

Nástroje pro zpracování a grafickou úpravu sekvenčních dat

Aplikovaná bioinformatika, Jaro 2014

ColorSeq

http://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_color.html

COLOR PROTEIN SEQUENCE

[Abstract] [[NPS@ help](#)] [Original server]

Sequence name (optional) :

Paste a protein sequence below : [help](#)

```
MKKITIIDLAELSGVSASAVSAILNGNWKRRISAKLAEKVTRIAEEQGYAINRQASML
R
SKKSHVIGMIIPKYDNRYFGSIAERFEEMARERGLLPITCTRRRPELEIEAVKAMLSW
Q
VDWVVATGATNPDKISALCQQAGVPTVNLDPGSLSPSVISDNYGGAKALTHKILANSA
R
RRGELAPLTFIGGRRATITPASVYAASTMRIASWGLACRRRIFWLPAIRKATLRTACRS
G
```

Output width :

Color :

- a predefined residue set :
- or your amino acid set :

Vyznačte v sekvenci všechny **tryptofany**,
tyrosiny a **cysteiny**.

Protein Colourer

<http://www.ebi.ac.uk/cgi-bin/proteincol/ProteinColourer.pl>

Default Colour Key: **A**GILPV **F**YW **DEN**QRHSTK **C**M

Colour Keys: You may change the assignment

Blue

Red

Green

Yellow

AGILPV

FYW

DENQRHSTK

CM

Input: Please paste a sequence below.

```
LENKAPEPAMARTINWALTERGITAADAMAGATAAGNESALANC  
ECILCEDRIKDALIDADANAEMILIEERIKEVAFILIPGERHAR  
DHERMINAKARELKATERINAMARLENAMARKETAVALDEMARA  
VLASTIMILA
```

Colour Protein

Reset Form

Results: Your Protein

```
LENKAPEPAM ARTINWALTE RGITAADAMA GATAAGNESA  
LANCECILCE DRIKDALIDA DANAEMILIE ERIKEVAFIL  
IPGERHARDH ERMINAKARE LKATERINAM ARLENAMARK  
ETAVALDEMA RAVLASTIMI LA
```

Obarvete si sekvenci...

Filter Protein/DNA

http://www.bioinformatics.org/sms2/filter_protein.html

http://www.bioinformatics.org/sms2/filter_dna.html

Sequence Manipulation Suite:

Filter Protein

Filter Protein removes non-protein characters from text. Use this program when you wish to remove digits and blank spaces from a sequence to make it suitable for other applications.

Paste the text into the text area below. Input limit is 500000 characters.

```
1 MEKVNEERDA VFEDHIGDRR RSVRSLLAEA FADEMEKTSY
41 DVEVADTPQP HIPIRFRHPP IAGPVHDFVG DAIHDIFQKM
81 MKRGQAVDFC HWVSHLIATE IDEKFSEVAF RDVQYNPDIY
121 VTDSTTEAKK LFNDKIWPAI DKILQNAET CPILSEKWSG
161 IHVSGDQLKG QRHKQEDRFL AYPNGQYMDR GEDPISVLAV
201 FDGHGGHECS QYAAGHLWET WLEVRKSRDP SDSLEDQLRK
```

Please check the [browser compatibility page](#) before using this program.

Sequence Manipulation Suite:

Filter DNA

Filter DNA removes non-DNA characters from text. Use this program when you wish to remove digits and blank spaces from a sequence to make it suitable for other applications.

Paste the text into the text area below. Input limit is 500000 characters.

```
1 ttaagatttg cgctttgccca actgtacacc caacctcggt
41 ttattgtcga acctcccgct tgtgccgcca tctgcatata
81 gatcccggtc agtccgctac attctgcca ttagtatcc
121 tcgaagtctt attccacgtg ctcaaagcaa gggatcgtg
161 cagtgataac cgcctcgtgc agatccaaat tctcgattaa
201 cactcaagta ctgatttta tcatcaggtg actaaaaact
```

Please check the [browser compatibility page](#) before using this program.

Three to One

http://www.bioinformatics.org/sms2/three_to_one.html

Sequence Manipulation Suite:

Three to One

Three to One converts three letter translations to single letter translations. Digits and blank spaces are removed automatically. Non-standard triplets are ignored.

Paste the raw sequence or one or more FASTA sequences into the text area below. Input limit is 100000 characters.

```
>sequence 1
AlaCysAspGluPheGlyHisIleLysAsxXaaGlx

>sequence 2
AsnProGlnArgSerThrValTrpTyr***
```

Please check the [browser compatibility page](#) before using this program.

Three to One results

```
>results for sequence "sequence 1" starting "AlaCysAspGlu"
ACDEFGHIKBXZ

>results for sequence "sequence 2" starting "AsnProGlnArg"
NPQRSTVWY*
```

One to Three

http://www.bioinformatics.org/sms2/one_to_three.html

Sequence Manipulation Suite:

One to Three

One to Three converts single letter translations to three letter translations.

Paste the raw sequence or one or more FASTA sequences into the text area below. Input limit is 100000 characters.

```
>sequence 1
ACDEFGHIKBXZ

>sequence 2
LMNPQRSTVWY*
```

Please check the [browser compatibility page](#) before using this program.

One to Three results

```
>results for 12 residue sequence "sequence 1" starting "ACDEFGHIKB"
AlaCysAspGluPheGlyHisIleLysAsxXaaGlx

>results for 12 residue sequence "sequence 2" starting "LMNPQRSTVW"
LeuMetAsnProGlnArgSerThrValTrpTyr***
```

Three- / one-letter code

http://molbiol.ru/eng/scripts/01_17.html

Name (not necessary):

Amino acid sequence:

(case insensitive, all symbols, except standard symbols of amino acids and stop-codons ("*", "****" and "end") are disregarded.)

```
LENKAPEPAMARTINWALTERGITAADAMAGATAAGNESALANCECILCE
DRIKDALIDADANAEMILIEERIKEVAFILIPGERHARDHERMINAKARE
LKATERINAMARLENAMARKETAVALDEMARAVLASTIMILA
```

Three... -> one...

One... -> three...

Reset

amino acids in one line;

capital letters (for one letter code);

print out the original sequence.

One letter sequence:

> 142 aminoacids; Mw=15457.77Da

```
LENKAPEPAMARTINWALTE
RGITAADAMAGATAAGNE SA
LANCECILCEDRIKDALIDA
DANAEMILIEERIKEVAFIL
IPGERHARDHERMINAKARE
LKATERINAMARLENAMARK
ETAVALDEMARAVLASTIMI
LA*
```

Three letter sequence:

> 142 aminoacids; Mw=15457.77Da

```
LeuGluAsnLysAlaProGluProAlaMetAlaArgThrIleAsnTrpAlaLeuThrGlu
ArgGlyIleThrAlaAlaAspAlaMetAlaGlyAlaThrAlaAlaGlyAsnGluSerAla
LeuAlaAsnCysGluCysIleLeuCysGluAspArgIleLysAspAlaLeuIleAspAla
AspAlaAsnAlaGluMetIleLeuIleGluGluArgIleLysGluValAlaPheIleLeu
IleProGlyGluArgHisAlaArgAspHisGluArgMetIleAsnAlaLysAlaArgGlu
LeuLysAlaThrGluArgIleAsnAlaMetAlaArgLeuGluAsnAlaMetAlaArgLys
GluThrAlaValAlaLeuAspGluMetAlaArgAlaValLeuAlaSerThrIleMetIle
LeuAla***
```

Reverse Transcription and Translation Tool

<http://www.attotron.com/cybertory/analysis/trans.htm>

Transcription and Translation Tool

Converts DNA to RNA to protein.

DNA sequence:

```
GGGGACCGCCGCACCGTTATCAGCCGTCA
TATCGACTACCGGAGGGCGAGACAGACGA
TCGGTGTAGCTACTTACATGGCGTTCGA
GAGTTGCTACGCGGTAGGCTTGACTCCAA
CTACAACGGAACGTGAATCTCATTTGGG
TTTTAGATATTGGGGTCGAATCCAGCGAA
AGCATTATTAAGGGGCTCCGTAACCTGGA
TGGAACATTGAGGTCTTTCAGTTCAACGA
ATCCTGGATAGGGCGCAACTCCCCTACA
CCAACCTTAACCTCACATTACCCTGTTCT
```

DNA (deoxyribonucleic acid)

- a permanent copy of genetic information.
- uses "T" instead of "U"
- no 2' OH group
- more stable than RNA
- lower error frequency during replication than RNA

transcribe>

<reverse transcribe

RNA sequence:

```
GGGGACCGCCGCACCGUUAUCAGCCGUCA
UAUCGACUACCGGAGGGCGAGACAGACGA
UCGGUGUUAGCUACUUAUCAUGGCGUUCGA
GAGUUGCUACGCGGUAGGCUUGACUCCAA
CUACAACGGAACGUGAAUCUCAUUUUGGG
UUUUAGAUUUUGGGGUCGAAUCCAGCGAA
AGCAUUUUUAAGGGGCUCCGUAACCUGGA
UGGAACAUUGAGGUCUUUCAGUUCAACGA
AUCCUGGAUAGGGCGCAACUCCCACUACA
CCAACUUUAACCUCACAUUACCCUGUUCU
UAUUGCGCAA
```

translate>

Protein sequence:

```
GDRRTVISRHIDYRRARQTIGVSYLHGVR
ELLRGRLDNSNYNGT . ISFWVLDIGVESSE
SIIKGLRNLDTLRSFSSTNPG . GATPTT
PTLTSHYPVLIQAQ
```

Protein

- consists of amino acids linked by aminoester ("peptide") bonds.
- most enzymes and many structural components of cells are made of proteins.

Pohrajte si s RNA...

Reverse Translate

http://www.bioinformatics.org/sms2/rev_trans.html

Sequence Manipulation Suite:

Reverse Translate

Reverse Translate accepts a protein sequence as input and uses a codon usage table to generate a DNA sequence representing the most likely non-degenerate coding sequence. A consensus sequence derived from all the possible codons for each amino acid is also returned. Use Reverse Translate when designing PCR primers to anneal to an unsequenced coding sequence from a related species.

Paste the raw sequence or one or more FASTA sequences into the text area below. Input limit is 20000 characters.

```
>sample sequence
LENKAPEPAMARTINWALTERGITAADAMAGATAAGNESALANCECILCEDRIK
DALIDADANAEMILIEERIKEVAFILIPGERHARDHERMINAKARELKATERIN
AMARLENAMARKETAVALDEMARAVLASTIMILA
```

Please check the [browser compatibility page](#) before using this program.

Enter the codon table you wish to use (in GCG format). The default codon usage table was generated using all the E. coli coding sequences in GenBank. It was obtained from the [Codon Usage Database](#).

| AmAcid | Codon | Number | /1000 | Fraction | .. |
|--------|-------|-----------|-------|----------|----|
| Gly | GGG | 50527.00 | 11.12 | 0.15 | |
| Gly | GGA | 39036.00 | 8.59 | 0.12 | |
| Gly | GGT | 114185.00 | 25.14 | 0.34 | |
| Gly | GGC | 130043.00 | 28.63 | 0.39 | |

Přeložte si protein...

Enter sequence here:

[Help](#)

Amino Acid Keypad

Peptide properties

Sequence: GERQKWFIPVYWF

Length: 13

Mass: 1754.8906

Isoelectric point (pI): 9.59

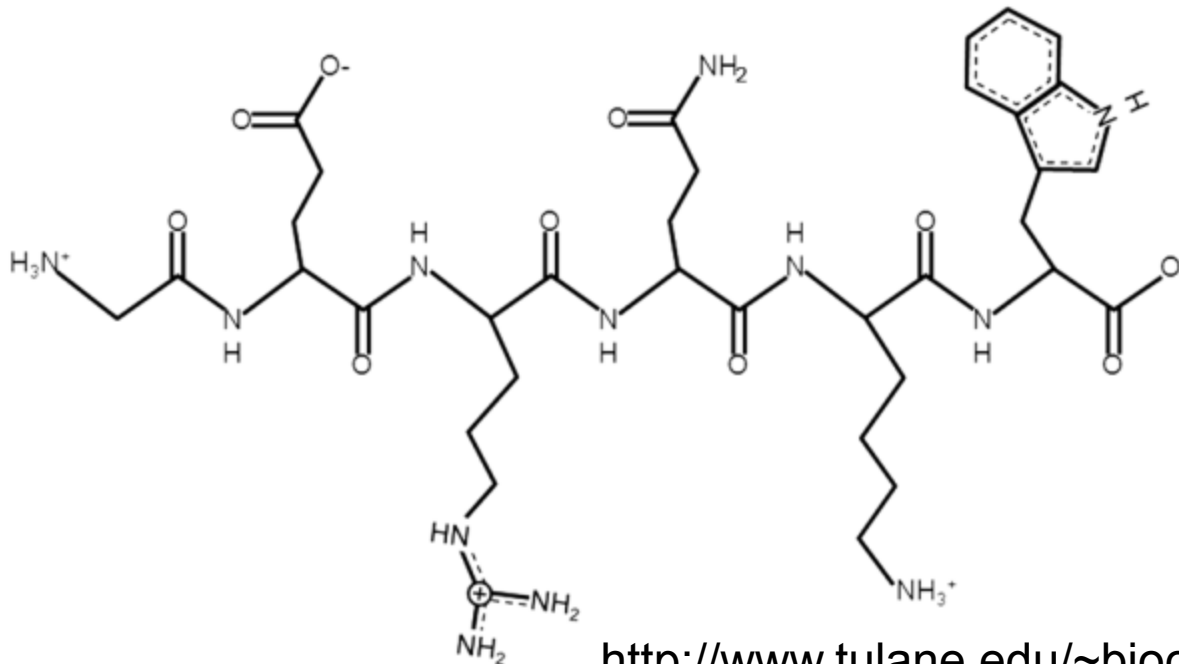
Net charge: +1

Hydrophobicity: +8.31 Kcal * mol⁻¹

Extinction coefficient¹: 12490 M⁻¹ * cm⁻¹

Extinction coefficient²: 12490 M⁻¹ * cm⁻¹

PEPDRAW



**Kolik aminokyselin
program zvládne?**

PepDraw

<http://www.tulane.edu/~biochem/WW/PepDraw/index.html>

POLYVIEW

<http://polyview.cchmc.org/>

[PDB deposited protein structure](#)

PDB ID considered as *Examples: 3ert, 1ttu, 1naq*

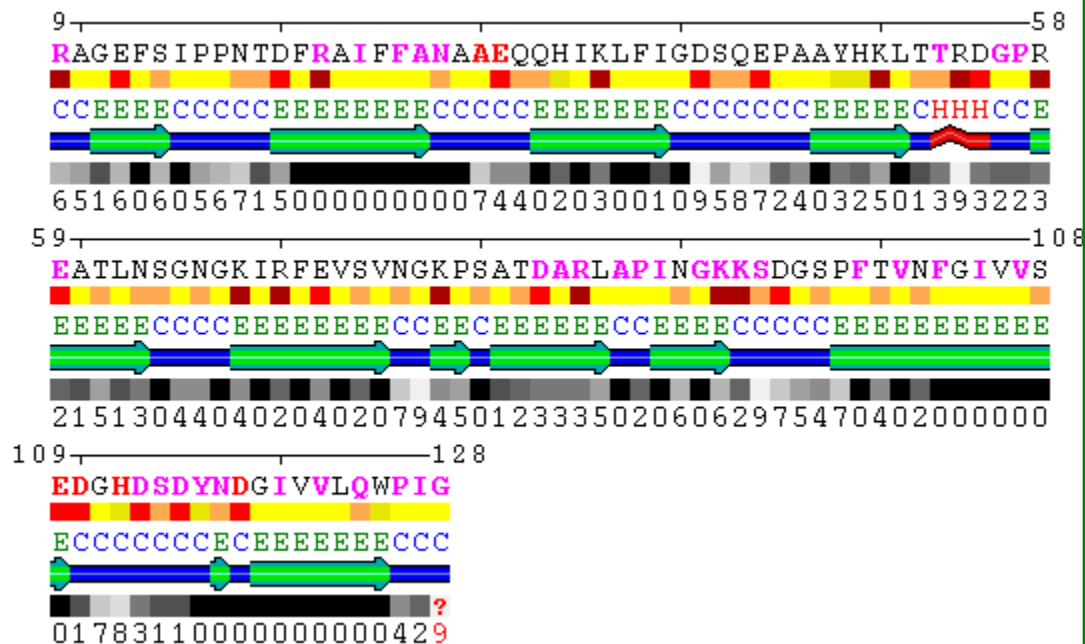
Get ID by keyword

Custom structure in the [PDB format](#)

File

Given coordinate file represents a multi-model structure, such as NMR (e.g., PDB ID 2kmv, 2kcj),
morph ([example](#)), or low-frequency motion ([example](#))

Structural Data from Predictions ([Help](#))



POLYVIEW

<http://polyview.cchmc.org/>

General settings [\(Help\)](#)

Structure unit

Representation of Secondary Structure

Background color [Pick color](#)

Number of residues per line

Start numeration from (Empty field means the original numeration)

Shown information [\(Help\)](#)

Hide

Show

- | | |
|---|--|
| <input type="checkbox"/> Residue numbering | <input checked="" type="checkbox"/> Chemical property profile |
| <input type="checkbox"/> Amino acid sequence | <input checked="" type="checkbox"/> Letter code for secondary structure |
| <input type="checkbox"/> Graphical secondary structure | |
| <input type="checkbox"/> Relative solvent accessibility | <input checked="" type="checkbox"/> Numerical relative solvent accessibility |

DSSP output

- Mark RSA for incorrectly resolved residues
- Show DSSP warnings

Legend

1



0 1 2 3 4 5 6 7 8 9



HAPNC



0 1 2 3 4 5 6 7 8 9

GLCFEPFERL

Description

Amino acid residue numeration

Protein secondary structure

H-alpha and other helices (model 1)

H-alpha and other helices (model 2)

E-beta-strand or bridge

C-coil

Relative solvent accessibility (RSA)

0-completely buried (0-9% RSA),

9-fully exposed (90-100% RSA)

Physical-chemical properties

H-hydrophobic: A,C,F,G,I,L,M,P,V

A-amphipathic: H,W,Y

P-polar: N,Q,S,T

N/C-charged: D,E-neg; R,K-pos

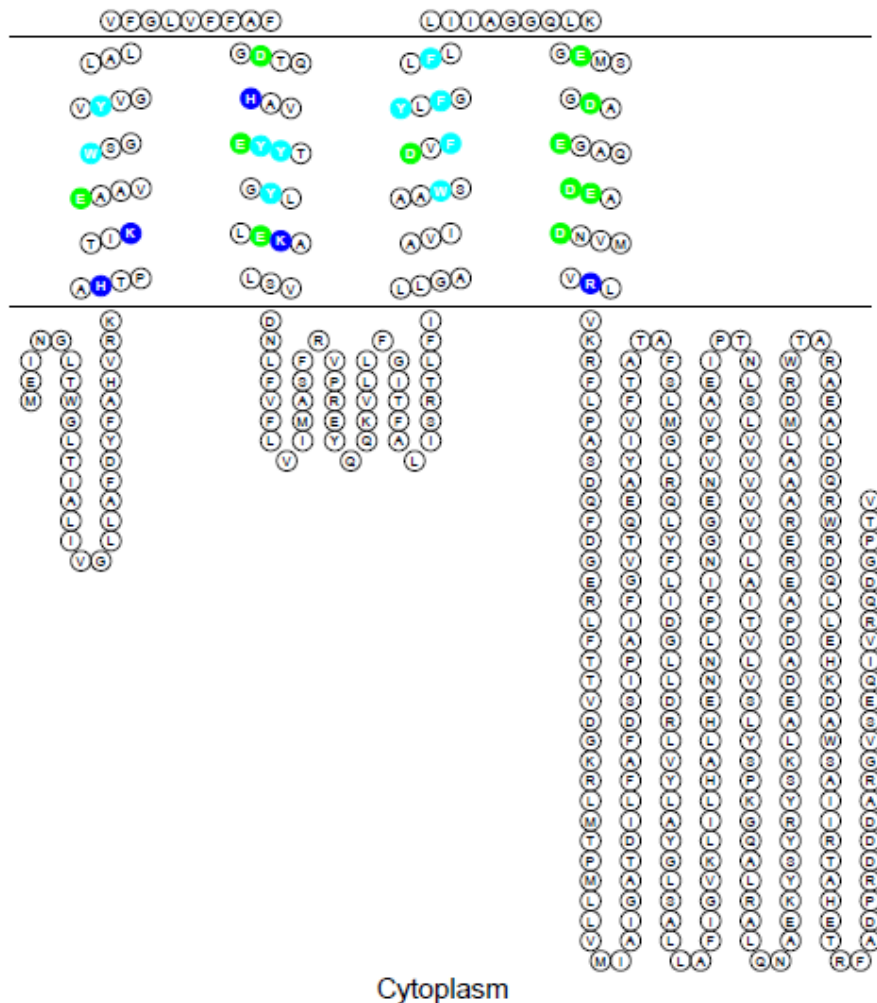
Confidence level of prediction

0-the lowest level,

9-the highest level

Transmembrane domain

Extracellular



TOPO2

<http://www.sacs.ucsf.edu/TOPO2/>

TOPO2 software is for creating transmembrane protein 2D topology images. It makes **no attempt to predict the TMDs** that it displays. The user needs to supply that information. Residues of interest can be highlighted, if desired.

MyDomains

<http://prosite.expasy.org/mydomains>

MyDomains - Image Creator
Input form




Protein/View data

Protein length Horizontal scale

Domain data

```
50 ,150 , 2,4, MY
300 ,400 , 3,2, DOMAIN

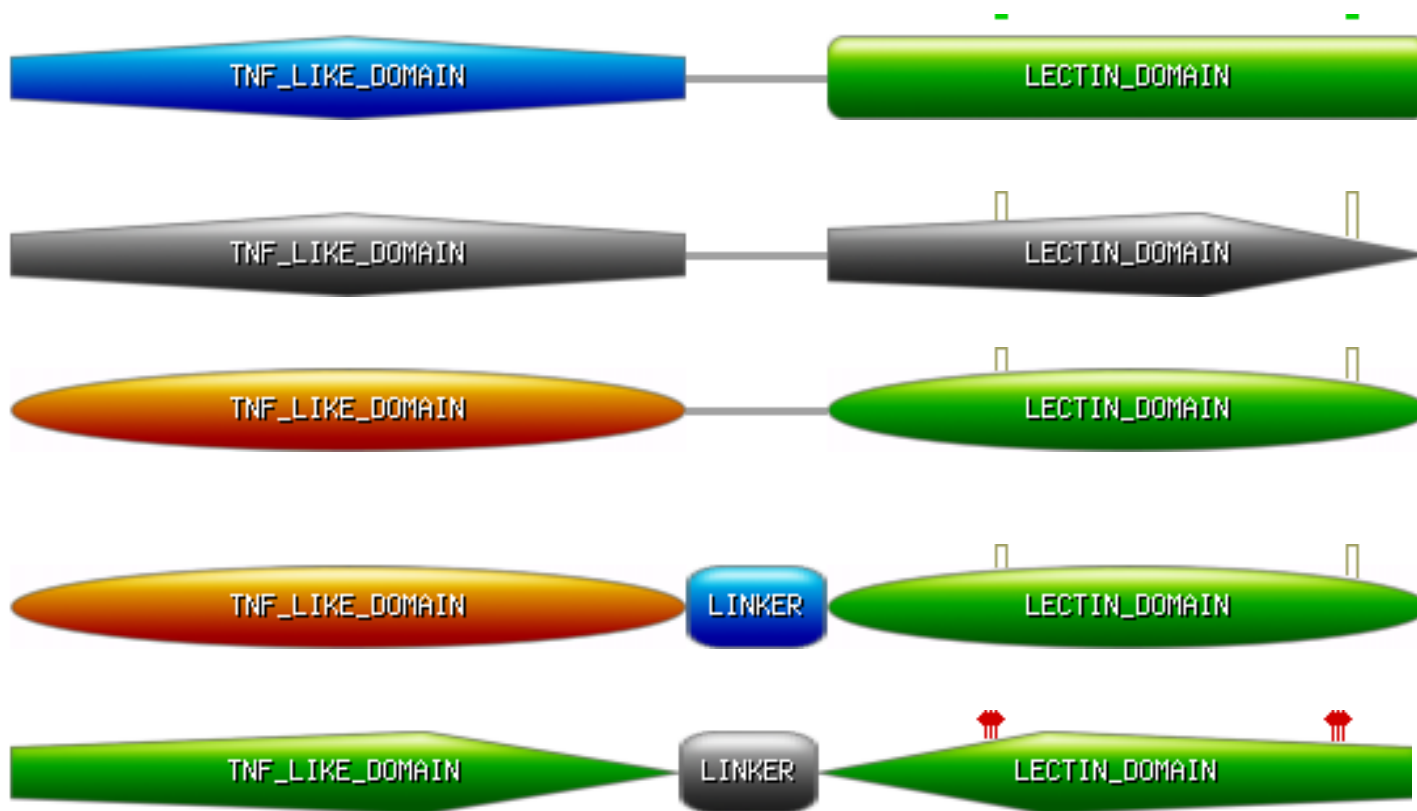
100 ,200 , 1
320 , 1
```

- To add a **domain**: start, stop, shape, color, text
 - Shape is any number between 1 and 6:

 - Color is any number between 1 and 4:

- To add a **range**: start, stop, type
 - Type is 0 or 1:
- To add a **site**: position, type
 - Type is 0 or 1: 

see result right below

PLLSASIVSAPVVTSETYVDIPGLYLDVAKAGIRDGKLQVILNVPTPYATGNNFPGIYFAI
 ATNQGVVADGCFTYSSKVPSTGRMPFTLVATIDVGSVTFVKGQWKSVRGSAMHIDSYAS
 LSAIWGTAAPSSQGSGNQGAETGGTGAGNIGGGGERDGTFNLPPIKFGVTALTHAANDQT
 IDIYIDDDPKPAATFKGAGAQQDQNLGTVLDSGNRVRVIVMANGRPSRLGSRQVDIFKKS
 YFGIIGSEDGADDDYNDGIVFLNWPLG

271 aa, 1-129 TNF like domain, 157-271 Lectin domain,
 189-191 vazebné miesto, 256-258 vazebné miesto



Protein/View data

271 Protein length 2 Horizontal scale

Domain data

```
1 ,129 , 3,2, TNF_LIKE_DOMAIN
130, 156, 1,4, LINKER
157 ,271 , 4,2, LECTIN_DOMAIN
```

```
189, 1
190, 1
191, 1
256, 1
257, 1
258,1
```

- To add a **domain**: start, stop, shape, color, text
 - Shape is any number between 1 and 6:



- Color is any number between 1 and 4:



- To add a **range**: start, stop, type
 - Type is 0 or 1:
- To add a **site**: position, type
 - Type is 0 or 1:

DRAW see result right below

undo changes




```

FEATURES             Location/Qualifiers
    source            1..248
                     /organism="Candidatus Pelagibacter ubique HTCC1062"
                     /strain="HTCC1062"
                     /db_xref="taxon:335992"
    Protein           1..248
                     /product="multi-domain protein"
    Region           13..61
                     /region_name="SH3_3"
                     /note="Bacterial SH3 domain; pfam08239"
                     /db_xref="CDD:254683"
    Region           <129..220
                     /region_name="Spr"
                     /note="Cell wall-associated hydrolases
                     (invasion-associated proteins) [Cell envelope biogenesis,
                     outer membrane]; COG0791"
                     /db_xref="CDD:223862"
    Region           141..>213
                     /region_name="NLPC_P60"
                     /note="NlpC/P60 family; cl17555"
                     /db_xref="CDD:266746"
    CDS              1..248
                     /locus_tag="SAR11_0214"
                     /coded_by="CP000084.1:215418..216164"
                     /note="SH3 and NLP/P60 domains (Pfam)"
                     /transl_table=11

```

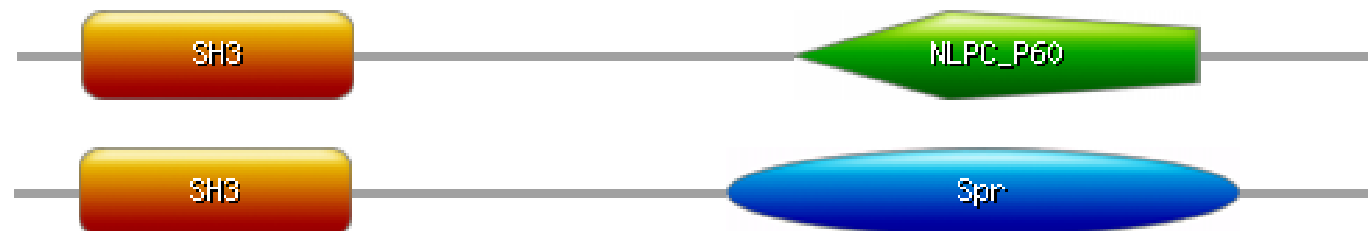
Vytvořte „doménové schéma“ proteinu.

```

ORIGIN
1  mkdnyfykqp lsniykkpna fsevtsqily gekfkiiskn knwikikvsf dnytgyiknk
61  yytkdhqpth kiftlkaniy nkqknktnkf lpfasrismi denkkfiefe knkwikkkdi
121 kkinhieky lkvllmflki kylwggktyr gidcsailql ffyynnkfyp rdtkdqikys
181 akknkskvfk kgdiifwqgh vavcinaqkl ihaygpekv limniketin riertakltv
241 kkispiky

```

//



Clustal Omega

[Input form](#) | [Web services](#) | [Help & Documentation](#)

[Tools](#) > [Multiple Sequence Alignment](#) > [Clustal Omega](#)

Results for job clustalo-I20140424-170544-0349-84275116-pg

[Alignments](#) | [Result Summary](#) | [Phylogenetic Tree](#) | [Submission Details](#)

[Download Alignment File](#) | [Show Colors](#) | [Send to ClustalW2_Phylogeny](#)

CLUSTAL O(1.2.1) multiple sequence alignment

BCLA
BCLD
BCLC
PA-IIL

BCLA
BCLD
BCLC
PA-IIL

BCLA
BCLD
BCLC

```
CLUSTAL O(1.2.1) multiple sequence alignmentBCLA -----
-----BCLD
LVIVDAVTLLSAYPEASRDPAAPTVIDGRHLYVVSPGDAA---QLGHNDSRLFTGLSPGDBCLC
-----PLLSASIV-----SAPV--VTSETYVDIPGLYLDVAKAGIRDGKLGKLVILNVP-PA-IIL
-----
-----BCLA -----
-----BCLD
QLHLRETALALRAEVSVLFRFALKDAGIVAPIELEVVRDAATAVPDADDLL-----BCLC
-----TPYATGNFPGIYFAIA-TNQGVVADGCFT---YSSKVPESTGRMPFTLVATIDPA-IIL
-----
-----BCLA -----
-----BCLD
HPSCRPLKDHYWRSVLAAGATTCTADFVAVCDRDGTVSGYFRWETSIEIA-GS-----QBCLC
VGGVTFVKGQWKSVRGSA---M-----HIDSYASLSAIWGTAAAPSSQGSNGQAETPA-IIL
-----
-----BCLA -----
-----
ADSQTSSNRAGEFSIPPNTDFRAIFFANAAEQQHIKLFIGDSQEPAA YHKLT TRDBCLD
PDKQPGFKPSSDRNGNFSLPPNTAFKAIFYANAADRQDLKLFIDDAPEPAATFVGNSEDBCLC
GGTGAGNIGGGGERDGTFLNPPHIKFGVTAALHAANDQTIDIYIDDDPKPAATFKGAGQAQA-IIL
-----ATQGVFTLPANTRFGVTAFAANSSGTQTVNVLVNNE--TAATFSGQSTN
*:*:* . * . : : : * : : : * : : * : : * : : * : : * : : * : : * : :
NGKIRFEVSVNGKPSATDARLAPINGKKSDBGSPFTVNFVIVVSEDGHBCLD GVRL--
FTLNSK-GGKIRIEASANGRQSATDARLAPLSAGD-----TVWLGWLGAEWGABCLC
DQNLGTKVLD SG-NGRVRVIVMANGRPSRLGSRQVDIFK-----KSYFGIIGSEDGAPA-IIL
NAVIGTQVLNSGSSGKVVQVQVSVNGRPSDLVSAQVILTNT-----ELNFALVGSSEDGT
.*:* * : : . * : : * : : * : : * : : * : : * : : * : : * : : * : :
BCLD DADYNDGIVILQWPITBCLC DDDYNDGIVFLNWPLGPA-IIL
DNDYNDVAVVINWPLG * * * * * : * : : * : : * : : * : : * : : * : :
```

BoxShade

http://embnet.vital-it.ch/software/BOX_form.html

Output format:

Font Size:

Consensus Line:

Fraction of sequences: (that must agree for shading)

Enter sequence number: only if 'consensus to a single sequence'

Query title (optional):

• When pasting MSF or ClustalW files, please make sure that the pasted text starts with the header line of the alignment contains no extra blank lines at the bottom.

Input sequence format:

Paste your multiple-alignment file:

```
BCLA      1  -----ADSQTSSNRAGEFSI
BCLD     139 CDRDGTVSGYFRWETSIEIA-GS-----QPDTKQPGFKPSSDRNGNFSL
BCLC     116 -HIDSYASLSAIWGTAA PSSQSGNQGAE TGGTGAGNIGGGGERDGT FNL
PA-IIL    1  -----ATQGVETL
consensus 151  . . . . . * *
```

```
BCLA      16  PPNTDFRAIFFANAAEQQH IKLFI GDSQEPAA YHKLTTRDGP RE--ATLN
BCLD     182  PPNTAFKAIIFYANAADRQDLKLFIDDAPEPAATFVGNSE DGVRL--FTLN
BCLC     165  PPHIKFGVTALTHAANDQTI DIYIDDDPKPAATFKGAGAQDQNLG TKVLD
PA-IIL    9   PANTRFGVTAEFANSSGTQTVNVLVNNE--TAATFSGOSTNNAVI GTQVLN
consensus 201  * . . . . * . . . . * . . . . * . . . . *
```

```
BCLA      64  SG-NGKIRFEVSVNGKPSATDARLAPINGKKS DSGSPFTVNF GIVVSEDGH
BCLD     230  SK-GGKIRIEASANGRQSATDARLAPLSAGD-----TVWLGWLGAE DGA
BCLC     215  SG-NGRVRVIVMANGRPSRLGSRQVDIFK-----KSYFGIIGSE DGA
PA-IIL    57  SGSSGKVQVQVSVNGRPSDLVSAQVILTN-----ELNFALVGS EDGT
consensus 251  * . * . . . . * . . . . * . . . . * . . . . *
```

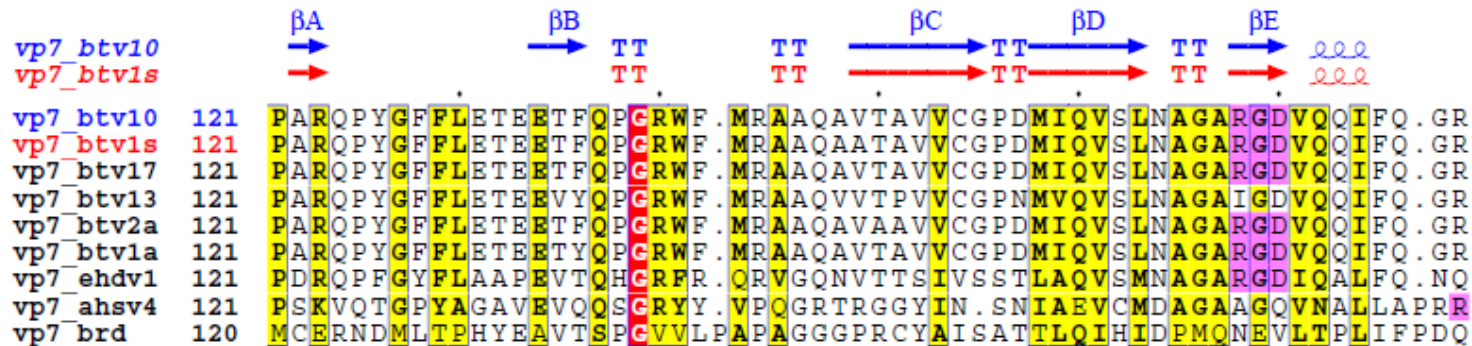
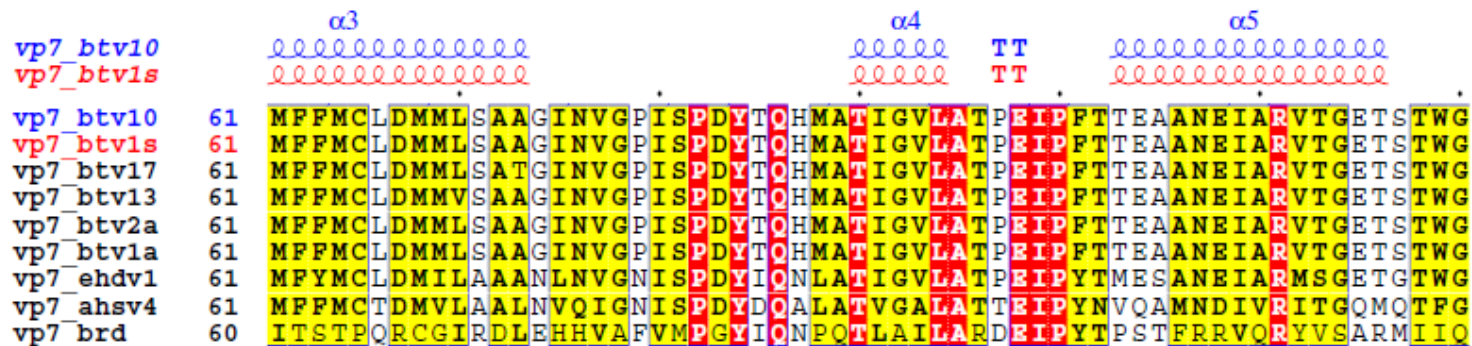
```
BCLA      113  DSDYNDGIVVLOWPIG
BCLD     273  DADYNDGIVVLOWPII
BCLC     256  DDDYNDGIVVELNWPLG
PA-IIL    99  DNDYNDAVVVINWPLG
consensus 301  * * * * * . . . . * . . . . *
```

ESPrict 3

<http://esprict.ibcp.fr/ESPrict/ESPrict/>

What is ESPrict?

- ESPrict, 'Easy Sequencing in PostScript', is a program which renders sequence similarities and secondary structure information from aligned sequences for analysis and publication purpose.



ESPrict 3

<http://esprict.ibcp.fr/ESPrict/ESPrict/>

ALN file
Example file • Tutorial

Number sequences

Secondary structure depiction

| Top secondary structures | Parameters |
|--|---|
| <p>Input file <i>Upload a file below OR click here:</i> PDB</p> <input type="text"/> <input type="button" value="Browse..."/> | <p><input checked="" type="radio"/> Sec. structure labels: $\alpha 1, \beta 1, \alpha 2, \beta 2, \dots$</p> <p><input type="radio"/> Sec. structure labels: $\alpha A, \beta A, \alpha B, \beta B, \dots$</p> <p><input type="radio"/> Sec. structure labels: $\alpha 1, \beta A, \alpha 2, \beta B, \dots$</p> |
| <p>Chain ID <input type="checkbox"/></p> <p>Relative accessibility <input type="checkbox"/></p> | |
| <p>Color scheme <input checked="" type="radio"/> Normal <input type="radio"/> Flashy <input type="radio"/> Thermal <input type="radio"/> Slide <input type="radio"/> B&W</p> <p>Orientation <input checked="" type="radio"/> Portrait <input type="radio"/> Landscape</p> <p>Paper size <input checked="" type="radio"/> A4 <input type="radio"/> A3 <input type="radio"/> A0 <input type="radio"/> US letter <input type="radio"/> Tapestry</p> <p>Footnotes <input type="text"/></p> | |
| <p>Font size <input type="text" value="7"/></p> <p>Number of columns <input type="text" value="60"/></p> | |

ESPrript 3

<http://esprript.ibcp.fr/ESPrript/ESPrript/>

```

CLUSTAL O(1.2.1) multiple sequence alignmentBCLA
-----BCLD
LVIVDAVTLLSAYPEASRDPAAPTVIDGRHLYVYVSPGDA---QLGHNDSRLFTGLSPGDBCLC
-----PLLSASIV-----SAPV--VTSETVYVDIPGLYLDVAKAGIRDGKLVILNVP-PA-IIL

-----BCLA
-----BCLD
QLHLRETALALRAEVSVLFIRFALKDAGIVAPIELEVRDAATAVPDADDLL-----BCLC
-----TPYATGNNFPGIYFAIA-TNQGVAADGCF---YSSKVPESTGRMPFTLVATIDPA-IIL

-----BCLA
-----BCLD
HPSCRPLKDHVYWRSDVLAAGATTCTADFVCDRDGTVSGYFRWETSIEIA-GS-----QBCLC
VSGSVTFVKGQWKSVRGS---M-----HIDSYASLSAIWGTAAAPSSQSGNQAETPA-II

-----BCLA
-----
ADSQTSSNRAGEFSIPPNTDFRAIFFANAEEQHQIKLFIGDSQEPAA YHKLTTRDBCLD
PDTKQPGFKPSSDRNGNFSLPNTAFKAIIFYANAADRQDLKLFIDDAPEPAATFVGNSEDBCLC
GGTGAGNIGGGGERDGTNLPPIHKFGVTA LTHAANDQTIDIYIDDDPKPAATFKGAGAOPA-IIL
-----ATQGVFTLPANTRFQVTA FANSSGTQTVNVLVNNE--TAATFSGQSTN
***** * : : : * : : : * : : : * : : : * : : : * : : : * : : : * : : :
NGKIRFEVSVNGKPSATDARLAPINGKKS DGSFPFVNFVGVVSEDGHBCLD GVRL--
FTLNSK-GGKIRIEASANGRQSATDARLAPLSAGD-----TVWLGWLGAEDEGABCLC
DQNLGTKVLD SG-NGRVRVIVMANGRPSRLGSRQVDIFK-----KSYFGIIGSEDEGAPA-IIL
NAVIGTQVLNSGSSGKVQVQVSVNGRPSDLVSAQVILT-----ELNFALVGSDEGT
.* * : : : * : : : * : : : * : : : * : : : * : : : * : : : * : : :
BCLD DADYNDGIVILQWPITBCLC DDDYNDGIVFLNWLPGA-IIL
DNDYNDAVVINWPLG ***** : : : * : : :
    
```

