

Package ‘apmsTools’

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Type Package

Title Tools for analysis of Affinity Purification Mass Spectrometry data

Version 0.1

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

Imports seqinr

License GPL-3

R topics documented:

apmsTools-package	1
readScaffoldSpecCountFile	2
setProteinLength	3
writeCRAPomeFile	4
writeSaintBaitFile	5
writeSaintInteractionFile	6
writeSaintPreyFile	7
Index	8

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)

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References

Not yet available

See Also

Not yet available

readScaffoldSpecCountFile

Parse scaffold spectral count export (.xls).

Description

Parses scaffold .xls and creates data.frame object.

Annotate replicates in scaffold file by adding replicate number to bait gene name.

IP-name: PPP2R1A-1 (as given in scaffold)

bait-name: PPP2R1A

Usage

```
readScaffoldSpecCountFile(file, sep = "\t", isControl = F, isUniprot = T)
```

Arguments

file	Path to Scaffold .xls File.
sep	the field separator character.
isControl	Does the file contain GFP control baits only
isUniprot	Uniprot Protein Accession Numbers TRUE/FALSE

Details

Not yet available

Value

Returns a data frame with the following structure:

rownames: protein accession numbers

df[,1:3]: "protein description", "gene name", "'approx.' protein length"

df[,4:]: bait-prey spectral count.

Note

Not yet available

Author(s)

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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)

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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)

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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)

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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)

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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:

```
sp|P30153|2AAA_HUMAN 650 PPP2R1A
sp|Q9BUJ2|HNRL1_HUMAN 960 HNRNPUL1
sp|P08107|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

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References

Not yet available

See Also

Not yet available

Index

*Topic `\textasciitildekw1`

- readScaffoldSpecCountFile, [2](#)
- setProteinLength, [3](#)
- writeCRAPomeFile, [4](#)
- writeSaintBaitFile, [5](#)
- writeSaintInteractionFile, [6](#)
- writeSaintPreyFile, [7](#)

*Topic `\textasciitildekw2`

- readScaffoldSpecCountFile, [2](#)
- setProteinLength, [3](#)
- writeCRAPomeFile, [4](#)
- writeSaintBaitFile, [5](#)
- writeSaintInteractionFile, [6](#)
- writeSaintPreyFile, [7](#)

*Topic **package**

- apmsTools-package, [1](#)

apmsTools (apmsTools-package), [1](#)

apmsTools-package, [1](#)

readScaffoldSpecCountFile, [2](#)

setProteinLength, [3](#)

writeCRAPomeFile, [4](#)

writeSaintBaitFile, [5](#)

writeSaintInteractionFile, [6](#)

writeSaintPreyFile, [7](#)