2.

Human Hemoglobin subunit alpha

AS-Sequenz:

```
10          20          30          40          50
MVLSPADKTN  VKAAWGKVGA  HAGEYGAEAL  ERMFLSFPTT  KTYFPHFDLS
        60          70          80          90          100
HGSAQVKGHG  KKVADALTNA  VAHVDDMPNA  LSALSDLHAH  KLRVDPVNFK
        110         120         130         140
LLSHCLLVTL  AAHLPAEFTP  AVHASLDKFL  ASVSTVLTSK  YR
```

Quelle: https://www.uniprot.org/uniprot/P69905

Human Hemoglobin subunit beta

```
 10          20          30          40          50
MVHLTPEEKS  AVTALWGKVN  VDEVGGEALG  RLLVVYPWTQ  RFFESFGDLS
        60          70          80          90          100
TPDAVMGNPK  VKAHGKKVLG  AFSDGLAHLD  NLKGTFATLS  ELHCDKLHVD
        110         120         130         140
PENFRLLGNV  LVCVLAHHFG  KEFTPPVQAA  YQKVVAGVAN  ALAHKYH
```

Quelle: https://www.uniprot.org/uniprot/P68871

```
MVLSPADKTN  VKAAWGKVGA  HAGEYGAEAL  ERMFLSFPTT  KTYFPHFDLS  HGSAQVKGHG
KKVADALTNA  VAHVDDMPNA  LSALSDLHAH  KLRVDPVNFK  LLSHCLLVTL  AAHLPAEFTP
AVHASLDKFL  ASVSTVLTSK  YR
```

MVHLTPEEKS AVTALWGKVN VDEVGGEALG RLLVVYPWTQ RFFESFGDLS TPDAVMGNPK VKAHGKKVLG
AFSDGLAHLD NLKGTFATLS ELHCDKLHVD PENFRLLGNV LVCVLAHHFG KEFTPPVQAA YQKVVAGVAN
ALAHKYH

3.

Globales Alignment: werden verwendet, wenn die 2 zu vergleichenden Sequenzen gleich lang sind und starke Homologien aufweisen.

Lokales Alignment: Alignment von 2 Teilsequenzen (Substrings), bei denen die Länge differenzieren und mehr Heterogenität aufkommen kann.

4.

(1)
```
# Program: stretcher
# Rundate: Mon  9 Jul 2018 22:28:41
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20180709-222837-0802-61100285-p2m.asequence
#    -bsequence emboss_stretcher-I20180709-222837-0802-61100285-p2m.bsequence
#    -datafile EBLOSUM62
#    -gapopen 10
#    -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: 10
# Extend_penalty: 2
#
# Length: 149
# Identity:      65/149 (43.6%)
# Similarity:    90/149 (60.4%)
# Gaps:           9/149 ( 6.0%)
# Score: 285
#
#
#=======================================

EMBOSS_001         1 MV-LSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHF-D     48
                     || |:|.:|:.|.|.|||| :..|.|.|||.|:.:.:|.|:..:|..| |
EMBOSS_001         1 MVHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGD     48

EMBOSS_001        49 LSH-----GSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKLR     93
                     ||.       |:.:||.|||||..|.:.:||:|::.....:.||:||..||.
EMBOSS_001        49 LSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLH     98

EMBOSS_001        94 VDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR    142
                     |||.||:||.:.|:..||.|...|||||.|.|:..|.:|.|:..|..||.
EMBOSS_001        99 VDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH    147
```

(2)
```
# Program: stretcher
# Rundate: Mon  9 Jul 2018 22:29:45
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20180709-222930-0927-92439638-p1m.asequence
#    -bsequence emboss_stretcher-I20180709-222930-0927-92439638-p1m.bsequence
#    -datafile EBLOSUM60
#    -gapopen 10
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################
```

```
#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM60
# Gap_penalty: 10
# Extend_penalty: 2
#
# Length: 149
# Identity:      65/149 (43.6%)
# Similarity:    91/149 (61.1%)
# Gaps:           9/149 ( 6.0%)
# Score: 272
#
#
#=======================================

EMBOSS_001         1 MV-LSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHF-D     48
                     || |:|.:|:.|.|.|||| :..|.|.|||.|:.:.:|.|:.:|..| |
EMBOSS_001         1 MVHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGD     48


EMBOSS_001        49 LS-----HGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKLR     93
                     ||      .|:.:||.|||||..|.::.:||:|::....:.||:||..||.
EMBOSS_001        49 LSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLH     98


EMBOSS_001        94 VDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR     142
                     |||.||:||:.:|:..||.|...||||.|:|:..|.:|.|:...|..||.
EMBOSS_001        99 VDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH     147
```

(3)

```
# Program: stretcher
# Rundate: Mon  9 Jul 2018 22:30:34
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20180709-223031-0655-56973340-p2m.asequence
#    -bsequence emboss_stretcher-I20180709-223031-0655-56973340-p2m.bsequence
#    -datafile EBLOSUM60
#    -gapopen 20
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
######################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM60
# Gap_penalty: 20
# Extend_penalty: 2
#
# Length: 149
# Identity:      63/149 (42.3%)
# Similarity:    89/149 (59.7%)
# Gaps:           9/149 ( 6.0%)
# Score: 239
#
#
#=======================================

EMBOSS_001         1 MV-LSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHF--     47
```

```
                          || |:|.:|:.|.|.|||| :..|.|.|||.|:.:.:|.|:.:|..|
EMBOSS_001        1 MVHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGD      48

EMBOSS_001       48 ----DLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKLR      93
                        |...|:.:||.|||||..|.:::.:||:|.....:.||:||..||.
EMBOSS_001       49 LSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLH      98

EMBOSS_001       94 VDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR      142
                        |||.||:||.:.|:..||.|...||||.|:|:..|.:|.|:..|..||.
EMBOSS_001       99 VDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH      147
```

Da auf Folie 9 keine Sequenz ist, wurde mit HBA_HUMAN auf Folie 11 verglichen:

--------VLSPADKTNVAAWGKVGA—HAGEYGAEALERMFLSPTTKTYFPHF

(1)
```
# Program: stretcher
# Rundate: Mon  9 Jul 2018 22:17:47
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20180709-221746-0876-38612629-p1m.asequence
#    -bsequence emboss_stretcher-I20180709-221746-0876-38612629-p1m.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: 149
# Identity:      19/149 (12.8%)
# Similarity:    28/149 (18.8%)
# Gaps:         107/149 (71.8%)
# Score: -162
#
#
#=======================================

EMBOSS_001        1 MVHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGD      48
                    :  |:|.:|:.|.| |||| :..|.|.|||.|:.:. |.|:.:|..|
EMBOSS_001        1 V--LSPADKTNVAA-WGKVGAHAGEYGAEALERMFLS-PTTKTYFPHF--      44

EMBOSS_001       49 LSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLH      98

EMBOSS_001       45 --------------------------------------------------      44

EMBOSS_001       99 VDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH      147

EMBOSS_001       45 --------------------------------------------------      44
```

(2)

```
#######################################
```

```
# Program: stretcher
# Rundate: Mon  9 Jul 2018 22:20:20
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20180709-222019-0033-54410676-p1m.asequence
#    -bsequence emboss_stretcher-I20180709-222019-0033-54410676-p1m.bsequence
#    -datafile EBLOSUM30
#    -gapopen 12
#    -gapextend 2
#    -aformat3 pair
#    -sprotein1
#    -sprotein2
# Align_format: pair
# Report_file: stdout
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM30
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 149
# Identity:      20/149 (13.4%)
# Similarity:    31/149 (20.8%)
# Gaps:         107/149 (71.8%)
# Score: -118
#
#
#=======================================

EMBOSS_001         1 MVHLTPEEKSAVTALWGKVNV--DEVGGEALGRLLVVYPWTQRFFESFGD     48
                     .  |:|.:|:.|:| ||||.:   .|:|.|||.|::. |.|..:|:
EMBOSS_001         1 V--LSPADKTNVAA-WGKVGAHAGEYGAEALERMFLS-PTTKTYFP----     42


EMBOSS_001        49 LSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLH     98

EMBOSS_001        43 --------------------------------------------------     42


EMBOSS_001        99 VDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH    147
                                          ||
EMBOSS_001        43 -------------------HF----------------------------     44



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

(3)

```
########################################
# Program: stretcher
# Rundate: Mon  9 Jul 2018 22:21:29
# Commandline: stretcher
#    -auto
#    -stdout
#    -asequence emboss_stretcher-I20180709-222128-0133-74154780-p1m.asequence
#    -bsequence emboss_stretcher-I20180709-222128-0133-74154780-p1m.bsequence
#    -datafile EBLOSUM62
#    -gapopen 10
#    -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: 10
# Extend_penalty: 2
#
# Length: 149
# Identity:      20/149 (13.4%)
# Similarity:    29/149 (19.5%)
# Gaps:         107/149 (71.8%)
# Score: -151
#
#
#=======================================

EMBOSS_001          1 MVHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGD     48
                      :  |:|.:|:.|.|  ||||  :..|.|.|||.|:.:. |.|:.:|.
EMBOSS_001          1 V--LSPADKTNVAA-WGKVGAHAGEYGAEALERMFLS-PTTKTYFP----     42

EMBOSS_001         49 LSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLH     98

EMBOSS_001         43 --------------------------------------------------     42

EMBOSS_001         99 VDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH    147
                                         ||
EMBOSS_001         43 --------------------HF----------------------------     44
```

(4)