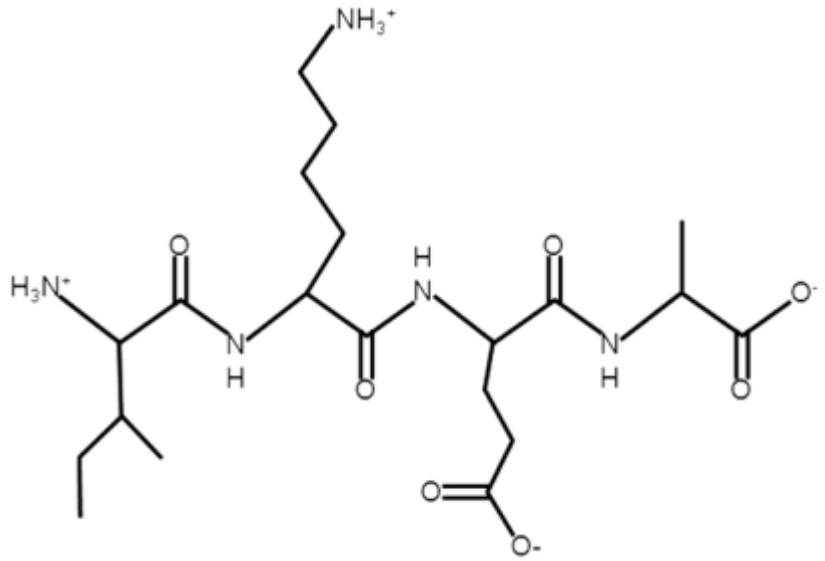


Nástroje pro zpracování a grafickou úpravu sekvenčních dat

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

```
MKKITIYDLAELSGVSASAVSAILNGNWKKRRISAKLAEKVTRIAEEQGYAINRQASML
R
SKKSHVIGMIIPKYDNRYFGSIAERFEEMARERGLLPIITCTRRRPELEIEAVKAMLSW
Q
VDWVVATGATNPDKISALCQQAGVPTVNLDLPGSLSPSVISDNYGGAKALTHKILANSA
R
RRGELAPLTFIGGRRATITPASVYAASTMRIASWGLACRRRIFWLPAIRKATLRTACRS
G
```

Output width : 70

Color :

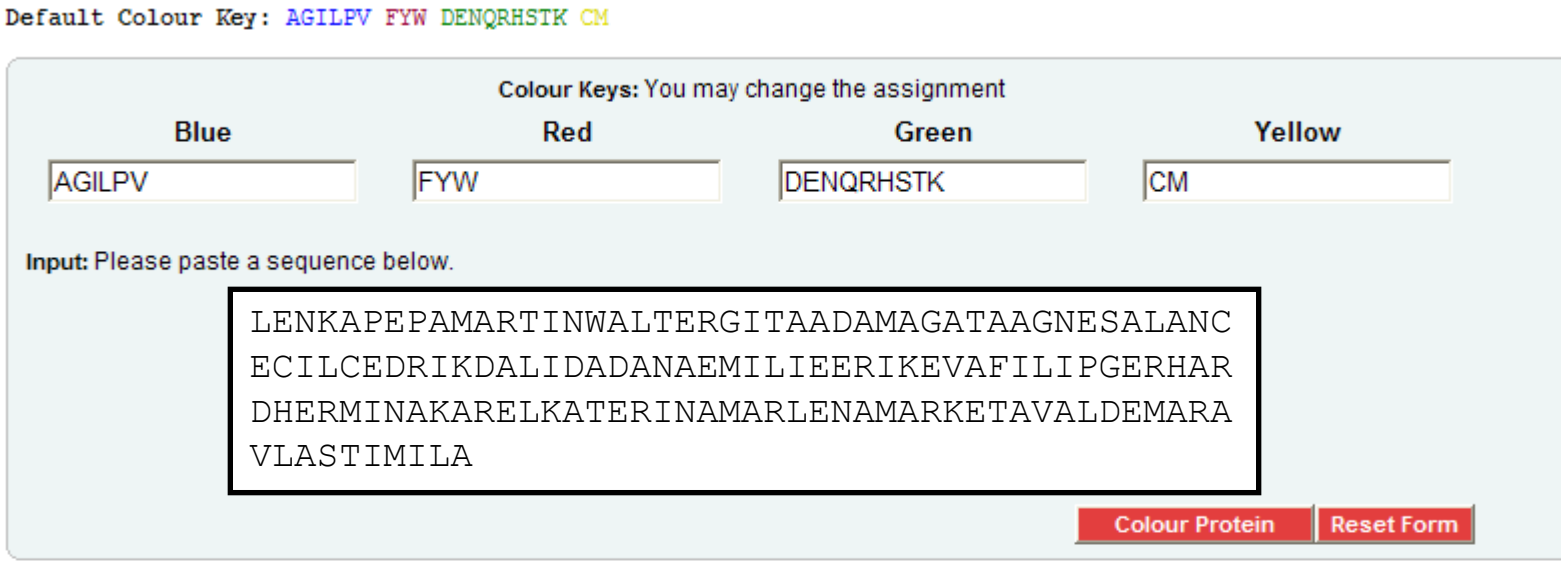
- a predefined residue set : Hydrophobic (ALIVMW)
- or your amino acid set :

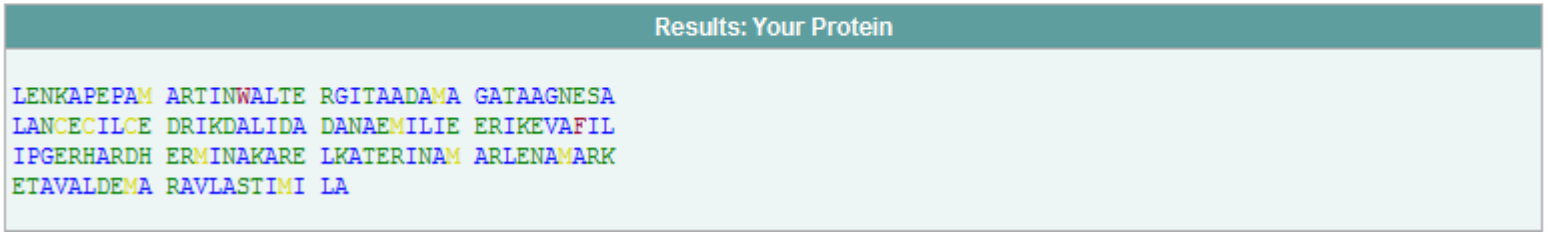
SUBMIT CLEAR

Vyznačte v sekvenci všechny tryptofany, tyrosiny a cysteiny.

Protein Colourer

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





Obarvěte 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 RSVRSLLEEA FADEMEKTSY
 41 DVEVADTPQP HIPIRFRHPP IAGPVHDVFG DAIHDIFQKM
 81 MKRGQAVDFC HWVSHLIATE IDEKFSEVAF RDVQYNPDIY
121 VTDSTTEAKK LFNDKIWPAI DKILQQNAET CPILSEKWSG
161 IHVSGDQLKG QRHKQEDRFL AYPNGQYMDR GEDPISVLAV
201 FDGHGGHECS QYAAGHLWET WLEVRKSRDP SDSLEDQLRK
```

Please check the browser compatibility page before using this program.

Submit Clear Reset

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 cgctttgcca actgtacacc caacctcggt
 41 ttattgtcga acctcccgct tgtgccgcca tctgcatata
 81 gatcccggtc agtccgtcac attctgccaa ttgagtatcc
121 tcgaagtctt attccacgtg ctcaaagcaa gggtatcgta
161 cagtgataac cgcctcgtgc agatccaaat tctcgattaa
201 cactcaagta ctgattttta tcatcaggta actaaaaact
```

Please check the browser compatibility page before using this program.

Submit Clear Reset

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.

Submit | Clear | Reset

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.

Submit | Clear | Reset

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

20 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
RGITAADAMAGATAAGNESA
LANCECILCEDRIKDALIDA
DANAEMILIEERIKEVAFIL
IPGERHARDHERMINAKARE
LKATERINAMARLENAMARK
ETAVALDEMARAVLASTIMI
LA*
```

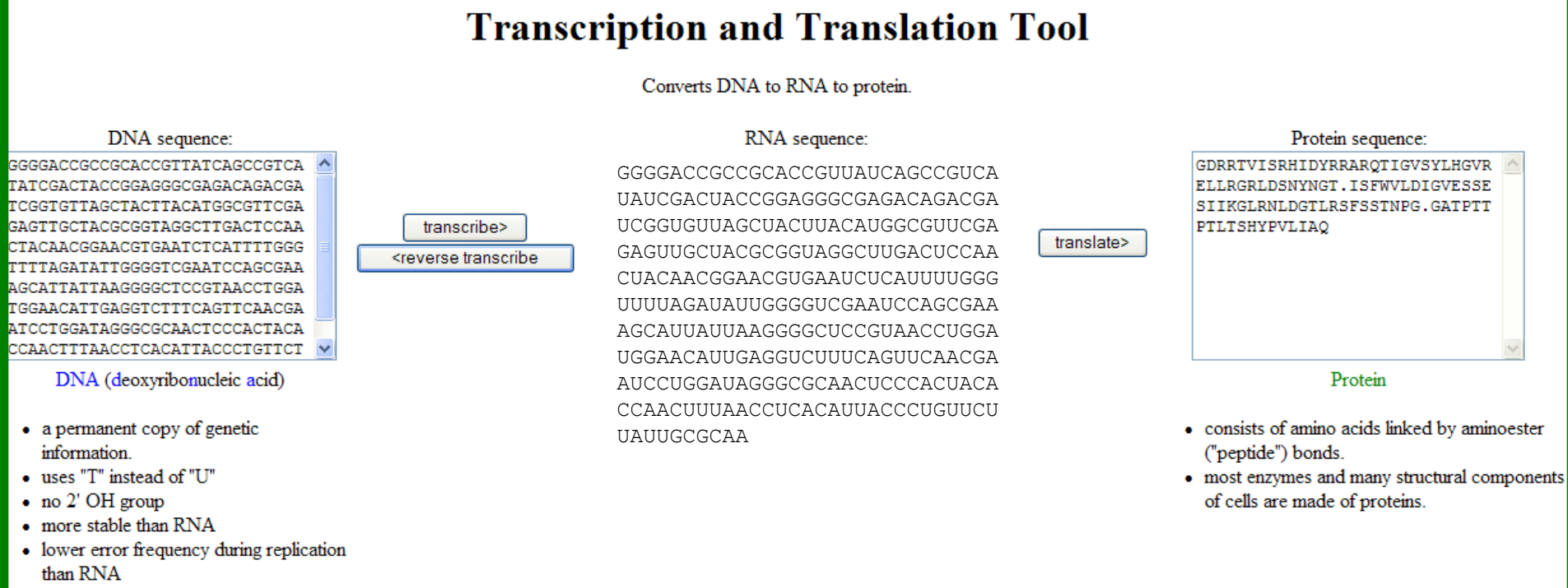
Three letter sequence:

> 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



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.

Submit | Clear | Reset

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: GERQKWFIPVYWF | Draw Peptide | Help

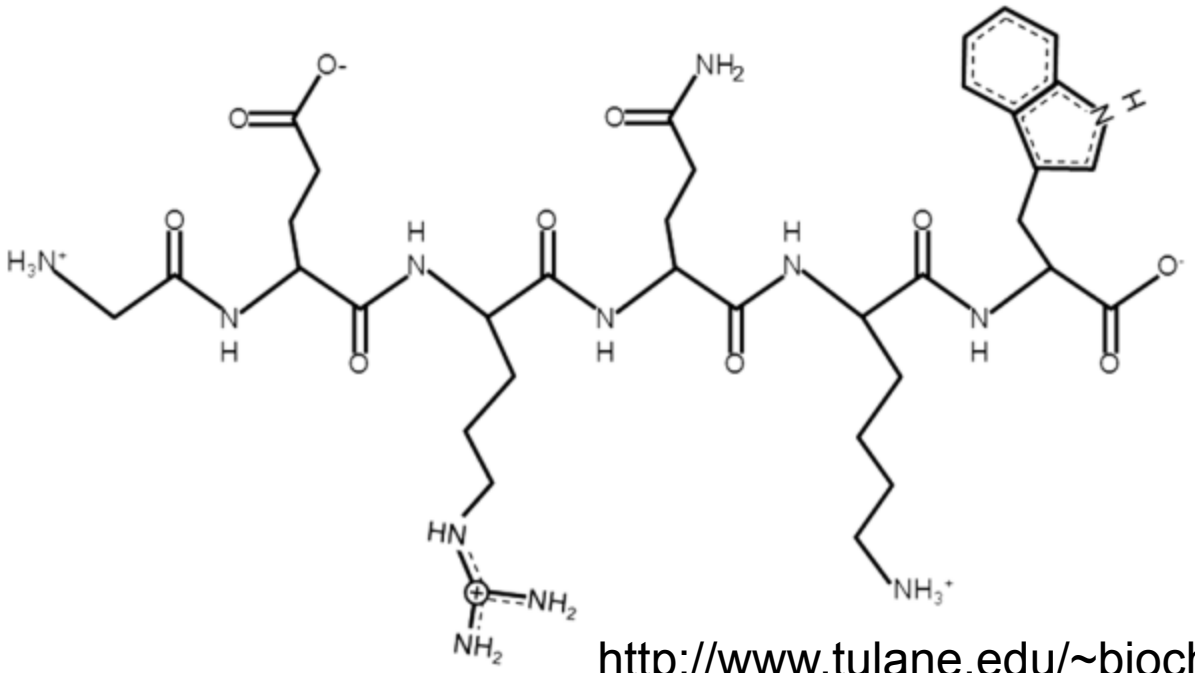
Amino Acid Keypad

Ala (A)	Arg (R)	Asn (N)	Asp (D)	Cys (C)
Gln (Q)	Glu (E)	Gly (G)	His (H)	Ile (I)
Leu (L)	Lys (K)	Met (M)	Phe (F)	Pro (P)
Ser (S)	Thr (T)	Trp (W)	Tyr (Y)	Val (V)

Peptide properties

Sequence:	GERQKWFIPVYWF
Length:	13
Mass:	1754.8906
Isoelectric point (pI):	9.59
Net charge:	+1
Hydrophobicity:	+8.31 Kcal * mol $^{-1}$
Extinction coefficient[1]:	12490 M^{-1} * cm^{-1}
Extinction coefficient[2]:	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 2vnv considered as Asymmetric unit *Examples: 3ert, 1ttu, 1naq*

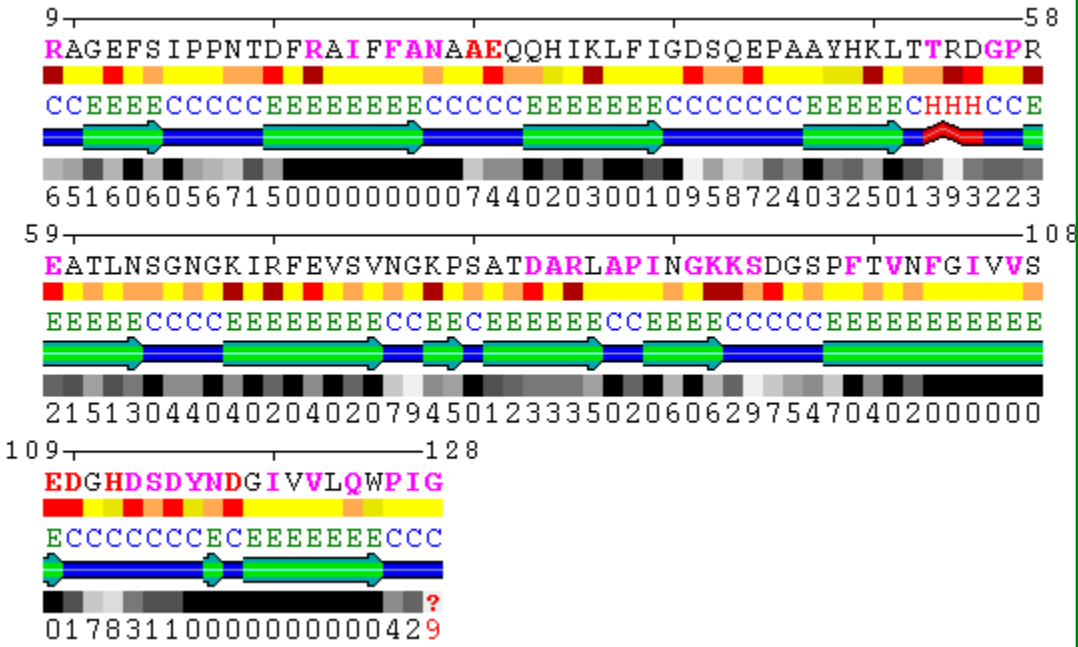
Get ID by keyword Find

Custom structure in the PDB format

File Browse...

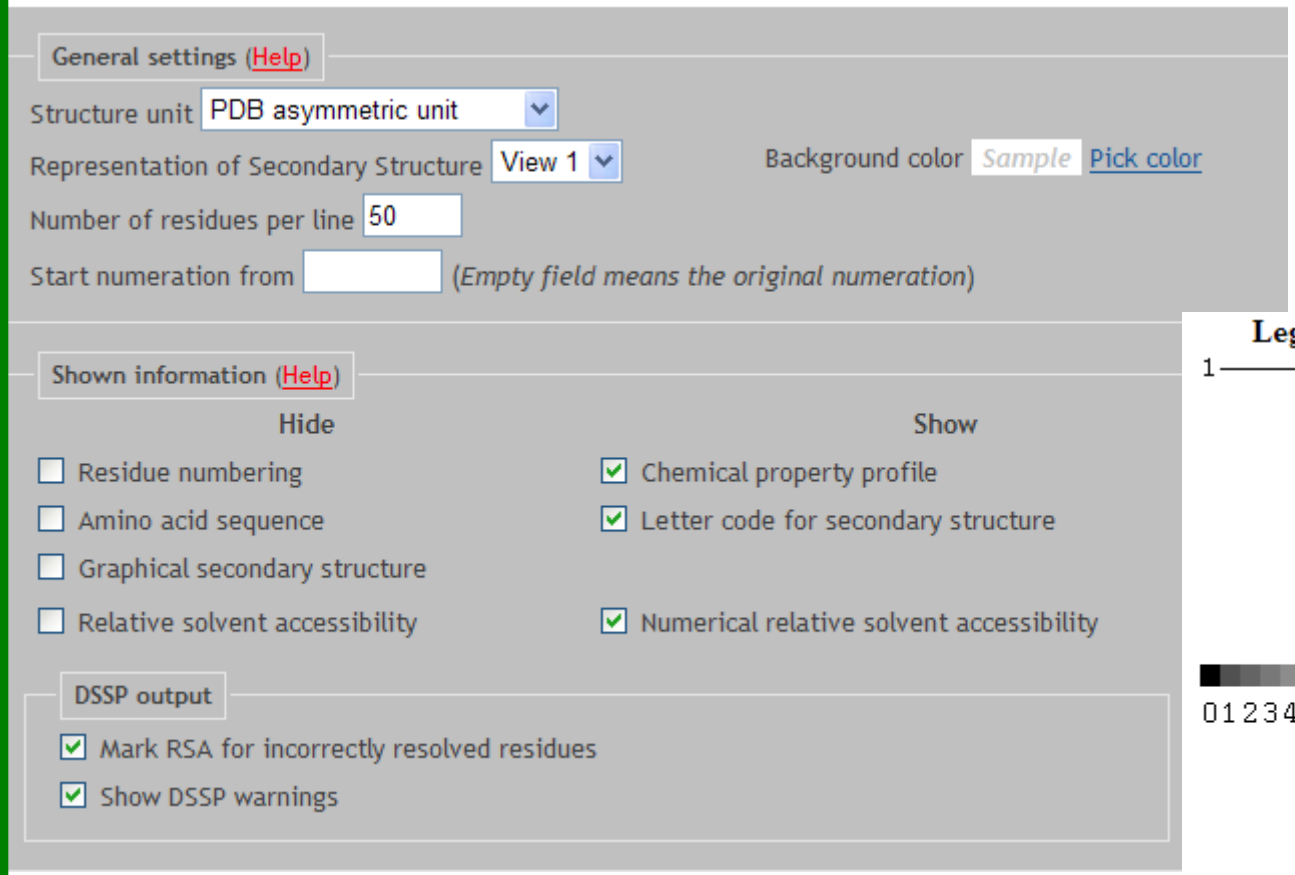
☐ Given coordinate file represents a multi-model structure, such as NMR (e.g., PDB ID 2kmv, 2kcj), morph (example), or low-frequency motion (example)

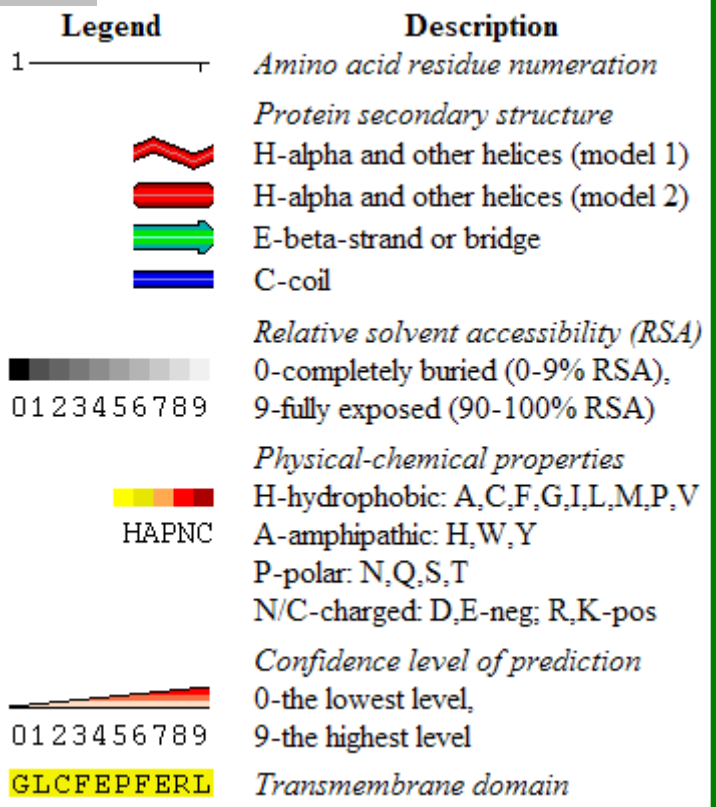
⊟ Structural Data from Predictions (Help)

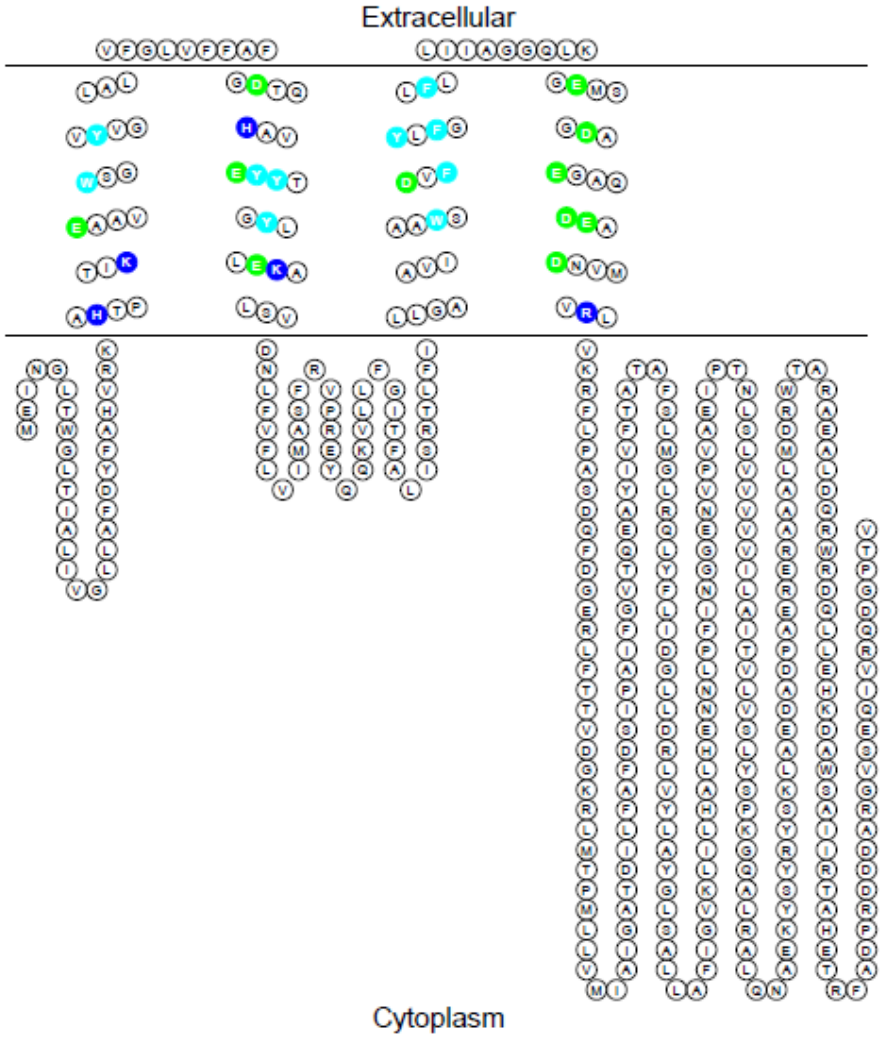


POLYVIEW

http://polyview.cchmc.org/







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

700 Protein length 0.8 Horizontal scale

Domain data

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

100 ,200 , 1
320 ,      1
```

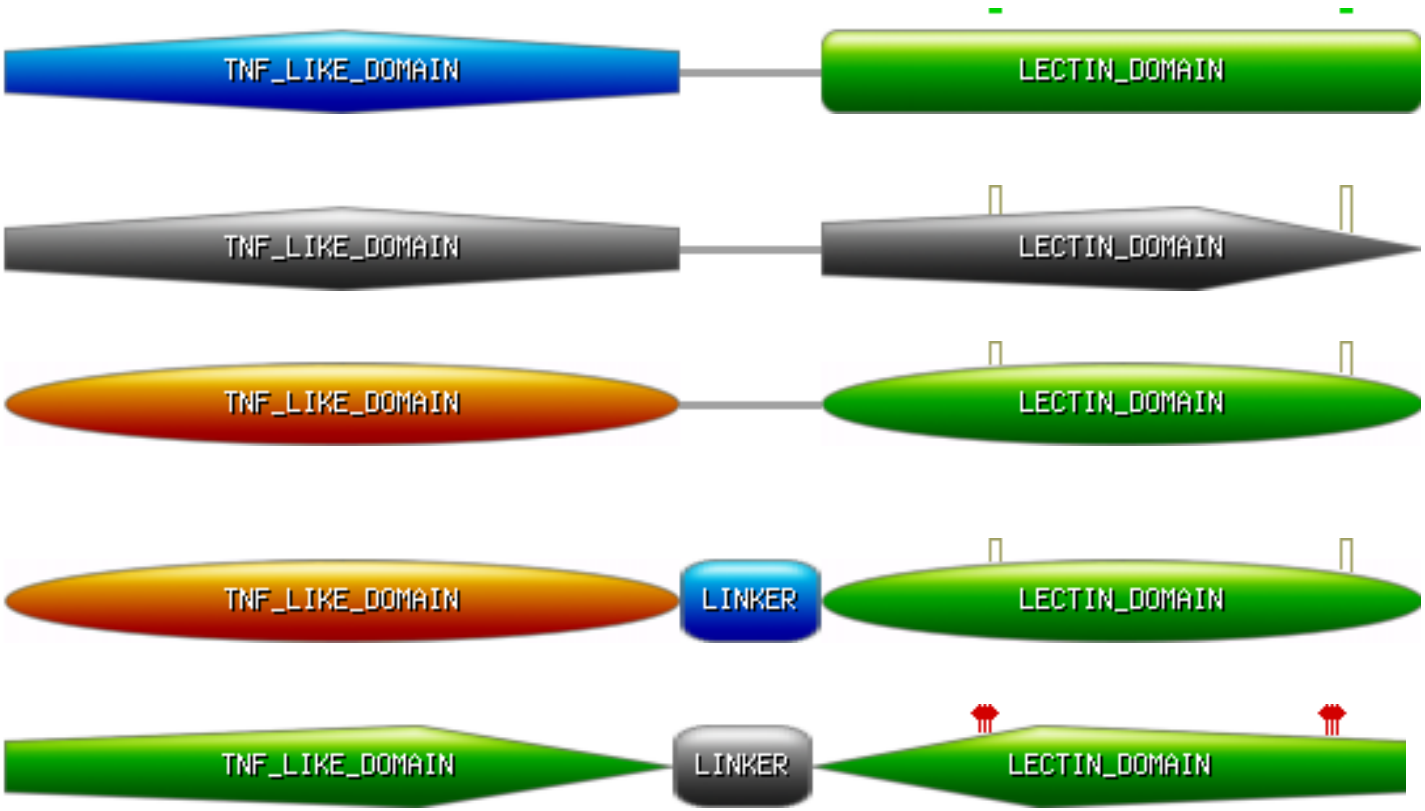
- To add a **domain**: `start, stop, shape, color, text`
  - Shape is any number between 1 and 6:
  - Color is any number between 1 and 4:
- To add a **range**: `start, stop, type`
  - Type is 0 or 1:
- To add a **site**: `position, type`
  - Type is 0 or 1:

DRAW see result right below

undo changes

PLLSASIVSAPVVTSETYVDIPGLYLDVAKAGIRDGKLQVILNVPTPYATGNNFPGIYFAI
ATNQGVVADGCFTYSSKVPESTGRMPFTLVATIDVGSGVTFVKGQWKSVRGSAMHIDSYAS
LSAIWGTAAPSSQGSGNQGAETGGTGAGNIGGGG**ERDGTFNLPPHIKFGVTALTHAANDQT**
IDIYIDDDPKPAATFKGAGAQDQNLGTKVLDSGNGRVRVIVMANGRPSRLGSRQVDIFKKS
YFGIIGSEDGADDDYNDGIVFLNWPLG

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



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
```

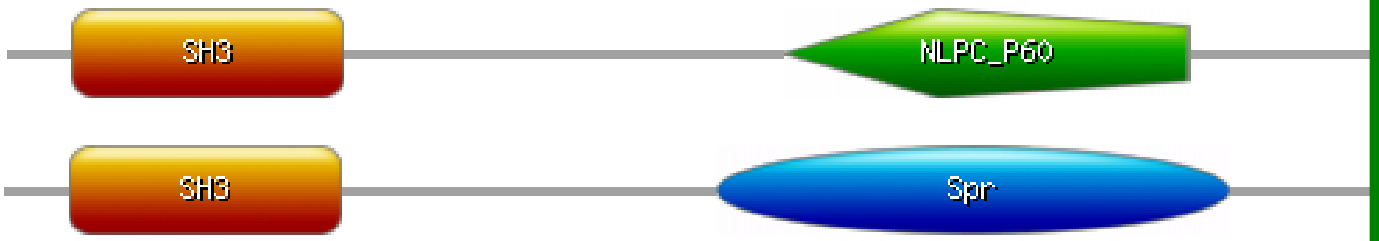
- To add a **domain**: `start, stop, shape, color, text`
  - Shape is any number between 1 and 6:
  - Color is any number between 1 and 4:
- To add a **range**: `start, stop, type`
  - Type is 0 or 1:
- To add a **site**: `position, type`
  - Type is 0 or 1:

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
ORIGIN
        1 mkdnyfykkp lsniykkpna fsevtsqily gekfkiiskn knwikikvsf dnytgyiknk
       61 yytkdhqpth kiftlkaniy nkqknktknf lpfasrismi denkkfiefe knkwikkkdi
      121 kkinhiekdy lkvlkmflki kylwggktyr gidcsailql ffyynnkfyp rdtkdqikys
      181 akknkskvfk kgdiifwkgh vavcinaqkl ihaygpekkv limniketin riertakltv
      241 kkispiky
//
```

Vytvořte „doménové schéma“ proteinu.



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        LVIVDAVTLLSAYPEASRDPAAPTVIDGRHLYVVSPGDA
BCLC        -------PLLSASIV-----SAPV--VTSETYVDIPGLY
PA-IIL      ----------------------------------------


BCLA        ----------------------------------------
BCLD        QLHLRETALALRAEVSVLFIRFALKDAGIVAPIELEVRD
BCLC        ------TPYATGNNFPGIYFAIA-TNQGVVADGCFT---
PA-IIL      ----------------------------------------


BCLA        ----------------------------------------
BCLD        HPSCRPLKDHYWRSDVLAAGATTCTADFAVCDRDGTVSG
BCLC        VGSGVTFVKGQWKSVRGSA---M--------HIDSYASL
```

```
CLUSTAL O(1.2.1) multiple sequence alignmentBCLA      ------------------------
-----------------------------------BCLD
LVIVDAVTLLSAYPEASRDPAAPTVIDGRHLYVVSPGDAA---QLGHNDSRLFTGLSPGDBCLC
 -------PLLSASIV-----SAPV--VTSETYVDIPGLYLDVAKAGIRDGKLQVILNVP-PA-IIL     -
------------------------------------------------------------
                                BCLA      ---------------------------------------
-------------------BCLD
QLHLRETALALRAEVSVLFIRFALKDAGIVAPIELEVRDAATAVPDADDLL---------BCLC      -
-----TPYATGNNFPGIYFAIA-TNQGVVADGCFT---YSSKVPESTGRMPFTLVATIDPA-IIL
------------------------------------------------------------
                                BCLA      ---------------------------------------
--------------------BCLD
HPSCRPLKDHYWRSDVLAAGATTCTADFAVCDRDGTVSGYFRWETSIEIA-GS------QBCLC
 VGSGVTFVKGQWKSVRGSA---M--------HIDSYASLSAIWGTAAPSSQGSGNQGAETPA-IIL
  ------------------------------------------------------------
                                   BCLA      -----
ADSQTSSNRAGEFSIPPNTDFRAIFFANAAEQQHIKLFIGDSQEPAAYHKLTTRDBCLD
PDTKQPGFKPSSDRNGNFSLPPNTAFKAIFYANAADRQDLKLFIDDAPEPAATFVGNSEDBCLC
 GGTGAGNIGGGGERDGTFNLPPHIKFGVTALTHAANDQTIDIYIDDDPKPAATFKGAGAQPA-IIL
  -----------ATQGVFTLPANTRFGVTAFANSSGTQTVNVLVNNE--TAATFSGQSTN
           * *.:* .  * .  :.::  * :.: : :   ** .    :BCLA      GPRE--ATLNSG-
NGKIRFEVSVNGKPSATDARLAPINGKKSDGSPFTVNFGIVVSEDGHBCLD      GVRL--
FTLNSK-GGKIRIEASANGRQSATDARLAPLSAGD------TVWLGWLGAEDGABCLC
DQNLGTKVLDSG-NGRVRVIVMANGRPSRLGSRQVDIFK--------KSYFGIIGSEDGAPA-IIL
NAVIGTQVLNSGSSGKVQVQVSVNGRPSDLVSAQVILTN--------ELNFALVGSEDGT
    .*:*   *:::. . .**: *   :  . :          :. : :*** BCLA      DSDYNDGIVVLQWPIG
BCLD      DADYNDGIVILQWPITBCLC      DDDYNDGIVFLNWPLGPA-IIL
DNDYNDAVVVINWPLG          * ****.:*.::**:
```

BoxShade

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

Output format: Postscript_portrait

Font Size: 10

Consensus Line: no consensus line

- no consensus line
- consensus line with letters
- consensus line with symbols

Fraction of sequences: 0.5 (that must agree for shading)

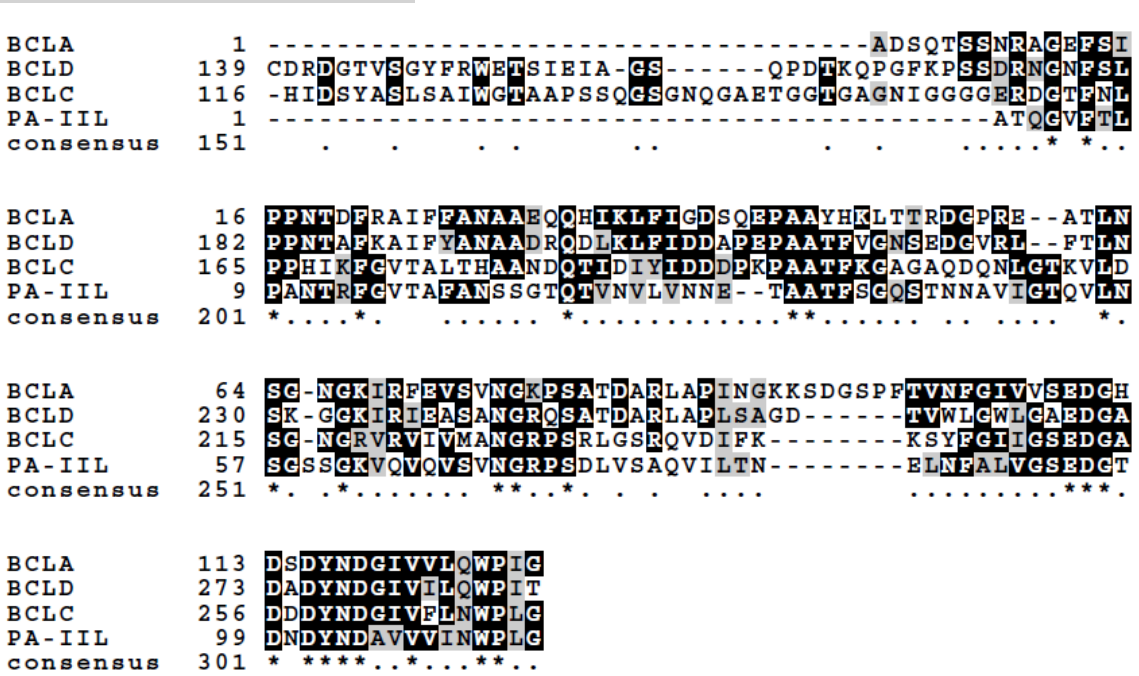
Enter sequence number: only if 'consensus to a single sequenc

Query title (optional):

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

Input sequence format: ALN

Paste your multiple-alignment file

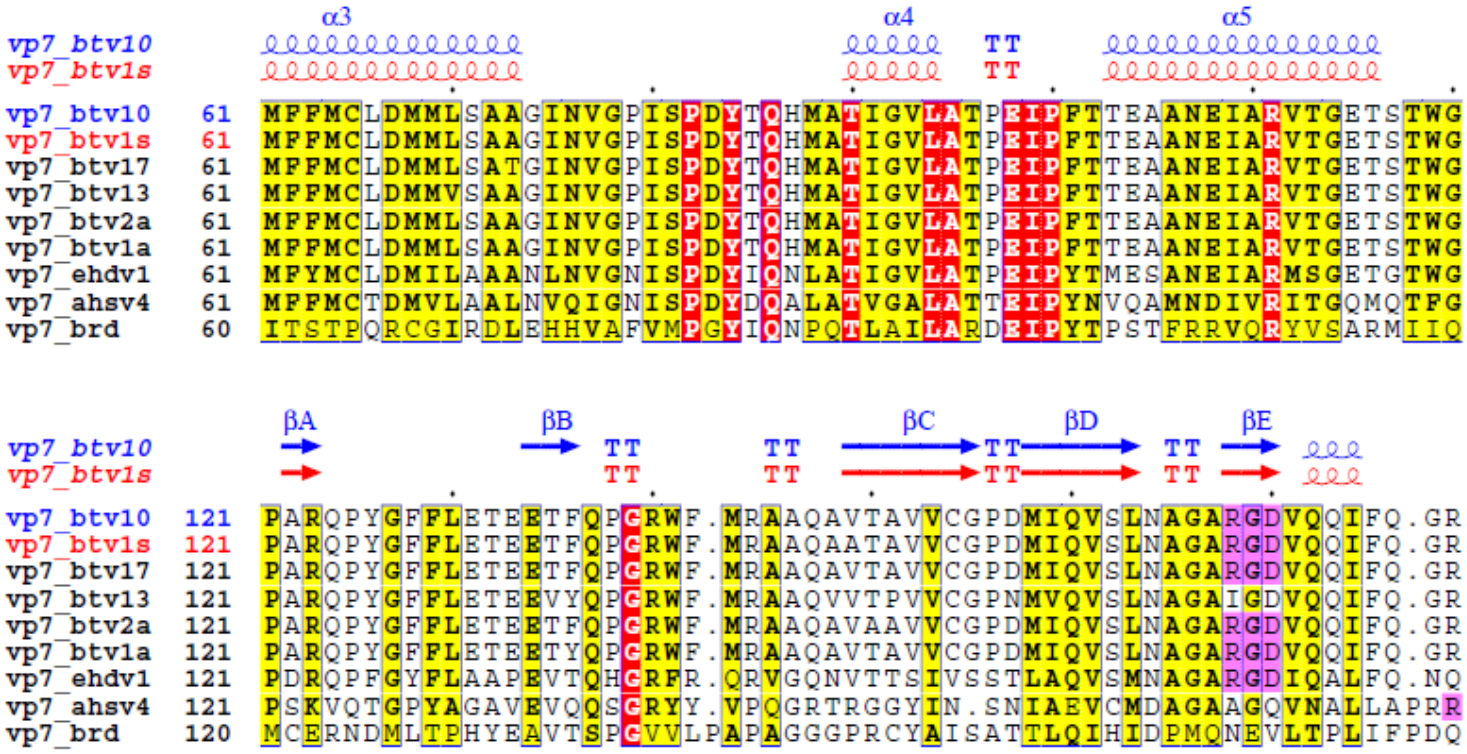


ESPript 3

http://espript.ibcp.fr/ESPript/ESPript/

What is ESPript?

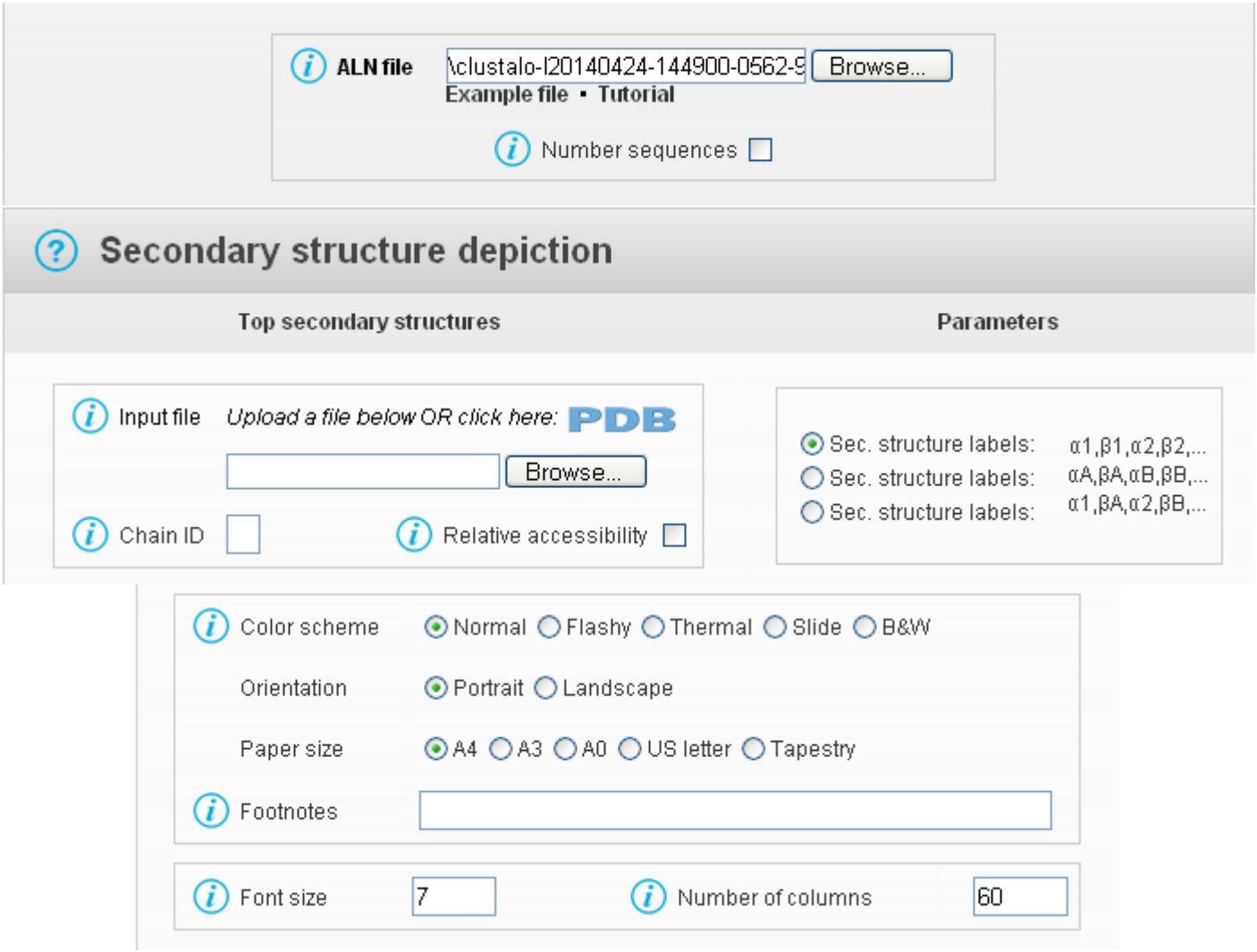
- **ESPript**, *'Easy Sequencing in PostScript'*, is a program which renders sequence similarities and secondary structure information from aligned sequences for analysis and publication purpose.



ESPript 3.0

ESPript 3

http://espript.ibcp.fr/ESPript/ESPript/



ESPript 3

http://espript.ibcp.fr/ESPript/ESPript/