



CPRISMA

COLORING PROTEINS BY INPUTS AND
SETS OF MULTIPLE ALIGNMENTS

CPRISMA USER'S GUIDE

Version 1.0

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DESCRIPTION

CPRISMA is a bioinformatics program that gives color to multiple sequence alignment based on an input of numerical data.

LICENSE

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1 Introduction

CPRISMA (**C**oloring **P**Roteins by **I**nputs and **S**ets of **M**ultiple **A**lignments) is a command-line program designed to give color to protein multiple sequence alignments. CPRISMA was written in Python language and runs on Unix systems. Since we often want to compare sets of numerical protein variables at the primary structural level, CPRISMA is an ideal program to visualize and/or detect possible differences in specific amino acids or protein regions through a color palette. CPRISMA is a versatile tool that allows the user to incorporate the features that are more convenient to highlight.

The development of this program was inspired by previous studies where we sought to highlight regions for the non-structural (NS) protein 1 from several *Flavivirus* with particular physical-chemistry or structural behavior [1, 2, 3]. We thought it would be interesting to have a capable tool to make relationships between numerical information and sequence alignments, but for any external data set.

In this documentation, we have divided the Chapters following a logical order and using practical examples to understand each CPRISMA parameter. In Chapter 2, the installation/uninstallation and the type of input and output (I/O) files needed to run a simulation in CPRISMA will be treated. Chapter 3 will describe the basic functions, and Chapters 4, 5, 6, and 7 more complex variables. These six Chapters, we used as examples the NS1 proteins from Zika virus (ZIKV), Dengue variant 2 (DENV2), and West Nile viruses (WNV). Regarding ZIKV, we employ two strains from Uganda (UG) and Brazil (BR). Finally, in Chapter 8, we show three practical examples that correlate directly with three publications where we explored *i*) p*K_a* shifts for several NS1_{ZIKV} [1], *ii*) B-cell epitope prediction for NS1_{WNV(176–352)} [2], and *iii*) the structural domains and biological interfaces for two ZIKV NS1 proteins [3].

Command lines, alert messages, or variables will be distinguished with the **Typewriter** font. Also, when a particular word/letter is preceded by a hyphen (-) in any title of this documentation it should be interpreted as a line command, otherwise, it should be interpreted



as a variable.

The current developer of CPRISMA is Sergio Alejandro Poveda Cuevas at the [Laboratory of Computational Biophysical Chemistry](#) (University of São Paulo). If you have any suggestions, bug reports, or general comments about CPRISMA, please contact us at seapovedac@gmail.com.



2 Setup

2.1 Installation/unistallation

To install CPRISMA you must directly download the code from the GitHub repositories <https://github.com/seapovedac/cprisma/> or by executing the following command:

```
git clone https://github.com/seapovedac/cprisma.git
```

Then, you can invoke in that directory:

```
pip install .
```

Now your program should be in the OS environment variables. Typing in the terminal:

```
cprisma1
```

or

```
python -m cprisma
```

should return an error, requesting one of the input files for execution. If you want to be sure that there are no problems with the program, you can try to generate outputs from the “examples” directory.

To uninstall the program you can simply do it through the following command:

```
pip uninstall cprisma
```

2.2 Inputs

To run CPRISMA, a basic knowledge of Python is required, so a good understanding of the data types that this language uses (*e.g.* sets, tuples, lists, etc.) is essential to achieve the

¹We will use this command throughout the documentation.



desired results².

Hereafter, we will use as an example a data set of pK_a 's³ for four NS1 from ZIKV (two different strains), DENV2, and WNV. Protein sequences were extracted from the NCBI (National Center for Biotechnology Information)⁴, and have the next accession codes: AY632535 (ZIKV-UG), KU365777 (ZIKV-BR), PR159-S1 (DENV2), and Q9Q6P4 (WNV). We will only take into account incomplete sequences (from residues 1 to 120) and the focus will be given to the titratable residues: Asp, Glu, Arg, His, Lys, and Tyr. Cys residues are not included, due to the fact that they are part of disulfide bridges.

⁵CPRISMA is a program that requires at least three file kinds in the run directory⁵:

1. The alignment to put the color called “alignment.dat”.
 2. A CSV file called “data_input.csv”.
 3. A Python script called “array_get.py”.

ZIKV-UG	DVGCSVDFSKKETRCGTVFIYNDVEAWRDRKYHPDSPRLLAAVKQAAWEEGICGISSV
ZIKV-BR	DVGCSVDFSKKETRCGTVFVYNDVEAWRDRKYHPDSPRLLAAVKQAAWEDGICGISSV
DENV2	DSCGVVSWKNKELKCGSGIFITDNVHTWEQYKFQPESPSSLASAIQKAHEEGICGISSV
WNV	DTGCAIDISRQLERCMSGVFIHNDVEAWMDRYKYYPTPQGLAKIIQKAHEGVCGLRSV
	* * * . . . * . * : * : * . : * : * . : * : * . : * : * . : * : * . : *
ZIKV-UG	SRMENIMWKSVEGELNAILEENGVQLTVVVGSVKNPWMWRGPQRLLPVVNELPHGWKAWGK
ZIKV-BR	SRMENIMWRSVEGELNAILEENGVQLTVVVGSVKNPWMWRGPQRLLPVVNELPHGWKAWGK
DENV2	TRLENLWMWKQTIPELNHLISENEVKLTIMTGDIGKQMAGKRSLRPQPTELKSYWSKTWKG
WNV	SRLHQMWAVEAVKDELNTLKLKENGVDSLSSVVEKQEGMYKSAKRLTATTEKLEIGWKAWGK
	* : * : * . * . : * : * . : * : * . : * : * . : * : * . : * : * . : *

Figure 2.2.1: MUSCLE output in ClustalW format.

In addition to these files, others directories will appear (*e.g.*, “cprisma”, “examples”, so on), which contain all the scripts and other stuff necessary for the program. For now, let us focus on the three files mentioned above. To get the alignment data, you can directly go to the website program called MUSCLE (MULTiple Sequence Comparison by Log-Expectation)⁶ and run it with the FASTA format protein sequences of your interest. You can modify the input parameters as wanted, nevertheless, it is essential that you keep ClustalW as the output format. You can also generate these multiple sequence alignments by invoking MUSCLE

²See also the official Python documentation: <https://docs.python.org/3.7/>.

³pK_a's were obtained through charges of ionizable residues calculated by Monte Carlo simulations [4, 5].

⁴ See <https://www.ncbi.nlm.nih.gov/>.

⁵These files can be found in the directory “examples/Example_0”.

⁶See <https://www.ebi.ac.uk/Tools/msa/muscle/>.



through Biopython⁷. A typical MUSCLE result appears in Figure 2.2.1. All the details about this type of output is previously described [6]. An improper alignment format can produce the following output:

The program stop! Improper alignment format. Check ClustalW format at <https://www.ebi.ac.uk/Tools/msa/muscle>.

	ZIKV-UG		ZIKV-BR		DENV2		WNV	
	A	B	C	D	E	F	G	H
1								
2	ASP	3.9	ASP	3.9	ASP	3.8899	ASP	3.7834
3	ASP	3.09737	ASP	3.38668	LYS	10.48393	ASP	3.39189
4	LYS	10.89431	LYS	10.99729	LYS	10.58842	ARG	12.78243
5	LYS	10.68626	LYS	10.69875	GLU	3.79962	GLU	3.99138
6	GLU	3.77967	GLU	3.98917	LYS	10.67679	ARG	12.39385
7	ARG	12.58017	ARG	12.2972	ASP	3.39033	HIS	6.69314
8	TYR	9.97794	TYR	9.98935	HIS	6.77441	ASP	3.58575
9	ASP	3.49226	ASP	3.79508	GLU	4.08867	GLU	4.38775
10	GLU	3.99375	GLU	4.09717	TYR	9.98403	ASP	3.48066
11	ARG	12.5932	ARG	13.38161	LYS	10.9964	ARG	12.89923
12	ASP	3.09964	ASP	2.68828	GLU	3.99943	TYR	9.79223
13	ARG	13.28718	ARG	12.97763	LYS	11.08543	LYS	11.18316
14	TYR	9.59769	TYR	9.59592	LYS	10.88321	TYR	10.19568
15	LYS	11.08461	LYS	10.99773	HIS	6.3864	TYR	9.49347

Figure 2.2.2: Data input with pK_a values for four proteins. All the information has not been shown.

Our second type of file with CSV extension is the numerical data that will be used as a basis for defining the color. Figure 2.2.2 shows an example of how this file should be. We are working with residues up to position 120, however, Figure 2.2.2 does not show all the charged amino acids up to that position. Each system is divided into 2 columns where the information on the residue kind (with code of three letters in capital) and the numerical value (in our case pK_a) will be contained.

Note: If, for example, you eliminated the pK_a value of 2.68828 from row 12 and column D, CPRISMA will consider the absence of it as equal to 0.

Notice that there are 4 data sets for the 4 systems. In our example, the absence of any 8

⁷For more details: <https://biopython.org/docs/1.75/api/Bio.Align.Applications.html>.



columns in the CSV file can return the following error message:

The program stop! Number of columns are not complete in data_input.csv.

```
def array_get():
    # Tuple of residues
    target_residues = ()

    # Tuple of sequences name
    name_sequence = ()

    # Operations
    descriptor_ope = { 'n' }

    # Color
    descriptor_col = { 'nc' }

    # Visualization
    descriptor_vis = { 'ReY', 'DeN', 'LeY' }

    # Maximum restriction
    descriptor_mxr = { 'nr' }

    # Array for comparisons
    dict_ref = {}

    # Array for operations
    dict_ope = {}

    # Array for color
    dict_col = {}

    # Array for visualization
    dict_vis = {}

    # Array for maximum restriction
    dict_mxr = {}

    return target_residues, name_sequence, descriptor_ope, descriptor_col, descriptor_vis, descriptor_mxr, dict_ref, dict_ope, dict_col, dict_vis, dict_mxr
```

Figure 2.2.3: Example of how looks like the Python script “array_get.py”.

On the other hand, the order as each protein appears in the alignment should match with the numerical data of the CSV file. For instance, the first dataset (highlighted by brackets) is related to the first protein (labeled as “ZIKV-UG”) in the alignment sequence and so on.

Note: The program does not have the ability to distinguish which data set each sequence belongs to, so it is your responsibility to put this information in the correct order.

Finally, it is crucial that the first row is empty, as indicated by the arrow in Figure 2.2.2.

Note: Sometimes the numerical data length will not be the same between the systems, however, you can ignore this as long as there is a match regarding the order of appearance between the alignment and numerical data files.

The third type of file is a Python script with the variables that will be used to give different instructions to the program and obtain the desired output (Figure 2.2.3)⁸.

⁸These variables and how they work will be better described in next Chapters.



2.3 Outputs

The two types of output files that CPRISMA generates are a log file called “cprisma.log” which shows relevant data from the comparisons that are made or data directly related to the input parameters, and a HTML file called “alignment.html” where the colored alignment will appear. As we will see later, due to the various features that CPRISMA has, it is better to observe with some examples how these two files work. Besides, it is worth mentioning that all the warning messages or error reports will appear in the log file. Finally, you can generate other types of files with specific commands (see Section [5.15](#)).



3 Basic commands

Our starting point will be the files located in "examples/Example_0". To run CPRISMA, you can simply type `cprisma` in the terminal (at the working directory). Based on the files previously created (*i.e.*, "alignment.dat", "data_input.csv", and "array_get.py"), something you will notice is that a new log file called "cprisma.log" has been generated in your directory. In this file will appear a count of all the amino acids per system registered from "alignment.dat" (Figure 3.0.1). On the other hand, a count of total charged or hydrophobic residues will also show right away (Figure 3.0.2).

--- Number of residues in alignment ---																					
	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	Z
ZIKV-UG	7	8	6	5	3	3	10	11	2	5	6	8	3	2	7	8	3	6	3	14	0
ZIKV-BR	7	9	6	6	3	3	9	11	2	4	6	7	3	2	7	8	3	6	3	15	0
DENV2	4	4	5	3	3	6	10	9	3	10	9	13	3	2	5	10	9	5	2	5	0
WNV	8	6	3	6	3	5	12	10	3	6	10	12	3	1	3	6	6	4	4	9	0

Figure 3.0.1: Amino acid count in the log file. Note that the last column is showing the residue called "Z", this is only a way to identify those residues that do not belong to the 20 essential amino acids.

```
--- Kind of residues in alignment ---  
ZIKV-UG charged=39 ['D', 'E', 'R', 'H', 'K', 'Y', 'C'], hydrophobic=50 ['A', 'I', 'L', 'M', 'F', 'P', 'W', 'V']  
ZIKV-BR charged=39 ['D', 'E', 'R', 'H', 'K', 'Y', 'C'], hydrophobic=50 ['A', 'I', 'L', 'M', 'F', 'P', 'W', 'V']  
DENV2 charged=38 ['D', 'E', 'R', 'H', 'K', 'Y', 'C'], hydrophobic=43 ['A', 'I', 'L', 'M', 'F', 'P', 'W', 'V']  
WNV charged=46 ['D', 'E', 'R', 'H', 'K', 'Y', 'C'], hydrophobic=44 ['A', 'I', 'L', 'M', 'F', 'P', 'W', 'V']  
Number of columns in data_input.csv is ok!
```

Figure 3.0.2: Kind of residues count in the log file.

Note: For our example, in the output shown in Figure 3.0.2 it was considered the Cys residues as charged, and this should not be. Nonetheless, CPRISMA by default counts all charged amino acids without discriminating whether or not Cys' belong to disulfide bridges.

You can see that the log file will report whether the number of columns in the CSV file is equivalent to the number of systems in the alignment file (see the last text in Figure 3.0.2).



Other additional information that appears in the log file will be the numerical data of the CSV file (Figure 3.0.3). Although it may be redundant information because you know about that in advance, what is sought with this is to propose the user a double-check of the numerical data to avoid future problems.

```
--- Information in data_input.csv ---
```

ZIKV-UG	ZIKV-UG_dat	ZIKV-BR	ZIKV-BR_dat	DENV2	DENV2_dat	WNV	WNV_dat
ASP	3.90000	ASP	3.90000	ASP	3.88990	ASP	3.78340
ASP	3.09737	ASP	3.38668	LYS	10.48393	ASP	3.39189
LYS	10.89431	LYS	10.99729	LYS	10.58842	ARG	12.78243
LYS	10.68626	LYS	10.69875	GLU	3.79962	GLU	3.99138
GLU	3.77967	GLU	3.98917	LYS	10.67679	ARG	12.39385
ARG	12.58017	ARG	12.29720	ASP	3.39033	HIS	6.69314
TYR	9.97794	TYR	9.98935	HIS	6.77441	ASP	3.58575
ASP	3.49226	ASP	3.79508	GLU	4.08867	GLU	4.38775
GLU	3.99375	GLU	4.09717	TYR	9.98403	ASP	3.48066
ARG	12.59320	ARG	13.38161	LYS	10.99640	ARG	12.89923
ASP	3.09964	ASP	2.68828	GLU	3.99943	TYR	9.79223
ARG	13.28718	ARG	12.97763	LYS	11.08543	LYS	11.18316
TYR	9.59769	TYR	9.59592	LYS	10.88321	TYR	10.19568
LYS	11.08461	LYS	10.99773	HIS	6.38640	TYR	9.49347
TYR	9.99884	TYR	9.68700	GLU	3.78878	GLU	3.99996
HIS	6.27657	HIS	6.19907	GLU	3.48118	LYS	10.69714

Figure 3.0.3: Numerical data in the log file. All the information has not been shown.

Assuming both the alignment and the numerical data match, the directory would be expected to have another new file called “alignment.html”, which contains the multiple sequence alignment with color. For our example, we will not get this file, instead, it displays the following message:

```
The program stop! Number of target-residues [ZIKV-UG] is not the same in the  
input files. Residue A: 0 (data_input.csv) != 7 (alignment.dat).
```

This error message is telling us that the number of Ala/Alanine residues (or A) for ZIKV-UG is not the same in both the alignment and the numerical data files. This error can be corrected by applying a specific command line, but, we must know the different possible parameters that can be used through CPRISMA at first. Executing:

```
cprisma -h
```



... the following optional arguments will be displayed:

-h --help	show this help message and exit
-v --version	show program's version number and exit
-ns [bool]	rename the sequences based on a tuple
-va [int]	method to visualize the alignment
-j [bool]	join sequences (only available for <code>va = 2</code>)
-hc [bool]	hide the conservation line
-n [int]	change the first and subsequent numbers in the alignment
-l [int]	number of residues per line
-tr [bool]	get a tuple of target-residues
-a [int]	define the accuracy of the input data
-t [bool]	get all information for the different comparisons in log file
-ck [bool]	check reference method
-rf [str]	method to compare sequences ('default', 'pair', 'multiple')
-lco [bool]	display a list of the available colors
-ico [int]	multiply the intensity of the color
-sco [int]	sequence color (when 'ssc' descriptor is applied)
-mco [int]	mutation color (when 'fmac' or 'pimc' descriptors are applied)
-tco [bool]	display color at the level of 3D structure through pymol script
-dop [bool]	get a operation descriptors dictionary (only available for <code>rf = 'multiple'</code>)
-dco [bool]	get a color descriptors dictionary (only available for <code>rf = 'multiple'</code>)
-dvi [bool]	get a visualization descriptors dictionary (only available for <code>rf = 'multiple'</code>)
-dmx [bool]	get a maximum restriction descriptors dictionary (only available for <code>rf = 'multiple'</code>)

Above you can see the possible flags implemented in CPRISMA. Note that the Python variable type is appearing inside of square brackets, and a short description is displayed as well.

Next, a description of them will be given in the next Sections and Chapters, bringing practical examples to better understand how they work. Some flags should be parsed in parallel with the "array_get.py" script to avoid future misinterpretations and others may be interdependent.

The positional arguments `-h` (`--help`) and `-v` (`--version`) are the default commands that will display the possible flags that can be written in the terminal and the version of the



program, respectively. As these two commands are by default and self-explicit, in the following sections we will just focus on the CPRISMA parameters.

3.1 Target-residues (-tr)

The problem with the residue A of ZIKV-UG shown above is caused by the absence of numerical data for that amino acid. A possible solution could be to include in the CSV file, new rows named “ALA” followed by a column with pK_a values equal to 0 and respecting the order in which they appear for each protein.

Note: Here we assume $pK_a = 0$ as equivalent to no color, but this may vary depending on the type of data.

But this process can become time-consuming because the pK_a values for residues of Val, Ser, Trp, and so on, would also have to be included in the CSV file. A more efficient way to exclude residues that are not needed is to run the `-tr` command. However, when running it you may find the following problem:

`The program stop! The variable to check the target-residues is True, but the tuple is equal to 0.`

The flag `-tr` is a Boolean command, which means that by default it is “False”, but when you invoke it becomes “True”. `-tr` calls the `target_residues` variable in the script “array_get.py” (Figure 2.2.3). This one is a *tuple*¹ that must contain residues in one-letter format. When `-tr` is executed, the correlation is made between the CSV file and the residues reported in the tuple. So you should try to use the same types of amino acids that appear in the numerical data file to build the tuple. Common errors that can occur in the construction of the tuple are listed below:

1. An empty tuple will return an error like the one we see above.
2. Do not put all the kinds of residues that appear in the CSV file in the tuple.
3. To include a residue in the tuple that is not in the CSV file.

For our example, the tuple should be as follows:

```
target_residues = ('D', 'E', 'R', 'H', 'K', 'Y')
```

¹See <https://docs.python.org/3.7/tutorial/datastructures.html#tuples-and-sequences>.



If we again run the program with the next command line:

```
cprisma -tr
```

... our log file will successfully return the following message:

```
Target-residues ('D', 'E', 'R', 'H', 'K', 'Y') match in alignment.dat and  
data_input.csv.
```

Note: It is important to mention that if you have the numerical values of all residues that appear in a specific multiple sequence alignment, it is not necessary to explicitly define a tuple with the 20 essential amino acids in the script “array_get.py” because the program already defines those 20 residues by default (see the practical example of Section 8.3).

3.2 Accuracy (-a)

Sometimes the color may not have enough intensity depending on the numerical data employed. This happens due to the limits that the HTML color code itself may have or because the limits of the human vision. To improve the color intensity to highlight the regions that matter most to us in the sequence alignment is necessary to make additional adjustments.

In this section, let us focus on the accuracy of the data, which is changeable by means of **-a** command². In Figure 3.0.3, it is observed that the precision of the data goes up to the fifth decimal place. As shown in Figure 3.2.1, after program processing one decimal per value will be displayed (which corresponds to the default condition). When two or more decimals are considered, it is necessary imperative to invoke the command **-a** followed by a positive integer number which refers to the decimal places, as follows:

```
cprisma -tr -a 3
```

In our example, we are ordering the program to only consider taking into account three decimal places. Remember that this command will only affect the possible values obtained from operations, and then, the color applied when a gradient is executed (see Chapters 4, 5, and 6, respectively). Nevertheless, some information in the log file will not be affected by this parameter, like the statistical data reported there (Figure 3.3.1).

²This is one of the possible methods to improve the color intensity. Other methods can also be applied (see Section 5.14 and Chapter 7).



--- Data processed ---

	ZIKV-UG	ZIKV-UG_dat	ZIKV-BR	ZIKV-BR_dat	DENV2	DENV2_dat	WNV	WNV_dat
0	ASP	3.9	ASP	3.9	ASP	3.9	ASP	3.8
1	ASP	3.1	ASP	3.4	XXX	0.0	ASP	3.4
2	XXX	0.0	XXX	0.0	LYS	10.5	XXX	0.0
3	LYS	10.9	LYS	11.0	XXX	0.0	ARG	12.8
4	LYS	10.7	LYS	10.7	LYS	10.6	XXX	0.0
5	GLU	3.8	GLU	4.0	GLU	3.8	GLU	4.0
6	ARG	12.6	ARG	12.3	LYS	10.7	ARG	12.4
7	TYR	10.0	TYR	10.0	XXX	0.0	HIS	6.7
8	XXX	0.0	XXX	0.0	ASP	3.4	XXX	0.0
9	ASP	3.5	ASP	3.8	XXX	0.0	ASP	3.6
10	GLU	4.0	GLU	4.1	HIS	6.8	GLU	4.4
11	ARG	12.6	ARG	13.4	XXX	0.0	XXX	0.0
12	ASP	3.1	ASP	2.7	GLU	4.1	ASP	3.5
13	ARG	13.3	ARG	13.0	XXX	0.0	ARG	12.9
14	TYR	9.6	TYR	9.6	TYR	10.0	TYR	9.8
15	LYS	11.1	LYS	11.0	LYS	11.0	LYS	11.2
16	TYR	10.0	TYR	9.7	XXX	0.0	TYR	10.2
17	HIS	6.3	HIS	6.2	XXX	0.0	TYR	9.5

Figure 3.2.1: Numerical data processed in the log file. Note that some rows are named “XXX”, which indicates that a gap has been inserted. These gaps are directly related to the alignment and are necessary for the reading and coloring of the sequences later. Notice that there is an index starting from 0 that number each row. All the information has not been shown.

3.3 Alignment visualization (-va)

At this point, you will have noticed that the file “alignment.html” appears in your directory (Figure 3.3.2). Note that the file does not have any color still³. By default, CPRISMA will separate each protein sequence keeping the conservation line for each of them [*i.e.*, the line that contains dots (“.”, “;”), asterisks (“*”) or spaces (“ ”)]. Now it seems not to have much relevance to observe our alignment without comparisons among sequences. Nevertheless, as described later this kind of visualization can be very useful to detect independent color behaviors from sets of numerical data.

Another way to visualize our alignment can be calling method 2 through the `-va` command, as follows:

```
cprisma -tr -va 2
```

³This aspect will be covered in Chapter 5.



--- Statistics ---

	ZIKV-UG	ZIKV-BR	DENV2	WNV
count	36.000000	36.000000	35.000000	43.000000
mean	8.027069	8.065460	7.998239	7.820189
std	3.957723	4.020073	3.578109	3.732822
min	3.097370	2.688280	3.390330	3.384640
25%	3.964313	3.990678	3.892795	3.993175
50%	9.787815	9.641460	9.984030	9.493470
75%	11.078850	11.322598	10.883975	11.034720
max	13.392970	13.485050	13.184100	13.491570

Figure 3.3.1: Statistical data for each protein in the log file.

```
1          20          40          60
ZIKV-UG DVGCSVDFSKKETRCGTGVFIYNDVEAWRDYKYHPDSPRRLAAAVKQAWEEGICGIGISSVSRMENIMWKSVEGELNAILE
* * * : . . :* . **: * : ; :* : * . **: * :; * : ** : ; :* . : * : * : * : * : * : * : * : * : * .
```



```
81          100         120
ZIKV-UG ENGVQLTVVVGSVKNPWRGPQR LPVPVNELPHGWKA WGK
*** *.*: : . . . . . * : * . * : ***: ***
```



```
1          20          40          60
ZIKV-BR DVGCSVDFSKKETRCGTGVFVYNDVEAWRDYKYHPDSPRRLAAAVKQAWEDGICGIGISSVSRMENIMWRSVEGELNAILE
* * * : . . :* . **: * : ; :* : * . **: * :; * : ** : ; :* . : * : * : * : * : * : * : * .
```



```
81          100         120
ZIKV-BR ENGVQLTVVVGSVKNPWRGPQR LPVPVNELPHGWKA WGK
*** *.*: : . . . . . * : * . * : ***: ***
```



```
1          20          40          60
DENV2 DSGCVVSWKNKELKGCGSIFITDNVHTWTEQYKFQPESPSKLASAIQKAHEEGICGIRSVRLENLMWKQITPELNHILS
* * * : . . :* . **: * : ; :* : * . **: * : ** : ; :* . : * : * : * : * : * : * : * .
```



```
81          100         120
DENV2 ENEVKLTIMTGDIKGIMQAGKRSLRPQPTELKYSWKTWGK
*** *.*: : . . . . . * : * . * : ***: ***
```



```
1          20          40          60
WNV DTGCAIDISRQELRCGSGVFIHNDVEAWMDRYKYYPETPQGLAKIIQKAHKEGVGLRSVSRLHEQMWEAVKDELNTLLK
* * * : . . :* . **: * : ; :* : * . **: * : ** : ; :* . : * : * : * : * : * : * .
```



```
81          100         120
WNV ENGVDSL VVVEKQEGMYKSAPKRLTATTEKLEIGWKA WGK
*** *.*: : . . . . . * : * . * : ***: ***
```

Figure 3.3.2: Alignment processed through visualization method 1 without sequence comparison.



An output using this method appears in Figure 3.6.1. Notice that each sequence is being labeled at the end with the word “comparison” followed by a number (see brackets in Figure 3.6.1). This means that CPRISMA is not comparing the sequences but only analyzing each protein separately, like in the previous method.

Note: We can apply these same visualization methods but comparing our sequences. To see this aspect in more detail it is recommended to check Sections 3.9 and 3.10.

3.4 Join (-j)

The -j command is a complement for the visualization method 2. With this command the space between the comparisons is reduced (compare Figures 3.6.1 and Figure 3.7.1). To get an alignment without spaces, you can invoke the following command:

```
cprisma -tr -va 2 -j
```

Practical examples using this flag appear in Chapter 8.

3.5 Numbering (-n)

To change the first and subsequent numbers that appear at the top of the alignment, the command -n can be executed followed by a positive integer number corresponding to the desired position. For instance, we can assume that our first number is 101, so:

```
cprisma -tr -va 2 -j -n 101
```

See the practical example of Section 8.2.

3.6 Number of residues per line (-l)

You can change the number of amino acids per line using the command -l followed by a positive integer number.

Note: Remember that 80 residues per line will appear by default, so we recommend only use values greater than and multiples of 80 to have an optimal display of the numbering. You can use whatever amount of residues per line you prefer, but there may be times when the numbers will be cut off.



ZIKV-UG	DVGCSVDFSKKETRCGTVFIYNDVEAWRDRYKHPDSPRLAAAVKQAWEEGICGISSVSRMENIMWKSVEGELNAILE	comparison 1
ZIKV-BR	DVGCSVDFSKKETRCGTVFVYNDVEAWRDRYKHPDSPRLAAAVKQAWEDGICGISSVSRMENIMWRSVEGELNAILE	comparison 2
DENV2	DSGCVVSWKNKEKCGSGIFITDNVHTWTEQYKFQPESPSKLASAIQKAHEEGICGIRSVTRLENLMWKQITPELNHILS	comparison 3
WNV	DTGCAIDISRQELRCGSGVFIHNDVEAWMDRYKYYPETPQGLAKIIQKAHKEGVCGLRSVSRLEHQMWEAVKDELNTLLK	comparison 4
	* * * : . . . * . * : * : ; * : * . * : * : * : * : * : * : * : * : * : * : * : * : * : * : * .	
81	100	120
ZIKV-UG	ENGVQLTVVVGSVKNPWMWRGPQRQLPVPVNELPHGWKAWGK	comparison 1
ZIKV-BR	ENGVQLTVVVGSVKNPWMWRGPQRQLPVPVNELPHGWKAWGK	comparison 2
DENV2	ENEVKLTIMTGDIGIMQAGKRSLRPQPTELKYSWKTWGK	comparison 3
WNV	ENGVDLSVVVEKQEGMYKSAPKRLTATTEKLEIGWKAWGK	comparison 4
	* * . * : : . . . * : * . * : * * *	

Figure 3.6.1: Alignment processed through visualization method 2 without sequence comparison.

Next, an example of a command-line for this feature appears:

```
cprisma -tr -va 2 -j -l 160
```

3.7 Name sequence (-ns)

Something that is useful when working with different sequences is renaming them with the command `-ns`. This command calls the variable `name_sequence` of the script “array_get.py” (Figure 2.2.3) and makes a relationship between this variable (which is a tuple) and the number of proteins analyzed. Let us imagine that we build the following tuple:

```
name_sequence = ("Sequence 1", "Sequence 2", "Sequence 3")
```

Then, the next command-line is executed:

```
cprisma -tr -va 2 -j -ns
```

Since the number of “name sequences” is only 3 and the total of proteins is 4, CPRISMA will return the following error:



```
Variable check_name_seq = True but the sequences' number does not match with
tuple input ('Sequence 1', 'Sequence 2', 'Sequence 3')
```

Adding one more name to the tuple ('Sequence 1', 'Sequence 2', 'Sequence 3', 'Sequence 4'), the program will finally return the following message:

```
Variable check_name_seq = True, so the sequences' names have been changed.
```

Now you can see that both your alignment (Figure 3.7.1) and all the information in the log file have changed the sequences' names.

```
1           20           40           60
Sequence 1 DVGCSVDFSKETRCGTGVFIYNDVEAWRDRYKYHPDSPRLAAAVKQAWEEGICGISSVSRMENIMWKSVEGELNAILE comparison 1
Sequence 2 DVGCSVDFSKKETRCGTGVFVYNDVEAWRDRYKYHPDSPRLAAAVKQAWEDGICGISSVSRMENIMWRSVEGELNAILE comparison 2
Sequence 3 DSGCVVSWKNKELKGSGIFITDNVHTWTEQYKFQPEPSKLASAIQKAHEEGICGIRSVTRLENLWMWKITPELNHILS comparison 3
Sequence 4 DTGCAIDISRQELRCGSGGVFIHNDVEAMDRYKYPPETPQGLAKIIQKAHKEGVCGRLRSVSRLHQMWEAVKDELNTLLK comparison 4
{ * *** :. . .:*. ***:*** :*: * :***: * :* * ** : :***:***: ***:***: * * : *** :*.

81           100          120
Sequence 1 ENGVQLTVVVGSVKNPMWRGPQRPLPVNVNELPHGWKAWGK comparison 1
Sequence 2 ENGVQLTVVVGSVKNPMWRGPQRPLPVNVNELPHGWKAWGK comparison 2
Sequence 3 ENEVVLTIMITGDIKGIMQAGKRSLRPQPTELKYSWKTWKGK comparison 3
Sequence 4 ENGVDSLSSVEKQEGMYKSAPKRLTATTEKLEIGWKAWGK comparison 4
{ ** *.***:.. . . . * :* .***:***
```

Figure 3.7.1: Alignment with renamed sequences.

3.8 Hide conservation line (-hc)

The -hc command hides the conservation line of the alignment (check the line with “*”, “.”, “:” and spaces “ ” in Figure 3.7.1, for instance). -hc can be invoked following the command-line:

```
cprisma -tr -hc
```

Hiding the conservation line can be useful when we are using transcendental comparison methods (see Section 3.10).

See the practical example of Section 8.2 where -hc is employed.

3.9 Check reference method (-ck)

So far you have surely noticed the following message in your log file:



```
No comparison among the data.

-- Set of comparisons: main_0 --

ZIKV-UG X no comparison

-- Set of comparisons: main_1 --

ZIKV-BR X no comparison

-- Set of comparisons: main_2 --

DENV2 X no comparison

-- Set of comparisons: main_3 --

WNV X no comparison
```

For our example, the data of the protein systems are not being compared. But if you want to apply mathematical operations between your numerical data (see Chapter 4), it will be mandatory to compare the sequences. For instance, in our previous study, we wanted to compare the pK_a 's of ionizable residues among NS1's proteins from several ZIKV strains [1]. For that, it was calculated the difference of pK_a 's (ΔpK_a) among proteins and they were visualized with specific colors (see Section 5.10 and the practical example described in Section 8.1 as well).

Before doing any calculation, you must inform the program that it is desired to compare the data by means of the `-ck` flag. The command line to execute comparisons between the protein sequences appears below:

```
cprisma -tr -ck
```

Now, the following information will be found in the log file:

```
-- Set of comparisons: main_0 --

ZIKV-UG X ZIKV-BR DENV2 WNV
```

Note that now the sequences are being compared, so ZIKV-UG is the reference sequence, and ZIKV-BR, DENV2, and WNV are the target-sequences. Also, this comparison is being coupled to a group of comparisons called “`main_0`”. This is not the same as what was seen previously where different “`main's`” were generated. At the same time, you will have perceived that your



HTML file (Figure 3.9.1) is different when compared to the previous outcomes (Figures 3.3.2 and 3.6.1). Technically, the alignment is the same as the input shown in Figure 2.2.1 but with a slightly different format.

Note: In Section 3.10, you will find more information on how to apply more transcendental comparisons.

1	20	40	60
ZIKV -UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYHDPSPRRLAAAVKQAWEEGICCGISSVSRMENIMWKSVEGELNAILE		
ZIKV -BR	DVGCSVDFSKKETRCGTGVFVYNDVEAWRDRYKYHDPSPRRLAAAVKQAWEDGICCGISSVSRMENIMWRSVEGELNAILE		
DENV2	DSGCVSVWKNKELKGSGIFITDNVHTWTEQYKFQPEPSKLASAIQKAHEEGICGIRSVTRLENLMWKQITPELNHILS		
WNV	DTGCAIDISRQELRCGSGVFIIHNDVEAMDRYKYYPETPQGLAKIIQKAHKEGVCGLRSVSRLHEQMWEAVKDELNTLLK * * * : . . . * . * * : * : ; :: * : * ; * : * : * : * : * : * : * : * : * : * : * : * : * : * .		
81	100	120	
ZIKV -UG	ENGVQLTVVVGSKNPMWRGPQRPLPVVNELPHGKAWGK		
ZIKV -BR	ENGVQLTVVVGSKNPMWRGPQRPLPVVNELPHGKAWGK		
DENV2	EDEVKLTIMTGDIGIMQAGKRSLRPQPTELKYSWKTWKG		
WNV	ENGVDSLSSVVEKQEGMYKSAPKRLTATTEKLEIGWKAWGK ** *.*::: * : * . * * : ***		

Figure 3.9.1: Alignment processed through visualization method 1 with sequence comparison.

3.10 Reference method (-rf)

Whether -ck was executed, other additional information will appear in the log file:

```
Method used 'default' for the array: | main_0 [{‘0’: [1, 2, 3]}] |
```

To understand what this means, a basic understanding of Python’s data structure is necessary. Let us go a little back, just to correctly interpret these outcomes. Based on the previous message, note that you have one comparison that belongs to `main_0`. Figure 3.10.1 is showing an example of the CPRISMA default variable when `-rf` is invoked (pay attention to the Roman numerals). In Python, whenever one string type (II) and any type variables (VI) appear separated by a colon (V) inside brackets (I), it will be interpreted by the language as a *dictionary*⁴. The numerals II and VI are also called *keys* and *values*, respectively. In our case, the key of our dictionary is the string ‘0’ and the value is a *list* of numbers from 1 to 3. Note that the lists have square brackets (III), which differentiates them from dictionaries⁵.

⁴See <https://docs.python.org/3.7/tutorial/datastructures.html#dictionaries>.

⁵See <https://docs.python.org/3.7/tutorial/datastructures.html#more-on-lists>.

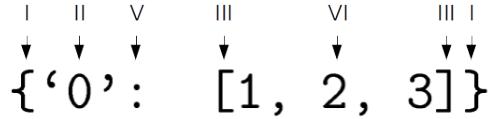


Figure 3.10.1: Dictionary created by CPRISMA. the meaning of Roman numerals is explained in the text.

Note: Based on the message cited at the beginning of this Section, see that your dictionary is also inside square brackets: `[{'0': [1, 2, 3]}]`⁶. In Subsection 3.10.3, we will explain in more detail the reason for that.

Please keep all these features in mind as they will be helpful in understanding the following sections. Furthermore, in some moments we will call the sets of comparisons as arrays.

To interpret the numbers in our dictionary (Figure 3.10.1), we simply have to relate the order of appearance for each sequence based on the multiple alignments. Thus, ‘0’ will be ZIKV-UG, ‘1’ will be ZIKV-BR, and so on.

There are three comparison methods used by CPRISMA: `default`, `pair`, and `multiple`, which are described below.

3.10.1 Default

The `default` method of CPRISMA compares the first sequence with the rest. You can explicitly invoke this method via the `-rf` flag followed by the word “default” like this:

```
cprisma -tr -ck -rf default
```

Note: Remember, due to this comparison method is the optional argument by default (as its name implies), CPRISMA will always return a dictionary with this structure when you run `-ck` (i.e., you do not need to type `-rf default`, explicitly)

3.10.2 Pair

Another comparison method is called `pair`. To invoke it, we can type in terminal:

```
cprisma -tr -ck -rf pair
```

⁶We have changed the color to purple for some square brackets to distinguish easily each list.



Now, our log file will contain the following information:

```
Method used 'pair' for the array: | main_0 [{0}: [1]] | | main_2 [{2}: [3]] |
```

```
-- Set of comparisons: main_0 --
```

```
ZIKV-UG X ZIKV-BR
```

```
-- Set of comparisons: main_2 --
```

```
DENV2 X WNV
```

Comparison: 1

1	20	40	60
ZIKV-UG	DVGCSVDFSKETRCGTGVFIYNDVEAWRDRYKYHPDSPRLAAVKQAWEEGICGISSVRMENIMWKSVEGELNAILE		
ZIKV-BR	DVGCSVDFSKETRCGTGVFYNDVEAWRDRYKYHPDSPRLAAVKQAWEDGICGISSVRMENIMWRSVEGELNAILE		
	* * * : . . : * . * * : * : * : . * : * : * : * : * : * : * : * : * : * : * : * : * : * .		
81	100	120	
ZIKV-UG	ENGVQLTVVVGSKNPMWRGPQRLLPVPVNELPHGKAWGK		
ZIKV-BR	ENGVQLTVVVGSKNPMWRGPQRLLPVPVNELPHGKAWGK		
	* * . * : : * : * . * * : * * : * * : * * : * * : * .		

Comparison: 2

1	20	40	60
DENV2	DSGCCVSWKNKELKGSGIFITDNVHTWTEQYKFQPEPSKLASAIQKAHEEGICGIRSVTRLENLMWKQITPELNHILS		
WNV	DTGCAIDISRQEELRCGSGVFIHNDEAWMDRYKYYPETPQGLAKIIQKAHKEGVCGLRSVSRLEHQMWAEAVKDELNTLLK		
	* * * : . . : * . * * : * : * : . * : * : * : * : * : * : * : * : * : * : * : * .		
81	100	120	
DENV2	ENEVKLTIMTGDIGIMQAGKRSLRQPTELKYSWKTWGK		
WNV	ENGVDSLSSVEKQEGMYKSAPKRLLTATTEKLEIGWKAWGK		
	* * . * : : * : * . * * : * * : * * : * * : * .		

Figure 3.10.2: Alignment processed with `pair` comparison method.

Note that two arrays have now been created, which can be interpreted as two independent sets of comparisons and they belong to the `main`'s: `main_0` and `main_2`. One where 0 (ZIKV-UG) and 1 (ZIKV-BR) sequences are the reference_{comparison1} and target_{comparison1}, respectively; and another where 2 (DENV2) and 3 (WNV) sequences are the reference_{comparison2} and



target_{comparison2}, respectively. This will also be reflected in our HTML file (Figure 3.10.2)⁷.

It is important to mention that for CPRISMA to work correctly with the `pair` comparison method, the total number of sequences is needed to be even. Otherwise, it will return to the method for `default` with the following message:

Attention!!! Method selected by user is ‘pair’ but number of sequences (=3⁸) is not a even number. The method return to ‘default’.

3.10.3 Multiple

Among all the comparison methods, `multiple` can be the most complex to understand. With this method, many types of comparisons can be made between a set of sequences (*e.g.* see all the practical examples in Chapter 8). However, before invoking it you must have built a dictionary compatible with the CPRISMA format array. In the script “array_get.py” a variable called `dict_ref` will appear (Figure 2.2.3). From this, you can build an array like this⁹:

```
dict_ref = { 'main_0' : [ {'0':[1, 2, 3]}, {'0':[]} ] ,  
            'main_1' : [ {'1':[0, 2]}, {'1':[0, 2, 3]} ] ,  
            'main_2' : [ {'2':[0]} ] }
```

At first glance, this type of arrangement may seem tricky, but give us a chance to explain it to make it easier.

The CPRISMA convention is going to call the “external layer” of the array with the names: “first-key” (or “main key”) and “first-value” (or “main value”). Then, the first-keys will be all `main`’s typed in the array, *i.e.*, `main_0`, `main_1`, and `main_2`; and the first-values will be the lists: `[{'0': [1, 2, 3]}, {'0': []}]`, `[{'1': [0, 2]}, {'1': [0, 2, 3]}]`, and `[{'2': [0]}]`¹⁰. Each element of the list/first-value is equivalent to a comparison and they have a “second-key” (or “subkey”) and a “second-value” (or “subvalue”). The subkeys are the string numbers that represent the sequence references and the subvalues are the lists with the target proteins. Notice that each cluster of first-key/first-value pairs is separated by a

⁷We suggest the user to also explore visualization method 2 (see Section 3.3).

⁸A data set of 3 proteins was used to compare them (only as an example).

⁹Note that we have differentiated each comparison with a different color to aid the reader.

¹⁰We have changed the color to purple for some square brackets to distinguish easily each list.



comma and they are so-called like “set of comparisons”¹¹. Besides, each comparison in the list/first-value is separated by a comma as well. Please, avoid confusing this! For the sake of convenience, in Figure 3.10.3, we have made a sketch for `main_0`, where you can follow each characteristic of the CPRISMA array.

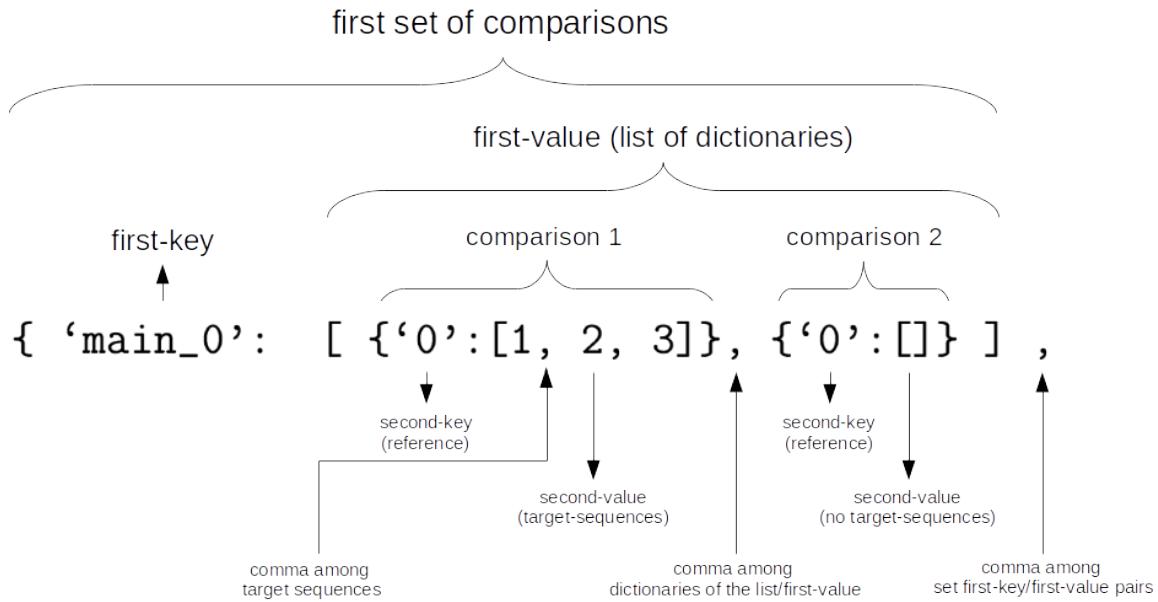


Figure 3.10.3: Example of the structure of the CPRISMA array when is used `multiple` method.

Maybe, you can also perceive that each `main` has the same reference number of a particular set of comparisons. For example, `main_1` has comparisons 3 and 4 which are `{'1': [0, 2]}` and `{'1': [0, 2, 3]}`, respectively, so the reference sequences ‘1’ match with the number of the `main` (*i.e.*, `main_1`). The same goes for `main_0` and `main_2`. However, it should be noted that you can use whatever name you prefer for each “`main`”, to better identify your comparisons. Just make sure they are different from each other. For practical purposes, we will use the standard name as already seen in the previous and following examples.

Note: Check that comparison 2 has a list with no elements or empty: {‘0’: []}. CPRISMA will interpret this dictionary as “without comparison” (or without target-sequences).

¹¹Identify this same structure when using the `default` and `pair` methods.



1	20	40	60
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYHPDSPRRLAAAVKQAWEEGICGISSVSRMENIMWKSVEGELNAILE	comparison 1	
ZIKV-BR	DVGCSVDFSKKETRCGTGVFVYNDVEAWRDRYKYHPDSPRRLAAAVKQAWEDGICGISSVSRMENIMWRSVEGELNAILE		
DENV2	DSGCVVSWKNKELKGSGIFITDNVHTWTEQYKFQPESPSKLASAIQKAHEEGICGIRSVTRLLENLMWKQITPELNHILS		
WNV	DTGCAIDISRQELRCGSGVFIHNDVEAWMDRYKYYPETPQGLAKITQKAHKEGVCGLRSVSRLEHQMWEAVKDELNTLLK		
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYHPDSPRRLAAAVKQAWEEGICGISSVSRMENIMWKSVEGELNAILE	comparison 2	
ZIKV-BR	DVGCSVDFSKKETRCGTGVFVYNDVEAWRDRYKYHPDSPRRLAAAVKQAWEDGICGISSVSRMENIMWRSVEGELNAILE	comparison 3	
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYHPDSPRRLAAAVKQAWEEGICGISSVSRMENIMWKSVEGELNAILE		
DENV2	DSGCVVSWKNKELKGSGIFITDNVHTWTEQYKFQPESPSKLASAIQKAHEEGICGIRSVTRLLENLMWKQITPELNHILS		
ZIKV-BR	DVGCSVDFSKKETRCGTGVFVYNDVEAWRDRYKYHPDSPRRLAAAVKQAWEDGICGISSVSRMENIMWRSVEGELNAILE	comparison 4	
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYHPDSPRRLAAAVKQAWEEGICGISSVSRMENIMWKSVEGELNAILE		
DENV2	DSGCVVSWKNKELKGSGIFITDNVHTWTEQYKFQPESPSKLASAIQKAHEEGICGIRSVTRLLENLMWKQITPELNHILS		
WNV	DTGCAIDISRQELRCGSGVFIHNDVEAWMDRYKYYPETPQGLAKITQKAHKEGVCGLRSVSRLEHQMWEAVKDELNTLLK		
DENV2	DSGCVVSWKNKELKGSGIFITDNVHTWTEQYKFQPESPSKLASAIQKAHEEGICGIRSVTRLLENLMWKQITPELNHILS	comparison 5	
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYHPDSPRRLAAAVKQAWEEGICGISSVSRMENIMWKSVEGELNAILE		
 * * * : . .: * .**:*: *: : * : * .*: *:: * ** : ::* .::*::: *: *: *: * : * *** :*.			

Figure 3.10.4: Alignment processed with `multiple` comparison method. Not all alignment is being shown.

If the array is well constructed, we can invoke the following command:

```
cprisma -tr -ck -rf multiple
```

Then, in our log file the comparisons will appear as follows:

```
-- Set of comparisons: main_0 --
ZIKV-UG X ZIKV-BR DENV2 WNV
ZIKV-UG X no comparison
-- Set of comparisons: main_1 --
ZIKV-BR X ZIKV-UG DENV2
ZIKV-BR X ZIKV-UG DENV2 WNV
-- Set of comparisons: main_2 --
DENV2 X ZIKV-UG
```



Our HTML file will show an output like the one shown in Figure 3.10.4 (to facilitate the visualization, method 2 was used, it is recommended to see Section 3.3).

Finally, if the array is not well built, CPRISMA will always return to the `default` value. In addition, it will inform you in detail where the errors are. Based on this, you can correct them yourself (the program will guide you). Warning/error messages for `multiple` command will not appear in this documentation, as we prefer that the user be trained in understanding the construction of CPRISMA arrays.

See in Chapter 8 the possibilities that can be declared in `dict_ref` using `multiple` comparison method .

3.11 Total information (-t)

To have the verbose version of the log file, you can invoke the following command:

```
cprisma -tr -t
```

Now, the log file will show in detail the operations that you are applying to each set of comparisons (see Chapter 4). In turn, a relationship between each comparison and the color assigned to it will be shown (see Chapter 5). Also, if a maximum restriction is applied (see Chapter 7), you can visualize the lists of values used to normalize the color displayed on the HTML file (whether or not math operations are performed).



4 Operation (descriptor_ope)

CPRISMA has a feature called “operation” that allows the user to compute basic mathematical operations among the data. To execute this feature, it is *mandatory* to have at least one comparison between a particular reference and target proteins. For the following examples, we will always assume the `default` comparison method (see Subsection 3.10.1), with the exception of Section 4.5.

Generally, the program will always read the variable called `descriptor_ope` from the Python script “array_get.py” (Figure 2.2.3). Then, CPRISMA will perform a certain operation between the vector $\mathbf{r} = [r_j]$ (reference) and the matrix $\mathbf{T} = [t_{ij}]$ [target(s)]. Based on the data processed and displayed in the log file, for our example using pK_a values, the vector \mathbf{r} , and matrix \mathbf{T} have dimensions 56×1 and 56×3 , respectively. Something that should be noted is that CPRISMA takes advantage of the `numpy` features to apply broadcasting and thus improve the speed of matrix operations. For this version of CPRISMA, you can perform 3 types of calculations: `delta/d` (Δ), absolute `delta/da` ($|\Delta|$), and multiplication/`m`. Although, it is possible to not calculate any operation (`none/n`) as well. For CPRISMA, these 4 possibilities are called *descriptors*.

Note: We highlight that this nomenclature (i.e., descriptor) also applies to other features in addition to operations, such as color, visualization, and maximum restriction (see Chapters 5, 6, and 7, respectively).

Finally, the numerical data generated through the operations will serve as the basis to put the color in the multiple sequence alignments.

4.1 None (n)

When it is desired to keep the same numerical values of the input (*i.e.*, the data of the CSV file), you can do this by declaring the descriptor `n` in the “array_get.py” file, as follows:

```
descriptor_ope = { 'n' }
```



Perceive that the `n` descriptor is a string variable inside a pair of brackets. This data structure corresponds to a *set* variable type and should not be confused with a dictionary¹.

After having run CPRISMA, your log file will have various information about the operation applied. For now, we should only focus on the next²:

```
main  comparison  descriptor
main_0          1           n
```

This statement is simply saying that `n` descriptor was considered for comparison 1, in the `main_0` comparison set.

Note: Sometimes, it could be declared this descriptor or another wrongly. To avoid that the program stops, it will always return to `n` descriptor (default parameter), with some additional error messages in your log file, which will guide you to correct the problem.

4.2 Delta (`d`)

When the `d` descriptor is invoked like this:

```
descriptor_ope = { 'd' }
```

... the program will do a conventional Δ calculation between \mathbf{r} and \mathbf{T} (Equation 4.2.1).

$$\mathbf{W} = \mathbf{T} - \mathbf{r}, \quad (4.2.1)$$

where \mathbf{W} is the new data to put color (see Chapter 5).

4.3 Absolute delta (`da`)

To declare the `da` descriptor, it is possible as follow:

```
descriptor_ope = { 'da' }
```

¹See <https://docs.python.org/3.7/tutorial/datastructures.html#sets>.

²When using a different operation descriptor, respectively, its letter will appear in the `descriptor` column.



CPRISMA will apply the Δ calculation as before (Section 4.2), but using the absolute value:

$$\mathbf{W} = |\mathbf{T} - \mathbf{r}| \quad (4.3.1)$$

4.4 Multiply (`m`)

To declare the `m` descriptor, you can invoke:

```
descriptor_ope = { 'm' }
```

The program will multiply the data as shown in Equation 4.4.1.

$$\mathbf{W} = \mathbf{T} \times \mathbf{r} \quad (4.4.1)$$

4.5 Operation descriptors dictionary (-dop)

One can run the following command using `multiple` comparison method:

```
cprisma -tr -ck -rf multiple
```

We have started from the next CPRISMA array (see Subsection 3.10.3)³:

```
dict_ref = { 'main_0': [ {'0': [1, 2, 3]}, {'0': []} ] ,  
            'main_1': [ {'1': [0, 2]}, {'1': [0, 2, 3]} ] ,  
            'main_2': [ {'2': [0]} ] }
```

Suppose we are doing a Δ operation (*i.e.*, `descriptor_ope = { 'd' }`). Then, the following information will appear in the log file:

Comparing `dict_ref` with `dict_ope`:

```
{'0': [1, 2, 3]} ..... d  
{'0': []} ..... d  
{'1': [0, 2]} ..... d
```

³Note that we have differentiated each comparison with a different color to aid the reader.



```
{'1': [0, 2, 3]} ..... d  
{'2': [0]} ..... d
```

The array of the feature ‘operation’ `dict_ope` is compatible with the array of comparison sequences `dict_ref`!

Note: Comparison 2 does not have a target-sequence (*i.e.*, `{'0': []}`), so operations like `d`, `da`, or `m` are not applied.

This information is showing us a relationship between each comparison and the type of operation that it is applied for each one. For all comparisons, a Δ is computed among its specific reference and target-sequences.

Nonetheless, we are not always going to calculate a single operation for all comparisons. To perform a different math calculation for each reference/target(s) relationship, an array of operation descriptors called `dict_ope` should be built in our “array_get.py” script. We shall follow very similar rules to those we saw earlier for the `multiple` method (see Subsection 3.10.3). Our dictionary of operations must have an equivalent number of `main`’s as well as in `dict_ref` (*i.e.*, `main_0`, `main_1`, and `main_2`). In turn, for each `main` (first-key), a list of operation descriptors (first-values) should be invoked⁴. Based on this, suppose we construct the following operation-array⁵:

```
dict_ope = { 'main_0' : [ {'d'} , {'n'} ] ,  
            'main_1' : [ {'m'} , {'d'} ] ,  
            'main_2' : [ {'da'} ] }
```

Invoking the `-dop` command you will order to CPRISMA to take into account the `dict_ope` dictionary of the “array_get.py” script:

```
cprisma -tr -ck -rf multiple -dop
```

Now, our log file will show the operation applied for each comparison:

Comparing `dict_ref` with `dict_ope`:

⁴For the other features (*i.e.*, color, visualization, and maximum restriction), these first-values will always be a list of descriptors with the same number of elements equivalent to the number of comparisons.

⁵Note that we have differentiated each operation descriptor for each comparison with a different color to aid the reader.



```
{'0': [1, 2, 3]} ..... d
{'0': []} ..... n
{'1': [0, 2]} ..... m
{'1': [0, 2, 3]} ..... d
{'2': [0]} ..... da
```

The array of the feature ‘operation’ `dict_ope` is compatible with the array of comparison sequences `dict_ref`!

... and the next table:

main	comparison	descriptor
main_0	1	d
main_0	2	n
main_1	3	m
main_1	4	d
main_2	5	da

It is important to mention that `-dop` will only work with the `multiple` comparison method.

Note: To check how the numerical calculations are applied between each row of the processed input file, the `-t` flag can be employed (see Section 3.11). Figure 7.0.1 shows an example of how that part of the log file looks like.

Note: If the array of `dict_ope` is wrongly built, all descriptors will be transformed to `n` (default parameter) for each comparison and additional information about where the errors are will be displayed.



5 Color (descriptor_col)

So far, we have intentionally seen situations where our multiple sequence alignment is colorless. This is because we did not want to work with many features simultaneously. This Chapter will describe how to use the CPRISMA feature called “color”.

Remember that the color applied is working with the HTML language. The file employed by CPRISMA to apply the color is located at “cprisma/colors.csv”. Figure 5.0.1 shows some rows from this file. The cells are divided into four columns with the heads “General”, “Name”, “Hex”, and “RGB”. CPRISMA will only invoke the column labeled RGB to give color, the other information is just to help the user to identify each color easily. It is important to mention that all this stuff is based on the official HTML site about color code¹. For quick access to this list of colors, you can invoke the `-lco` command described in Section 5.16.

	A	B	C	D
1	General	Name	Hex	RGB
2	Red HTML	IndianRed	#CD5C5C	rgb(205, 92, 92)
3	Red HTML	LightCoral	#F08080	rgb(240, 128, 128)
4	Red HTML	Salmon	#FA8072	rgb(250, 128, 114)
5	Red HTML	DarkSalmon	#E9967A	rgb(233, 150, 122)
6	Red HTML	LightSalmon	#FFA07A	rgb(255, 160, 122)
7	Red HTML	Crimson	#DC143C	rgb(220, 20, 60)
8	Red HTML	Red	#FF0000	rgb(255, 0, 0)

Figure 5.0.1: CSV file with color information. All the rows have not been shown.

For the color feature, we also have a set variable called `descriptor_col` in the script “array_get.py” (Figure 2.2.3). The color feature has 10 different descriptors (`nc`, `ssc`, `fsc`, `fac`, `fmac`, `pic`, `pimc`, `tc`, `tmc`, and `pkac`) that will be described below.

For most next examples the following command is being executed:

¹See <https://htmlcolorcodes.com/color-names/>.



```
cprisma -tr -ck
```

Furthermore, the variable `descriptor_ope` in the Python script “array_get.py” was typed as follows:

```
descriptor_ope = { 'd' }
```

5.1 No color (nc)

To use the descriptor `nc`, you can declare it like this:

```
descriptor_col = { 'nc' }2
```

As the name implies, you are not adding any color to the alignment. Now, your log file will have various information about the color feature applied. We should only focus on the next:

main	comparison	descriptor	sequence	residue	mutation	style	threshold
main_0	1	nc	NaN	NaN	NaN	NaN	NaN

This table is simply saying that the `nc` descriptor was considered for comparison 1, in the `main_0` comparison set (for now ignore the rest of columns in that log message).

Note: Sometimes, some descriptors can be declared wrongly. To avoid that the program stops, it will always return to the nc descriptor (default parameter), with some additional error messages in your log file, which will guide you to correct the problem.

5.2 Same sequence color (ssc)

Suppose that you want to color a set of sequences with the same color. For this we declare:

```
descriptor_col = { 'ssc' }
```

The log file will report as `[same]` in the `sequence` column:

main	comparison	descriptor	sequence	residue	mutation	style	threshold
main_0	1	ssc	[same]	NaN	NaN	NaN	NaN

Furthermore, the HTML file now has a colored alignment (Figure 5.2.1).

²For all alignment examples of Chapter 3, this was the variable executed.



Figure 5.2.1: Alignment colored through `ssc` descriptor.

Note that only the target-residues in all the proteins are being colored with Red (see Section 3.1) and the reference (*i.e.*, ZIKV-UG) is not being examined. The default color for the `ssc` descriptor is Red, which corresponds to the 6th row when executed `-lco` (see Section 5.16). You can change that color by invoking the `-sco` flag described in Section 5.12.

5.3 Free sequence color (fsc)

To give a different color to each *target-sequence*, the descriptor `fsc` can be declared as follows:

```
descriptor_col = { 'fsc' : [6, 54, 94] }
```

Notice that now is not being invoked a set variable type but a dictionary. Our key will be the descriptor `fsc` (string type) and our value is a list of number colors (see Section 5.16) that corresponds to the total number of target-sequences and their order of appearance (*i.e.*, colors 6, 54, and 94 for ZIKV-BR, DENV2, and WNV, respectively). After running the program, the log file will show the following information:

```
main comparison descriptor      sequence residue mutation style threshold
main_0          1           fsc  [6, 54, 94]       NaN      NaN      NaN      NaN
```

... and the HTML file will now display a color for each target-sequence (Figure 5.3.1). Assuming you will do quick tests and do not care about the color kind assigned to each target-sequence, it is possible to declare your variable like this:

```
descriptor_col = { 'fsc' : ['random'] }
```



When the word ‘random’ is typed into the list, CPRISMA will give each target-sequence a random color.

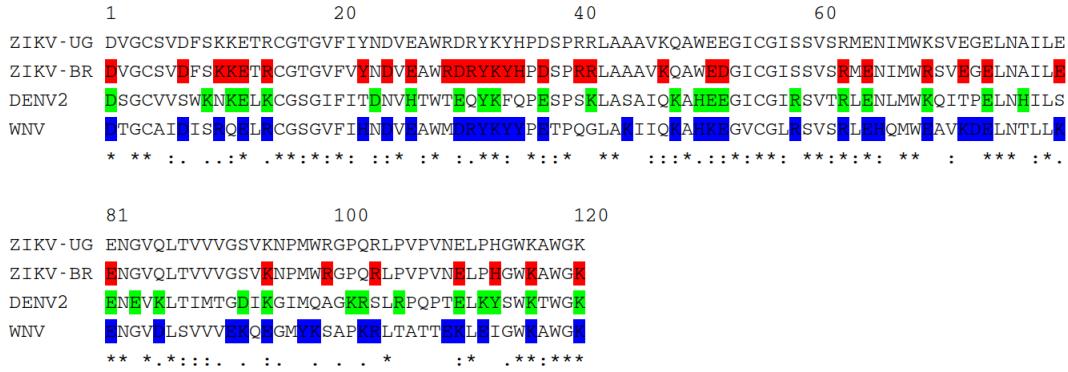


Figure 5.3.1: Alignment colored through `fsc` descriptor.

5.4 Free amino acid color (fac)

To color each *target-residue* for the target-sequence(s), the `descriptor_col` can be invoked like this:

```
descriptor_col = { 'fac' : [6, 20, 22, 54, 94, 46] }
```

Look at the list has 6 different color numbers. That number of elements is correlated to the number of target-residues declared in the tuple `target_residues` of the script “array_get.py” (see Section 3.1).

Note: If you need to assess the 20 essential amino acids, you will need to declare 20 color numbers in that list or use random option.

Later, the log file will report this list of color numbers in the `residue` column like this:

```
main  comparison  descriptor  sequence      residue  mutation  style  threshold
main_0          1           fac        NaN  [6, 20...]

```

... and the HTML file will now display a color for each target-residue (Figure 5.4.1). As with the `fsc` descriptor, random colors for your target-residues can be declared as follows:

```
descriptor_col = { 'fac' : ['random'] }
```

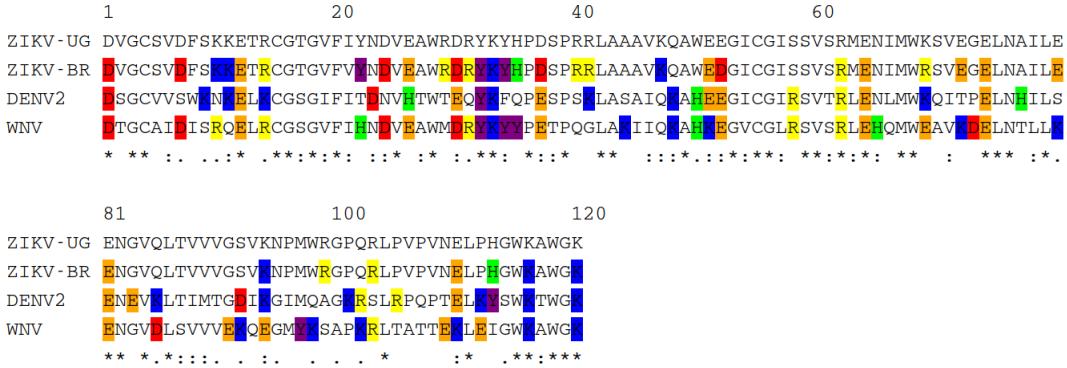


Figure 5.4.1: Alignment colored through `fac` descriptor.

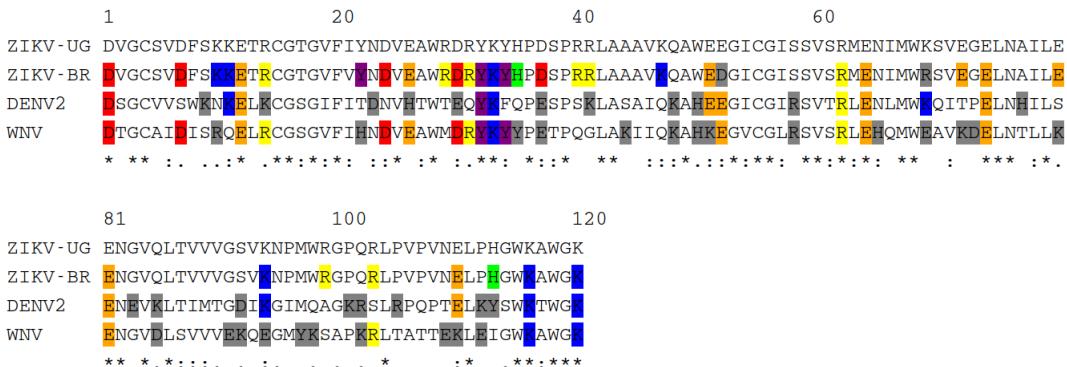


Figure 5.4.2: Alignment colored through `fmac` descriptor.

5.5 Free amino acid and mutation color (`fmac`)

The `fmac` descriptor is a copy of the `fac` one, but with the capacity to distinguish regions where there are mutations between the reference and target-sequence(s). To execute it, you can declare your variable `descriptor_col` like this:

```
descriptor_col = { 'fmac' : [6, 20, 22, 54, 94, 46]3 }
```

Now the log file will also inform you that mutations are being differentiated by means of the `True` Boolean in the `mutation` column:

³Remember that the `random` method could be employed here.



```
main  comparison  descriptor  sequence      residue  mutation  style  threshold
main_0          1           fmac        NaN  [6, 20...]     True     NaN      NaN
```

A typical HTML outcome using the descriptor `fmac` appears in Figure 5.4.2. See that mutations are colored in gray. Whether you want to change the Gray color of the mutations (default), it is possible through the `-mco` command (see Section 5.13).

5.6 Color by position index (pic)

When it is desired to highlight only specific regions of the alignment, the `pic` descriptor can be invoked⁴:

```
descriptor_col = { 'pic' : [ { '1' : [6, 'n', '1-2', '3', '4-8'] } ,
                            { '1' : [94, 'b', '11-27'] } ,
                            { '2' : [75, 'd', '3', '30-55'] } ,
                            { '3' : [54, 'u', '20-35'] } ] }
```

This can be one of the most complex color descriptors to implement. The descriptor `pic` is a dictionary type where its key will be the string '`'pic'`', and the value is a list of dictionaries with several parameters (the orange square brackets delimit the list and purple brackets the dictionaries).

We have seen this arrangement structure before (see Subsection 3.10.3). However, when `pic` is called, we have some differences. Our second-key will be a number (string type), from one of the target-sequence(s) (for our example, '`1`', '`2`', and '`3`', or ZIKV-BR, DENV2, and WNV, respectively).

Note: It is imperative that you respect the order in which the target-sequences appear in a specific comparison. However, note that you can call the same sequence more than once as '`1`' in our example.

The second-value is a list of parameters where the first (in red letters) and second (in green letters) refer, respectively, to the positive integer color number (see Section 5.16) and the font style [`'n'` ("none"), `'b'` ("bold"), `'i'` ("italic"), `'d'` ("deleted"), and `'u'` ("underlined")].

⁴Some brackets, letters, and numbers are colored to aid the reader.



From the third (in blue), we find the intervals (string type) that we want to color with the format: ‘number₁-number₂’. The intervals must be from a lower to a higher number and sometimes only one can be considered (for our example see ‘3’ in blue). You should respect this consistency! The numbers of the intervals that you must implement are the same when the input data is processed (see the index of each row in Figure 3.2.1 or the “Data processed” section of the log file). Remember, your intervals should be related to that index and not the alignment position!

Note: Be careful about overlaps that can occur between the intervals.

When CPRISMA is run, the program will display the following information in the log file:

Figure 5.6.1: Alignment colored through `pic` descriptor.

Notice that for the **pic** descriptor, the **sequence** column is not showing the color as we saw with the **fsc** descriptor, instead, it is displaying the number of the target protein that is being colored. To find the color, you must see the first element in the list that appears in the **residue** column [for our example the color values will be 6 (Red), 94 (Blue), 75 (Cyan), and 54 (Lime)].



The next elements on the same list will be the highlighted residues⁵. Moreover, the font letter that is being applied for each region will appear in the `style` column. The HTML file is going to display specific regions based on the position index of the processed data (Figure 5.6.1). Make correlations with both that graph and the table above. Note that if the interval matches with a gap, this region will not be colored. For instance, the interval ‘1-2’ (sequence₁/ZIKV-BR) presents a gap at position 2 (Figure 3.2.1), as this position coincides with a Lys residue for DENV2 and one Ser residue for ZIKV-BR, no color should be assigned to that region of ZIKV-BR, due to the Ser is not a target-residue.

```

      1          20          40          60
ZIKV-UG DVGCSVDFSKKETRCGTGVFIYNDVEAWDRYKYHDPSPRLAAAVQQAWEEGICGIGISSVSRMENIMWKSVEGELNAILE
ZIKV-BR DVGCSVLFSSKKETRCGTGVFVYNDVEAWDRYKYHDPSPRLAAAVQQAWEEDGICGIGISSVSRMENIMWRSVEGELNAILE
DENV2   DSGCVVSWKNKELKGSGIFITDNVHTWTEQYKFQPESPSKLASAIQKAHEEGICGIRSVTRLENLMWKQITPELNHILS
WNV     DTGCAIDISRQELRGSGGVFIHNDVEAWMDRYKYYPETPQGLAKIIQKAHKPGVCGLRSVSLEHQMWAEVKDPLNTLLK
* * * : . . . * . * * : * * : . . * : * : * : * * : * : * : * * : * * : * * : * * : * .
```



```

      81          100         120
ZIKV-UG ENGVQLTVVVGSVKNPWRGPQRLLPVNELPHGKAWGK
ZIKV-BR ENGVQLTVVVGSVKNPWRGPQRLLPVNELPHGKAWGK
DENV2   ENGVQLTIMTGSIKGIMQAGKRSLSPPQPTELKYSWKTWGK
WNV     ENGVDSLSSVVEKQEGMYKSAPKRLTATTEKLEIGWKAWGK
* * * . * : . . . . . * : * . * * : * * :
```

Figure 5.6.2: Alignment colored through `pimc` descriptor.

5.7 Color by position index and mutation (`pimc`)

The `pimc` descriptor can be declared when it is desired to put color based on an index and distinguish point mutations⁶. `pimc` is a copy of `pic`, so we can simply change `pic` by `pimc` from the previous array to get the following information:

main	comparison	descriptor	sequence	residue	mutation	style	threshold
main_0	1	pimc	[1]	[6...]	True	n	NaN
main_0	1	pimc	[1]	[94...]	True	b	NaN
main_0	1	pimc	[2]	[75...]	True	d	NaN
main_0	1	pimc	[3]	[54...]	True	u	NaN

⁵In the table they are being replaced by points.

⁶Imagine that this descriptor is equivalent to `fmac` or `tmc` (see Sections 5.5 or 5.9, respectively).



Check that the `mutation` column appears with the Boolean value equal to `True`. If you prefer another color for the mutations, remember that it is also possible to implement the `-mco` flag (see Section 5.13).

The HTML file will be like shown in Figure 5.6.2.

A practical example using this descriptor appears in Section 8.3. Also, the implementation of the `pimc` descriptor appears in a previously published study [3].



Figure 5.7.1: Alignment colored through `tc` descriptor.

5.8 Color by threshold (tc)

To discriminate the numeric values of the input data by means of color and using a threshold, it is possible through the following declaration:

```
descriptor_col = { 'tc' : [94, 0.1, '>='] }
```

The descriptor `tc` is a dictionary where its value is a list with three elements. In the first position of that list, you must put a positive integer number that is related to the type of color desired (see Section 5.16). In the second position, there is an `int/float` number that defines the threshold, and the third element, must be a string that refers to a symbol of order relation (*i.e.*, `'>='`, `'<='`, `'>`, `'<`, `'=='`, `'!='`). For our example, we are ordering the program to color in Blue only those ΔpK_a of the target-residues that are greater equal than 0.1.

Subsequently, the log file will report the color number in the `sequence` column, and the two last parameters of the `tc` descriptor list in the `threshold` column, like this:



```
main  comparison  descriptor  sequence  residue  mutation  style  threshold
main_0           1          tc      [94]       NaN       NaN       NaN    0.1, >=
```

The HTML file will now display a color for each target-residue following the threshold condition (Figure 5.7.1).

A practical example using this descriptor appears in Section 8.2. The implementation of the `tc` descriptor appears in a previously published study [2].

The figure shows a sequence alignment of four viruses: ZIKV-UG, ZIKV-BR, DENV2, and WNV. The alignment is color-coded based on the `tmc` descriptor. The top row shows positions 1, 20, 40, and 60. The bottom row shows positions 81, 100, and 120. Residues are colored according to their mutation status relative to the reference sequence (ZIKV-UG). Blue boxes indicate mutations, while grey boxes indicate conserved residues. The alignment highlights specific mutations in the ZIKV-BR and DENV2 strains compared to the reference.

Figure 5.8.1: Alignment colored through `tmc` descriptor.

5.9 Color by threshold and mutation (tmc)

The descriptor `tmc` is the version of `tc` that will simultaneously discriminate mutations. This follows the same `tc` rules and is invoked as follows:

```
descriptor_col = { 'tmc' : [94, 0.1, '>='] }
```

The log file will report the next information:

```
main  comparison  descriptor  sequence  residue  mutation  style  threshold
main_0           1          tc      [94]       NaN      True     NaN    0.1, >=
```

Look that a Boolean value equal to `True` appears in the `mutation` column. If you prefer another color for the mutations remember that it is also possible to implement the `-mco` flag (see Section 5.13).



The HTML file will be like shown in Figure 5.8.1. Note that CPRISMA only taking into account mutations that are matching the declared threshold condition.

5.10 pK_a color (pkac)

To use the `pkac` descriptor you must always do a Δ operation among *ionizable residues* (see Section 4.2). To execute this descriptor, your “`array_get.py`” script should contain the following instructions:

```
descriptor_col = { 'pkac' : True/False7 }
```

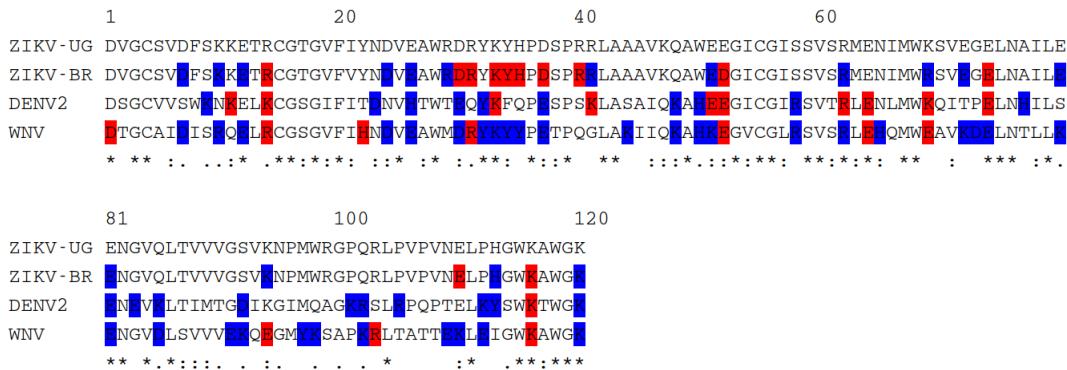


Figure 5.10.1: Alignment colored through `pkac` descriptor and invoking `False` as value.

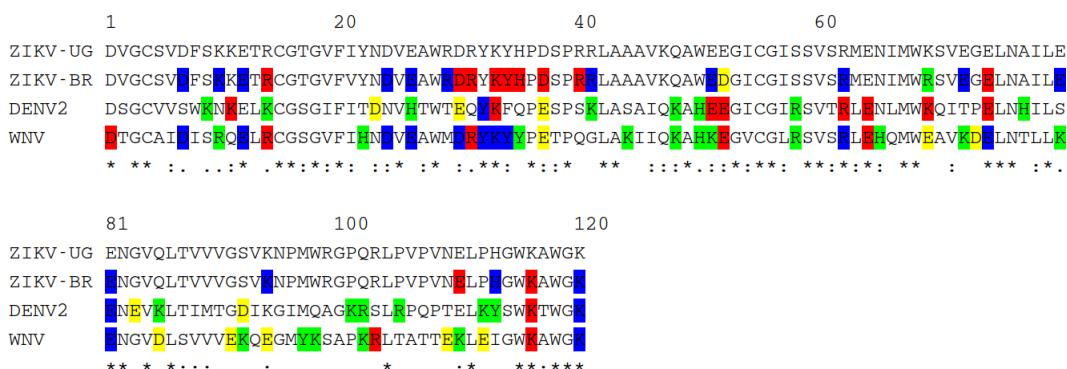


Figure 5.10.2: Alignment colored through `pkac` descriptor and invoking `True` as value.

⁷Select only one Boolean option.



The descriptor `pkac` is able to distinguish between those negative and positive ΔpK_a of the ionizable groups and will assign Red and Blue colors, respectively. Observe that the `descriptor_col` dictionary has a Boolean variable as a value. You can interpret `False` or `True` for cases where you do not require (as `fac/pic/tc` descriptors) or require (as `fmac/pimc/tmc` descriptors) to differentiate point mutations, respectively. If `True`, mutations will be highlighted in two ways:

1. When there is a shift from acid residue to a basic one (Lime color will be assigned).
2. Vice versa (Yellow color will be assigned).

A typical output in the log file when the `pkac` descriptor is invoked with `False` Boolean appears below:

```
main  comparison  descriptor  sequence      residue  mutation  style  threshold
main_0          1            pkac        NaN  [ionizable]      NaN      NaN      NaN
```

Note: Remember, if you invoke the Boolean `True` as a value in the dictionary of `pkac` descriptor, then this parameter will be displayed on the `mutation` column as `True`.

Whenever the `pkac` descriptor is run, the `residue` column will show the information: `[ionizable]`. Examples of colored alignments by means of the `pkac` descriptor using `False` and `True` appear in Figures 5.10.1 and 5.10.2, respectively. See that this descriptor can be quite useful for data with negative or positive numbers even if they are not pK_a values!

A practical example appears in Section 8.1. Nevertheless, note that for these cases other features are being incorporated, such as color gradient (see Chapter 6). The implementation of the `pkac` descriptor appears in a previously published study [1].

5.11 Color descriptors dictionary (-dco)

When the `multiple` comparison method is executed, maybe you need to distinguish each reference/target(s) relationship with a specific color descriptor. For that, we must build an array of color descriptors through the `dict_col` variable of the script “array_get.py”. To build it, you should follow the same rules as for `dict_ope` (see Section 4.5). For this example, we used the same dictionary for the `multiple` method as a base (see Subsection 3.10.3). Then,



our CPRISMA color-array will be as follows⁸:

```
dict_col = { 'main_0' : [ { 'pimc' : [ { '1' : [63, 'b', '0-20'] } , { '3' : [96, 'u', '20-35'] } ] } , { 'ssc' } ] , 'main_1' : [ { 'fsc' : [2,80] } , { 'pkac' : True } ] , 'main_2' : [ { 'fac' : ['6, 20, 22, 54, 94, 46'] } ] }
```

Now we can execute the `-dco` flag to call the array `dict_col`.⁹

```
cprisma -tr -ck -rf multiple -va 2 -hc -sco 20 -mco 75 -dco
```

1	20	40	60		
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYH	PDSPRRLAAAVQQA	EEGICGISSVS	RMENIMWKSVEGELNAILE	comparison 1
ZIKV-BR	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYH	PDSPRRLAAAVQQA	EEGICGISSVS	RMENIMWKSVEGELNAILE	
DENV2	DSGCVVSWKNKELKGCGSIFICITDNVHTWTEQYKFQPEPSK	LASAIQKAHEEGICG	IERSVTRLENLMWK	QITPELNHILS	
WNV	DTGCAIDISRQELRGSGVFIHNDVEAWMDRYKYPETPQGLAKIIQKAHK	GVCGLRSVS	LEQMWEAVKD	LNLLKK	
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYH	PDSPRRLAAAVQQA	EEGICGISSVS	RMENIMWKSVEGELNAILE	comparison 2
ZIKV-BR	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYH	PDSPRRLAAAVQQA	EEGICGISSVS	RMENIMWKSVEGELNAILE	
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYH	PDSPRRLAAAVQQA	EEGICGISSVS	RMENIMWKSVEGELNAILE	comparison 3
DENV2	DSGCVVSWKNKELKGCGSIFICITDNVHTWTEQYKFQPEPSK	LASAIQKAHEEGICG	IERSVTRLENLMWK	QITPELNHILS	
ZIKV-BR	DVGCSVDFSKKETRCGTGVFYNDVEAWRDRYKYH	PDSPRRLAAAVQQA	EEGICGISSVS	RMENIMWKSVEGELNAILE	comparison 4
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYH	PDSPRRLAAAVQQA	EEGICGISSVS	RMENIMWKSVEGELNAILE	
DENV2	DSGCVVSWKNKELKGCGSIFICITDNVHTWTEQYKFQPEPSK	LASAIQKAHEEGICG	IERSVTRLENLMWK	QITPELNHILS	
WNV	DTGCAIDISRQELRGSGVFIHNDVEAWMDRYKYPETPQGLAKIIQKAHK	GVCGLRSVS	LEQMWEAVKD	LNLLKK	
DENV2	DSGCVVSWKNKELKGCGSIFICITDNVHTWTEQYKFQPEPSK	LASAIQKAHEEGICG	IERSVTRLENLMWK	QITPELNHILS	comparison 5
ZIKV-UG	DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYH	PDSPRRLAAAVQQA	EEGICGISSVS	RMENIMWKSVEGELNAILE	

Figure 5.11.1: Alignment for `multiple` comparison method and colored through an array of color descriptors `dict_col`. Not all alignment is being shown.

The log file will show the relationships between each comparison and color descriptor:

Comparing `dict_ref` with `dict_col`:

```
{'0': [1, 2, 3]} ..... { 'pimc' : ... }
```

⁸Note that we have differentiated each color descriptor for each comparison with a different color to aid the reader.

⁹Notice that additional parameters are being implemented.



```
{'0':  []} ..... { 'ssc' }
```

```
{'1':  [0, 2]} ..... { 'fsc' :  [2,80] }
```

```
{'1':  [0, 2, 3]} ..... { 'pkac' :  True }
```

```
{'2':  [0]} ..... { 'fac' :  [6, 20, 22...]} }
```

The array of the feature ‘color’ `dict_col` is compatible with the array of comparison sequences `dict_ref`!

... and a table with a summary for all color descriptor information per comparison:

main	comparison	descriptor	sequence	residue	mutation	style	threshold
main_0	1	pimc	[1]	[63...]	True	b	NaN
main_0	1	pimc	[3]	[96...]	True	u	NaN
main_0	2	ssc	[same]	NaN	NaN	NaN	NaN
main_1	3	fsc	[2, 80]	NaN	NaN	NaN	NaN
main_1	4	pkac	NaN	[ionizable]	True	NaN	NaN
main_2	5	fac	NaN	[6...]	NaN	NaN	NaN

Figure 5.11.1 shows the alignment for the typed commands and the built `dict_col` array.

Note: If the array of `dict_col` is wrongly built, all descriptors will be transformed to `nc` (default parameter) for each comparison and additional information about where the errors are will be displayed.

Note: Remember that these complex color-arrays can be simultaneously combined (or not) with other transcendental CPRISMA arrangements of the other features as well (*i.e.*, operation, visualization, and maximum restriction described in Sections 4.5, 6.1, and 7.14). See also the practical examples in Chapter 8.

5.12 Color sequence (-sco)

To change the default color of the `ssc` descriptor, you should leave your variable `descriptor_col` as declared above in Section 5.2 and execute the `-sco` flag followed by a positive integer number in the terminal, as follows:



```
cprisma -tr -ck -sco 51
```

Remember that this number should be equivalent to a positive integer number less equal than 142. For the command above we have changed the alignment color from Red to GreenYellow, which is at row-position 51 when `-lco` is executed (see Section [5.16](#)).

5.13 Color mutation (`-mco`)

It is possible to change the color of the mutations by executing a command like the one below:

```
cprisma -tr -ck -mco 75
```

Remember to use the same rules as for the `-sco` flag (see Section [5.12](#)). For the command above, the color of point mutations was changed from Gray to Cyan.

Note: The flag `-mco` only works for `fmac`, `pimc`, and `tmc` color descriptors (see Sections [5.5](#), [5.7](#), and [5.9](#), respectively).

5.14 Color intensity (`-ico`)

Sometimes when we apply a gradient color (see Chapter [6](#)) the intensity of this can not be the best due to several problems (as mentioned earlier in Section [3.2](#)). An alternative to fix these dilemmas is to multiply the intensity of the color by a positive integer number invoking the `-ico` flag. As an example, you can execute it as appears below:

```
cprisma -tr -ck -ico 4
```

For the previous command line, we are multiplying by 4 the intensity of the color. We recommend the user to test with gradient colors and implement `-ico`.

5.15 Color on three-dimensional structure (`-tco`)

To observe the regions colored by CPRISMA at the three-dimensional structure level, the `-tco` flag can be useful. Using the case of Section [5.10](#) as an example^{[10](#)}, we can execute:

```
cprisma -tr -ck -tco
```

¹⁰Differences between mutations are being considered.

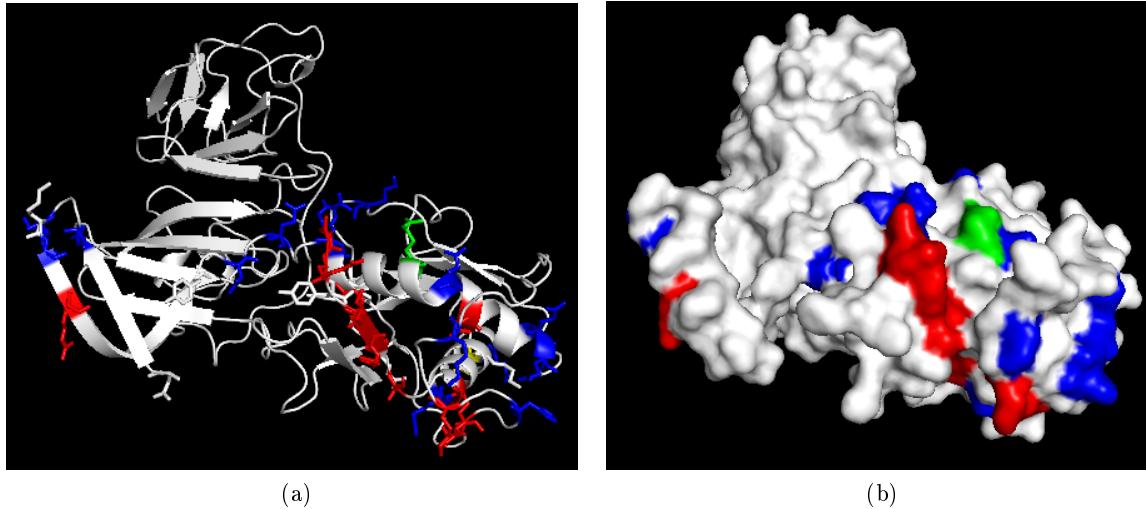


Figure 5.15.1: Three-dimensional structure for the monomeric NS1_{ZIKV-BR} (PDB id 5GS6) using the pkac descriptor. (a) Ribbons representation (target-residues appear as sticks). (b) Surface representation. Visualizations were made from Pymol scripts generated through the -tco flag.

This command will generate a directory called “3D_representation” with various Pymol scripts for all proteins and comparisons. To visualize the protein, type the next command line:

```
pymol your-protein.pdb 3D_representation/main_0/main_0_comparison1_your-protein.pml
```

An example for ZIKV-BR appears in Figure 5.15.1. Notice that only the target-residues are taken into account. Furthermore, only the first 120 amino acids are being evaluated.

5.16 List of colors (-lco)

To have quick access to the list of colors you can execute the command:

```
cprisma -lco
```

Figure 5.16.1 shows the first 10 rows displayed in the terminal as an example. See that an index appears numbering each color. This index will be useful to access the colors that CPRISMA applies. Remember, these colors are based on the website <https://htmlcolorcodes.com/color-names/>.



Note: The possible number of colors is from 0 to 142.

	General	Name	Hex	RGB
0	Red HTML	IndianRed	#CD5C5C	rgb(205, 92, 92)
1	Red HTML	LightCoral	#F08080	rgb(240, 128, 128)
2	Red HTML	Salmon	#FA8072	rgb(250, 128, 114)
3	Red HTML	DarkSalmon	#E9967A	rgb(233, 150, 122)
4	Red HTML	LightSalmon	#FFA07A	rgb(255, 160, 122)
5	Red HTML	Crimson	#DC143C	rgb(220, 20, 60)
6	Red HTML	Red	#FF0000	rgb(255, 0, 0)
7	Red HTML	FireBrick	#B22222	rgb(178, 34, 34)
8	Red HTML	DarkRed	#8B0000	rgb(139, 0, 0)
9	Pink HTML	Pink	#FFC0CB	rgb(255, 192, 203)
10	Pink HTML	LightPink	#FFB6C1	rgb(255, 182, 193)

Figure 5.16.1: First 10 rows when invoked `-lco` command.



6 Visualization (descriptor_vis)

Previously, in Chapters 3 and 5, we already saw some commands and variables that alter the display of alignments. In this Chapter, we will give an expansion focusing on three possible functionalities available on CPRISMA through the so-called “visualization” feature:

1. Reference display (`Re`).
2. Target-sequence(s) degrade (`De`).
3. Visualization of the letters (`Le`).

These three variables will be the descriptors of the “visualization” feature, and they are always declared simultaneously through the `descriptor_vis` of the “array_get.py” script (Figure 2.2.3), as follows:

```
descriptor_vis = { 'ReY', 'DeN', 'LeY' }
```

The `descriptor_vis` is a set variable with three elements. Besides, each descriptor is accompanied by a letter Y (Yes) or N (No), which indicates whether or not this visualization feature is enabled, respectively.

Suppose we respectively declare the operation (see Chapter 4) and color (see Chapter 5) variables like this,

```
descriptor_ope = { 'd' }

descriptor_col = { 'pkac' : True }

... and we run the next command1:
```

```
cprisma -tr -ck
```

You may have noticed that your log file shows the following information:

¹It is important to mention that for most of the examples in this Chapter we have used this command and these variables as declared.



1 20 40 60
 ZIKV-BR DVGCSVDFSKKETRCGTGVFVYNDVIAWRDRYKYHPSPRDLAAAVKQAWPDGICGISSVSRMENIMWRSVGEELNAILE
 DENV2 DSGCVSVWNKELKGSGSIFITDNVHTWTEQKFQPEPSKLASAIQAHHEEGICGIVSVTRLENLMWKQITPELNHILS
 WNV DTGCAIDISRQELRCGSVFIHNDVIAWMDRYKYYPETPQGLAKIIQAHKEGVCGLSVSRLEHQMWAEAVDDELNTLLK
 * * . . . : * . * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * .

81 100 120
 ZIKV-BR ENGVQLTVVVGSVNPMPWRGPQRPLPVVNELPHGWKAWGK
 DENV2 ENEVKLTIMTGDIKGIMQACKRSLQPQPTELKYSWKTWKG
 WNV ENGVDSLSSVVEKQEGMYKSAPKRLTATTEKLEIGWKAWGK
 * * . * : : * : * . * : * : * : * .

(a)

1 20 40 60
 ZIKV-UG DVGCSVDFSKKETRCGTGVFIYNDVEAWRDRYKYHPDSPRLLAAAVKQAWEEGICGISSVSRMENIMWKSVEGELNAILE
 ZIKV-BR DVGCSVDFSKKETRCGTGVFVYNDVIAWRDRYKYHPDSPRLLAAAVKQAWEDGICGISSVSRMENIMWRSVEGELNAILE
 DENV2 DSGCVSVWNKELKGSGSIFITDNVHTWTEQKFQPEPSKLASAIQAHHEEGICGIVSVTRLENLMWKQITPELNHILS
 WNV DTGCAIDISRQELRCGSVFIHNDVIAWMDRYKYYPETPQGLAKIIQAHKEGVCGLSVSRLEHQMWAEAVDDELNTLLK
 * * . . . : * . * : * : * : * : * : * : * : * : * : * : * : * : * .

81 100 120
 ZIKV-UG ENGVQLTVVVGSVKNPMPWRGPQRPLPVVNELPHGWKAWGK
 ZIKV-BR ENGVQLTVVVGSVKNPMPWRGPQRPLPVVNELPHGWKAWGK
 DENV2 ENEVKLTIMTGDIKGIMQACKRSLQPQPTELKYSWKTWKG
 WNV ENGVDSLSSVVEKQEGMYKSAPKRLTATTEKLEIGWKAWGK
 * * . * : : * : * . * : * : * : * .

-13.3 13.3
 acid mutation basic mutation

(b)

1 20 40 60
 ZIKV-UG
 ZIKV-BR
 DENV2
 WNV
 * * . . . : * . * : * : * : * : * : * : * : * : * : * .

81 100 120
 ZIKV-UG
 ZIKV-BR
 DENV2
 WNV
 ** . * : : * : * . * : * : * : * .

(c)

Figure 6.0.1: Several alignments using different visualization descriptors. (a) Re descriptor with False Boolean (N). (b) De descriptor with True Boolean (Y). (c) Le descriptor with False Boolean (N).



main	comparison	reference	degraded	letters
main_0	1	True	False	True

Now, for each visualization descriptor, a Boolean variable is shown based on the relations: Y (True) and N (False).

Note: Sometimes, some descriptors can be declared wrongly. To avoid that the program stops, it will always return to ‘ReY’, ‘DeN’, ‘LeY’ descriptors (default parameters), with some additional error messages in your log file, which will guide you to correct the problem.

Early, the output alignment for these initial parameters was displayed (Figure 5.10.2). But now, let us change reference descriptor from ReY to ReN, as follows:

```
descriptor_vis = { 'ReN', 'DeN', 'LeY' }
```

As shown in Figure 6.0.1a, the “reference line” has disappeared. Since this sequence may not be relevant because it does not have any color, the Re descriptor allows us to remove it or not as appropriate.

Enabling the degrade, like this:

```
descriptor_vis = { 'ReY', 'DeY', 'LeY' }
```

... we can see the effect that our operations have when it is invoked the d descriptor on the descriptor_ope (Figure 6.0.1b). Check that the color is on a scale from -13.3 to 13.3. This scale is normalized based on the maximum value derived from Δ operation². We observe that the point mutations have a greater impact on the rest of the ΔpK_a values. Nevertheless, it is possible to apply maximum restriction methods to improve the color alignment display (see Chapter 7).

Finally, if we are not interested in visualizing the letters of the protein sequences, you could eliminate them by means of the following declaration:

```
descriptor_vis = { 'ReY', 'DeN', 'LeN' }
```

Figure 6.0.1c shows an alignment without the letters.

We recommend checking the practical examples in Sections 8.1 and 8.2 for a better understanding of the visualization descriptors.

²See explicitly the Δ calculations in your log file with the -t flag (see Section 3.11).



6.1 Visualization descriptors dictionary (-dvi)

When it is applied complex comparisons with the `multiple` method (see Subsection 3.10.3), perhaps you will require to make a specific visualization based on `Re`, `De`, and `Le`, for each reference/target(s) relationship. For this, we can invoke the `-dvi` flag to get a visualization descriptors dictionary `dict_vis` from the “array_get.py” script. It is important to mention that the same rules as already described for `dict_ope` were followed (see Section 4.5). For our example, the `dict_col` arrangement mentioned in Section 5.11 was employed. On the other hand, it will be assumed to be `d` for all comparisons (*i.e.*, `descriptor_ope = { 'd' }`) and the same array of comparisons described in Subsection 3.10.3. Our `dict_vis` variable will be declared as follows³:

```
dict_vis = { 'main_0' : [ { 'ReN', 'DeN', 'LeY' } , { 'ReY', 'DeY', 'LeY' } ] ,  
            'main_1' : [ { 'ReY', 'DeN', 'LeN' } , { 'ReY', 'DeY', 'LeY' } ] ,  
            'main_2' : [ { 'ReN', 'DeY', 'LeY' } ] }
```

Now we can execute the `-dvi` flag to call the array `dict_vis`⁴:

```
cprisma -tr -ck -rf multiple -va 2 -hc -sco 20 -mco 75 -dco -dvi
```

The log file will show the relationships between each comparison and visualization descriptors:

Comparing `dict_ref` with `dict_vis`:

```
{'0': [1, 2, 3]} ..... ['ReN', 'DeN', 'LeY']  
{'0': []} ..... ['ReY', 'DeY', 'LeY']  
{'1': [0, 2]} ..... ['ReY', 'DeN', 'LeN']  
{'1': [0, 2, 3]} ..... ['ReY', 'DeY', 'LeY']  
{'2': [0]} ..... ['ReN', 'DeY', 'LeY']
```

The array of the feature ‘visualization’ `dict_vis` is compatible with the array of comparison sequences `dict_ref`!

³Note that we have differentiated each set of visualization descriptors for each comparison with a different color to aid the reader.

⁴Notice that additional parameters are being implemented.



... and a table with a summary for all visualization descriptor information per comparison:

main	comparison	reference	degraded	letters
main_0	1	False	False	True
main_0	2	True	True	True
main_1	3	True	False	False
main_1	4	True	True	True
main_2	5	False	True	True

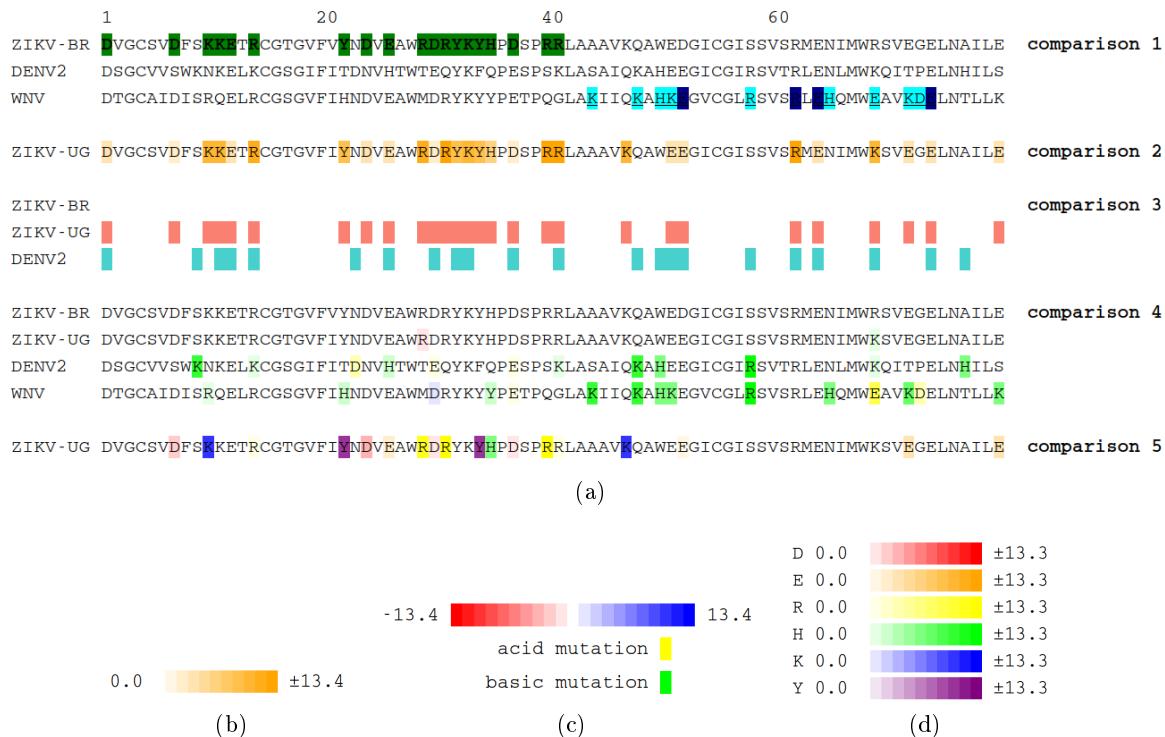


Figure 6.1.1: (a) Alignment for `multiple` comparison method and colored through the arrays of color (`dict_col`) and visualization (`dict_vis`) descriptors. Not all alignment is being shown. (b) Scale for comparison 2. (c) Scale for comparison 4. (d) Scale for comparison 5.

The HTML output for the previous conditions invoked is displayed in Figure 6.1.1a. Make the respective relationships between the previous table and that graph. Since we are invoking DeY for comparisons 2, 4, and 5, we are obtaining, respectively, their scales in the log file (Figures 6.1.1b, 6.1.1c, and 6.1.1d). Although comparison 2 does not have any target-sequence (*i.e.*,



{‘0’ : []}), the gradient color that you are seeing for this case is related to the reference protein. The case of comparison 4 is similar to what we saw earlier (Figure 6.0.1b), but now the reference sequence is ZIKV-BR. Finally, see that comparison 5 has separated a different color scale for each target-residue. This is because the color descriptor `fac` is being declared for that comparison (see Section 5.4). Nevertheless, the scale is normalized based on the greater value of the result of the operation `d` that is being applied for that comparison (*i.e.*, ± 13.3). You can see the independent behavior for each amino acid, but for that, you need to apply special maximum restriction methods (see Section 7.13).

Note: Whether the array of `dict_vis` is wrongly built, all descriptors will be transformed to ReY, DeN, LeY (default parameters) for each comparison and additional information about where the errors are will be displayed.



7 Maximum restriction (descriptor_mxr)

To understand how the CPRISMA feature called “maximum restriction” works, let us suppose the next declared variables in the “array_get.py” script¹:

```
descriptor_ope = { 'd' }

descriptor_col = { 'pkac' : True }

descriptor_vis = { 'ReY', 'DeY', 'LeY' }
```

Then the following command is run in terminal²:

```
cprisma -tr -ck -t
```

The HTML output for this example was already cited earlier (Figure 6.0.1b). Although this output is correct, we are not clearly observing the pK_a shifts for many target-residues. Since we have invoked the `-t` flag (see Section 3.11), our log file will show in the operation feature part, how the Δ data is being obtained (see Figure 7.0.1 as an example). The value of ΔpK_a highlighted in row 13 (*i.e.*, -13.3) is based on the subtraction $pK_{a-\text{DENV2}} - pK_{a-\text{ZIKV-UG}}$. This value matches with a mutation, due to a genetic indel (see row 13 in Figure 3.2.1). Thus, the scale of Figure 6.0.1b is being normalized as a function of this value, which corresponds to the maximum among the entire data set. Nonetheless, the regions that should be more Red or Blue cannot display that color because their ΔpK_a are very low with respect to the greater value. For instance, when is calculated $|0.1^{\Delta pK_a} / -13.3^{\Delta pK_a(\max)}|$, it is observed that 0.1 is 7.5×10^{-3} smaller than the maximum value. From the point of view of the HTML code, this is negligible and the color should be equal to White.

To improve the color displayed when is invoked a gradient by DeY (see Chapter 6), we can use a maximum restriction method like: `rm`, `ra`, `ram`, `rpi`, `rt`, `rs`, `rsm`, `rsa`, `rsam`, `rspi`, and `rspim`, through the variable `descriptor_mxr` of the script “array_get.py” (Figure 2.2.3).

¹For a further explanation of these variables see Chapters 4, 5, and 6, respectively.

²Most of the examples below are using this command line.



ZIKV-UG X ZIKV-BR DENV2 WNV

	0	1	2	3	d	->	0.0	0.0	-0.1
0	3.9	3.9	3.9	3.8	->	0.0	0.0	0.0	-0.1
1	3.1	3.4	0.0	3.4	->	0.3	-3.1	0.3	
2	0.0	0.0	10.5	0.0	->	0.0	10.5	0.0	
3	10.9	11.0	0.0	12.8	->	0.1	-10.9	1.9	
4	10.7	10.7	10.6	0.0	->	0.0	-0.1	-10.7	
5	3.8	4.0	3.8	4.0	->	0.2	0.0	0.2	
6	12.6	12.3	10.7	12.4	->	-0.3	-1.9	-0.2	
7	10.0	10.0	0.0	6.7	->	0.0	-10.0	-3.3	
8	0.0	0.0	3.4	0.0	->	0.0	3.4	0.0	
9	3.5	3.8	0.0	3.6	->	0.3	-3.5	0.1	
10	4.0	4.1	6.8	4.4	->	0.1	2.8	0.4	
11	12.6	13.4	0.0	0.0	->	0.8	-12.6	-12.6	
12	3.1	2.7	4.1	3.5	->	-0.4	1.0	0.4	
13	13.3	13.0	0.0	12.9	->	-0.3	13.3	-0.4	
14	9.6	9.6	10.0	9.8	->	0.0	0.4	0.2	
15	11.1	11.0	11.0	11.2	->	-0.1	-0.1	0.1	
16	10.0	9.7	0.0	10.2	->	-0.3	-10.0	0.2	
17	6.3	6.2	0.0	9.5	->	-0.1	-6.3	3.2	

Figure 7.0.1: Example of the pK_a data for each target protein and its ΔpK_a obtained after running `d` as an operation. The number highlighted in blue refers to the maximum value for this data set. All the information has not been shown.

7.1 No restriction (nr)

When it is not considered maximum restrictions we declare the `descriptor_mxr` as follows:

```
descriptor_mxr = { 'nr' }3
```

Note that `nr` descriptor is a string variable inside a pair of brackets.

When we run CPRISMA, our log file will show the following information:

main	comparison	descriptor	sequence	residue	position	mutation	threshold	separate
main_0	1	nr	NaN	NaN	NaN	NaN	NaN	NaN

This statement is simply saying that the `nr` descriptor was considered for comparison 1, in the `main_0` comparison set (for now ignore the rest of the columns in that log message). Besides this table, in the maximum restriction part of the log file, you will find a list with all values for the operations invoked, like this⁴:

³For all alignment examples of the preceding Chapters, this was the variable executed.

⁴These lists only appear when -t flag is executed (see Section 3.11).



```
list_max = [0.0, 0.3, 0.0, 0.1, 0.0, 0.2, -0.3, 0.0, 0.0, 0.3, 0.1, 0.8, -0.4, -0.3, 0.0, -0.1, -0.3, -0.1, -0.5, -0.2, 0.1, 0.0, 0.0, 0.0, 0.0, 0.1, -0.6, 0.0, 0.1, 0.0, 0.0, 1.7, 0.2, 0.0, -0.1, 0.0, 0.1, 0.3, 0.0, 0.0, 0.0, 0.0, 0.0, 0.1, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, -0.2, 0.0, 0.1, -0.5, 0.3, 0.0, -3.1, 10.5, -10.9, -0.1, 0.0, -1.9, -10.0, 3.4, -3.5, 2.8, -12.6, 1.0, -13.3, 0.4, -0.1, -10.0, -6.3, 0.7, -13.0, -1.8, 0.0, -11.0, 10.9, 6.4, -0.3, -0.8, 12.9, -0.2, -0.1, 0.0, -0.2, -3.8, 0.0, -0.2, 6.8, -4.2, 0.1, 4.2, 10.8, 0.0, 3.5, 0.0, 0.0, 0.0, -12.7, 10.2, 12.4, -12.9, 12.6, 0.0, 0.0, 11.2, 3.3, -0.2, 0.1, -0.1, 0.3, 0.0, 1.9, -10.7, 0.2, -0.2, -3.3, 0.0, 0.1, 0.4, -12.6, 0.4, -0.4, 0.2, 0.1, 0.2, 3.2, 0.7, -13.0, -12.9, 10.7, -11.0, 10.6, 6.1, 6.5, -0.9, 13.2, 0.1, -0.2, 6.8, -7.3, 7.9, 3.4, 0.1, 0.0, 7.2, 0.2, 0.0, 3.7, 4.0, 11.5, -6.7, 9.9, 10.9, -12.7, 0.0, 10.2, -0.5, 0.0, 3.6, 7.6, 4.2, -6.4, -0.1, 0.2]
```

A summary of this information should appear immediately, as follows:

main	minimum (abs)	maximum (abs)	length
main_0	0.0	13.3	168

Notice that this table is showing the maximum and minimum numbers for the last list after applying the absolute value. This is because the HTML code will only work with positive numbers. Furthermore, the column `length` is showing us the total number of elements for that list ($56^{\text{rows}} \times 3^{\text{target-proteins}} = 168$). As no restriction applies, all data is being considered.

Note: Sometimes, some descriptors can be declared wrongly. To avoid that the program stops, it will always return to the `nr` descriptor (default parameter), with some additional error messages in your log file, which will guide you to correct the problem.

7.2 Restriction by mutation (rm)

For our example, notice that most of the high ΔpK_a values correspond to regions where mutations occurred (compare Figures 3.2.1 and 7.0.1). We can declare the `rm` descriptor to avoid taking into account these “high ΔpK_a values” through:

```
descriptor_mxr = { 'rm' }
```

After executing the program, our table for this CPRISMA feature will appear in the log file like this:

main	comparison	descriptor	sequence	residue	position	mutation	threshold	separate
main_0	1	rm	NaN	NaN	NaN	True	NaN	NaN

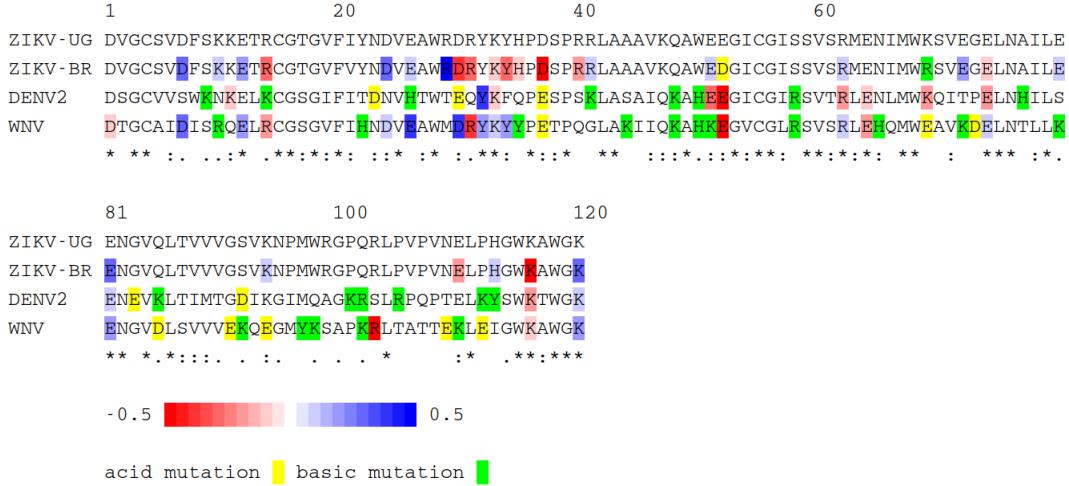


Figure 7.2.1: Alignment colored applying `rm` descriptor.

Notice that the `mutation` column has a Boolean equal to `True`. The list of ΔpK_a values that are being considered to normalize the color now is reduced:

```
list_max = [0.0, 0.2, 0.0, -0.1, 0.1, 0.0, -0.1, 0.3, -0.5, 0.3, 0.0, 0.0, 0.4, -0.1, -0.2, -0.1, -0.2, 0.1, -0.2, 0.1, -0.1, 0.2, 0.2, 0.1, 0.1, -0.2, 0.1, 0.2, -0.1, 0.2]
```

main	minimum (abs)	maximum (abs)	length
main_0	0.0	0.5	30

Note: For the following sections, this information will not be displayed or discussed anymore. When a maximum restriction is invoked, it is understood that CPRISMA is removing or transforming the data to normalize and improve the color visual quality of the alignment.

Changing the scale of these data allows us to observe with greater definition the color for each pK_a shifts (Figure 7.2.1). At this point, we can finally see the impact of the numerical data of the CSV input file after the Δ operation is applied.

7.3 Restriction by amino acid (ra)

Suppose you do not want to consider the numerical values of some target-residues (see Section 3.1). To delete them you can invoke the `ra` descriptor, as mentioned below:

```
descriptor_mxr = { 'ra' : [ 'R', 'K' ] }
```

The dictionary structure of the `ra` descriptor is composed by a key as a string (*i.e.*, '`ra`') and



a value as a list of target-residues (*i.e.*, `['R', 'K']`). For this example, CPRISMA is being instructed to do not take into account the numerical values of the row where Arg and Lys residues match in the processed data (for instance, row 2, 3, and 4 in Figure 3.2.1).

Note: When the `ra` descriptor is run, CPRISMA will looks for all the rows where the residue declared appears and the program will “remove” the entire row if it matches. Later, CPRISMA will calculate the maximum from these transformations. However, it is possible to use other specific descriptors like `rsa` (see Section 7.9) to have a more refined definition of maximum restriction.

The log file will display the following information:

```
main  comparison  descriptor  sequence      residue  position  mutation  threshold  separate
main_0        1          ra        NaN  ['R', 'K']       NaN       NaN       NaN       NaN
```

See that the `residue` column is showing the list declared. The color scale is now normalized based on this condition.



Figure 7.3.1: Scale example invoking `ram` descriptor.

7.4 Restriction by amino acid and mutation (ram)

The numerical values of target-residues and mutations can simultaneously constrained by means of:

```
descriptor_mxr = { 'ram' :  ['R', 'K'] }
```

The `ram` descriptor is a combination of `rm` (see Section 7.2) and `ra` (see Section 7.3), therefore it will follow the same rules as for those descriptors.

The log file will display the following information:

```
main  comparison  descriptor  sequence      residue  position  mutation  threshold  separate
main_0        1          ram        NaN  ['R', 'K']       NaN      True       NaN       NaN
```



Notice that the `mutation` column has a Boolean equal to `True`. Removing rows with Arg and Lys residues has changed the color scale. Now, it is displays a maximum of ± 0.4 instead of ± 0.5 (Figures 7.3.1 and 7.2.1, respectively).

7.5 Restriction by index position (rpi)

To have a maximum restriction for the exact position of specific operation values, the variable `descriptor_mxr` can be declared like this:

```
descriptor_mxr = { 'rpi' : [13, 45, 48] }
```

The `rpi` descriptor has a dictionary structure similar to `ra` (see Section 7.3). Although the list has numbers that match with the row index of the processed data (Figures 3.2.1 and 7.0.1), instead to target-residues. Remember, the numbers of the list should be related to that index and not the alignment position!

Note: When the `rpi` descriptor is typed, CPRISMA will looks for all the rows based on the index positions declared and the program will “remove” the entire row if matches. Later, CPRISMA will calculate the maximum from these transformations. Nevertheless, it is possible to use other specific descriptors like `rspi` (see Section 7.11) to have a more refined definition of maximum restriction.

The log file will display the following information:

main	comparison	descriptor	sequence	residue	position	mutation	threshold	separate
main_0	1	rpi	NaN	NaN	[13, 45, 48]	NaN	NaN	NaN

See that in the `position` column, the list declared for the `rpi` descriptor appears. Based on this, the color scale will be normalized.

7.6 Restriction by threshold (rt)

A maximum restriction based on a threshold can be invoked through:

```
descriptor_mxr = { 'rt' : [0.0, '>='] }
```

Look that `rt` descriptor has a dictionary structure. The value of the dictionary is a list with two elements where the first shows a numerical value (float type), meanwhile the second is a



string that refers to a symbol of order relation (*i.e.*, ‘ \geq ’, ‘ \leq ’, ‘ $>$ ’, ‘ $<$ ’, ‘ \equiv ’, ‘ \neq ’). Based on our example, we are telling the program to only take into account those rows with values greater equal than 0.0. Whether the row presents any number in any column that does not meet that condition, then the value will be converted to 0.0 immediately.

Note: Occasionally, too strict threshold can be invoked and this could cause all values to be ignored. To avoid the program stops, by default, CPRISMA will normalize everything based on 1.0.

The table when invoked `rt` descriptor looks like this:

```
main  comparison  descriptor  sequence  residue  position  mutation  threshold  separate
main_0        1          rt        NaN       NaN       NaN      NaN  [0.0, >=]      NaN
```

When `-t` flag is invoked (see Section 3.11), the log file will display the following information:

```
main  minimum (abs)  maximum (abs)  lenght
main_0           0.0           13.2       168
```

See that the `length` column reports the same amount of data as when we have no restriction (*i.e.*, when `nr` is applied [see Section 7.1]). This is because all values that do not satisfy the threshold condition are being converted to 0.0 and are not being “eliminated”.

Finally, the new maximum for the color scale will be 13.2. Our maximum constraint has not changed much despite the conversion of the highest negative value (*i.e.*, from -13.3 to 0.0). As the threshold condition cited above does not take into account values less than 0.0, the problem persists because, even with this restriction, the data still have “high” positive values like 13.2.

Note: Based on the last statement, it is important to mention that `rt` descriptor is more suitable for data with only one type of mathematical sign. For that, you could use `da` as an operation descriptor (see Section 4.3).

7.7 Restriction by sequence (rs)

In CPRISMA you can not consider the data of a whole sequence by invoking `descriptor_mxr` like this:



```
descriptor_mxr = { 'rs' : [2] }
```

The dictionary structure of the **rs** descriptor is similar to **ra** (see Section 7.3) or **rpi** (see Section 7.5). But now, the number in the list refers to a target-sequence.

The log file will display the following information:

```
main  comparison  descriptor  sequence  residue  position  mutation  threshold  separate
main_0        1          rs        [2]       NaN       NaN       NaN       NaN       NaN
```

For our example, we are not taking into account the data of the DENV2 sequence. Based on this, the color scale will be normalized.

*Note: Regarding the descriptor **rs**, the pair comparison method, array of comparisons like `{# : []}`, or cases where `-ck` is not invoked, CPRISMA will always return to the default value of the maximum restriction feature (i.e., `nr`).*

If you want to restrict the maximum values of target-residues or row position index from a specific sequence, we recommend Sections 7.9 and 7.11, respectively.

7.8 Restriction by sequence and mutation (**rsm**)

The data from a sequence and the places where mutations appear can simultaneously “removed” by means of:

```
descriptor_mxr = { 'rsm' : [2] }
```

The descriptor **rsm** is a combination of **rm** (see Section 7.2) and **rs** (see Section 7.7), so the same rules will apply for it.

The log file will display the following information:

```
main  comparison  descriptor  sequence  residue  position  mutation  threshold  separate
main_0        1          rsm        [2]       NaN       NaN      True       NaN       NaN
```

Notice that the **mutation** column has a Boolean equal to `True`. The scale of your HTML output will be normalized based on these parameters.



7.9 Restriction by sequence and amino acid (`rsa`)

Sometimes, it could be very radical to apply `ra` (see Section 7.3) due to many rows with useful values may be being removed. Nevertheless, to focus only on target-residues of a specific sequence, the `rsa` descriptor can be invoked. To declare this maximum restriction descriptor you can do it as follows:

```
descriptor_mxr = { 'rsa' : [ { '1' : ['R', 'K'] }, { '2' : ['D', 'Y'] } ] }
```

Notice that we saw this array structure before (see Subsection 3.10.3). Now, our value is a list of dictionaries. Each second-key represents the target-sequences of interest (*i.e.*, ‘1’ and ‘2’) and the second-values are the lists of target-residues to be discard (*i.e.*, ['R', 'K'] and ['D', 'Y'], respectively). For our example, CPRISMA is being instructed to just consider the sequences of ZIKV-BR (‘1’) and DENV2 (‘2’) and “to delete” the Arg and Lys residues; and the Asp and Tyr residues of that proteins, respectively. The descriptor `rsa` follows similar rules like `ra` but just examining the target-residues of the target-sequence of interest.

The log file will display the following information:

main	comparison	descriptor	sequence	residue	position	mutation	threshold	separate
main_0	1	rsa	[1]	['R', 'K']		NaN	NaN	NaN
main_0	1	rsa	[2]	['D', 'Y']		NaN	NaN	NaN

The color scale will be normalized based on these conditions.

*Note: Regarding the descriptor `rsa`, the pair comparison method, array of comparisons like `{# : []}`, or cases where `-ck` is not invoked, CPRISMA will always return to the default value of the maximum restriction feature (*i.e.*, `nr`).*

7.10 Restriction by sequence, amino acid, and mutation (`rsam`)

We can use a version of `rsa` that also restricts mutations simultaneously. For that, we invoke the maximum restriction variable by means of:

```
descriptor_mxr = { 'rsam' : [ { '1' : ['R', 'K'] }, { '2' : ['D', 'Y'] } ] }
```

The `rsam` is a combination of `rm` and `rsa` descriptors (see Sections 7.2 and 7.9, respectively), so it will follow similar rules as them. For this case, `rsam` will not take into account the mutations



that occur between the target-sequence of the second-keys [for our example, ‘1’ (ZIKV-BR) and ‘2’ (DENV2)] and the reference sequence [for our example, ‘0’ (ZIKV-UG)].

The log file will display the following information:

main	comparison	descriptor	sequence	residue	position	mutation	threshold	separate
main_0	1	rsa	[1]	['R', 'K']	NaN	True	NaN	NaN
main_0	1	rsa	[2]	['D', 'Y']	NaN	True	NaN	NaN

Notice that the `mutation` column has a Boolean equal to `True`. The color scale will be normalized based on these conditions.

7.11 Restriction by sequence and index position (`rspi`)

The `rspi` descriptor is similar to `rsa`, however, the second-value must have the index positions of the processed data (see the index in Figure 7.0.1). To declare `rspi`, we can do it by means of:

```
descriptor_mxr = { 'rspi' : [ { '1' : [0, 29] } , { '2' : [48] } ] }
```

The `rspi` descriptor shares the same rules as `rpi` (see Section 7.5) and `rsa` (see Section 7.9). For our example, CPRISMA is being instructed to just “delete” the positions 0 and 29 of ZIKV-BR (‘1’) and 48 of DENV2 (‘2’).

The log file will display the following information:

main	comparison	descriptor	sequence	residue	position	mutation	threshold	separate
main_0	1	rspi	[1]	NaN	[0, 29]	NaN	NaN	NaN
main_0	1	rspi	[2]	NaN	[48]	NaN	NaN	NaN

The color scale will be normalized based on these conditions.

Note: Regarding the descriptor `rspi`, the pair comparison method, array of comparisons like `{# : []}`, or cases where `-ck` is not invoked, CPRISMA will always return to the default value of the maximum restriction feature (i.e., `nr`).



7.12 Restriction by sequence, index position, and mutation (rspim)

The version of `rspi` that restricts places where point mutations occur is called `rspim` and can be declared as follows:

```
descriptor_mxr = { 'rspim' : [ { '1' : [0, 29] } , { '2' : [48] } ] }
```

The `rspim` is a combination of `rm` and `rspi` descriptors (see Sections 7.4 and 7.11, respectively), so it will follow similar rules as them⁵.

The log file will display the following information:

main	comparison	descriptor	sequence	residue	position	mutation	threshold	separate
main_0	1	rspim	[1]	NaN	[0, 29]	True	NaN	NaN
main_0	1	rspim	[2]	NaN	[48]	True	NaN	NaN

Notice that the `mutation` column has a Boolean equal to `True`. The scale of your HTML output will be normalized taking into account these parameters.

7.13 Restrictions by target-residues (Y)

Sometimes some target-residues have more influence than others when we apply a maximum restriction method. We can evaluate the independent maximum behavior for each target-residue by adding the letter '`Y`' to our descriptor in the following way:

```
descriptor_mxr = { 'nrY' }
```

When we run CPRISMA, our log file will show the following information:

main	comparison	descriptor	sequence	residue	position	mutation	threshold	separate
main_0	1	nr	NaN	NaN	NaN	NaN	NaN	True

Notice that the `separate` column is showing a Boolean variable as `True`. Whether `-t` flag is invoked (see Section 3.11), the log file will display the following information:

⁵See other considerations on how numerical data is removed at the places where mutations happen in Section 7.10 (although `rsam` and `rspim` are different maximum restriction methods they follow the same pattern of execution)



```
main    minimum (abs)           maximum (abs)   lenght
main_0      0.0  [3.7, 7.3, 13.2, 6.8, 11.5, 9.9]     NaN
```

Now, the `maximum (abs)` column is displaying the maximum for each target-residue. In other words, the values for each amino acid will be normalized according to their respective maxima. This list and its order will match according to the target-residues that were declared in the tuple `target_residues` (see Section 3.1). The alignment of the HTML file for this new condition appears in Figure 7.13.1. Note that the scale for each target-residue can be observed. A first impression may seem like there is no difference between what we got earlier (Figure 6.0.1b). Although some regions are fainter in color (see some amino acids between positions 20 and 40 on the alignment). The intensity of the color is still not enough because of the maximum values are still very high due to the presence of mutations.

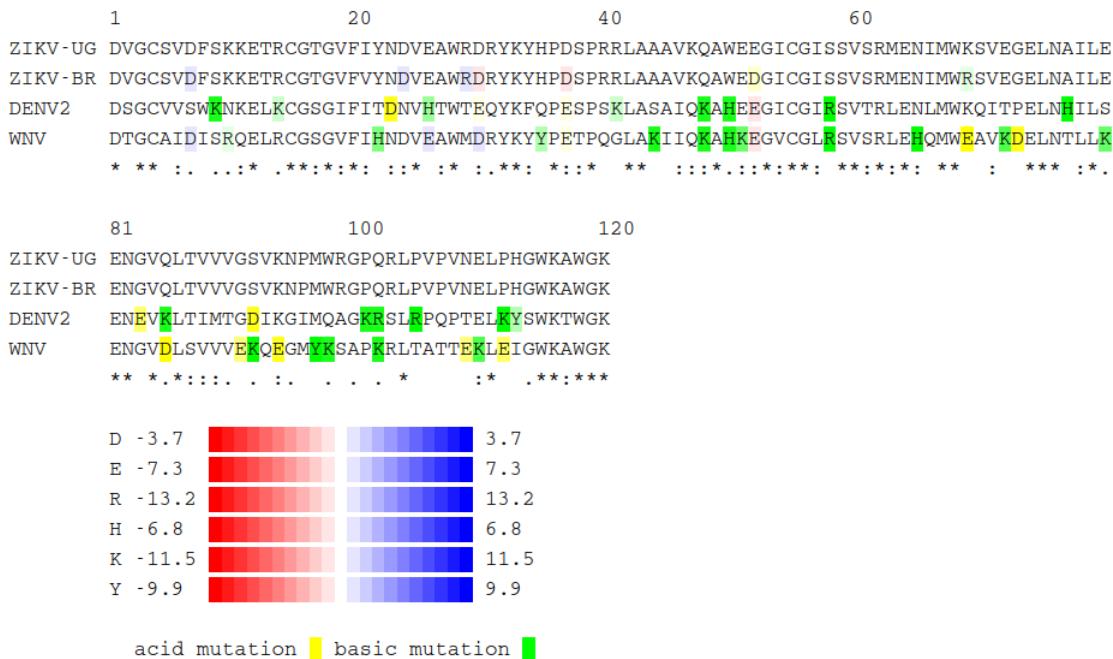


Figure 7.13.1: Alignment colored applying `nr` descriptor and the condition `Y` to separate the maximum per target-residue.

We can confirm this by invoking the color descriptor like this:

```
descriptor_col = { 'fac' : [6, 20, 22, 54, 94, 46] }
```



Based on that, we can clearly see the influence of the maximum for each target-residue (Figure 7.13.2). Furthermore, check how the most intense colors match with mutations.

Finally, you can test different descriptors and observe the behavior separately based on maximums for each target-residue. The base structure for invoking these conditions is shown as follows:

```
descriptor_mxr = { 'maximum_descriptorY' }  
  
descriptor_mxr = { 'maximum_descriptorY' : additional_parameters }
```

Note that we are considering situations where descriptors can be sets (e.g. `nr`, `rm`, and so on) or dictionaries (e.g., `rt`, `rsa`, `rspi`, and so on), respectively.

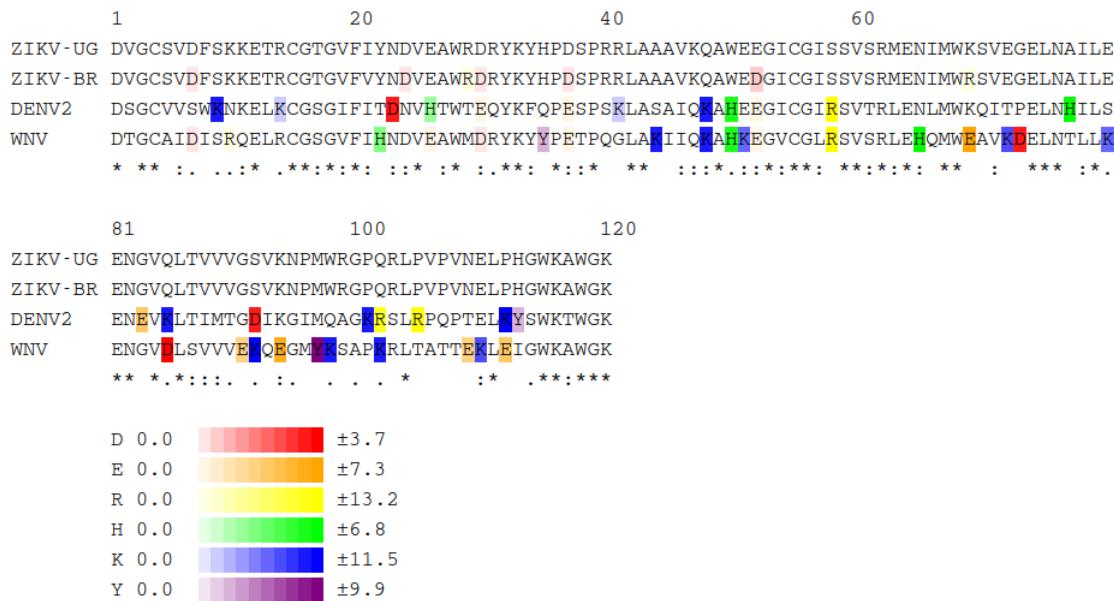


Figure 7.13.2: Alignment colored applying `nr` descriptor and the condition `Y` to separate the maximum per target-residue but using `fac` descriptor.

Note: We recommend the user to test different combinations of maximum restriction and color (see Chapter 5) descriptors, to examine the impact of each case. Keep in mind the same rules for each maximum restriction descriptor that we saw previously.



7.14 Maximum restriction descriptors dictionary (-dmx)

When the `multiple` comparison method is declared, it is possible that you need to distinguish each reference/target(s) relationship with a specific maximum restriction descriptor. For that, we must build an array of maximum descriptors through the `dict_mxr` variable of the script “array_get.py”. To build it, you should follow the same rules as for `dict_ope` (see Section 4.5). For this example, we used the same dictionary for the `multiple` method as a base (see Subsection 3.10.3). The CPRISMA maximum-restriction-array will be declared as follows⁶:

```
dict_mxr = { 'main_0' : [ { 'rmY' } , { 'nr' } ] ,  
            'main_1' : [ { 'rspim' : [ { '2' : [ 47, 48, 50 ] } ] } ,  
                         { 'rsaY' : [ { '0' : [ 'R' ] } , { '3' : [ 'D' ] } ] }  
            ,  
            'main_2' : [ { 'rt' : [ 0, '>=' ] } ] }
```

Now we can execute the `-dmx` flag to call the array `dict_mxr`⁷:

```
cprisma -tr -ck -rf multiple -dmx
```

The log file will show the relationships between each comparison and maximum restriction descriptors:

Comparing `dict_ref` with `dict_mxr`:

```
{'0': [1, 2, 3]} ..... { 'rmY' }  
{'0': []} ..... { 'nr' }  
{'1': [0, 2]} ..... { 'rspim' : ... }  
{'1': [0, 2, 3]} ..... { 'rsaY' : ... }  
{'2': [0]} ..... { 'rt' : [0, '>=' ] }
```

The array of the feature ‘maximum’ `dict_mxr` is compatible with the array of comparison sequences `dict_ref`!

⁶Note that we have differentiated each maximum restriction descriptor for each comparison with a different color to aid the reader.

⁷Notice that additional parameters are being implemented.



... and a table with a summary for all maximum descriptor information per comparison:

main	comparison	descriptor	sequence	residue	position	mutation	threshold	separate
main_0	1	rmY	NaN	NaN	NaN	True	NaN	True
main_0	2	nr	NaN	NaN	NaN	NaN	NaN	NaN
main_1	3	rspim	2	NaN	[47...]	True	NaN	NaN
main_1	4	rsaY	0	[R]	NaN	NaN	NaN	True
main_1	4	rsaY	3	[D]	NaN	NaN	NaN	True
main_2	5	rt	NaN	NaN	NaN	NaN	[0, >=]	NaN

Note: If the array of dict_mxr is wrongly built, all descriptors will be transformed to nr (default parameter) for each comparison and additional information about where the errors are will be displayed.



8 Practical Examples

The following examples bring together some of the features that we described earlier. Each is related to a previously published study [1, 2]. Furthermore, in the “examples” directory, you will find the scripts, alignments and other files that help as the basis for achieving the desired visualizations. Many details will not be given as we wish to motivate the reader to test and explore the characteristics of each example on their own. Each case follows the next order:

1. Command-line invoked.
2. Declared variables (as shown in Figure 2.2.3).
3. An image of the alignment.

Each example tries to approximate a certain image from a specific publication. In example 1 (see Section 8.1) we try to reproduce Figure 8 [1], in example 2 (see Section 8.2) Figure 5 (only chain A) [2], and in example 3 (see Section 8.3) Figure 1a [3].

Note: For more details on the methodological aspects, data collection, purpose, and others, you can find them in the respective publication.

8.1 Example 1: ΔpK_a for several NS1_{ZIKV}

Command-line:

```
cprisma -tr -ns -ck -rf multiple -va 2 -j -sco 142 -dop -dco -dvi -dmx
```

Variables:

```
target_residues = ('D', 'E', 'R', 'H', 'K', 'Y')

name_sequence = ('UG_chA_x-ray', 'UG_chB_x-ray', 'UG_chA_mod1', 'UG_chA_mod2',
'SE_chA_mod1', 'CAR_chA_mod1', 'MA_chA_mod1', 'TH_chA_mod1', 'YAP_chA_mod1',
'BR_chA_x-ray', 'BR_chB_x-ray', 'BR_chA_mod1', 'BR_chA_mod2', '')

descriptor_ope = {'n'}
```



```
descriptor_col = { 'nc' }

descriptor_vis = { 'ReY', 'DeN', 'LeY' }

descriptor_mxr = { 'nr' }
```

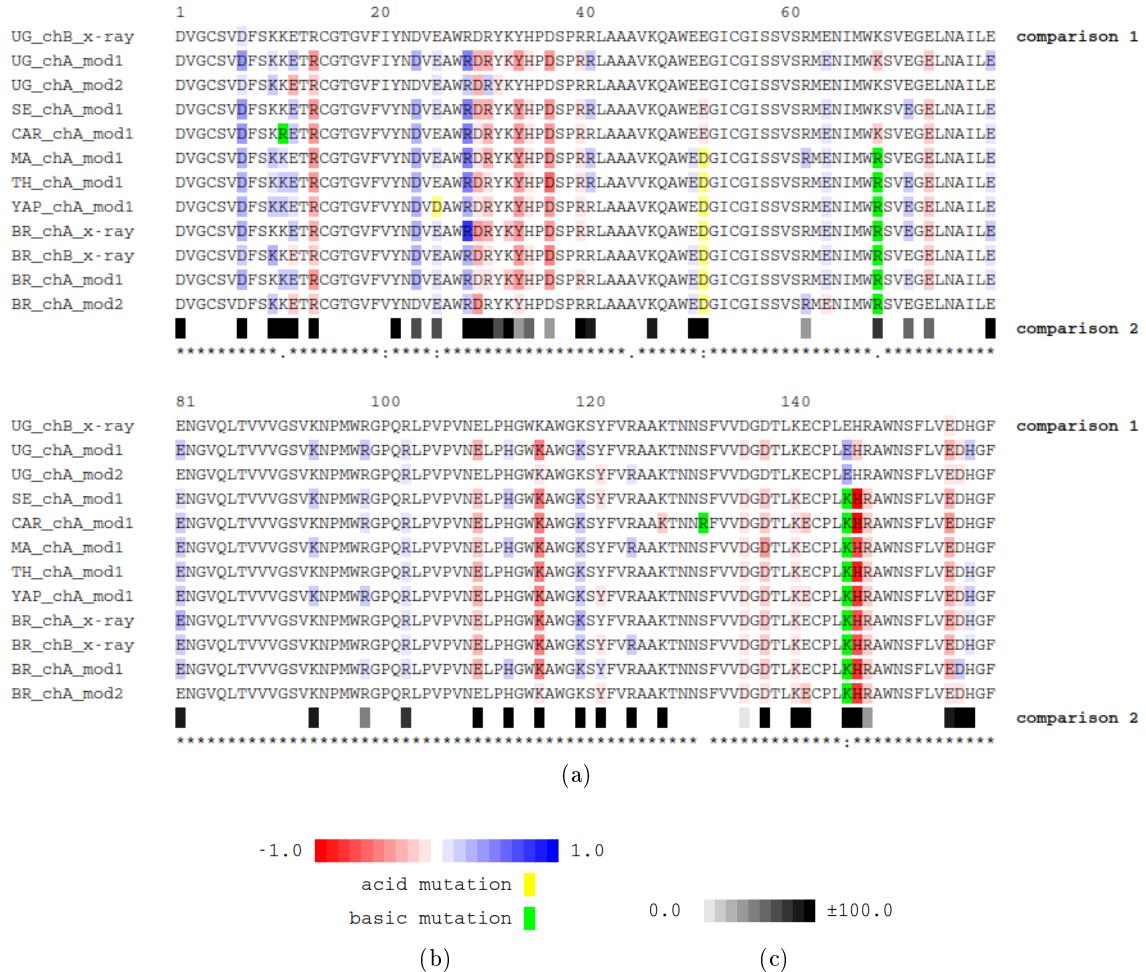


Figure 8.1.1: (a) Alignment for Example 1. Not all alignment is being shown. (b) Scale for comparison 1. (c) Scale for comparison 2.

```
dict_ref = { 'main_0' : [ { '0' : [ 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 ] } ] ,  
            'main_13' : [ { '13' : [ ] } ] }
```



```
dict_ope = { 'main_0' : [ { 'd' } ] ,  
            'main_13' : [ { 'n' } ] }  
  
dict_col = { 'main_0' : [ { 'pkac' : True } ] ,  
            'main_13' : [ { 'ssc' } ] }  
  
dict_vis = { 'main_0' : [ { 'ReN', 'DeY', 'LeY' } ] ,  
            'main_13' : [ { 'ReY', 'DeN', 'LeN' } ] }  
  
dict_mxr = { 'main_0' : [ { 'rm' } ] ,  
            'main_13' : [ { 'nr' } ] }
```

From these input parameters, we obtain the alignment that appears in Figure 8.1.1. Note that the last element of the tuple `name_sequence` does not have a name. Due to that, the alignment will not display any name for that sequence.

8.2 Example 2: B-cell epitope predictions on NS1_{WNV(176–352)}

Command-line:

```
cprisma -tr -ck -rf multiple -ns -va 2 -j -hc -n 176 -sco 142 -a 3 -dop -dco  
-dvi
```

Variables

```
target_residues = ('D', 'E', 'R', 'H', 'K', 'Y')  
  
name_sequence = ('SASA', 'pKa_NS1 (alone)', 'PROCEEDpKa', 'PISA', 'DiscoTope',  
                 'ElliPro', 'SEPPA2', 'SEPPA3', 'Consensus', '')  
  
descriptor_ope = { 'n' }  
  
descriptor_col = { 'nc' }  
  
descriptor_vis = { 'ReY', 'DeN', 'LeY' }  
  
descriptor_mxr = { 'nr' }  
  
dict_ref = { 'main_0' : [ {'0' : [] } ] ,  
            'main_1' : [ {'1' : [2] } ] ,
```



```
'main_3' : [ {'3' : []} ] ,
'main_4' : [ {'4' : []} ] ,
'main_5' : [ {'5' : []} ] ,
'main_6' : [ {'6' : []} ] ,
'main_7' : [ {'7' : []} ] ,
'main_8' : [ {'8' : []} ] ,
'main_9' : [ {'9' : []} ] }

dict_ope = { 'main_0' : [ { 'n' } ] ,
'main_1' : [ { 'da' } ] ,
'main_3' : [ { 'n' } ] ,
'main_4' : [ { 'n' } ] ,
'main_5' : [ { 'n' } ] ,
'main_6' : [ { 'n' } ] ,
'main_7' : [ { 'n' } ] ,
'main_8' : [ { 'n' } ] ,
'main_9' : [ { 'n' } ] }

dict_col = { 'main_0' : [ { 'tc' : [54, 0, '>'] } ] ,
'main_1' : [ { 'tc' : [6, 0.007, '>'] } ] ,
'main_3' : [ { 'tc' : [75, 0, '>'] } ] ,
'main_4' : [ { 'tc' : [20, -6.85, '>='] } ] ,
'main_5' : [ { 'tc' : [64, 0, '>'] } ] ,
'main_6' : [ { 'tc' : [22, 0.049, '>='] } ] ,
'main_7' : [ { 'tc' : [96, 0.093, '>='] } ] ,
'main_8' : [ { 'tc' : [92, 0, '>'] } ] ,
'main_9' : [ { 'ssc' } ] }
```

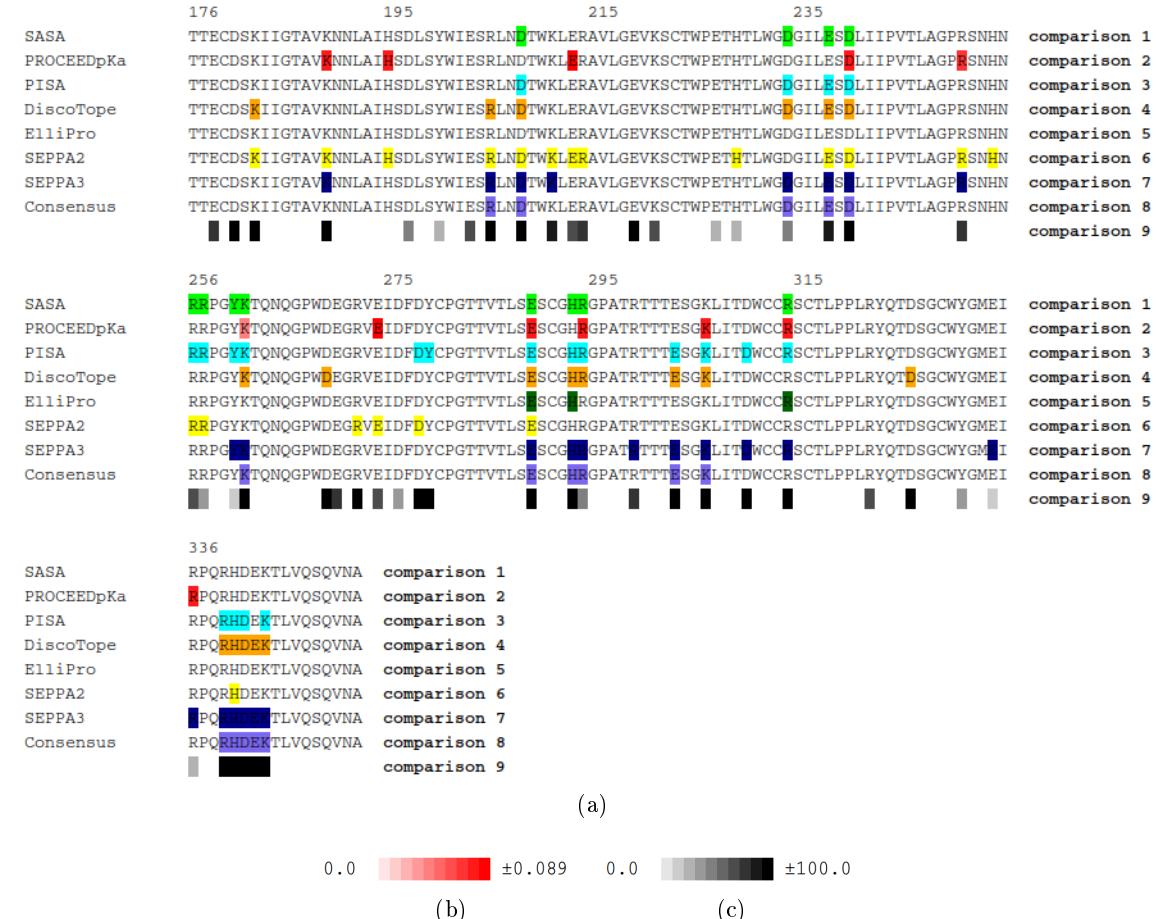


Figure 8.2.1: (a) Alignment for Example 2. (b) Scale for comparison 2. (c) Scale for comparison 9.

```
dict_vis = { 'main_0' : [ { 'ReY', 'DeN', 'LeY' } ] ,
    'main_1' : [ { 'ReN', 'DeY', 'LeY' } ] ,
    'main_3' : [ { 'ReY', 'DeN', 'LeY' } ] ,
    'main_4' : [ { 'ReY', 'DeN', 'LeY' } ] ,
    'main_5' : [ { 'ReY', 'DeN', 'LeY' } ] ,
    'main_6' : [ { 'ReY', 'DeN', 'LeY' } ] ,
    'main_7' : [ { 'ReY', 'DeN', 'LeY' } ] ,
```



```

'main_8' : [ { 'ReY', 'DeN', 'LeY' } ] ,
'main_9' : [ { 'ReY', 'DeY', 'LeN' } ] }

dict_mxr={}

```

As we are implementing the `tc` color descriptor (see Section 5.8) and the numerical data is dependent on the threshold, we recommend taking care with the accuracy. The output for example 2 appears in Figure 8.2.1. To obtain this outcome, we have considered an accuracy of 3 decimal places with the `-a` flag (see Section 3.2).

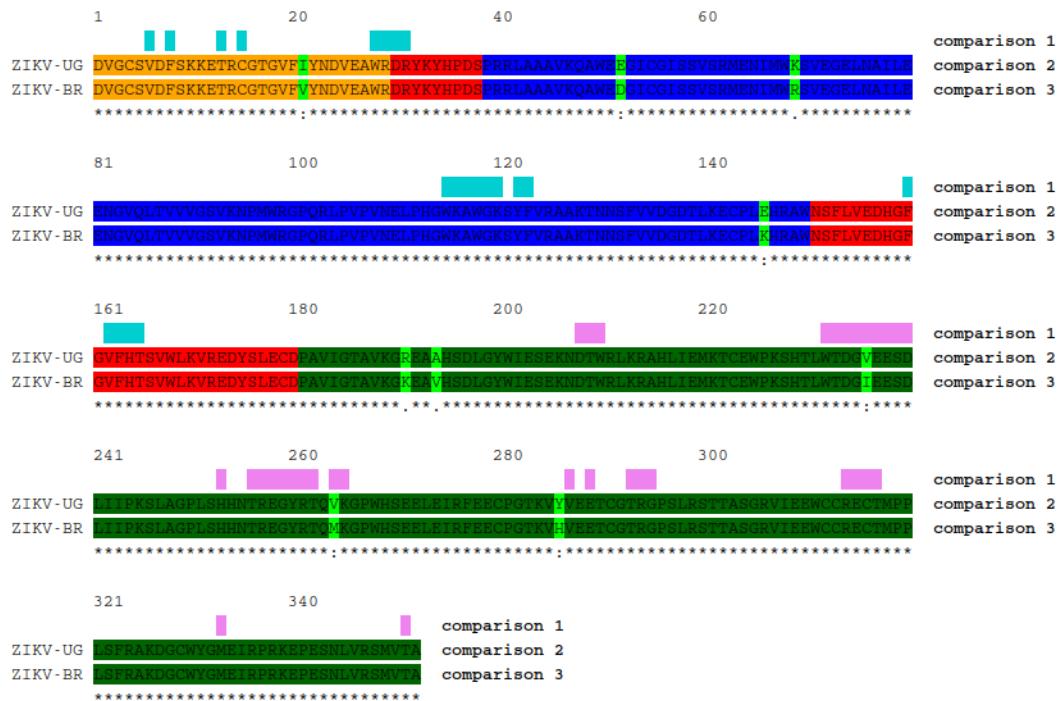


Figure 8.2.2: Alignment for Example 3.

8.3 Example 3: Protein structural domains for two NS1_{ZIKV} and its biological interfaces

Command-line:

```
cprisma -va 2 -j -ns -ck -rf multiple -mco 54 -dco -dvi
```



Variables:

```
target_residues = ()  
name_sequence = ('', 'ZIKV-UG', 'ZIKV-BR')  
descriptor_ope = { 'n' }  
descriptor_col = { 'nc' }  
descriptor_vis = { 'ReY', 'DeN', 'LeY' }  
descriptor_mxr = { 'nr' }  
dict_ref = { 'main_0' : [ {'0' : []} ] ,  
            'main_2' : [ {'2' : [1]} ] ,  
            'main_1' : [ {'1' : [2]} ] }  
dict_ope = {}  
dict_col = { 'main_0' : [ { 'pic' : [ { '0' : [81, 'n', '5', '7', '12', '14',  
                                         '27-30', '114-119', '121-122',  
                                         '159', '161-164'] } ,  
                           { '0' : [35, 'n', '207-209', '231-239',  
                                     '252', '255-261', '263-264',  
                                     '286', '288', '292-294',  
                                     '313-316', '332', '350'] } ] } ] ,  
            'main_2' : [ { 'pimc' : [ { '1' : [20, 'n', '0-28'] } ,  
                                      { '1' : [6, 'n', '29-37'] } ,  
                                      { '1' : [94, 'n', '38-149'] } ,  
                                      { '1' : [6, 'n', '150-179'] } ,  
                                      { '1' : [64, 'n', '180-351'] } ] } ] ,  
            'main_1' : [ { 'pimc' : [ { '2' : [20, 'n', '0-28'] } ,  
                                      { '2' : [6, 'n', '29-37'] } ] } ] }
```



```
{ '2' : [94, 'n', '38-149'] } ,  
{ '2' : [6, 'n', '150-179'] } ,  
{ '2' : [64, 'n', '180-351'] } ] } }  
  
dict_vis = { 'main_0' : [ { 'ReY', 'DeN', 'LeN' } ] ,  
             'main_2' : [ { 'ReN', 'DeN', 'LeY' } ] ,  
             'main_1' : [ { 'ReN', 'DeN', 'LeY' } ] }  
  
dict_mxr = {}
```

The output for example 3 appears in Figure 8.2.2. See that for `pimc` descriptor to distinguish the mutations (see Section 5.7), the `main`'s 1 and 2 in `dict_ref` have the sequences exchanged and we have hidden the references with the `ReN` visualization method (see Chapter 6).



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“One should never try to prove anything that is not almost obvious”

Alexander Grothendieck