VIOLIN Programming Utilities

VIOLIN programming utilities (V-Utilities) provide a set of tools for access to the entire VIOLIN database for vaccine related information. The data can be currently retrieved with a known pathogen. The retrieved data is returned in XML format. The XML Schema is used to define the returned XML file.

Query database using GET method

With known pathogen

URL: **http://www.violinet.org/v-utilities/fpathogen.php**

Parameters:

Select pathogen (one of the following)

ptg = pathogen identifier (*prefix_value*)

prefix can be either “p_” (pathogen id #), “n_” (pathogen name), or “t_” (taxonomy id #)

value is the value corresponding to a given prefix

example: ptg=p_31 *or* ptg=n_ Haemophilus%20influenzae *or* ptg=t_727

Fetch the type of data from the database

datafield = type of data

the type(s) of data can be:

```
pathogen_id, pathogen_name, taxonomy_id, pathogensis,
disease_name, protective_immunity, host_range, introduction,
pathogen_gene, host_gene, vaccine, reference
```

special parameters when datafield = pathogen_gene or host_gene or vaccine or reference

returntype = return type for the parameters with a list of data

return type can be any combination of letters, with each letter representing a field to be returned:

special keyword: list

equivalent to letter ‘n’, representing all the fields of a given datafield

allowed values for datafield = pathogen_gene or host_gene

```
"n"=>"gene_name"
"h"=>"ncbi_gene_id"
"x"=>"xrefs"
"f"=>"phi_annotation"
"k"=>"dna_sequence"
"q"=>"protein_sequence"
"j"=>"strain"
"t"=>"taxonomy_id"
"b"=>"ncbi_protein_id"
"v"=>"protein_refseq"
"y"=>"protein_name"
"c"=>"chromosome"
"m"=>"segment"
"g"=>"gene_locus_tag"
"s"=>"gene_start"
"e"=>"gene_end"
"d"=>"gene_strand"
"r"=>"gene_refseq"
```

```
"o"=>"protein_note"
"a"=>"protein_annotation"
"i"=>"protein_pi"
"w"=>"protein_weight"
"l"=>"protein_length"
"u"=>"phi_function"
"p"=>"plasmid"
```

allowed values for datafield = vaccine

```
"n"=>"vaccine_name"
"p"=>"pathogen_id"
"t"=>"type"
"d"=>"description"
"a"=>"adjuvant"
"s"=>"storage"
"v"=>"virulence"
"r"=>"preparation"
"b"=>"brand_name"
"g"=>"antigen"
```

allowed values for datafield = reference

```
"n"=>"reference_name"
"t"=>"reference_type"
"a"=>"authors"
"i"=>"title"
"y"=>"year"
"v"=>"volume"
"i"=>"issue"
"p"=>"pages"
"j"=>"journal_book_name"
"b"=>"publisher"
"l"=>"publisher_location"
"e"=>"book_editors"
"c"=>"isbn"
"s"=>"university"
"n"=>"university_location"
"d"=>"degree"
"m"=>"pmid"
"u"=>"url"
"f"=>"file_name"
```

Examples

http://www.violinet.org/v-utilities/fpathogen.php?ptg=p_32&datafield=introduction

http://www.violinet.org/v-utilities/fpathogen.php?ptg=p_13&datafield=vaccine&returntype=ndr

http://www.violinet.org/v-utilities/fpathogen.php?ptg=t_1773&datafield=host_gene&returntype=nkse

With known vaccine

URL: **http://www.violinet.org/v-utilities/fvaccine.php**

Parameters:

Select vaccine (one of the following)

vacn = pathogen identifier (*prefix_value*)

prefix can be either “v_” (vaccine id #), “n_” (vaccine name) *value* is the value corresponding to a given prefix

example: vacn=v_36 *or* vacn=n_ F1%20antigen

Fetch the type of data from the database

datafield = type of data

the type(s) of data can be:

```
vaccine_id, pathogen_id, vaccine_name, type, description,
adjuvant, storage, virulence, preparation, brand_name, antigen,
host_response, reference
```

special parameters when datafield = host_response or reference

returntype = return type for the parameters with a list of data

return type can be any combination of letters, with each letter representing a field to be returned:

special keyword: list

equivalent to letter ‘n’, representing all the fields of a given datafield

allowed values for datafield = host_response

```
"n"=>"pathogen_id",
"v"=>"vaccine_id"
"h"=>"host_id"
"r"=>"immune_response"
"s"=>"host_strain"
"t"=>"vaccination_protocol"
"o"=>"route"
"p"=>"persistance"
"e"=>"protection_efficacy"
"f"=>"side_effects"
"c"=>"challenge_protocol"
"d"=>"description"
```

allowed values for datafield = reference

```
"n"=>"reference_name"
"t"=>"reference_type"
"a"=>"authors"
"i"=>"title"
"y"=>"year"
"v"=>"volume"
"i"=>"issue"
"p"=>"pages"
"j"=>"journal_book_name"
"b"=>"publisher"
"l"=>"publisher_location"
"e"=>"book_editors"
"c"=>"isbn"
"s"=>"university"
"n"=>"university_location"
"d"=>"degree"
"m"=>"pmid"
"u"=>"url"
```

```
"f"=>"file_name"
```

Examples

http://www.violinet.org/v-utilities/fvaccine.php?vacn=v_36&datafield=description
http://www.violinet.org/v-utilities/fvaccine.php?vacn=v_36&datafield=host_response&returntype=vtd
http://www.violinet.org/v-utilities/fvaccine.php?vacn=n_F1%20antigen&datafield=preparation

Query database using web service

The VIOLIN database is also accessible by the use of web service. The web service description language (WSDL) describes the web service currently available. Simple Object Access Protocol (SOAP) is the protocol used for accessing the web services.

WSDL file for the web service is located at http://www.violinet.org/v-utilities/wsutil.wsdl