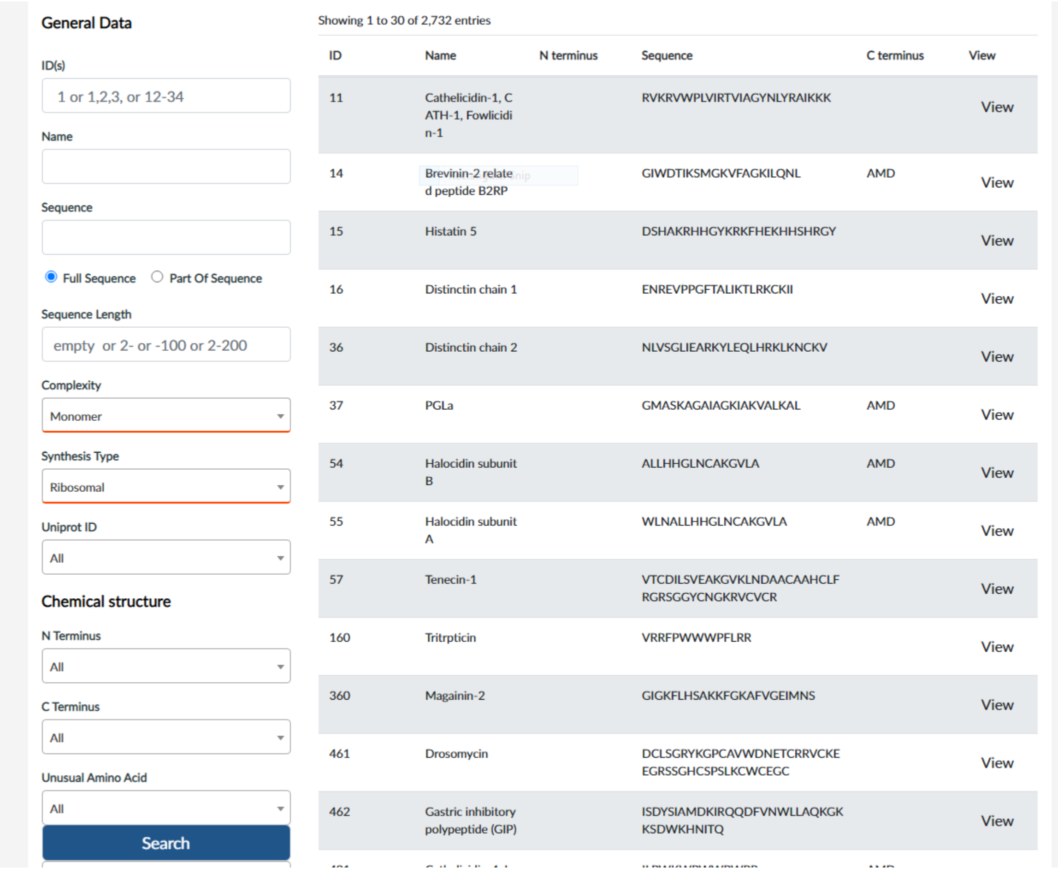


General Data

ID(s): 1 or 1,2,3, or 12-34

Name:

Sequence:

● Full Sequence ○ Part Of Sequence

Sequence Length: empty or 2- or -100 or 2-200

Complexity: Monomer

Synthesis Type: Ribosomal

Uniprot ID: All

Chemical structure

N Terminus: All

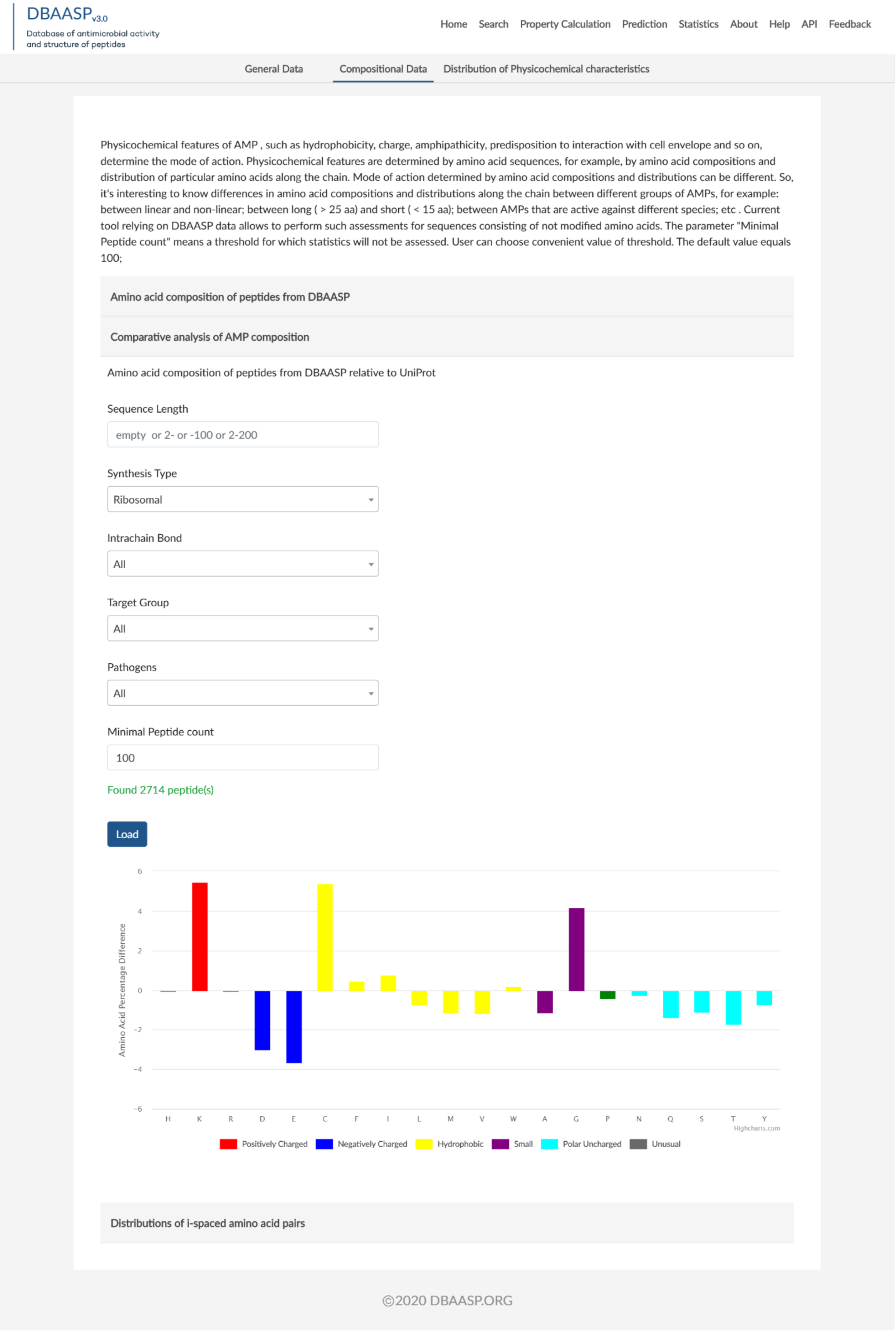
C Terminus: All

Unusual Amino Acid: All

Showing 1 to 30 of 2,732 entries

ID	Name	N terminus	Sequence	C terminus	View
11	Cathelicidin-1, CATH-1, Fowlicidin-1		RVKRVWPLVIRTVIAGYNLYRAIKKK		View
14	Brevinin-2 related peptide B2RP		GIWDTIKSMGKVFAGKILQNL	AMD	View
15	Histatin 5		DSHAKRHHGYKRKFHEKHHSHRGY		View
16	Distinctin chain 1		ENREVPPGFTALIKTLRKCKII		View
36	Distinctin chain 2		NLVSGLIEARKYLEQLHRKLKNCKV		View
37	PGLa		GMASKAGAIAGKIAKVALKAL	AMD	View
54	Halocidin subunit B		ALLHHGLNCAKGVLA	AMD	View
55	Halocidin subunit A		WLNALLHHGLNCAKGVLA	AMD	View
57	Tenecin-1		VTCDILSVEAKGVKLNDAACAAHCLFRGRSGGYCNGKRVCVCR		View
160	Tritrpticin		VRRFPWWWPFLRR		View
360	Magainin-2		GIGKFLHSAKKFGKAFVGEIMNS		View
461	Drosomycin		DCLSGRYKGPCAVWDNETCRRVCKEEGRSSGHCSPSLKCWCEGC		View
462	Gastric inhibitory polypeptide (GIP)		ISDYSIAMDKIRQQDFVNWLLAQKGKKSDWKHNITQ		View

Figure S1 . Screenshot of the “Search” page



Physicochemical features of AMP , such as hydrophobicity, charge, amphipathicity, predisposition to interaction with cell envelope and so on, determine the mode of action. Physicochemical features are determined by amino acid sequences, for example, by amino acid compositions and distribution of particular amino acids along the chain. Mode of action determined by amino acid compositions and distributions can be different. So, it's interesting to know differences in amino acid compositions and distributions along the chain between different groups of AMPs, for example: between linear and non-linear; between long (> 25 aa) and short (< 15 aa); between AMPs that are active against different species; etc . Current tool relying on DBAASP data allows to perform such assessments for sequences consisting of not modified amino acids. The parameter "Minimal Peptide count" means a threshold for which statistics will not be assessed. User can choose convenient value of threshold. The default value equals 100;

Amino acid composition of peptides from DBAASP relative to UniProt

Sequence Length: empty or 2- or -100 or 2-200

Synthesis Type: Ribosomal

Intrachain Bond: All

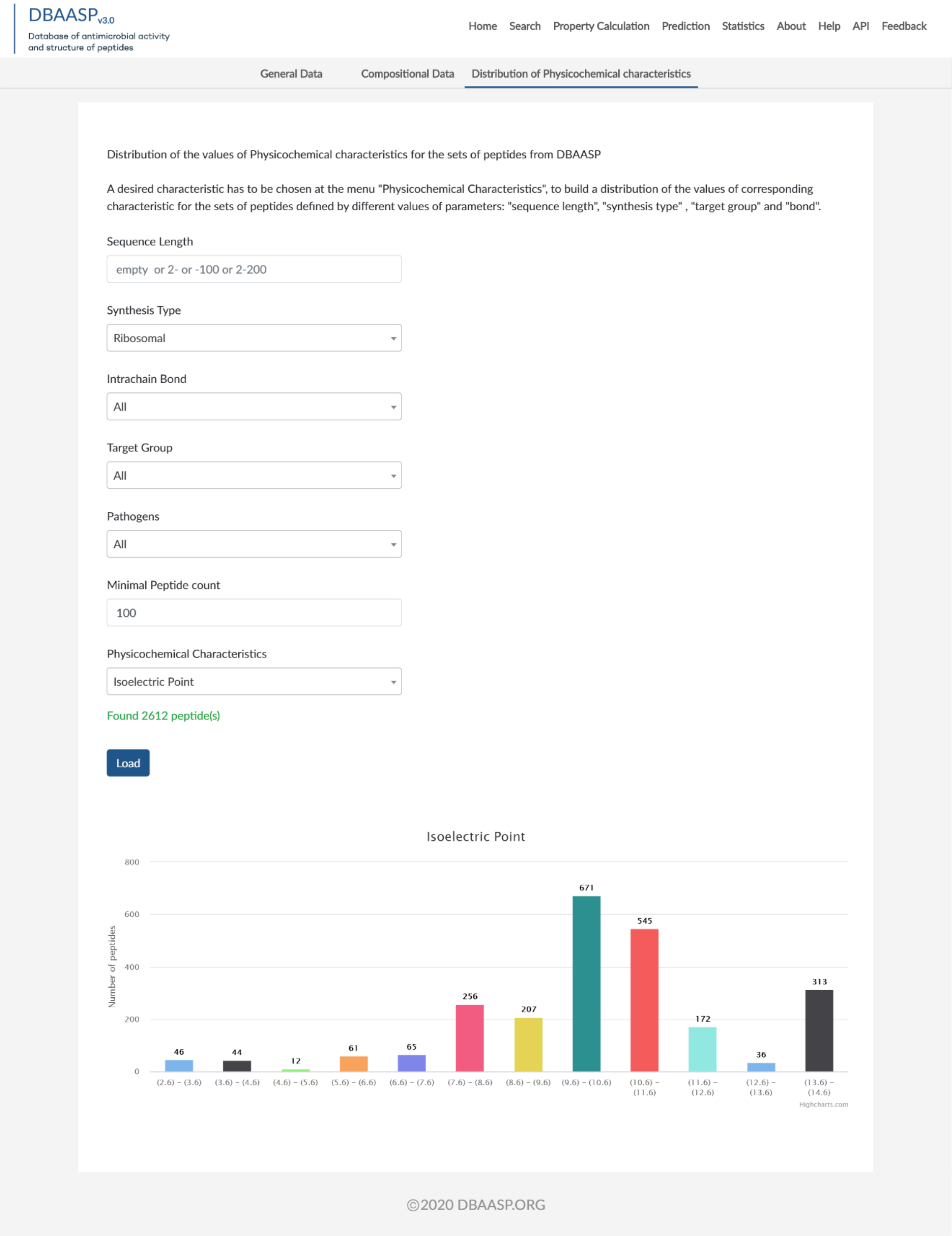
Target Group: All

Pathogens: All

Minimal Peptide count: 100

Found 2714 peptide(s)

Figure S2. Screenshot of the subpage of the "Statistics" titled "Comparative analysis of AMP composition"



Distribution of the values of Physicochemical characteristics for the sets of peptides from DBAASP

A desired characteristic has to be chosen at the menu "Physicochemical Characteristics", to build a distribution of the values of corresponding characteristic for the sets of peptides defined by different values of parameters: "sequence length", "synthesis type" , "target group" and "bond".

Sequence Length: empty or 2- or -100 or 2-200

Synthesis Type: Ribosomal

Intrachain Bond: All

Target Group: All

Pathogens: All

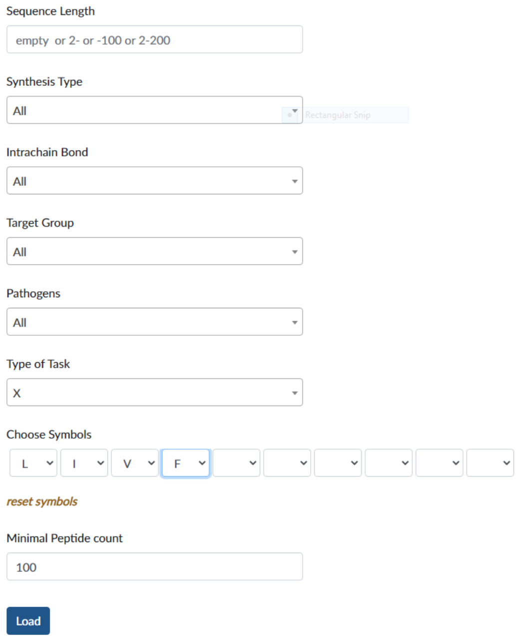
Minimal Peptide count: 100

Physicochemical Characteristics: Isoelectric Point

Found 2612 peptide(s)

Figure S3. Screenshot of the subpage of the "Statistics" titled "Distribution of Physicochemical characteristics "

a)



Sequence Length
empty or 2- or -100 or 2-200

Synthesis Type
All

Intrachain Bond
All

Target Group
All

Pathogens
All

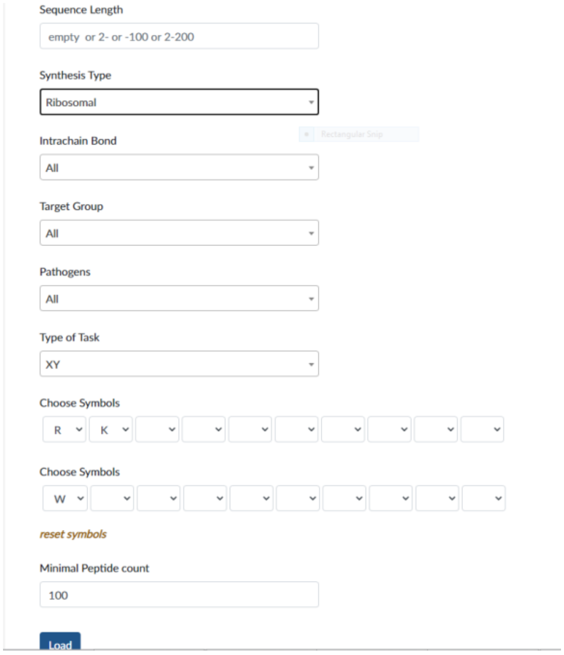
Type of Task
X

Choose Symbols
L I V F

reset symbols

Minimal Peptide count
100

b)



Sequence Length
empty or 2- or -100 or 2-200

Synthesis Type
Ribosomal

Intrachain Bond
All

Target Group
All

Pathogens
All

Type of Task
XY

Choose Symbols
R K

Choose Symbols
W

reset symbols

Minimal Peptide count
100

Figure S4. Screenshots of the subpage of the “statistics” titled “Distribution of i-spaced amino acid pairs” for two different options of the parameters from the drop-down menu of the "type of task": a) when X option is selected and b) when XY option is selected