C-Scanner - Operation Manual

Content:

What is C-Scanner?

The C-Scanner allows you to rank the selected epitopes (or any other peptide sequences) according to their complexity.

When selecting epitope sequences using various software (EpiQuest-B, A or other platforms) you would like to end up with a *unique* epitope – whether you plan developing a specific antibody or using this peptide epitope as an antigen in antibody assays.

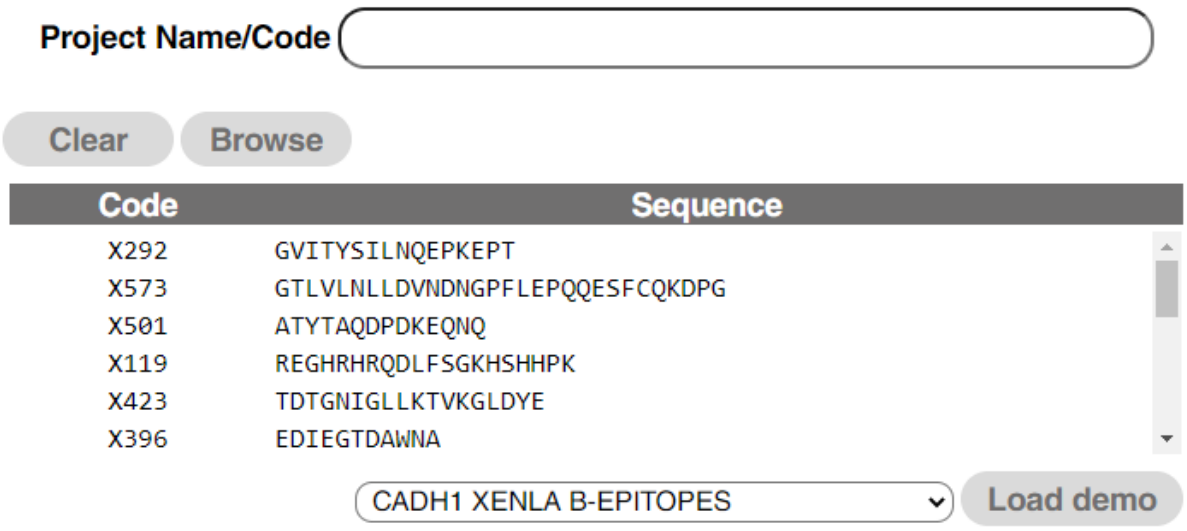
The C-Scanner allows you to scan a group of peptide sequences and determine the most unique ones. Uniqueness of epitopes greatly define the specificity of an antibody prepared against it i.e. the sequences with low complexity will likely be present in proteins other that the target one.

The software also allows you to define a shorter, more specific, sequence within the long epitope sequences, and thus ensure the specificity of epitope used in your antibody or assay development project.

Species specificity

The matrix C1.3 is based on the complexity of proteins in *higher mammals.* Sequences from i.e. lower invertebrates, fungi, etc. may receive a lower overall score in comparison to mammals, but still, the scanning allows you to establish the most unique sequences. Whether making an antibody or looking for epitopes recognised by natural antibodies, we aim to look at the immune response in higher mammals, so the uniqueness of the tested epitopes should be defined for these types of animals.

Entering the Data



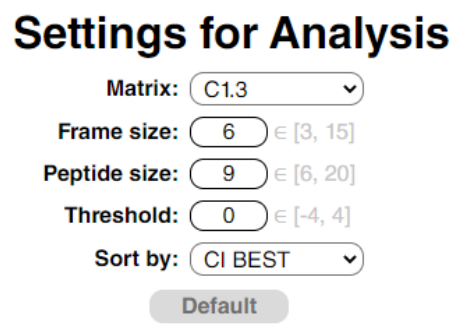
To test the program, select Demo sequences and click ***Load demo***. In the window for sequences the two columns will appear: ***Code*** and ***Sequence***.

To empty the window, click ***Clear***.

To load your own data, it should be presented in ***XLS*** or ***XLSL*** format (MS-***Excel***) and to contain only *one dataset* with data per file. The data should be presented as two columns. The first should be named and contain ***Code*** (just your number or other identifier for the peptide; we do not recommend going above 15 signs, letters, numbers, and dash signs allowed) and ***Sequence*** (sequences of the peptides to be tested in a single letter code; we do not recommend going above 100 amino acids each,).

You may ***Browse*** for the location of the file and click on it to load.

Settings for Complexity analysis



Currently only one ***Matrix*** C1.3 – is available.

You can adjust your cut-off level for weak/functionally negative epitopes by changing the ***Threshold*** (positive numbers to decrease the sensitivity, negative – to increase). We do not recommend going beyond (-2) or (+2).

Frame size defines the size of the context analysed for every position in the sequence, we recommend keeping it at 6 (the default value).

Peptide size defines the size of epitope you are looking for in your peptides. If the tested sequences are of different length (i.e. your data set includes 10-mers, 20-mers, other), we recommend keeping it at 9, since very few epitopes and practically none of the specific ones are shorter than 9 amino acids. In case you wish to compare a set of peptides of different length and to select the best of them, set the size of the shortest one as the reported peptide size.

Sort by. You can select the data to be reported in several ways:

Start: the results will be sorted according to the order of the analysed peptides in your data file. If you analyse 19-20 mers and have defined the *Peptide size* as 9, your results will contain multiple 9-mers for every original peptide with AGI (antigenicity) defined for every 9-mer. In Results the data will be sorted according to the order of the peptide in the original sequence.

View Save **Report for "Analysis of epitopes complexity":**

Code	Sequence	Start	End	Peptide	CI	CPB
X292	GVITYSILNQEPKEPT	1	9	GVITYSILN	*90*	*10*
X292	GVITYSILNQEPKEPT	2	10	VITYSILNQ	*57*	*6*
X292	GVITYSILNQEPKEPT	3	11	ITYSILNQE	*21*	*2*
X292	GVITYSILNQEPKEPT	4	12	TYSILNQEP	*-12*	*-1*
X292	GVITYSILNQEPKEPT	5	13	YSILNQEPK	*-37*	*-4*
X292	GVITYSILNQEPKEPT	6	14	SILNQEPKE	*-55*	*-6*
X292	GVITYSILNQEPKEPT	7	15	ILNQEPKEP	*-63*	*-7*
X292	GVITYSILNQEPKEPT	8	16	LNQEPKEPT	*-63*	*-7*

CI: all results will be sorted according to the order of the analysed peptides in the data file, for every analysed sequence they will be presented from the best to the worst.

CI ALL: the results will be sorted according to the AGI values of the detected peptides of the defined peptide length (say, 9) irrespective of their origin from different original sequences, from the best to the worst.

View Save **Report for "Analysis of epitopes complexity":**

Code	Sequence	Start	End	Peptide	CI	CPB
X669	NVTKLHITICQ	1	9	NVTKLHITI	*162*	*18*
X669	NVTKLHITICQ	2	10	VTKLHITIC	*155*	*17*
X852	ALNDWGPRFTKLADMYGGDED	1	9	ALNDWGPRF	*146*	*16*
X852	ALNDWGPRFTKLADMYGGDED	2	10	LNDWGPRFT	*139*	*15*
X669	NVTKLHITICQ	3	11	TKLHITICQ	*137*	*15*
X852	ALNDWGPRFTKLADMYGGDED	3	11	NDWGPRFTK	*135*	*15*
X852	ALNDWGPRFTKLADMYGGDED	4	12	DWGPRFTKL	*125*	*13*
X852	ALNDWGPRFTKLADMYGGDED	5	13	WGPRFTKLA	*102*	*11*

CI BEST: the data will be presented by *only* the best peptide form every sequence in the order from the highest to the lowest (here only 1 9-mer is shown for the original 4 peptides of various lengths.

View Save **Report for "Analysis of epitopes complexity":**

Code	Sequence	Start	End	Peptide	CI	CPB
X669	NVTKLHITICQ	1	9	NVTKLHITI	*162*	*18*
X852	ALNDWGPRFTKLADMYGGDED	1	9	ALNDWGPRF	*146*	*16*
X292	GVITYSILNQEPKEPT	1	9	GVITYSILN	*90*	*10*
X423	TDTGNIGLLKTVKGLDYE	8	16	LLKTVKGLD	*82*	*9*
X634	AIVTGQSILELRP	1	9	AIVTGQSIL	*60*	*6*
X158	SENEKGPFPKRI	4	12	EKGPFPKRI	*59*	*6*
X119	REGHRHRQDLFSGKHSHHPK	3	11	GHRHRQDLF	*57*	*6*
X396	FDTEGTDAWNA	1	9	FDTEGTDAW	*57*	*6*

Viewing and saving the Results

You may ***View*** all results in new window or ***Save*** them for your records as HTML file. You can always import such file into your spreadsheet program or simply copy the selected areas of interest in other file formats.

Report: Relative complexity of epitopes (C-Scanner)

Date & Time: 05.11.2020 19:08:51
Project name:
Program: EpiQuest C-Scanner v1.0.0.1
Matrix: C1.3
Peptide size: 9
Frame size: 6
Threshold: 0
Sorted by: CI BEST

Code	Sequence	Start	End	Peptide	CI	CPB
X669	NVTKLHITICQ	1	9	NVTKLHITI	*162*	*18*
X852	ALNDWGPRFTKLADMYGGDED	1	9	ALNDWGPRF	*146*	*16*
X292	GVITYSILNQEPKEPT	1	9	GVITYSILN	*90*	*10*
X423	TDTGNIGLLKTVKGLDYE	8	16	LLKTVKGLD	*82*	*9*
X634	AIVTGQSILELRP	1	9	AIVTGQSIL	*60*	*6*
X158	SENEKGPFPKRI	4	12	EKGPFPKRI	*59*	*6*
X119	REGHRHRQDLFSGKHSHHPK	3	11	GHRHRQDLF	*57*	*6*
X396	EDIEGTDAWNA	1	9	EDIEGTDAW	*57*	*6*
X786	PQYRPRPANPDEIGNFIDENLN	10	18	PDEIGNFID	*50*	*5*
X753	GEEDQDFDLSQLHRGLDARP	4	12	DQDFDLSQL	*43*	*4*
X85	YIKNPAKMKD	1	9	YIKNPAKMK	*37*	*4*
X573	GTLVLNLLDVNDNGPFLEPQQESFCQKDPG	21	29	QESFCQKDP	*20*	*2*
X360	VMDTNDNPPVFD	4	12	TNDNPPVFD	*15*	*1*
X242	IIIKVQDQN	1	9	IIIKVQDQN	*-13*	*-1*
X501	ATYTAQDPDKEQNQ	1	9	ATYTAQDPD	*-15*	*-1*
X726	KKVVKEPLL	1	9	KKVVKEPLL	*-21*	*-2*
X834	ASLSSLNSPNSDLDQDY	9	17	PNSDLDQDY	*-25*	*-2*

Demo Sequences

For Demo, we supply several files with either tested selections of epitopes or selected sets of sequences for training.