

A

ALIGNMENT LENGTH

Number of residues in each sequence

4057

DOWNLOAD RESULTS

Download DiMA results

JSON XLSX

G

PROTEIN NAME

Name of the protein being analysed

MERS Spike

SUPPORT THRESHOLD

Minimum support required per position

30

POSITION SUPPORT

Support at the selected k-mer position

449

DISTINCT PEPTIDES

Distinct peptides at current k-mer position

2

B

POSITION ENTROPY

Shannon's entropy for the current position

0.03

SELECTED POSITION

Currently selected k-mer position

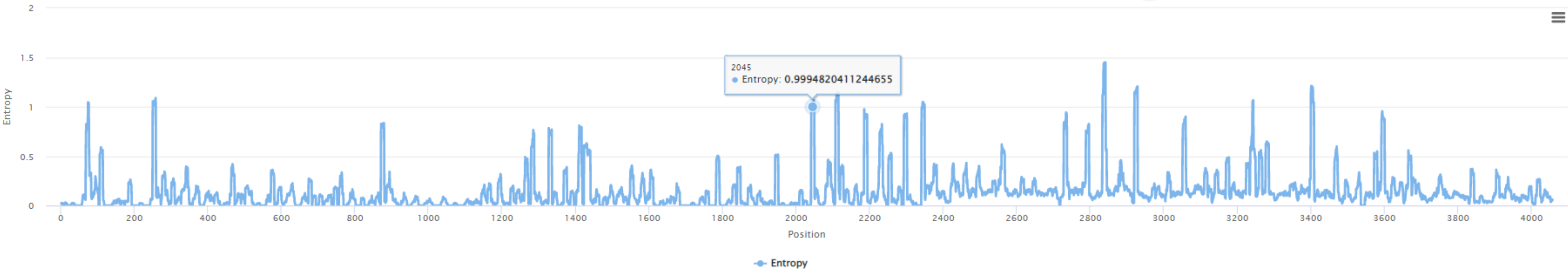
13

K-MER POSITION ENTROPY

Shannon's entropy of the generated k-mer positions

C

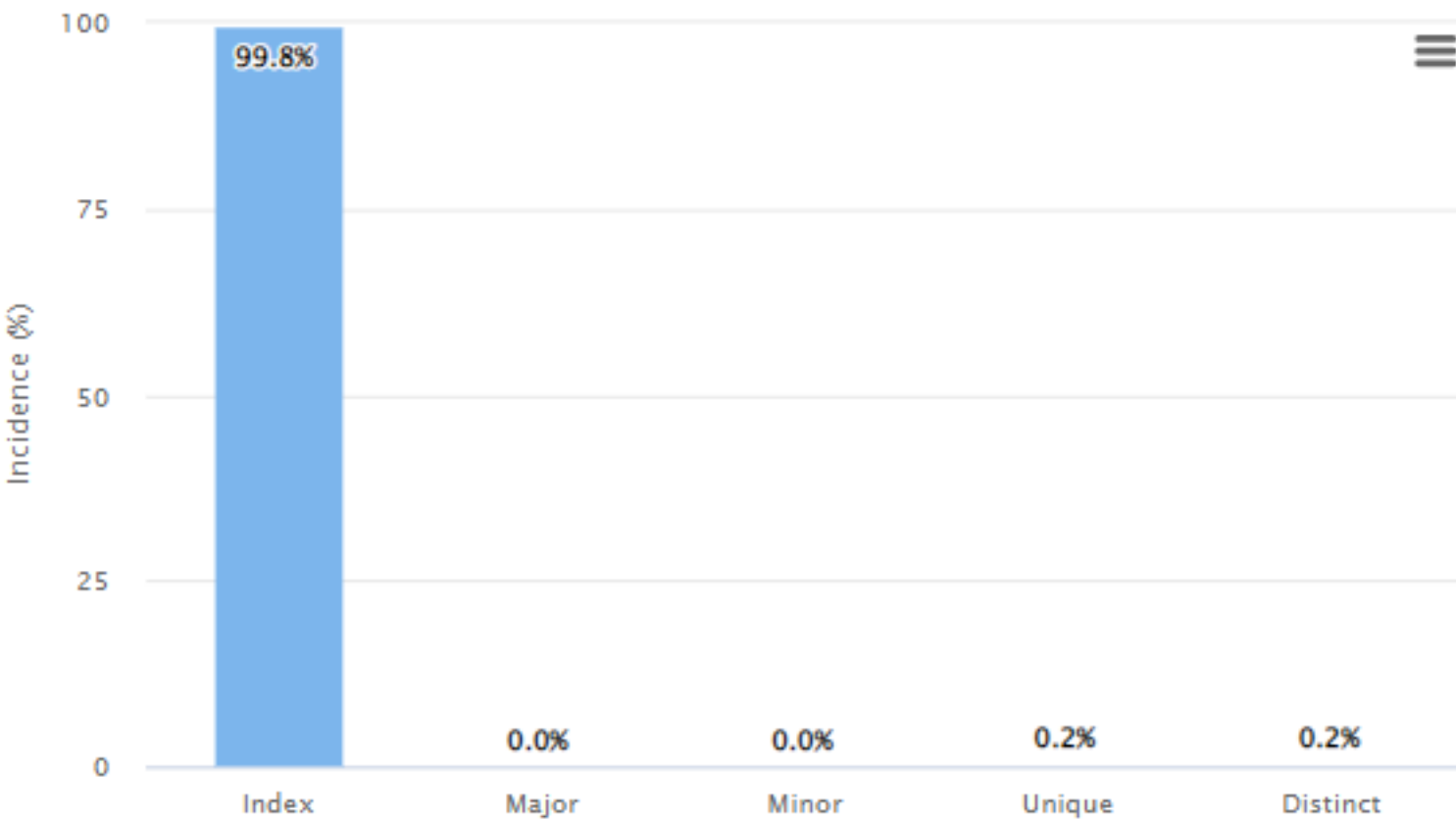
Click & Drag to zoom in



MOTIF DISTRIBUTION

The distribution of motifs at k-mer position 13

D



K-MER POSITION PEPTIDES

Distinct peptides observed at the k-mer position 13

E

Sequence	↓ Frequency	Incidence	Motif Class
gtgtttcta	448	99.777	Index
gtgtatcta	1	0.223	Unique

1 row selected

1-2 of 2

PEPTIDE METADATA

Metadata of the selected distinct peptide

F

