

Package ‘apmsTools’

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Type Package

Title Tools for analysis of Affinity Purification Mass Spectrometry data

Version 0.1

Date 2014-04-01

Author Erik Ahrne

Maintainer Erik Ahrne <erik.ahrne@unibas.ch>

Description Several functions for handling/analyzing Spectral Count data from Affinity Purification Mass Spectrometry experiments

Imports seqinr

License GPL-3

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apmsTools-package	<i>Tools for analysis of Affinity Purification Mass Spectrometry data</i>
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Description

Several functions for handling/analyzing Spectral Count data from Affinity Purification Mass Spectrometry experiments

Details

Package: apmsTools
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Author(s)

Erik Ahrne

Maintainer: Erik Ahrne <erik.ahrne@unibas.ch>

References

Not yet available

See Also

Not yet available

setProteinLength	<i>Update protein lengths</i>
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Description

Updates protein lengths (extracted from .fasta) in apmsExp object,

Usage

```
setProteinLength(apmsExp, fastaFile)
```

Arguments

apmsExp	An object of class apmsExp.
fastaFile	Full path to .fasta file

Details

Not yet available

Value

An updated apmsExp object

specCountDf	data.frame, df
	df[,1:3]: "protein description", "gene name", "protein length"
	df[,4:n] bait-prey spec counts

Note

Not yet available

Author(s)

Erik Ahrne
erik.ahrne@unibas.ch

References

Not yet available

See Also

Not yet available

writeCRAPomeFile	<i>Write CRAPome input file</i>
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Description

Write CRAPome input file

Example:

```
PROTID GENEID PROTLIN C1_SPC C2_SPC HDAC5_1_SPC HDAC5_2_SPC
```

```
PROTID GENEID PROTLIN C C HDAC5 HDAC5
```

```
Q9Y6M1 IGF2BP2 599 9 2 2 0
```

```
Q9Y697 NFS1 457 0 0 14 8
```

```
Q9Y618 NCOR2 2525 0 0 19 16
```

Usage

```
writeCRAPomeFile(apmsExp, file, verbose = F)
```

Arguments

apmsExp	An object of class apmsExp.
file	Full path to output file.
verbose	verbose

Details

Not yet available

Note

Not yet available

Author(s)

Erik Ahrne
erik.ahrne@unibas.ch

References

Not yet available

See Also

Not yet available

writeSaintBaitFile	<i>Write bait SAINT input file</i>
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Description

Write bait SAINT input file

Example:

PPP2R1A PPP2R1A T

PPP2CB PPP2CB T

PPME1 PPME1 T

TP53 TP53 T

GFP1 GFP1 C

GFP2 GFP2 C

GFP3 GFP3 C

GFP4 GFP4 C

Usage

```
writeSaintBaitFile(apmsExp, file, verbose = F)
```

Arguments

apmsExp	An object of class apmsExp.
file	Full path to output file.
verbose	verbose

Details

Not yet available

Note

Not yet available

Author(s)

Erik Ahrne
erik.ahrne@unibas.ch

References

Not yet available

See Also

Not yet available

writeSaintInteractionFile

Write interaction SAINT input file.

Description

Write interaction SAINT input file.

Example:

```
PPP2R1A PPP2R1A splP30153l2AAA_HUMAN 64
PPP2R1A PPP2R1A splQ9BUJ2lHNRL1_HUMAN 62
PPP2R1A PPP2R1A splP08107lHSP71_HUMAN 29
```

Usage

```
writeSaintInteractionFile(apmsExp, file, verbose = F)
```

Arguments

apmsExp	An object of class apmsExp.
file	Full path to output file.
verbose	verbose

Details

Not yet available

Note

Not yet available

Author(s)

Erik Ahrne
erik.ahrne@unibas.ch

References

Not yet available

See Also

Not yet available

writeSaintPreyFile	<i>Write prey SAINT input file</i>
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Description

Write prey SAINT input file

Example:

```
splP30153|2AAA_HUMAN 650 PPP2R1A  
splQ9BUJ2|HNRL1_HUMAN 960 HNRNPUL1  
splP08107|HSP71_HUMAN 700 HSPA1A
```

Usage

```
writeSaintPreyFile(apmsExp, file, verbose = F)
```

Arguments

apmsExp	An object of class apmsExp.
file	Full path to output file.
verbose	verbose

Details

Not yet available

Note

Not yet available

Author(s)

Erik Ahrne
erik.ahrne@unibas.ch

References

Not yet available

See Also

Not yet available

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