300

301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF    350
    ..................................................
301 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    350

351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ    400
    ..............................................||||
351 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKSPQ    400

401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450
    ||||||||............................|||||||||||||.
401 VMPIEEFQXXXXXXXXXXXXXXXXXXXXXXXXXXXXTRGQHCQHCRLGYX    450

451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500
    ...............|||||||||.....................|||||
451 XXXXXXXXXXXXXXXCNCNQIGSVXXXXXXXXXXXXXXXXXXXXXDDCLP    500

501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550
    |||||||||......||||||||||||..........|..||||||||.|
501 THYWRQGCYXXXXXXDQLLCQNGGTCLXXXXXXXXXXYXXVRCEQPRCXP    550

551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
    .||..................................
551 XDDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX    587


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141030-071213-0791-57584196-es

```
########################################
# Program: stretcher
# Rundate: Thu 30 Oct 2014 07:12:14
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141030-071213-0791-57584196-es.aupfile
#    -bsequence emboss_stretcher-I20141030-071213-0791-57584196-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     264/587 (45.0%)
# Similarity:   266/587 (45.3%)
# Gaps:           0/587 ( 0.0%)
# Score: 1202
#
#
#=======================================

                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                     ......|||:||||||||||..............................
                   1 XXXXXXLFLYCLPLASGDYDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     50
```

```
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE     100
    ........||||||||||||||||||||||||||||||............
 51 XXXXXXXXITCGDPPERFCSHENPYLCSNECDASNPDLXXXXXXXXXXXX     100

101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV     150
    ......||||||||||||||||||||||||||||||||||..........
101 XXXXXXWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTXXXXXXXXXX     150

151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS     200
    ..|||||||||||||||||||||||||||.....................
151 XXKSLDNGRTWQPYQFYAEDCMEAFGMSAXXXXXXXXXXXXXXXXXXXXX     200

201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT     250
    ..................................................
201 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX     250

251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE     300
    ....................................|||||||||||||.
251 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCKCNLHANLCSMRX     300

301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF     350
    .|||||||.......................||||||||||||||.||||
301 XSLQCECEXXXXXXXXXXXXXXXXXXXXXXXSYLPLPHGSPNACAAAGSF     350

351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ     400
    |............................|||||||||||||||||||||
351 GXXXXXXXXXXXXXXXXXXXXXXXXXXXXAAAPAPAKGYKLFQLKPKSPQ     400

401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY     450
    |||.|||||||||||||||||||||||||||||||....|||||||||..
401 VMPXEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHXXXXQHCQHCRLGXX     450

451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP     500
    .|||||||||||||..............................||||||
451 XNGSAELDDENVCIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCDDCLP     500

501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP     550
    ||........||||||||||||||||||||....................
501 THXXXXXXXXNVCDDDQLLCQNGGTCLQNQXXXXXXXXXXXXXXXXXXXX     550

551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR     587
    ..................||||:||||||||||||..
551 XXXXXXXXXXXXXXXXXXPATLIGCLLLLGLAARLXX     587


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141029-101147-0897-16362380-pg

```
########################################
# Program: stretcher
# Rundate: Wed 29 Oct 2014 10:11:48
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141029-101147-0897-16362380-pg.aupfile
#    -bsequence emboss_stretcher-I20141029-101147-0897-16362380-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     585/587 (99.7%)
# Similarity:   586/587 (99.8%)
# Gaps:           0/587 ( 0.0%)
# Score: 3278
#
#
#=======================================

                     1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
                     1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
```

```
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100

101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150

151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS    200
    ||||||||||||||||||||||||||||||:|||||||||||||||||||
151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARQARDMSSSSAHRVLCTEEYS    200

201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250

251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300

301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF    350
    |||||||||||||||||||||||||||||||||||||||||||||.||||
301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACAAAGSF    350

351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ    400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ    400

401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450

451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500

501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550

551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
    |||||||||||||||||||||||||||||||||||||
551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587


#---------------------------------------
#---------------------------------------
```

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EMBOSS Stretcher

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Results for job emboss_stretcher-I20141029-101340-0856-98043844-es

```
########################################
# Program: stretcher
# Rundate: Wed 29 Oct 2014 10:13:41
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141029-101340-0856-98043844-es.aupfile
#    -bsequence emboss_stretcher-I20141029-101340-0856-98043844-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     586/587 (99.8%)
# Similarity:   586/587 (99.8%)
# Gaps:           0/587 ( 0.0%)
# Score: 3282
#
#
#=======================================

                     1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
                     1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
```

```
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE     100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE     100

101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV     150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV     150

151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS     200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS     200

201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT     250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT     250

251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE     300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE     300

301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF     350
    |||||||||||||||||||||||||||||||||||||||||||||.||||
301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACAAAGSF     350

351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ     400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ     400

401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY     450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY     450

451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP     500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP     500

501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP     550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP     550

551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
    |||||||||||||||||||||||||||||||||||||
551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587


#---------------------------------------
#---------------------------------------
```

Human vs MezmayskayaNea

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Results for job emboss_stretcher-I20141113-061852-0842-34597676-es

```
########################################
# Program: stretcher
# Rundate: Thu 13 Nov 2014 06:18:53
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141113-061852-0842-34597676-es.aupfile
#    -bsequence emboss_stretcher-I20141113-061852-0842-34597676-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     349/587 (59.5%)
# Similarity:   349/587 (59.5%)
# Gaps:           0/587 ( 0.0%)
# Score: 1744
#
#
#=======================================

                     1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                       .........................................|||||||||
                     1 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKVMRLKDYV     50
```

```
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100
    |||||||||||||||||||||....|||||||||||||||..........
 51 KVKVEPSGITCGDPPERFCSHXXXXLCSNECDASNPDLAHXXXXXXXXXX    100

101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150
    .....|||||||||||||......||||||||||||||.|||||||||||
101 XXXXXYWQSITWSRYPSPXXXXXXLSWNKTVELTDDVVXTFEYGRPTVMV    150

151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS    200
    |||||||...........|||||||||||||..............|||||
151 LEKSLDNXXXXXXXXXXXEDCMEAFGMSARRXXXXXXXXXXXXXXTEEYS    200

201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250
    ||||||||||||||||||||||.|||||||||||||||||||||||||||
201 RWAGSKKEKHVRFEVRDRFAIFXGPDLRNMDNLYTRLESAKGLKEFFTLT    250

251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300
    |||..|||||||||||||||||||||||||||||||||||||||......
251 DLRXXLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANXXXXXX    300

301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF    350
    .....|||||.||||||||||||...........................
301 XXXXXECEHNITGPDCGKCKKNFXXXXXXXXXXXXXXXXXXXXXXXXXXX    350

351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ    400
    .......................||||||||||||...............
351 XXXXXXXXXXXXXXXXXXXXXXXEAVGTPAAAPAPXXXXXXXXXXXXXXX    400

401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450
    .........|||||||||||||||||||||||||||||......||||||
401 XXXXXXXXXCECYGHSNRCSYIDFLNVVTCVSCKHNTRXXXXXXCRLGYY    450

451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500
    ||||||||||||||.|||||||||||||||||.............|||||
451 RNGSAELDDENVCIXCNCNQIGSVHDRCNETGXXXXXXXXXXXXXDDCLP    500

501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550
    ||||||||||||||||||||||||||||...........|||||||||||
501 THYWRQGCYPNVCDDDQLLCQNGGTCLQXXXXXXXXXXXGVRCEQPRCDP    550

551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
    .................|||||||||||.........
551 XXXXXXXXXXXXXXXXXRPATLLGCLLLXXXXXXXXX    587


#---------------------------------------
#---------------------------------------
```

Human vs chimpanzee

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141030-041142-0278-79313696-es

```
########################################
# Program: stretcher
# Rundate: Thu 30 Oct 2014 04:11:43
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141030-041142-0278-79313696-es.aupfile
#    -bsequence emboss_stretcher-I20141030-041142-0278-79313696-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     585/587 (99.7%)
# Similarity:   586/587 (99.8%)
# Gaps:           0/587 ( 0.0%)
# Score: 3279
#
#
#=======================================

                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
                   1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
```

```
  51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE     100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE     100

 101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV     150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV     150

 151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS     200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS     200

 201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT     250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT     250

 251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE     300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE     300

 301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF     350
     |||||||||||||||||||||||||||||||||||||||||||||.||||
 301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACAAAGSF     350

 351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ     400
     ||||||||||||||||||||:|||||||||||||||||||||||||||||
 351 GKWTRPSTAAPLSSRWSQVAARAEAVGTPAAAPAPAKGYKLFQLKPKSPQ     400

 401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY     450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY     450

 451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP     500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP     500

 501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP     550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP     550

 551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR     587
     |||||||||||||||||||||||||||||||||||||
 551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR     587


#---------------------------------------
#---------------------------------------
```

Human vs marmoset

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Results for job emboss_stretcher-I20141030-050745-0739-85030227-pg

```
########################################
# Program: stretcher
# Rundate: Thu 30 Oct 2014 05:07:46
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141030-050745-0739-85030227-pg.aupfile
#    -bsequence emboss_stretcher-I20141030-050745-0739-85030227-pg.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 587
# Identity:     575/587 (98.0%)
# Similarity:   577/587 (98.3%)
# Gaps:           0/587 ( 0.0%)
# Score: 3227
#
#
#=======================================

                     1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
                     1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
```

```
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE    100

101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150
    |||.||||||||||||||||||||||||||||||||||||||||||||||
101 EGLVTYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV    150

151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS    200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS    200

201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT    250

251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE    300
    |||||||||||||||||||||||||||||||||||||||||||||||:||
251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSVRE    300

301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGSF    350
    ||||||||||||||||||||||||||||||||||||||||||||:.||||
301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACSAAGSF    350

351 GKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQ    400
    |||||||||||||.|||||..|||||||||.|||||||.|||||||||||
351 GKWTRPSTAAPLSGRWSQVVVRAEAVGTPATAPAPAKGSKLFQLKPKSPQ    400

401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRLGYY    450

451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 RNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDDCLP    500

501 THYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550
    ||||||||||||||||||||.|||||||||||||||||||||||||||||
501 THYWRQGCYPNVCDDDQLLCLNGGTCLQNQRCACPRGYTGVRCEQPRCDP    550

551 ADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR    587
    |||||||||||||||||.||||||||||||||||||.
551 ADDDGGLDCDRAPGAAPHPATLLGCLLLLGLAARLGH    587


#---------------------------------------
#---------------------------------------
```

Human vs mouse

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EMBOSS Stretcher

Tools > Pairwise Sequence Alignment > EMBOSS Stretcher

Results for job emboss_stretcher-I20141029-101504-0513-95492894-es

```
########################################
# Program: stretcher
# Rundate: Wed 29 Oct 2014 10:15:05
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20141029-101504-0513-95492894-es.aupfile
#    -bsequence emboss_stretcher-I20141029-101504-0513-95492894-es.bupfile
#    -datafile EBLOSUM62
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 590
# Identity:     537/590 (91.0%)
# Similarity:   554/590 (93.9%)
# Gaps:           4/590 ( 0.7%)
# Score: 2993
#
#
#=======================================

                  1 MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
                    ||.|||||||||||.|||||||||||||||||||||||||||||||||||
                  1 MLRLLALFLHCLPLVSGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYV     50
```

```
     51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDKEE     100
        |||||||||||||||||||||||||||||||||||||||||||||||:|:
     51 KVKVEPSGITCGDPPERFCSHENPYLCSNECDASNPDLAHPPRLMFDRED     100

    101 EGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMV     150
        |||||||||:|||||||||||||||||||:||||||||:|||||||||||
    101 EGLATYWQSVTWSRYPSPLEANITLSWNKSVELTDDVVVTFEYGRPTVMV     150

    151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYS     200
        ||||||||||||||||||||||||||||||||||||.|||||||||||||
    151 LEKSLDNGRTWQPYQFYAEDCMEAFGMSARRARDMSPSSAHRVLCTEEYS     200

    201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESAKGLKEFFTLT     250
        ||||||||||||||||||||||||||||||||||||:|||||||||||.|
    201 RWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRMESAKGLKEFFTFT     250

    251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMRE     300
        ||||||||||||||||||||||||||||||||||||||||||||||::||
    251 DLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCTVRE     300

    301 GSLQCECEHNTTGPDCGKCKKNFRTRSWRAGSYLPLPHGSPNACATAGS-     349
        |||||||||||||||||:||||||||:||||||||||||||||||.|||
    301 GSLQCECEHNTTGPDCGRCKKNFRTRAWRAGSYLPLPHGSPNACAAAGSA     350

    350 FGKWTRPSTAAPL--SSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPK     397
        ||..|:|.|.|||  ||.|.||:|.||||....|.|:.||...||:|||:
    351 FGSQTKPPTMAPLGDSSFWPQVSSSAEAVAISVAVPSQAKDSTLFELKPR     400

    398 SPQVMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRL     447
        ||||:|||||||||||||||||||||||||||||||||||||||||||||
    401 SPQVIPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNTRGQHCQHCRL     450

    448 GYYRNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAAGPKCDD     497
        |||||||||||||||||||||||||||||||||||||||||||.||||||
    451 GYYRNGSAELDDENVCIECNCNQIGSVHDRCNETGFCECREGAVGPKCDD     500

    498 CLPTHYWRQGCYPNVCDDDQLLCQNGGTCLQNQRCACPRGYTGVRCEQPR     547
        |||||||||||||||||||||||||||||.||||||||.||||:||||||
    501 CLPTHYWRQGCYPNVCDDDQLLCQNGGTCQQNQRCACPPGYTGIRCEQPR     550

    548 CDPADDDGGLDCDRAPGAAPRPATLLGCLLLLGLAARLGR     587
        ||.||| .|.|||||||..|||.|||||||||||||||..
    551 CDLADD-AGPDCDRAPGIVPRPDTLLGCLLLLGLAARLAC     589


#---------------------------------------
#---------------------------------------
```