

# Package ‘MSGFplus’

April 10, 2015

**Type** Package

**Title** An interface between R and MS-GF+

**Version** 1.0.5

**Date** 2015-02-03

**Author** Thomas Lin Pedersen

**Maintainer** Thomas Lin Pedersen <thomasp85@gmail.com>

**Description** This package contains function to perform peptide identification using MS-GF+

**License** GPL (>= 2)

**VignetteBuilder** knitr

**SystemRequirements** Java (>= 1.7)

**LazyLoad** yes

**biocViews** MassSpectrometry, Proteomics

**Depends** methods

**Imports** mzID

**Suggests** gWidgets, knitr, testthat

**Collate** 'MSGFplus-package.R' 'aaa.R' 'generics.R' 'msgfAsync.R'  
'msgfParTolerance.R' 'msgfParTda.R' 'msgfParProtocol.R'  
'msgfParNtt.R' 'msgfParModification.R'  
'msgfParModificationList.R' 'msgfParMatches.R'  
'msgfParLengthRange.R' 'msgfParIsotopeError.R'  
'msgfParInstrument.R' 'msgfParFragmentation.R'  
'msgfParEnzyme.R' 'msgfParChargeRange.R' 'msgfPar.R'  
'msgfPar-getters.R' 'msgfParGUI.R' 'zzz.R'

## R topics documented:

MSGFplus-package	2
chargeRange	3
db	4
enzyme	5

fragmentation	7
getMSGFpar	8
instrument	9
isotopeError	11
lengthRange	12
matches	13
mods	15
msgfPar	17
msgfPar-class	20
msgfParChargeRange-class	23
msgfParEnzyme-class	24
msgfParFragmentation-class	26
msgfParFromID	27
msgfParGUI	28
msgfParInstrument-class	29
msgfParIsotopeError-class	30
msgfParLengthRange-class	32
msgfParMatches-class	33
msgfParModification-class	35
msgfParModificationList-class	37
msgfParNtt-class	39
msgfParProtocol-class	41
msgfParTda-class	42
msgfParTolerance-class	44
ntt	45
protocol	47
runMSGF	48
running	50
tda	51
tolerance	53

## Index 56

---

MSGFplus-package      *An interface between R and MS-GF+*

---

### Description

This package comes bundled with the peptide database search tool MS-GF+ and provides means of running peptide searches from within R with automatic result import and easy handling of parameters.

### Details

The version bundled with this package is: MS-GF+ Beta (v10072) (11/11/2013)

### Author(s)

Thomas Lin Pedersen with contributions from Laurent Gatto

---

chargeRange	<i>Get and set the charge range in msgfPar objects</i>
-------------	--

---

**Description**

These functions allow you to retrieve and set the charge range in the msgfPar object of interest

**Usage**

```
chargeRange(object)

chargeRange(object) <- value

## S4 method for signature msgfPar
chargeRange(object)

## S4 replacement method for signature msgfPar,numeric
chargeRange(object) <- value

## S4 replacement method for signature msgfPar,msgfParChargeRange
chargeRange(object) <- value
```

**Arguments**

object	An msgfPar object
value	Either a numeric vector of length 2 or an msgfParChargeRange object

**Value**

In case of the getter a numeric vector with the named elements 'min' and 'max'

**Methods (by class)**

- msgfPar: Get the charge range
- object = msgfPar, value = numeric: Set the charge range using lower and upper bounds
- object = msgfPar, value = msgfParChargeRange: Set the charge range using a dedicated msgfParChargeRange object

**See Also**

Other msgfPar-getter\_setter: [db, db, msgfPar-method, db<-, db<-, msgfPar, character-method, enzyme, enzyme, msgfPar-method, enzyme<-, enzyme<-, msgfPar, character-method, enzyme<-, msgfPar, msgfParEnzy](#)  
[enzyme<-, msgfPar, numeric-method; fragmentation, fragmentation, msgfPar-method, fragmentation<-,](#)  
[fragmentation<-, msgfPar, character-method, fragmentation<-, msgfPar, msgfParFragmentation-method,](#)  
[fragmentation<-, msgfPar, numeric-method; instrument, instrument, msgfPar-method, instrument<-,](#)  
[instrument<-, msgfPar, character-method, instrument<-, msgfPar, msgfParInstrument-method,](#)  
[instrument<-, msgfPar, numeric-method; isotopeError, isotopeError, msgfPar-method, isotopeError<-,](#)

```
isotopeError<-,msgfPar,msgfParIsotopeError-method, isotopeError<-,msgfPar,numeric-method;
lengthRange,lengthRange,msgfPar-method,lengthRange<- ,lengthRange<- ,msgfPar,msgfParLengthRange-method;
lengthRange<- ,msgfPar,numeric-method; matches,matches,msgfPar-method,matches<- ,
matches<- ,msgfPar,msgfParMatches-method,matches<- ,msgfPar,numeric-method; mods,mods,msgfPar-method,
mods<- ,mods<- ,msgfPar,msgfParModificationList-method,nMod,nMod,msgfPar-method,nMod<- ,
nMod<- ,msgfPar,numeric-method; ntt,ntt,msgfPar-method,ntt<- ,ntt<- ,msgfPar,msgfParNtt-method,
ntt<- ,msgfPar,numeric-method; protocol,protocol,msgfPar-method,protocol<- ,protocol<- ,msgfPar,character-method;
protocol<- ,msgfPar,msgfParProtocol-method,protocol<- ,msgfPar,numeric-method; tda,
tda,msgfPar-method,tda<- ,tda<- ,msgfPar,logical-method,tda<- ,msgfPar,msgfParTda-method;
tolerance,tolerance,msgfPar-method,tolerance<- ,tolerance<- ,msgfPar,character-method,
tolerance<- ,msgfPar,msgfParTolerance-method,toleranceRange,toleranceRange,msgfPar-method,
toleranceRange<- ,toleranceRange<- ,msgfPar,numeric-method,toleranceUnit,toleranceUnit,msgfPar-method,
toleranceUnit<- ,toleranceUnit<- ,msgfPar,character-method
```

## Examples

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
chargeRange(parameters) <- c(2, 4)
chargeRange(parameters)
```

---

db

*Get and set database in msgfPar objects*

---

## Description

These functions allow you to retrieve and set the location of the database fasta file in the msgfPar object of interest

## Usage

```
db(object)
```

```
db(object) <- value
```

```
## S4 method for signature msgfPar
db(object)
```

```
## S4 replacement method for signature msgfPar,character
db(object) <- value
```

## Arguments

object	An msgfPar object
value	A string matching the location of a fasta file

## Value

In case of the getter a character vector with the location of the database file

**Methods (by class)**

- msgfPar: Get the database location
- object = msgfPar, value = character: Set the database location

**See Also**

Other msgfPar-getter\_setter: [chargeRange](#), [chargeRange](#), [msgfPar-method](#), [chargeRange<-](#), [chargeRange<-](#), [msgfPar](#), [m](#), [chargeRange<-](#), [msgfPar](#), [numeric-method](#); [enzyme](#), [enzyme](#), [msgfPar-method](#), [enzyme<-](#), [enzyme<-](#), [msgfPar](#), [character-method](#), [enzyme<-](#), [msgfPar](#), [msgfParEnzyme-method](#), [enzyme<-](#), [msgfPar](#), [numeric-method](#); [fragmentation](#), [fragmentation](#), [msgfPar-method](#), [fragmentation<-](#), [fragmentation<-](#), [msgfPar](#), [character-method](#), [fragmentation<-](#), [msgfPar](#), [msgfParFragmentation-method](#), [fragmentation<-](#), [msgfPar](#), [numeric-method](#); [instrument](#), [instrument](#), [msgfPar-method](#), [instrument<-](#), [instrument<-](#), [msgfPar](#), [character-method](#), [instrument<-](#), [msgfPar](#), [msgfParInstrument-method](#), [instrument<-](#), [msgfPar](#), [numeric-method](#); [isotopeError](#), [isotopeError](#), [msgfPar-method](#), [isotopeError<-](#), [isotopeError<-](#), [msgfPar](#), [msgfParIsotopeError-method](#), [isotopeError<-](#), [msgfPar](#), [numeric-method](#); [lengthRange](#), [lengthRange](#), [msgfPar-method](#), [lengthRange<-](#), [lengthRange<-](#), [msgfPar](#), [msgfParLengthRange-method](#), [lengthRange<-](#), [msgfPar](#), [numeric-method](#); [matches](#), [matches](#), [msgfPar-method](#), [matches<-](#), [matches<-](#), [msgfPar](#), [msgfParMatches-method](#), [matches<-](#), [msgfPar](#), [numeric-method](#); [mods](#), [mods](#), [msgfPar-method](#), [mods<-](#), [mods<-](#), [msgfPar](#), [msgfParModification-method](#), [nMod](#), [nMod](#), [msgfPar-method](#), [nMod<-](#), [nMod<-](#), [msgfPar](#), [numeric-method](#); [ntt](#), [ntt](#), [msgfPar-method](#), [ntt<-](#), [ntt<-](#), [msgfPar](#), [msgfParNtt-method](#), [ntt<-](#), [msgfPar](#), [numeric-method](#); [protocol](#), [protocol](#), [msgfPar-method](#), [protocol<-](#), [protocol<-](#), [msgfPar](#), [character-method](#), [protocol<-](#), [msgfPar](#), [msgfParProtocol-method](#), [protocol<-](#), [msgfPar](#), [numeric-method](#); [tda](#), [tda](#), [msgfPar-method](#), [tda<-](#), [tda<-](#), [msgfPar](#), [logical-method](#), [tda<-](#), [msgfPar](#), [msgfParTda-method](#); [tolerance](#), [tolerance](#), [msgfPar-method](#), [tolerance<-](#), [tolerance<-](#), [msgfPar](#), [character-method](#), [tolerance<-](#), [msgfPar](#), [msgfParTolerance-method](#), [toleranceRange](#), [toleranceRange](#), [msgfPar-method](#), [toleranceRange<-](#), [toleranceRange<-](#), [msgfPar](#), [numeric-method](#); [toleranceUnit](#), [toleranceUnit](#), [msgfPar-method](#), [toleranceUnit<-](#), [toleranceUnit<-](#), [msgfPar](#), [character-method](#)

**Examples**

```
parameters <- msgfPar()
db(parameters) <- system.file(package=MSGFplus, extdata, milk-proteins.fasta)
db(parameters)
```

---

enzyme

*Get and set enzyme in msgfPar objects*

---

**Description**

These functions allow you to retrieve and set the enzyme used for digestion during sample treatment.

**Usage**

```
enzyme(object)

enzyme(object) <- value

## S4 method for signature msgfPar
```

```

enzyme(object)

## S4 replacement method for signature msgfPar,numeric
enzyme(object) <- value

## S4 replacement method for signature msgfPar,character
enzyme(object) <- value

## S4 replacement method for signature msgfPar,msgfParEnzyme
enzyme(object) <- value

```

### Arguments

object	An msgfPar object
value	Either an integer, string or msgfParEnzyme object

### Value

In case of the getter a named integer

### Methods (by class)

- msgfPar: Get the enzyme currently used
- object = msgfPar, value = numeric: Set the enzyme to use using the key for the enzyme
- object = msgfPar, value = character: Set the enzyme to use using the name of the enzyme
- object = msgfPar, value = msgfParEnzyme: Set the enzyme to use using an msgfParEnzyme object

### See Also

Other msgfPar-getter\_setter: [chargeRange](#), [chargeRange](#), [msgfPar-method](#), [chargeRange<-](#), [chargeRange<-](#), [msgfPar, numeric-method](#); [db](#), [db](#), [msgfPar-method](#), [db<-](#), [db<-](#), [msgfPar, character-method](#); [fragmentation](#), [fragmentation](#), [msgfPar-method](#), [fragmentation<-](#), [fragmentation<-](#), [msgfPar, character-method](#), [fragmentation<-](#), [msgfPar, msgfParFragmentation-method](#), [fragmentation<-](#), [msgfPar, numeric-method](#); [instrument](#), [instrument](#), [msgfPar-method](#), [instrument<-](#), [instrument<-](#), [msgfPar, character-method](#), [instrument<-](#), [msgfPar, msgfParInstrument-method](#), [instrument<-](#), [msgfPar, numeric-method](#); [isotopeError](#), [isotopeError](#), [msgfPar-method](#), [isotopeError<-](#), [isotopeError<-](#), [msgfPar, msgfParIsotopeError-method](#), [isotopeError<-](#), [msgfPar, numeric-method](#); [lengthRange](#), [lengthRange](#), [msgfPar-method](#), [lengthRange<-](#), [lengthRange<-](#), [msgfPar, msgfParLengthRange-method](#), [lengthRange<-](#), [msgfPar, numeric-method](#); [matches](#), [matches](#), [msgfPar-method](#), [matches<-](#), [matches<-](#), [msgfPar, msgfParMatches-method](#), [matches<-](#), [msgfPar, numeric-method](#); [mods](#), [mods](#), [msgfPar-method](#), [mods<-](#), [mods<-](#), [msgfPar, msgfParModification-method](#), [mods<-](#), [msgfPar, numeric-method](#); [ntt](#), [ntt](#), [msgfPar-method](#), [ntt<-](#), [ntt<-](#), [msgfPar, msgfParNtt-method](#), [ntt<-](#), [msgfPar, numeric-method](#); [protocol](#), [protocol](#), [msgfPar-method](#), [protocol<-](#), [protocol<-](#), [msgfPar, character-method](#), [protocol<-](#), [msgfPar, msgfParProtocol-method](#), [protocol<-](#), [msgfPar, numeric-method](#); [tda](#), [tda](#), [msgfPar-method](#), [tda<-](#), [tda<-](#), [msgfPar, logical-method](#), [tda<-](#), [msgfPar, msgfParTda-method](#); [tolerance](#), [tolerance](#), [msgfPar-method](#), [tolerance<-](#), [tolerance<-](#), [msgfPar, character-method](#), [tolerance<-](#), [msgfPar, msgfParTolerance-method](#),

```
toleranceRange, toleranceRange, msgfPar-method, toleranceRange<-, toleranceRange<-, msgfPar, numeric-method  
toleranceUnit, toleranceUnit, msgfPar-method, toleranceUnit<-, toleranceUnit<-, msgfPar, character-method
```

## Examples

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))  
enzyme(parameters) <- Trypsin  
enzyme(parameters) <- 3  
enzyme(parameters)
```

---

fragmentation	<i>Get and set fragmentation in msgfPar objects</i>
---------------	---

---

## Description

These functions allow you to retrieve and set the fragmentation method used during acquisition

## Usage

```
fragmentation(object)  
  
fragmentation(object) <- value  
  
## S4 method for signature msgfPar  
fragmentation(object)  
  
## S4 replacement method for signature msgfPar,numeric  
fragmentation(object) <- value  
  
## S4 replacement method for signature msgfPar,character  
fragmentation(object) <- value  
  
## S4 replacement method for signature msgfPar,msgfParFragmentation  
fragmentation(object) <- value
```

## Arguments

object	An msgfPar object
value	Either an integer, string or msgfParFragmentation object

## Value

In case of the getter a named integer

**Methods (by class)**

- msgfPar: Get the fragmentation method currently used
- object = msgfPar, value = numeric: Set the fragmentation method using the key for the method
- object = msgfPar, value = character: Set the fragmentation method using the name of the method
- object = msgfPar, value = msgfParFragmentation: Set the fragmentation method using an msgfParFragmentation object

**See Also**

Other msgfPar-getter\_setter: `chargeRange`, `chargeRange`, `msgfPar-method`, `chargeRange<-`, `chargeRange<-`, `msgfPar`, `m`, `chargeRange<-`, `msgfPar`, `numeric-method`; `db`, `db`, `msgfPar-method`, `db<-`, `db<-`, `msgfPar`, `character-method`; `enzyme`, `enzyme`, `msgfPar-method`, `enzyme<-`, `enzyme<-`, `msgfPar`, `character-method`, `enzyme<-`, `msgfPar`, `msgfParEnzy`, `enzyme<-`, `msgfPar`, `numeric-method`; `instrument`, `instrument`, `msgfPar-method`, `instrument<-`, `instrument<-`, `msgfPar`, `character-method`, `instrument<-`, `msgfPar`, `msgfParInstrument-method`, `instrument<-`, `msgfPar`, `numeric-method`; `isotopeError`, `isotopeError`, `msgfPar-method`, `isotopeError<-`, `isotopeError<-`, `msgfPar`, `msgfParIsotopeError-method`, `isotopeError<-`, `msgfPar`, `numeric-method`; `lengthRange`, `lengthRange`, `msgfPar-method`, `lengthRange<-`, `lengthRange<-`, `msgfPar`, `msgfParLengthRange-method`, `lengthRange<-`, `msgfPar`, `numeric-method`; `matches`, `matches`, `msgfPar-method`, `matches<-`, `matches<-`, `msgfPar`, `msgfParMatches-method`, `matches<-`, `msgfPar`, `numeric-method`; `mods`, `mods`, `msgfPar-method`, `mods<-`, `mods<-`, `msgfPar`, `msgfParModificationList-method`, `nMod`, `nMod`, `msgfPar-method`, `nMod<-`, `nMod<-`, `msgfPar`, `numeric-method`; `ntt`, `ntt`, `msgfPar-method`, `ntt<-`, `ntt<-`, `msgfPar`, `msgfParNtt-method`, `ntt<-`, `msgfPar`, `numeric-method`; `protocol`, `protocol`, `msgfPar-method`, `protocol<-`, `protocol<-`, `msgfPar`, `character-method`, `protocol<-`, `msgfPar`, `msgfParProtocol-method`, `protocol<-`, `msgfPar`, `numeric-method`; `tda`, `tda`, `msgfPar-method`, `tda<-`, `tda<-`, `msgfPar`, `logical-method`, `tda<-`, `msgfPar`, `msgfParTda-method`; `tolerance`, `tolerance`, `msgfPar-method`, `tolerance<-`, `tolerance<-`, `msgfPar`, `character-method`, `tolerance<-`, `msgfPar`, `msgfParTolerance-method`, `toleranceRange`, `toleranceRange`, `msgfPar-method`, `toleranceRange<-`, `toleranceRange<-`, `msgfPar`, `numeric-method`, `toleranceUnit`, `toleranceUnit`, `msgfPar-method`, `toleranceUnit<-`, `toleranceUnit<-`, `msgfPar`, `character-method`

**Examples**

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
fragmentation(parameters) <- CID
fragmentation(parameters) <- 3
fragmentation(parameters)
```

---

getMSGFpar

*Get a string representation of an msgfPar-related object*

---

**Description**

The string representation is defined as the arguments that should get appended to the call when running MSGF+ in the terminal/command prompt

**Usage**

```
getMSGFpar(object)
```

**Arguments**

object            An msgfPar object or a related object

**Value**

A string that can be appended to a `system()` call to specify the parameters for the MSGF+ analysis

**See Also**

[msgfPar-class](#)

**Examples**

```
parameters <- msgfPar(  
  database=system.file(package=MSGFplus, extdata, milk-proteins.fasta),  
  tolerance=20 ppm,  
  instrument=TOF,  
  enzyme=Lys-C  
)  
getMSGFpar(parameters)
```

---

instrument

*Get and set instrument in msgfPar objects*

---

**Description**

These functions allow you to retrieve and set the instrument type used for acquisition

**Usage**

```
instrument(object)
```

```
instrument(object) <- value
```

```
## S4 method for signature msgfPar
```

```
instrument(object)
```

```
## S4 replacement method for signature msgfPar,numeric
```

```
instrument(object) <- value
```

```
## S4 replacement method for signature msgfPar,character
```

```
instrument(object) <- value
```

```
## S4 replacement method for signature msgfPar,msgfParInstrument
```

```
instrument(object) <- value
```

**Arguments**

object	An msgfPar object
value	Either an integer, string or msgfParInstrument object

**Value**

In case of the getter a named integer

**Methods (by class)**

- msgfPar: Get the instrument currently used
- object = msgfPar, value = numeric: Set the instrument using the key for the instrument
- object = msgfPar, value = character: Set the instrument using the name of the instrument
- object = msgfPar, value = msgfParInstrument: Set the instrument using an msgfParInstrument object

**See Also**

Other msgfPar-getter\_setter: [chargeRange](#), [chargeRange](#), [msgfPar-method](#), [chargeRange<-](#), [chargeRange<-](#), [msgfPar](#), [msgfPar-method](#), [chargeRange<-](#), [msgfPar](#), [numeric-method](#); [db](#), [db](#), [msgfPar-method](#), [db<-](#), [db<-](#), [msgfPar](#), [character-method](#); [enzyme](#), [enzyme](#), [msgfPar-method](#), [enzyme<-](#), [enzyme<-](#), [msgfPar](#), [character-method](#), [enzyme<-](#), [msgfPar](#), [msgfParEnzyme-method](#); [enzyme<-](#), [msgfPar](#), [numeric-method](#); [fragmentation](#), [fragmentation](#), [msgfPar-method](#), [fragmentation<-](#), [fragmentation<-](#), [msgfPar](#), [character-method](#), [fragmentation<-](#), [msgfPar](#), [msgfParFragmentation-method](#), [fragmentation<-](#), [msgfPar](#), [numeric-method](#); [isotopeError](#), [isotopeError](#), [msgfPar-method](#), [isotopeError<-](#), [isotopeError<-](#), [msgfPar](#), [msgfParIsotopeError-method](#), [isotopeError<-](#), [msgfPar](#), [numeric-method](#); [lengthRange](#), [lengthRange](#), [msgfPar-method](#), [lengthRange<-](#), [lengthRange<-](#), [msgfPar](#), [msgfParLengthRange-method](#), [lengthRange<-](#), [msgfPar](#), [numeric-method](#); [matches](#), [matches](#), [msgfPar-method](#), [matches<-](#), [matches<-](#), [msgfPar](#), [msgfParMatches-method](#), [matches<-](#), [msgfPar](#), [numeric-method](#); [mods](#), [mods](#), [msgfPar-method](#), [mods<-](#), [mods<-](#), [msgfPar](#), [msgfParModificationList-method](#), [nMod](#), [nMod](#), [msgfPar-method](#), [nMod<-](#), [nMod<-](#), [msgfPar](#), [numeric-method](#); [ntt](#), [ntt](#), [msgfPar-method](#), [ntt<-](#), [ntt<-](#), [msgfPar](#), [msgfParNtt-method](#), [ntt<-](#), [msgfPar](#), [numeric-method](#); [protocol](#), [protocol](#), [msgfPar-method](#), [protocol<-](#), [protocol<-](#), [msgfPar](#), [character-method](#); [protocol<-](#), [msgfPar](#), [msgfParProtocol-method](#), [protocol<-](#), [msgfPar](#), [numeric-method](#); [tda](#), [tda](#), [msgfPar-method](#), [tda<-](#), [tda<-](#), [msgfPar](#), [logical-method](#), [tda<-](#), [msgfPar](#), [msgfParTda-method](#); [tolerance](#), [tolerance](#), [msgfPar-method](#), [tolerance<-](#), [tolerance<-](#), [msgfPar](#), [character-method](#), [tolerance<-](#), [msgfPar](#), [msgfParTolerance-method](#), [toleranceRange](#), [toleranceRange](#), [msgfPar-method](#), [toleranceRange<-](#), [toleranceRange<-](#), [msgfPar](#), [numeric-method](#), [toleranceUnit](#), [toleranceUnit](#), [msgfPar-method](#), [toleranceUnit<-](#), [toleranceUnit<-](#), [msgfPar](#), [character-method](#)

**Examples**

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
instrument(parameters) <- TOF
instrument(parameters) <- 3
instrument(parameters)
```

---

isotopeError	<i>Get and set isotope error in msgfPar objects</i>
--------------	---

---

**Description**

These functions allow you to retrieve and set the isotope error used when calculating the parent ion error range

**Usage**

```
isotopeError(object)

isotopeError(object) <- value

## S4 method for signature msgfPar
isotopeError(object)

## S4 replacement method for signature msgfPar,numeric
isotopeError(object) <- value

## S4 replacement method for signature msgfPar,msgfParIsotopeError
isotopeError(object) <- value
```

**Arguments**

object	An msgfPar object
value	Either an integer vector or an msgfParIsotopeError object

**Value**

In case of the getter an integer vector

**Methods (by class)**

- msgfPar: Get the isotope error currently used
- object = msgfPar, value = numeric: Set the isotope error with an integer vector
- object = msgfPar, value = msgfParIsotopeError: Set the isotope error with an msgfParIsotopeError object

**See Also**

Other msgfPar-getter\_setter: [chargeRange](#), [chargeRange](#), [msgfPar-method](#), [chargeRange<-](#), [chargeRange<-](#), [msgfPar](#), [m](#), [chargeRange<-](#), [msgfPar](#), [numeric-method](#); [db](#), [db](#), [msgfPar-method](#), [db<-](#), [db<-](#), [msgfPar](#), [character-method](#); [enzyme](#), [enzyme](#), [msgfPar-method](#), [enzyme<-](#), [enzyme<-](#), [msgfPar](#), [character-method](#), [enzyme<-](#), [msgfPar](#), [msgfParEnzy](#), [enzyme<-](#), [msgfPar](#), [numeric-method](#); [fragmentation](#), [fragmentation](#), [msgfPar-method](#), [fragmentation<-](#), [fragmentation<-](#), [msgfPar](#), [character-method](#), [fragmentation<-](#), [msgfPar](#), [msgfParFragmentation-method](#), [fragmentation<-](#), [msgfPar](#), [numeric-method](#); [instrument](#), [instrument](#), [msgfPar-method](#), [instrument<-](#),

```

instrument<-,msgfPar,character-method,instrument<-,msgfPar,msgfParInstrument-method,
instrument<-,msgfPar,numeric-method,lengthRange,lengthRange,msgfPar-method,lengthRange<-,
lengthRange<-,msgfPar,msgfParLengthRange-method,lengthRange<-,msgfPar,numeric-method;
matches,matches,msgfPar-method,matches<-,matches<-,msgfPar,msgfParMatches-method,
matches<-,msgfPar,numeric-method;mods,mods,msgfPar-method,mods<-,mods<-,msgfPar,msgfParModification
nMod,nMod,msgfPar-method,nMod<-,nMod<-,msgfPar,numeric-method;ntt,ntt,msgfPar-method,
ntt<-,ntt<-,msgfPar,msgfParNtt-method,ntt<-,msgfPar,numeric-method;protocol,protocol,msgfPar-method,
protocol<-,protocol<-,msgfPar,character-method,protocol<-,msgfPar,msgfParProtocol-method,
protocol<-,msgfPar,numeric-method;tda,tda,msgfPar-method,tda<-,tda<-,msgfPar,logical-method,
tda<-,msgfPar,msgfParTda-method;tolerance,tolerance,msgfPar-method,tolerance<-,
tolerance<-,msgfPar,character-method,tolerance<-,msgfPar,msgfParTolerance-method,
toleranceRange,toleranceRange,msgfPar-method,toleranceRange<-,toleranceRange<-,msgfPar,numeric-method
toleranceUnit,toleranceUnit,msgfPar-method,toleranceUnit<-,toleranceUnit<-,msgfPar,character-method

```

### Examples

```

parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
isotopeError(parameters) <- c(0, 3)
isotopeError(parameters)

```

---

lengthRange

*Get and set peptide length range in msgfPar objects*

---

### Description

These functions allow you to retrieve and set the residue length allowed for the peptides search for in MS-GF+

### Usage

```
lengthRange(object)
```

```
lengthRange(object) <- value
```

```
## S4 method for signature msgfPar
```

```
lengthRange(object)
```

```
## S4 replacement method for signature msgfPar,numeric
```

```
lengthRange(object) <- value
```

```
## S4 replacement method for signature msgfPar,msgfParLengthRange
```

```
lengthRange(object) <- value
```

### Arguments

object            An msgfPar object

value            Either an integer vector or an msgfParLengthRange object

**Value**

In case of the getter an integer vector of length 2 giving the lower and upper bounds of the length range

**Methods (by class)**

- `msgfPar`: Get the lower and upper bounds of peptide lengths
- `object = msgfPar, value = numeric`: Set the lower and upper bounds of peptide lengths using an integer vector
- `object = msgfPar, value = msgfParLengthRange`: Set the lower and upper bounds of peptide lengths using an `msgfParLengthRange`

**See Also**

Other `msgfPar`-getter\_setter: `chargeRange`, `chargeRange`, `msgfPar-method`, `chargeRange<-`, `chargeRange<-`, `msgfPar`, `m`, `chargeRange<-`, `msgfPar`, `numeric-method`; `db`, `db`, `msgfPar-method`, `db<-`, `db<-`, `msgfPar`, `character-method`; `enzyme`, `enzyme`, `msgfPar-method`, `enzyme<-`, `enzyme<-`, `msgfPar`, `character-method`, `enzyme<-`, `msgfPar`, `msgfParEnzy`, `enzyme<-`, `msgfPar`, `numeric-method`; `fragmentation`, `fragmentation`, `msgfPar-method`, `fragmentation<-`, `fragmentation<-`, `msgfPar`, `character-method`, `fragmentation<-`, `msgfPar`, `msgfParFragmentation-method`, `fragmentation<-`, `msgfPar`, `numeric-method`; `instrument`, `instrument`, `msgfPar-method`, `instrument<-`, `instrument<-`, `msgfPar`, `character-method`, `instrument<-`, `msgfPar`, `msgfParInstrument-method`, `instrument<-`, `msgfPar`, `numeric-method`; `isotopeError`, `isotopeError`, `msgfPar-method`, `isotopeError<-`, `isotopeError<-`, `msgfPar`, `msgfParIsotopeError-method`, `isotopeError<-`, `msgfPar`, `numeric-method`; `matches`, `matches`, `msgfPar-method`, `matches<-`, `matches<-`, `msgfPar`, `msgfParMatches-method`, `matches<-`, `msgfPar`, `numeric-method`; `mods`, `mods`, `msgfPar-method`, `mods<-`, `mods<-`, `msgfPar`, `msgfParModification`, `nMod`, `nMod`, `msgfPar-method`, `nMod<-`, `nMod<-`, `msgfPar`, `numeric-method`; `ntt`, `ntt`, `msgfPar-method`, `ntt<-`, `ntt<-`, `msgfPar`, `msgfParNtt-method`, `ntt<-`, `msgfPar`, `numeric-method`; `protocol`, `protocol`, `msgfPar-method`, `protocol<-`, `protocol<-`, `msgfPar`, `character-method`, `protocol<-`, `msgfPar`, `msgfParProtocol-method`, `protocol<-`, `msgfPar`, `numeric-method`; `tda`, `tda`, `msgfPar-method`, `tda<-`, `tda<-`, `msgfPar`, `logical-method`, `tda<-`, `msgfPar`, `msgfParTda-method`; `tolerance`, `tolerance`, `msgfPar-method`, `tolerance<-`, `tolerance<-`, `msgfPar`, `character-method`, `tolerance<-`, `msgfPar`, `msgfParTolerance-method`, `toleranceRange`, `toleranceRange`, `msgfPar-method`, `toleranceRange<-`, `toleranceRange<-`, `msgfPar`, `numeric-method`; `toleranceUnit`, `toleranceUnit`, `msgfPar-method`, `toleranceUnit<-`, `toleranceUnit<-`, `msgfPar`, `character-method`

**Examples**

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
lengthRange(parameters) <- c(6, 40)
lengthRange(parameters)
```

---

matches

*Get and set the number of matches in msgfPar objects*

---

**Description**

These functions allow you to retrieve and set the number of matches per spectrum returned by MS-GF+

**Usage**

```

matches(object)

matches(object) <- value

## S4 method for signature msgfPar
matches(object)

## S4 replacement method for signature msgfPar,numeric
matches(object) <- value

## S4 replacement method for signature msgfPar,msgfParMatches
matches(object) <- value

```

**Arguments**

object	An msgfPar object
value	Either an integer or an msgfParMatches object

**Value**

In case of the getter an integer

**Methods (by class)**

- msgfPar: Get the number of matches reported per spectrum
- object = msgfPar, value = numeric: Set the number of matches reported per spectrum using an integer
- object = msgfPar, value = msgfParMatches: Set the number of matches reported per spectrum using an msgfParMatches object

**See Also**

Other msgfPar-getter\_setter: [chargeRange](#), [chargeRange](#), [msgfPar-method](#), [chargeRange<-](#), [chargeRange<-](#), [msgfPar](#), [m](#), [chargeRange<-](#), [msgfPar](#), [numeric-method](#); [db](#), [db](#), [msgfPar-method](#), [db<-](#), [db<-](#), [msgfPar](#), [character-method](#); [enzyme](#), [enzyme](#), [msgfPar-method](#), [enzyme<-](#), [enzyme<-](#), [msgfPar](#), [character-method](#), [enzyme<-](#), [msgfPar](#), [msgfParEnzy](#), [enzyme<-](#), [msgfPar](#), [numeric-method](#); [fragmentation](#), [fragmentation](#), [msgfPar-method](#), [fragmentation<-](#), [fragmentation<-](#), [msgfPar](#), [character-method](#), [fragmentation<-](#), [msgfPar](#), [msgfParFragmentation-method](#), [fragmentation<-](#), [msgfPar](#), [numeric-method](#); [instrument](#), [instrument](#), [msgfPar-method](#), [instrument<-](#), [instrument<-](#), [msgfPar](#), [character-method](#), [instrument<-](#), [msgfPar](#), [msgfParInstrument-method](#), [instrument<-](#), [msgfPar](#), [numeric-method](#); [isotopeError](#), [isotopeError](#), [msgfPar-method](#), [isotopeError<-](#), [isotopeError<-](#), [msgfPar](#), [msgfParIsotopeError-method](#), [isotopeError<-](#), [msgfPar](#), [numeric-method](#); [lengthRange](#), [lengthRange](#), [msgfPar-method](#), [lengthRange<-](#), [lengthRange<-](#), [msgfPar](#), [msgfParLengthRange-method](#), [lengthRange<-](#), [msgfPar](#), [numeric-method](#); [mods](#), [mods](#), [msgfPar-method](#), [mods<-](#), [mods<-](#), [msgfPar](#), [msgfParModificati](#), [nMod](#), [nMod](#), [msgfPar-method](#), [nMod<-](#), [nMod<-](#), [msgfPar](#), [numeric-method](#); [ntt](#), [ntt](#), [msgfPar-method](#), [ntt<-](#), [ntt<-](#), [msgfPar](#), [msgfParNtt-method](#), [ntt<-](#), [msgfPar](#), [numeric-method](#); [protocol](#), [protocol](#), [msgfPar-method](#), [protocol<-](#), [protocol<-](#), [msgfPar](#), [character-method](#), [protocol<-](#), [msgfPar](#), [msgfParProtocol-method](#), [protocol<-](#), [msgfPar](#), [numeric-method](#); [tda](#), [tda](#), [msgfPar-method](#), [tda<-](#), [tda<-](#), [msgfPar](#), [logical-method](#),

```

tda<-,msgfPar,msgfParTda-method; tolerance, tolerance,msgfPar-method, tolerance<-,
tolerance<-,msgfPar,character-method, tolerance<-,msgfPar,msgfParTolerance-method,
toleranceRange, toleranceRange,msgfPar-method, toleranceRange<-, toleranceRange<- ,msgfPar,numeric-method
toleranceUnit, toleranceUnit,msgfPar-method, toleranceUnit<-, toleranceUnit<- ,msgfPar,character-method

```

## Examples

```

parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
matches(parameters) <- 5
matches(parameters)

```

---

mods

*Get and set the modifications in msgfPar objects*

---

## Description

These functions allow you to retrieve and set the specific modifications allowed on peptides during MS-GF+ search, as well as the number allowed on each peptide

## Usage

```
mods(object)
```

```
mods(object) <- value
```

```
nMod(object)
```

```
nMod(object) <- value
```

```
## S4 method for signature msgfPar
mods(object)
```

```
## S4 replacement method for signature msgfPar,msgfParModificationList
mods(object) <- value
```

```
## S4 method for signature msgfPar
nMod(object)
```

```
## S4 replacement method for signature msgfPar,numeric
nMod(object) <- value
```

## Arguments

object            An msgfPar object

value            An msgfParModificationList object or in the case of nMod an integer

**Value**

For the getter an msgfParModificationList object or an integer (in the case of nMod)

**Methods (by class)**

- msgfPar: Get the list of modifications allowed during peptide search
- object = msgfPar, value = msgfParModificationList: Set the list of modifications allowed during peptide search
- msgfPar: Get the number of peptides allowed per peptide during search
- object = msgfPar, value = numeric: Set the number of peptides allowed per peptide during search using an integer

**See Also**

Other msgfPar-getter\_setter: [chargeRange](#), [chargeRange](#), [msgfPar-method](#), [chargeRange<-](#), [chargeRange<-](#), [msgfPar](#), [msgfPar-method](#), [chargeRange<-](#), [msgfPar](#), [numeric-method](#); [db](#), [db](#), [msgfPar-method](#), [db<-](#), [db<-](#), [msgfPar](#), [character-method](#); [enzyme](#), [enzyme](#), [msgfPar-method](#), [enzyme<-](#), [enzyme<-](#), [msgfPar](#), [character-method](#), [enzyme<-](#), [msgfPar](#), [msgfParEnzyme-method](#), [enzyme<-](#), [msgfPar](#), [numeric-method](#); [fragmentation](#), [fragmentation](#), [msgfPar-method](#), [fragmentation<-](#), [fragmentation<-](#), [msgfPar](#), [character-method](#), [fragmentation<-](#), [msgfPar](#), [msgfParFragmentation-method](#), [fragmentation<-](#), [msgfPar](#), [numeric-method](#); [instrument](#), [instrument](#), [msgfPar-method](#), [instrument<-](#), [instrument<-](#), [msgfPar](#), [character-method](#), [instrument<-](#), [msgfPar](#), [msgfParInstrument-method](#), [instrument<-](#), [msgfPar](#), [numeric-method](#); [isotopeError](#), [isotopeError](#), [msgfPar-method](#), [isotopeError<-](#), [isotopeError<-](#), [msgfPar](#), [msgfParIsotopeError-method](#), [isotopeError<-](#), [msgfPar](#), [numeric-method](#); [lengthRange](#), [lengthRange](#), [msgfPar-method](#), [lengthRange<-](#), [lengthRange<-](#), [msgfPar](#), [msgfParLengthRange-method](#), [lengthRange<-](#), [msgfPar](#), [numeric-method](#); [matches](#), [matches](#), [msgfPar-method](#), [matches<-](#), [matches<-](#), [msgfPar](#), [msgfParMatches-method](#), [matches<-](#), [msgfPar](#), [numeric-method](#); [ntt](#), [ntt](#), [msgfPar-method](#), [ntt<-](#), [ntt<-](#), [msgfPar](#), [msgfParNtt-method](#), [ntt<-](#), [msgfPar](#), [numeric-method](#); [protocol](#), [protocol](#), [msgfPar-method](#), [protocol<-](#), [protocol<-](#), [msgfPar](#), [character-method](#), [protocol<-](#), [msgfPar](#), [msgfParProtocol-method](#), [protocol<-](#), [msgfPar](#), [numeric-method](#); [tda](#), [tda](#), [msgfPar-method](#), [tda<-](#), [tda<-](#), [msgfPar](#), [logical-method](#), [tda<-](#), [msgfPar](#), [msgfParTda-method](#); [tolerance](#), [tolerance](#), [msgfPar-method](#), [tolerance<-](#), [tolerance<-](#), [msgfPar](#), [character-method](#), [tolerance<-](#), [msgfPar](#), [msgfParTolerance-method](#), [toleranceRange](#), [toleranceRange](#), [msgfPar-method](#), [toleranceRange<-](#), [toleranceRange<-](#), [msgfPar](#), [numeric-method](#); [toleranceUnit](#), [toleranceUnit](#), [msgfPar-method](#), [toleranceUnit<-](#), [toleranceUnit<-](#), [msgfPar](#), [character-method](#)

**Examples**

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
nMod(parameters) <- 2
mods(parameters)[[1]] <- msgfParModification(
    name=Carbamidomethyl,
    composition=C2H3N1O1,
    residues=C,
    type=fix,
    position=any
)
mods(parameters)
```



**Details**

Please consult the MS-GF+ documentation for full description of the parameters

Fragmentation is usually specified as an integer according to the following lookup

- 0** As written in the spectrum or CID if no info
- 1** CID
- 2** ETD
- 3** HCD
- 4** Merge spectra from the same precursor

It is possible to use the full name of the description for a more literal function call

Instrument can likewise be specified as an integer or as a name according to this list

- 0** LowRes
- 1** HighRes
- 2** TOF
- 3** QExactive

Enzymes are specified in the same manner using the following list

- 0** Unspecific cleavage
- 1** Trypsin
- 2** Chymotrypsin
- 3** Lys-C
- 4** Lys-N
- 5** glutamyl endopeptidase (Glu-C)
- 6** Arg-C
- 7** Asp-N
- 8** alphaLP
- 9** No cleavage

The protocol informs MS-GF+ whether a special sample treatment has been performed as part of the analysis. The protocol is specified according to the following list

- 0** No protocol
- 1** Phosphorylation
- 2** iTRAQ
- 3** iTRAQPhospho

**Value**

An msgfPar object

## References

[MS-GF+](#)

## See Also

Other msgfParClasses: `[[], msgfParModificationList, numeric, missing-method, [[<- , msgfParModificationList, n`  
`getMSGFpar, msgfParModificationList-method, length, msgfParModificationList-method,`  
`msgfParModificationList, msgfParModificationList-class, show, msgfParModificationList-method;`  
`getMSGFpar, msgfPar-method, length, msgfPar-method, msgfPar-class, runMSGF, msgfPar-method,`  
`show, msgfPar-method; getMSGFpar, msgfParChargeRange-method, length, msgfParChargeRange-method,`  
`msgfParChargeRange, msgfParChargeRange-class, show, msgfParChargeRange-method; getMSGFpar, msgfParEnzyme-`  
`length, msgfParEnzyme-method, msgfParEnzyme, msgfParEnzyme-class, show, msgfParEnzyme-method;`  
`getMSGFpar, msgfParFragmentation-method, length, msgfParFragmentation-method, msgfParFragmentation,`  
`msgfParFragmentation-class, show, msgfParFragmentation-method; getMSGFpar, msgfParInstrument-method,`  
`length, msgfParInstrument-method, msgfParInstrument, msgfParInstrument-class, show, msgfParInstrument-me`  
`getMSGFpar, msgfParIsotopeError-method, length, msgfParIsotopeError-method, msgfParIsotopeError,`  
`msgfParIsotopeError-class, show, msgfParIsotopeError-method; getMSGFpar, msgfParLengthRange-method,`  
`length, msgfParLengthRange-method, msgfParLengthRange, msgfParLengthRange-class, show, msgfParLengthRange`  
`getMSGFpar, msgfParMatches-method, length, msgfParMatches-method, msgfParMatches, msgfParMatches-class,`  
`show, msgfParMatches-method; getMSGFpar, msgfParModification-method, msgfParModification,`  
`msgfParModification-class, show, msgfParModification-method; getMSGFpar, msgfParNtt-method,`  
`length, msgfParNtt-method, msgfParNtt, msgfParNtt-class, show, msgfParNtt-method; getMSGFpar, msgfParProto`  
`length, msgfParProtocol-method, msgfParProtocol, msgfParProtocol-class, show, msgfParProtocol-method;`  
`getMSGFpar, msgfParTda-method, length, msgfParTda-method, msgfParTda, msgfParTda-class,`  
`show, msgfParTda-method; getMSGFpar, msgfParTolerance-method, length, msgfParTolerance-method,`  
`msgfParTolerance, msgfParTolerance-class, show, msgfParTolerance-method`

## Examples

```
# Example of specifying all parameters - usually not necessary
parameters <- msgfPar(
  database=system.file(package=MSGFplus, extdata, milk-proteins.fasta),
  tolerance=20 ppm,
  isotopeError=c(0, 2),
  tda=TRUE,
  fragmentation=CID,
  instrument=TOF,
  enzyme=Lys-C,
  protocol=No protocol,
  ntt=2,
  modification=list(
    nMod=2,
    modifications=list(
      list(name=Carbamidomethyl,
           composition=C2H3N1O1,
           residues=C,
           type=fix,
           position=any
      ),
      list(name=Oxidation,
```

```

                                mass=15.994915,
                                residues=M,
                                type=opt,
                                position=any
                                )
                                )
                                ),
                                lengthRange=c(6,40),
                                chargeRange=c(2,7),
                                matches=1
                                )
parameters

```

---

msgfPar-class

*A class to contain parameters used in an MS-GF+ analysis*


---

### Description

This class collects and stores parameters for an MS-GF+ analysis and is the starting point for peptide identification

### Usage

```

## S4 method for signature msgfPar
show(object)

## S4 method for signature msgfPar
length(x)

## S4 method for signature msgfPar
getMSGFpar(object)

## S4 method for signature msgfPar
runMSGF(object, rawfiles, savenames, import = TRUE,
        memory = 10000, async = FALSE, msgfPath)

```

### Arguments

object	An msgfPar object
x	An msgfPar object
rawfiles	A character vector holding the filepath to the spectrum files to be analysed (currently supported formats: *.mzML, *.mzXML, *.mgf, *.ms2, *.pkl or *_dta.txt)
savenames	An optional vector of same length as rawfiles. Specifies the name used to save the results. If omitted the results will be saved with the same name as the rawfile, but with an .mzid extension.
import	Logical (default=TRUE). Should the results be imported in to R after the analysis is finished.

memory	An integer (default=10000). How much memory should be allocated to the java virtual machine during execution (in mb)
async	An Logical (default=FALSE). Should MS-GF+ be run asynchronously?
msgfPath	The path to an alternative MSGFPlus.jar file if the bundled one is not desired

### Details

This class contains a range of other classes, each handling a different set of parameters. Often these classes are simple containers that only takes care of errorchecking and generating command line arguments, but in some cases, as with msgfParModificationList, the class is a bit more complex.

### Value

length: 1 if a database is defined, 0 otherwise.

getMSGFpar: A stringified version of the parameters compliant with MS-GF+.

runMSGF: If import=TRUE an mzID or mzIDCollection object. If async=TRUE an msgfAsync object. Otherwise NULL

### Methods (by generic)

- show: Short summary of msgfPar object
- length: Report the length of an msgfPar object
- getMSGFpar: Get [system](#) compliant function call
- runMSGF: Initiate an MS-GF+ analysis using the selected msgfPar object

### Slots

database The location of the database fasta file used for the analysis.

tolerance An msgfParTolerance object holding the m/z tolerance used in the search.

isotopeError An msgfParIsotopeError object holding the isotope errors permitted in the search.

tda An msgfParTda object saying whether FDR should be estimated using the target-decoy approach.

fragmentation An msgfParFragmentation object holding the type of fragmentation expected from the experiment.

instrument An msgfParInstrument object holding which type of instrument was used for collecting the data.

enzyme An msgfParEnzyme object holding which enzyme was used for digestion

protocol An msgfParProtocol object defining whether a specific protocol should be used in the search.

ntt An msgfParNtt object defining the number of tolerable termini allowed in the peptides.

modification An msgfParModificationList object holding the modifications accepted in the search.

lengthRange An msgfParLengthRange object setting the limits on the peptide length in residues that the search allows.

chargeRange An msgfParChargeRange object defining which charges should be included in the search.

matches An msgfParMatches object defining the number of matches per PSM that gets reported in the output.

### Objects from the class

Objects can be created using the `msgfPar` constructor, or with `msgfParGUI` for a simple graphical user interface

### References

<http://proteomics.ucsd.edu/Software/MSGFPlus.html>

### See Also

`msgfParGUI`

Other msgfParClasses: `[[], msgfParModificationList, numeric, missing-method, [[<-], msgfParModificationList, msgfParModificationList-method, length, msgfParModificationList-method, msgfParModificationList, msgfParModificationList-class, show, msgfParModificationList-method; getMSGFpar, msgfParChargeRange-method, length, msgfParChargeRange-method, msgfParChargeRange, msgfParChargeRange-class, show, msgfParChargeRange-method; getMSGFpar, msgfParEnzyme-method, length, msgfParEnzyme-method, msgfParEnzyme, msgfParEnzyme-class, show, msgfParEnzyme-method; getMSGFpar, msgfParFragmentation-method, length, msgfParFragmentation-method, msgfParFragmentation, msgfParFragmentation-class, show, msgfParFragmentation-method; getMSGFpar, msgfParInstrument-method, length, msgfParInstrument-method, msgfParInstrument, msgfParInstrument-class, show, msgfParInstrument-method; getMSGFpar, msgfParIsotopeError-method, length, msgfParIsotopeError-method, msgfParIsotopeError, msgfParIsotopeError-class, show, msgfParIsotopeError-method; getMSGFpar, msgfParLengthRange-method, length, msgfParLengthRange-method, msgfParLengthRange, msgfParLengthRange-class, show, msgfParLengthRange-method; getMSGFpar, msgfParMatches-method, length, msgfParMatches-method, msgfParMatches, msgfParMatches-class, show, msgfParMatches-method; getMSGFpar, msgfParModification-method, msgfParModification, msgfParModification-class, show, msgfParModification-method; getMSGFpar, msgfParNtt-method, length, msgfParNtt-method, msgfParNtt, msgfParNtt-class, show, msgfParNtt-method; getMSGFpar, msgfParProtocol-method, length, msgfParProtocol-method, msgfParProtocol, msgfParProtocol-class, show, msgfParProtocol-method; getMSGFpar, msgfParTda-method, length, msgfParTda-method, msgfParTda, msgfParTda-class, show, msgfParTda-method; getMSGFpar, msgfParTolerance-method, length, msgfParTolerance-method, msgfParTolerance, msgfParTolerance-class, show, msgfParTolerance-method; msgfPar`

### Examples

```
parameters <- msgfPar(
  database=system.file(package=MSGFplus, extdata, milk-proteins.fasta),
  tolerance=20 ppm,
  instrument=TOF,
  enzyme=Lys-C
)
getMSGFpar(parameters)
## Not run:
parameters <- msgfPar(
  database=system.file(package=MSGFplus, extdata, milk-proteins.fasta),
```

```

        tolerance=20 ppm,
        instrument=TOF,
        enzyme=Lys-C
    )
runMSGF(parameters, c(file1.mzML, file2.mzML))

## End(Not run)

```

---

msgfParChargeRange-class

*A class handling charge ranges*

---

### Description

This class defines a charge range and provides methods to get correct system call parameters.

### Usage

```

## S4 method for signature msgfParChargeRange
show(object)

## S4 method for signature msgfParChargeRange
length(x)

## S4 method for signature msgfParChargeRange
getMSGFpar(object)

msgfParChargeRange(value)

```

### Arguments

object	An msgfParChargeRange object
x	An msgfParChargeRange object
value	A numeric vector of length 2. The first element must be smaller than the last

### Value

For length() An integer.  
 For getMSGFpar() A string.  
 For msgfParChargeRange() An msgfParChargeRange object.

### Methods (by generic)

- show: Short summary of msgfParChargeRange object
- length: Report the length of an msgfParChargeRange object
- getMSGFpar: Get [system](#) compliant function call

**Slots**

value A numeric vector of length 2 describing the upper and lower bounds of the charge range

**See Also**

Other msgfParClasses: `[[], msgfParModificationList, numeric, missing-method, [[<- , msgfParModificationList, n`  
`getMSGFpar, msgfParModificationList-method, length, msgfParModificationList-method,`  
`msgfParModificationList, msgfParModificationList-class, show, msgfParModificationList-method;`  
`getMSGFpar, msgfPar-method, length, msgfPar-method, msgfPar-class, runMSGF, msgfPar-method,`  
`show, msgfPar-method; getMSGFpar, msgfParEnzyme-method, length, msgfParEnzyme-method,`  
`msgfParEnzyme, msgfParEnzyme-class, show, msgfParEnzyme-method; getMSGFpar, msgfParFragmentation-method,`  
`length, msgfParFragmentation-method, msgfParFragmentation, msgfParFragmentation-class,`  
`show, msgfParFragmentation-method; getMSGFpar, msgfParInstrument-method, length, msgfParInstrument-method,`  
`msgfParInstrument, msgfParInstrument-class, show, msgfParInstrument-method; getMSGFpar, msgfParIsotopeEr`  
`length, msgfParIsotopeError-method, msgfParIsotopeError, msgfParIsotopeError-class,`  
`show, msgfParIsotopeError-method; getMSGFpar, msgfParLengthRange-method, length, msgfParLengthRange-meth`  
`msgfParLengthRange, msgfParLengthRange-class, show, msgfParLengthRange-method; getMSGFpar, msgfParMatches`  
`length, msgfParMatches-method, msgfParMatches, msgfParMatches-class, show, msgfParMatches-method;`  
`getMSGFpar, msgfParModification-method, msgfParModification, msgfParModification-class,`  
`show, msgfParModification-method; getMSGFpar, msgfParNtt-method, length, msgfParNtt-method,`  
`msgfParNtt, msgfParNtt-class, show, msgfParNtt-method; getMSGFpar, msgfParProtocol-method,`  
`length, msgfParProtocol-method, msgfParProtocol, msgfParProtocol-class, show, msgfParProtocol-method;`  
`getMSGFpar, msgfParTda-method, length, msgfParTda-method, msgfParTda, msgfParTda-class,`  
`show, msgfParTda-method; getMSGFpar, msgfParTolerance-method, length, msgfParTolerance-method,`  
`msgfParTolerance, msgfParTolerance-class, show, msgfParTolerance-method; msgfPar`

**Examples**

```
charges <- msgfParChargeRange(c(2, 5))
```

---

msgfParEnzyme-class    *A class handling enzyme selection*

---

**Description**

This class defines a digestion enzyme selection and provides methods to get correct system call parameters.

**Usage**

```
## S4 method for signature msgfParEnzyme
show(object)
```

```
## S4 method for signature msgfParEnzyme
length(x)
```

```
## S4 method for signature msgfParEnzyme
```

getMSGFpar(object)

msgfParEnzyme(enzyme)

### Arguments

object	An msgfParEnzyme object
x	An msgfParEnzyme object
enzyme	Either an integer or a string

### Value

For length() An integer.

For getMSGFpar() A string.

For msgfParEnzyme() An msgfParEnzyme object.

### Methods (by generic)

- show: Short summary of msgfParEnzyme object
- length: Report the length of an msgfParEnzyme object
- getMSGFpar: Get [system](#) compliant function call

### Slots

enzyme An integer specifying the selection of enzyme. See the detail section of [msgfPar](#)

### See Also

Other msgfParClasses: [\[\[\],msgfParModificationList,numeric,missing-method,\[<- ,msgfParModificationList,nu](#)  
[getMSGFpar,msgfParModificationList-method,length,msgfParModificationList-method,](#)  
[msgfParModificationList,msgfParModificationList-class,show,msgfParModificationList-method;](#)  
[getMSGFpar,msgfPar-method,length,msgfPar-method,msgfPar-class,runMSGF,msgfPar-method,](#)  
[show,msgfPar-method;getMSGFpar,msgfParChargeRange-method,length,msgfParChargeRange-method,](#)  
[msgfParChargeRange,msgfParChargeRange-class,show,msgfParChargeRange-method;getMSGFpar,msgfParFragmen](#)  
[length,msgfParFragmentation-method,msgfParFragmentation,msgfParFragmentation-class,](#)  
[show,msgfParFragmentation-method;getMSGFpar,msgfParInstrument-method,length,msgfParInstrument-metho](#)  
[msgfParInstrument,msgfParInstrument-class,show,msgfParInstrument-method;getMSGFpar,msgfParIsotopeEr](#)  
[length,msgfParIsotopeError-method,msgfParIsotopeError,msgfParIsotopeError-class,](#)  
[show,msgfParIsotopeError-method;getMSGFpar,msgfParLengthRange-method,length,msgfParLengthRange-meth](#)  
[msgfParLengthRange,msgfParLengthRange-class,show,msgfParLengthRange-method;getMSGFpar,msgfParMatches](#)  
[length,msgfParMatches-method,msgfParMatches,msgfParMatches-class,show,msgfParMatches-method;](#)  
[getMSGFpar,msgfParModification-method,msgfParModification,msgfParModification-class,](#)  
[show,msgfParModification-method;getMSGFpar,msgfParNtt-method,length,msgfParNtt-method,](#)  
[msgfParNtt,msgfParNtt-class,show,msgfParNtt-method;getMSGFpar,msgfParProtocol-method,](#)  
[length,msgfParProtocol-method,msgfParProtocol,msgfParProtocol-class,show,msgfParProtocol-method;](#)  
[getMSGFpar,msgfParTda-method,length,msgfParTda-method,msgfParTda,msgfParTda-class,](#)  
[show,msgfParTda-method;getMSGFpar,msgfParTolerance-method,length,msgfParTolerance-method,](#)  
[msgfParTolerance,msgfParTolerance-class,show,msgfParTolerance-method;msgfPar](#)

**Examples**

```
enzyme <- msgfParEnzyme(1)
enzyme <- msgfParEnzyme(Trypsin)
```

---

msgfParFragmentation-class

*A class handling Fragmentation types*

---

**Description**

This class defines a fragmentation type and provides methods to get correct system call parameters.

**Usage**

```
## S4 method for signature msgfParFragmentation
show(object)

## S4 method for signature msgfParFragmentation
length(x)

## S4 method for signature msgfParFragmentation
getMSGFpar(object)

msgfParFragmentation(method)
```

**Arguments**

object	An msgfParFragmentation object
x	An msgfParFragmentation object
method	An integer specifying the method

**Value**

For length() An integer.

For getMSGFpar() A string.

For msgfParFragmentation() An msgfParFragmentation object.

**Methods (by generic)**

- show: Short summary of msgfParFragmentation object
- length: Report the length of an msgfParFragmentation object
- getMSGFpar: Get [system](#) compliant function call

**Slots**

method An integer between 0 and 4 giving the selected method

**See Also**

Other msgfParClasses: [[\[,msgfParModificationList,numeric,missing-method](#), [\[\[<- ,msgfParModificationList,numeric](#), [getMSGFpar,msgfParModificationList-method,length,msgfParModificationList-method](#), [msgfParModificationList,msgfParModificationList-class,show,msgfParModificationList-method](#); [getMSGFpar,msgfPar-method,length,msgfPar-method,msgfPar-class,runMSGF,msgfPar-method,show,msgfPar-method](#); [getMSGFpar,msgfParChargeRange-method,length,msgfParChargeRange-method,msgfParChargeRange,msgfParChargeRange-class,show,msgfParChargeRange-method](#); [getMSGFpar,msgfParEnzyme-method,length,msgfParEnzyme-method,msgfParEnzyme,msgfParEnzyme-class,show,msgfParEnzyme-method](#); [getMSGFpar,msgfParInstrument-method,length,msgfParInstrument-method,msgfParInstrument,msgfParInstrument-class,show,msgfParInstrument-method](#); [getMSGFpar,msgfParIsotopeError-method,length,msgfParIsotopeError-method,msgfParIsotopeError,msgfParIsotopeError-class,show,msgfParIsotopeError-method](#); [getMSGFpar,msgfParLengthRange-method,length,msgfParLengthRange-method,msgfParLengthRange,msgfParLengthRange-class,show,msgfParLengthRange-method](#); [getMSGFpar,msgfParMatches-method,length,msgfParMatches-method,msgfParMatches,msgfParMatches-class,show,msgfParMatches-method](#); [getMSGFpar,msgfParModification-method,msgfParModification,msgfParModification-class,show,msgfParModification-method](#); [getMSGFpar,msgfParNtt-method,length,msgfParNtt-method,msgfParNtt,msgfParNtt-class,show,msgfParNtt-method](#); [getMSGFpar,msgfParProtocol-method,length,msgfParProtocol-method,msgfParProtocol,msgfParProtocol-class,show,msgfParProtocol-method](#); [getMSGFpar,msgfParTda-method,length,msgfParTda-method,msgfParTda,msgfParTda-class,show,msgfParTda-method](#); [getMSGFpar,msgfParTolerance-method,length,msgfParTolerance-method,msgfParTolerance,msgfParTolerance-class,show,msgfParTolerance-method](#); [msgfPar](#)

**Examples**

```
fragmentation <- msgfParFragmentation(1)
fragmentation <- msgfParFragmentation(CID)
```

---

msgfParFromID

*Extract parameters from mzIdentML result file*

---

**Description**

This function analyses an mzIdentML file generated using MS-GF+ and returns an msgfPar object with parameters matching the ones used to generate the mzIdentML file. If the mzIdentML file does not origin from an MS-GF+ analysis it throws an error.

**Usage**

```
msgfParFromID(file)
```

**Arguments**

file            The mzIdentML file to extract the parameters from

**Details**

NOTE: At the moment the number of allowed modifications per peptide is not written to the result file and can thus not be extracted. It defaults to 2

**Value**

An msgfPar object with parameters matching the input file

**See Also**

[msgfPar-class msgfPar](#)

**Examples**

```
## Not run:  
parameters <- msgfParFromID(result1.mzid)  
  
## End(Not run)
```

---

msgfParGUI

*A simple GUI to create msgfPar objects*

---

**Description**

This function presents the user with a GUI where the different parameters can be filled out interactively. When the window appears the different values already present reflects the default values for MS-GF+ so leaving them as is equals to not setting them in advance.

**Usage**

```
msgfParGUI()
```

**Details**

NOTE: This functions requires gWidgets and checks for the existance beforehand. MSGFplus does not import gWidgets and gWidgets does thus not necessarily exist on your system. In addition at least one of the gWidgetsXXX packages are needed.

**Value**

A msgfPar object with parameters set according to the final state of the GUI

**See Also**

[msgfPar-class](#)

**Examples**

```
## Not run:  
parameters <- msgfParGUI()  
  
## End(Not run)
```

---

`msgfParInstrument-class`*A class handling instrument types*

---

## Description

This class defines an instrument type and provides methods to get correct system call parameters.

## Usage

```
## S4 method for signature msgfParInstrument
show(object)
```

```
## S4 method for signature msgfParInstrument
length(x)
```

```
## S4 method for signature msgfParInstrument
getMSGFpar(object)
```

```
msgfParInstrument(instrument)
```

## Arguments

<code>object</code>	An <code>msgfParInstrument</code> object
<code>x</code>	An <code>msgfParInstrument</code> object
<code>instrument</code>	An integer specifying the instrument type

## Value

For `length()` An integer.

For `getMSGFpar()` A string.

For `msgfParInstrument()` An `msgfParInstrument` object.

## Methods (by generic)

- `show`: Short summary of `msgfParInstrument` object
- `length`: Report the length of an `msgfParInstrument` object
- `getMSGFpar`: Get [system](#) compliant function call

## Slots

`instrument` An integer specifying the instrument type

**See Also**

Other msgfParClasses: `[[], msgfParModificationList, numeric, missing-method, [[<- , msgfParModificationList, nu`  
`getMSGFpar, msgfParModificationList-method, length, msgfParModificationList-method,`  
`msgfParModificationList, msgfParModificationList-class, show, msgfParModificationList-method;`  
`getMSGFpar, msgfPar-method, length, msgfPar-method, msgfPar-class, runMSGF, msgfPar-method,`  
`show, msgfPar-method; getMSGFpar, msgfParChargeRange-method, length, msgfParChargeRange-method,`  
`msgfParChargeRange, msgfParChargeRange-class, show, msgfParChargeRange-method; getMSGFpar, msgfParEnzyme-`  
`length, msgfParEnzyme-method, msgfParEnzyme, msgfParEnzyme-class, show, msgfParEnzyme-method;`  
`getMSGFpar, msgfParFragmentation-method, length, msgfParFragmentation-method, msgfParFragmentation,`  
`msgfParFragmentation-class, show, msgfParFragmentation-method; getMSGFpar, msgfParIsotopeError-method,`  
`length, msgfParIsotopeError-method, msgfParIsotopeError, msgfParIsotopeError-class,`  
`show, msgfParIsotopeError-method; getMSGFpar, msgfParLengthRange-method, length, msgfParLengthRange-meth`  
`msgfParLengthRange, msgfParLengthRange-class, show, msgfParLengthRange-method; getMSGFpar, msgfParMatches-`  
`length, msgfParMatches-method, msgfParMatches, msgfParMatches-class, show, msgfParMatches-method;`  
`getMSGFpar, msgfParModification-method, msgfParModification, msgfParModification-class,`  
`show, msgfParModification-method; getMSGFpar, msgfParNtt-method, length, msgfParNtt-method,`  
`msgfParNtt, msgfParNtt-class, show, msgfParNtt-method; getMSGFpar, msgfParProtocol-method,`  
`length, msgfParProtocol-method, msgfParProtocol, msgfParProtocol-class, show, msgfParProtocol-method;`  
`getMSGFpar, msgfParTda-method, length, msgfParTda-method, msgfParTda, msgfParTda-class,`  
`show, msgfParTda-method; getMSGFpar, msgfParTolerance-method, length, msgfParTolerance-method,`  
`msgfParTolerance, msgfParTolerance-class, show, msgfParTolerance-method; msgfPar`

**Examples**

```
instrument <- msgfParInstrument(1)
instrument <- msgfParInstrument(HighRes)
```

---

msgfParIsotopeError-class

*A class handling isotope errors*

---

**Description**

This class defines a set of isotopes that should be included for error correction and provides methods to get correct system call parameters.

**Usage**

```
## S4 method for signature msgfParIsotopeError
show(object)
```

```
## S4 method for signature msgfParIsotopeError
length(x)
```

```
## S4 method for signature msgfParIsotopeError
getMSGFpar(object)
```

```
msgfParIsotopeError(range)
```

**Arguments**

object	An msgfParIsotopeError object
x	An msgfParIsotopeError object
range	An integer vector with isotopes

**Value**

For length() An integer.

For getMSGFpar() A string.

For msgfParIsotopeError() An msgfParIsotopeError object.

**Methods (by generic)**

- show: Short summary of msgfParIsotopeError object
- length: Report the length of an msgfParIsotopeError object
- getMSGFpar: Get [system](#) compliant function call

**Slots**

range An integer vector with lower and upper bounds of isotopes to error correct

**See Also**

Other msgfParClasses: `[[,msgfParModificationList,numeric,missing-method,[[-,msgfParModificationList,n  
getMSGFpar,msgfParModificationList-method,length,msgfParModificationList-method,  
msgfParModificationList,msgfParModificationList-class,show,msgfParModificationList-method;  
getMSGFpar,msgfPar-method,length,msgfPar-method,msgfPar-class,runMSGF,msgfPar-method,  
show,msgfPar-method;getMSGFpar,msgfParChargeRange-method,length,msgfParChargeRange-method,  
msgfParChargeRange,msgfParChargeRange-class,show,msgfParChargeRange-method;getMSGFpar,msgfParEnzyme-  
length,msgfParEnzyme-method,msgfParEnzyme,msgfParEnzyme-class,show,msgfParEnzyme-method;  
getMSGFpar,msgfParFragmentation-method,length,msgfParFragmentation-method,msgfParFragmentation,  
msgfParFragmentation-class,show,msgfParFragmentation-method;getMSGFpar,msgfParInstrument-method,  
length,msgfParInstrument-method,msgfParInstrument,msgfParInstrument-class,show,msgfParInstrument-me  
getMSGFpar,msgfParLengthRange-method,length,msgfParLengthRange-method,msgfParLengthRange,  
msgfParLengthRange-class,show,msgfParLengthRange-method;getMSGFpar,msgfParMatches-method,  
length,msgfParMatches-method,msgfParMatches,msgfParMatches-class,show,msgfParMatches-method;  
getMSGFpar,msgfParModification-method,msgfParModification,msgfParModification-class,  
show,msgfParModification-method;getMSGFpar,msgfParNtt-method,length,msgfParNtt-method,  
msgfParNtt,msgfParNtt-class,show,msgfParNtt-method;getMSGFpar,msgfParProtocol-method,  
length,msgfParProtocol-method,msgfParProtocol,msgfParProtocol-class,show,msgfParProtocol-method;  
getMSGFpar,msgfParTda-method,length,msgfParTda-method,msgfParTda,msgfParTda-class,  
show,msgfParTda-method;getMSGFpar,msgfParTolerance-method,length,msgfParTolerance-method,  
msgfParTolerance,msgfParTolerance-class,show,msgfParTolerance-method;msgfPar`

**Examples**

```
isotopeError <- msgfParIsotopeError(c(0, 2))
```

---

 msgfParLengthRange-class

*A class handling length ranges*


---

## Description

This class defines a length range and provides methods to get correct system call parameters.

## Usage

```
## S4 method for signature msgfParLengthRange
show(object)
```

```
## S4 method for signature msgfParLengthRange
length(x)
```

```
## S4 method for signature msgfParLengthRange
getMSGFpar(object)
```

```
msgfParLengthRange(value)
```

## Arguments

object	An msgfParLengthRange object
x	An msgfParLengthRange object
value	A numeric vector of length 2. The first element must be smaller than the last

## Value

For length() An integer.

For getMSGFpar() A string.

For msgfParLengthRange() An msgfParLengthRange object.

## Methods (by generic)

- show: Short summary of msgfParLengthRange object
- length: Report the length of an msgfParLengthRange object
- getMSGFpar: Get [system](#) compliant function call

## Slots

value A numeric vector of length 2 describing the upper and lower bounds of the length range

**See Also**

Other msgfParClasses: [[\[,msgfParModificationList,numeric,missing-method](#), [[\[<- ,msgfParModificationList,n](#), [getMSGFpar,msgfParModificationList-method,length,msgfParModificationList-method](#), [msgfParModificationList,msgfParModificationList-class,show,msgfParModificationList-method](#); [getMSGFpar,msgfPar-method,length,msgfPar-method,msgfPar-class,runMSGF,msgfPar-method,show,msgfPar-method](#); [getMSGFpar,msgfParChargeRange-method,length,msgfParChargeRange-method,msgfParChargeRange,msgfParChargeRange-class,show,msgfParChargeRange-method](#); [getMSGFpar,msgfParEnzyme-length,msgfParEnzyme-method,msgfParEnzyme,msgfParEnzyme-class,show,msgfParEnzyme-method](#); [getMSGFpar,msgfParFragmentation-method,length,msgfParFragmentation-method,msgfParFragmentation,msgfParFragmentation-class,show,msgfParFragmentation-method](#); [getMSGFpar,msgfParInstrument-method,length,msgfParInstrument-method,msgfParInstrument,msgfParInstrument-class,show,msgfParInstrument-me](#); [getMSGFpar,msgfParIsotopeError-method,length,msgfParIsotopeError-method,msgfParIsotopeError,msgfParIsotopeError-class,show,msgfParIsotopeError-method](#); [getMSGFpar,msgfParMatches-method,length,msgfParMatches-method,msgfParMatches,msgfParMatches-class,show,msgfParMatches-method](#); [getMSGFpar,msgfParModification-method,msgfParModification,msgfParModification-class,show,msgfParModification-method](#); [getMSGFpar,msgfParNtt-method,length,msgfParNtt-method,msgfParNtt,msgfParNtt-class,show,msgfParNtt-method](#); [getMSGFpar,msgfParProtocol-method,length,msgfParProtocol-method,msgfParProtocol,msgfParProtocol-class,show,msgfParProtocol-method](#); [getMSGFpar,msgfParTda-method,length,msgfParTda-method,msgfParTda,msgfParTda-class,show,msgfParTda-method](#); [getMSGFpar,msgfParTolerance-method,length,msgfParTolerance-method,msgfParTolerance,msgfParTolerance-class,show,msgfParTolerance-method](#); [msgfPar](#)

**Examples**

```
lengths <- msgfParLengthRange(c(6, 40))
```

---

`msgfParMatches-class` *A class handling number of matches*

---

**Description**

This class defines a number of matches and provides methods to get correct system call parameters.

**Usage**

```
## S4 method for signature msgfParMatches
show(object)

## S4 method for signature msgfParMatches
length(x)

## S4 method for signature msgfParMatches
getMSGFpar(object)

msgfParMatches(value)
```

**Arguments**

object	An msgfParMatches object
x	An msgfParMatches object
value	An integer giving the number of matches that should be returned per spectrum

**Value**

For length() An integer.  
 For getMSGFpar() A string.  
 For msgfParMatches() An msgfParMatches object.

**Methods (by generic)**

- show: Short summary of msgfParMatches object
- length: Report the length of an msgfParMatches object
- getMSGFpar: Get [system](#) compliant function call

**Slots**

value An integer giving the number of matches per spectrum reported by MS-GF+

**See Also**

Other msgfParClasses: `[[,msgfParModificationList,numeric,missing-method,[<- ,msgfParModificationList,numeric,length,msgfParModificationList-method,length,msgfParModificationList-method,msgfParModificationList,msgfParModificationList-class,show,msgfParModificationList-method;getMSGFpar,msgfPar-method,length,msgfPar-method,msgfPar-class,runMSGF,msgfPar-method,show,msgfPar-method;getMSGFpar,msgfParChargeRange-method,length,msgfParChargeRange-method,msgfParChargeRange,msgfParChargeRange-class,show,msgfParChargeRange-method;getMSGFpar,msgfParEnzyme-length,msgfParEnzyme-method,msgfParEnzyme,msgfParEnzyme-class,show,msgfParEnzyme-method;getMSGFpar,msgfParFragmentation-method,length,msgfParFragmentation-method,msgfParFragmentation,msgfParFragmentation-class,show,msgfParFragmentation-method;getMSGFpar,msgfParInstrument-method,length,msgfParInstrument-method,msgfParInstrument,msgfParInstrument-class,show,msgfParInstrument-method;getMSGFpar,msgfParIsotopeError-method,length,msgfParIsotopeError-method,msgfParIsotopeError,msgfParIsotopeError-class,show,msgfParIsotopeError-method;getMSGFpar,msgfParLengthRange-method,length,msgfParLengthRange-method,msgfParLengthRange,msgfParLengthRange-class,show,msgfParLengthRange-method;getMSGFpar,msgfParModification-method,msgfParModification,msgfParModification-class,show,msgfParModification-method;getMSGFpar,msgfParNtt-method,length,msgfParNtt-method,msgfParNtt,msgfParNtt-class,show,msgfParNtt-method;getMSGFpar,msgfParProtocol-method,length,msgfParProtocol-method,msgfParProtocol,msgfParProtocol-class,show,msgfParProtocol-method;getMSGFpar,msgfParTda-method,length,msgfParTda-method,msgfParTda,msgfParTda-class,show,msgfParTda-method;getMSGFpar,msgfParTolerance-method,length,msgfParTolerance-method,msgfParTolerance,msgfParTolerance-class,show,msgfParTolerance-method;msgfPar`

**Examples**

```
matches <- msgfParMatches(5)
```

---

 msgfParModification-class

*A class handling modification characteristics*


---

### Description

This class defines a single modification type that can be searched for by MS-GF+. Modifications are collected in a [msgfParModificationList](#) before adding them to [msgfPar](#) objects.

### Usage

```
## S4 method for signature msgfParModification
getMSGFpar(object)
```

```
## S4 method for signature msgfParModification
show(object)
```

```
msgfParModification(name, composition = "", mass = as.numeric(NA), residues,
  type, position)
```

### Arguments

object	An msgfParModification object
name	The name of the modification
composition	The molecular formular as a string for the modification. Loss of atoms are denoted with negative integers (e.g. O-1 for loss of oxygen)
mass	The monoisotopic mass change between a peptide without and with the given modification. Either composition or mass must be defined.
residues	The amino acids that the modification applies to. Given as their one-letter code in upper-case without any separation. Use '*' for all residues
type	Either 'fix' or 'opt' for fixed or optional
position	Where the modification can be. Either 'any', 'c-term', 'n-term', 'prot-c-term' or 'prot-n-term'.

### Value

For getMSGFpar() A string.

For msgfParModification() An msgfParModification object.

### Methods (by generic)

- getMSGFpar: Get [system](#) compliant function call
- show: Short summary of msgfParModification object

**Slots**

composition The molecular formula for the modification.  
 mass The monoisotopic mass of the modification  
 residues The amino acids the modification applies to  
 type Whether the modification is optional or always present  
 position The possible position of the modification  
 name The name of the modification

**See Also**

Other msgfParClasses: `[[], msgfParModificationList, numeric, missing-method, [[<- , msgfParModificationList, n`  
`getMSGFpar, msgfParModificationList-method, length, msgfParModificationList-method,`  
`msgfParModificationList, msgfParModificationList-class, show, msgfParModificationList-method;`  
`getMSGFpar, msgfPar-method, length, msgfPar-method, msgfPar-class, runMSGF, msgfPar-method,`  
`show, msgfPar-method; getMSGFpar, msgfParChargeRange-method, length, msgfParChargeRange-method,`  
`msgfParChargeRange, msgfParChargeRange-class, show, msgfParChargeRange-method; getMSGFpar, msgfParEnzyme-`  
`length, msgfParEnzyme-method, msgfParEnzyme, msgfParEnzyme-class, show, msgfParEnzyme-method;`  
`getMSGFpar, msgfParFragmentation-method, length, msgfParFragmentation-method, msgfParFragmentation,`  
`msgfParFragmentation-class, show, msgfParFragmentation-method; getMSGFpar, msgfParInstrument-method,`  
`length, msgfParInstrument-method, msgfParInstrument, msgfParInstrument-class, show, msgfParInstrument-me`  
`getMSGFpar, msgfParIsotopeError-method, length, msgfParIsotopeError-method, msgfParIsotopeError,`  
`msgfParIsotopeError-class, show, msgfParIsotopeError-method; getMSGFpar, msgfParLengthRange-method,`  
`length, msgfParLengthRange-method, msgfParLengthRange, msgfParLengthRange-class, show, msgfParLengthRang`  
`getMSGFpar, msgfParMatches-method, length, msgfParMatches-method, msgfParMatches, msgfParMatches-class,`  
`show, msgfParMatches-method; getMSGFpar, msgfParNtt-method, length, msgfParNtt-method,`  
`msgfParNtt, msgfParNtt-class, show, msgfParNtt-method; getMSGFpar, msgfParProtocol-method,`  
`length, msgfParProtocol-method, msgfParProtocol, msgfParProtocol-class, show, msgfParProtocol-method;`  
`getMSGFpar, msgfParTda-method, length, msgfParTda-method, msgfParTda, msgfParTda-class,`  
`show, msgfParTda-method; getMSGFpar, msgfParTolerance-method, length, msgfParTolerance-method,`  
`msgfParTolerance, msgfParTolerance-class, show, msgfParTolerance-method; msgfPar`

**Examples**

```
# Using composition
modification1 <- msgfParModification(
  name=Carbamidomethyl,
  composition=C2H3N1O1,
  residues=C,
  type=fix,
  position=any
)

# Using exact mass
modification2 <- msgfParModification(
  name=Oxidation,
  mass=15.994915,
  residues=M,
  type=opt,
  position=any
)
```

---

msgfParModificationList-class

*A class handling a list of modifications*

---

## Description

This class defines a set of modifications and a maximum number of modifications allowed per peptide.

## Usage

```
## S4 method for signature msgfParModificationList
show(object)

## S4 method for signature msgfParModificationList
length(x)

## S4 method for signature msgfParModificationList
getMSGFpar(object)

## S4 method for signature msgfParModificationList,numeric,missing
x[[i, j, ...]]

## S4 replacement method for signature
## msgfParModificationList,numeric,missing,msgfParModification
x[[i,
  j, ...]] <- value

msgfParModificationList(nMod, modifications = list())
```

## Arguments

object	An msgfParModificationList object
x	An msgfParModificationList object
i	The index of the modification
j	Ignored
...	Ignored
value	An msgfParModification object
nMod	The maximum allowed number of modifications to expect on any peptide
modifications	A list of <a href="#">msgfParModification</a> objects

**Value**

For length() An integer.

For getMSGFpar() A string.

For '[[[' A msgfParModification object

For msgfParModificationList() An msgfParModificationList object.

**Methods (by generic)**

- show: Short summary of msgfParModificationList object
- length: Report the length of an msgfParModificationList object
- getMSGFpar: Get [system](#) compliant function call
- [[[: Get the i`th modification
- [[<-: Set or change the i`th modification

**Slots**

nMod The maximum allowed number of modifications to expect on any peptide

modifications A list of [msgfParModification](#) objects

**See Also**

Other msgfParClasses: [getMSGFpar](#), [msgfPar-method](#), [length](#), [msgfPar-method](#), [msgfPar-class](#), [runMSGF](#), [msgfPar-method](#), [show](#), [msgfPar-method](#); [getMSGFpar](#), [msgfParChargeRange-method](#), [length](#), [msgfParChargeRange-method](#), [msgfParChargeRange](#), [msgfParChargeRange-class](#), [show](#), [msgfParChargeRange-method](#); [getMSGFpar](#), [msgfParEnzyme-method](#), [length](#), [msgfParEnzyme-method](#), [msgfParEnzyme](#), [msgfParEnzyme-class](#), [show](#), [msgfParEnzyme-method](#); [getMSGFpar](#), [msgfParFragmentation-method](#), [length](#), [msgfParFragmentation-method](#), [msgfParFragmentation](#), [msgfParFragmentation-class](#), [show](#), [msgfParFragmentation-method](#); [getMSGFpar](#), [msgfParInstrument-method](#), [length](#), [msgfParInstrument-method](#), [msgfParInstrument](#), [msgfParInstrument-class](#), [show](#), [msgfParInstrument-method](#); [getMSGFpar](#), [msgfParIsotopeError-method](#), [length](#), [msgfParIsotopeError-method](#), [msgfParIsotopeError](#), [msgfParIsotopeError-class](#), [show](#), [msgfParIsotopeError-method](#); [getMSGFpar](#), [msgfParLengthRange-method](#), [length](#), [msgfParLengthRange-method](#), [msgfParLengthRange](#), [msgfParLengthRange-class](#), [show](#), [msgfParLengthRange-method](#); [getMSGFpar](#), [msgfParMatches-method](#), [length](#), [msgfParMatches-method](#), [msgfParMatches](#), [msgfParMatches-class](#), [show](#), [msgfParMatches-method](#); [getMSGFpar](#), [msgfParModification-method](#), [msgfParModification](#), [msgfParModification-class](#), [show](#), [msgfParModification-method](#); [getMSGFpar](#), [msgfParNtt-method](#), [length](#), [msgfParNtt-method](#), [msgfParNtt](#), [msgfParNtt-class](#), [show](#), [msgfParNtt-method](#); [getMSGFpar](#), [msgfParProtocol-method](#), [length](#), [msgfParProtocol-method](#), [msgfParProtocol](#), [msgfParProtocol-class](#), [show](#), [msgfParProtocol-method](#); [getMSGFpar](#), [msgfParTda-method](#), [length](#), [msgfParTda-method](#), [msgfParTda](#), [msgfParTda-class](#), [show](#), [msgfParTda-method](#); [getMSGFpar](#), [msgfParTolerance-method](#), [length](#), [msgfParTolerance-method](#), [msgfParTolerance](#), [msgfParTolerance-class](#), [show](#), [msgfParTolerance-method](#); [msgfPar](#)

**Examples**

```
modification1 <- msgfParModification(
                                name=Carbamidomethyl,
                                composition=C2H3N1O1,
                                residues=C,
```

```

                                type=fix,
                                position=any
                                )
modification2 <- msgfParModification(
                                name=Oxidation,
                                mass=15.994915,
                                residues=M,
                                type=opt,
                                position=any
                                )
modificationlist <- msgfParModificationList(
                                nMod=2,
                                modifications=list(
                                    modification1,
                                    modification2
                                )
                                )
modificationlist[[3]] <- msgfParModification(
                                name=Gln->pyro-Glu,
                                composition=H-3N-1,
                                residues=Q,
                                type=opt,
                                position=N-term
                                )

```

---

msgfParNtt-class      *A class handling cleavage specificity*

---

## Description

This class defines cleavage specificity and provides methods to get correct system call parameters.

## Usage

```
## S4 method for signature msgfParNtt
show(object)
```

```
## S4 method for signature msgfParNtt
length(x)
```

```
## S4 method for signature msgfParNtt
getMSGFpar(object)
```

```
msgfParNtt(value)
```

## Arguments

object	An msgfParNtt object
x	An msgfParNtt object

value An integer between 0 and 2 that specifies the specificity (2: full cleavage, 1: semi specific cleavage, 0: no specificity)

### Value

For length() An integer.

For getMSGFpar() A string.

For msgfParNtt() An msgfParNtt object.

### Methods (by generic)

- show: Short summary of msgfParNtt object
- length: Report the length of an msgfParNtt object
- getMSGFpar: Get [system](#) compliant function call

### Slots

value An integer between 0 and 2 that specifies the specificity (2: full cleavage, 1: semi specific cleavage, 0: no specificity)

### See Also

Other msgfParClasses: [\[,msgfParModificationList,numeric,missing-method,\[<- ,msgfParModificationList,n](#)  
[getMSGFpar,msgfParModificationList-method,length,msgfParModificationList-method,](#)  
[msgfParModificationList,msgfParModificationList-class,show,msgfParModificationList-method;](#)  
[getMSGFpar,msgfPar-method,length,msgfPar-method,msgfPar-class,runMSGF,msgfPar-method,](#)  
[show,msgfPar-method;getMSGFpar,msgfParChargeRange-method,length,msgfParChargeRange-method,](#)  
[msgfParChargeRange,msgfParChargeRange-class,show,msgfParChargeRange-method;getMSGFpar,msgfParEnzyme-](#)  
[length,msgfParEnzyme-method,msgfParEnzyme,msgfParEnzyme-class,show,msgfParEnzyme-method;](#)  
[getMSGFpar,msgfParFragmentation-method,length,msgfParFragmentation-method,msgfParFragmentation,](#)  
[msgfParFragmentation-class,show,msgfParFragmentation-method;getMSGFpar,msgfParInstrument-method,](#)  
[length,msgfParInstrument-method,msgfParInstrument,msgfParInstrument-class,show,msgfParInstrument-me](#)  
[getMSGFpar,msgfParIsotopeError-method,length,msgfParIsotopeError-method,msgfParIsotopeError,](#)  
[msgfParIsotopeError-class,show,msgfParIsotopeError-method;getMSGFpar,msgfParLengthRange-method,](#)  
[length,msgfParLengthRange-method,msgfParLengthRange,msgfParLengthRange-class,show,msgfParLengthRang](#)  
[getMSGFpar,msgfParMatches-method,length,msgfParMatches-method,msgfParMatches,msgfParMatches-class,](#)  
[show,msgfParMatches-method;getMSGFpar,msgfParModification-method,msgfParModification,](#)  
[msgfParModification-class,show,msgfParModification-method;getMSGFpar,msgfParProtocol-method,](#)  
[length,msgfParProtocol-method,msgfParProtocol,msgfParProtocol-class,show,msgfParProtocol-method;](#)  
[getMSGFpar,msgfParTda-method,length,msgfParTda-method,msgfParTda,msgfParTda-class,](#)  
[show,msgfParTda-method;getMSGFpar,msgfParTolerance-method,length,msgfParTolerance-method,](#)  
[msgfParTolerance,msgfParTolerance-class,show,msgfParTolerance-method;msgfPar](#)

### Examples

```
ntt <- msgfParNtt(2)
```

---

msgfParProtocol-class *A class handling protocol choice*

---

### Description

This class defines a protocol and provides methods to get correct system call parameters.

### Usage

```
## S4 method for signature msgfParProtocol
show(object)

## S4 method for signature msgfParProtocol
length(x)

## S4 method for signature msgfParProtocol
getMSGFpar(object)

msgfParProtocol(protocol)
```

### Arguments

object	An msgfParProtocol object
x	An msgfParProtocol object
protocol	An integer or string specifying the protocol to use.

### Value

For length() An integer.  
For getMSGFpar() A string.  
For msgfParProtocol() An msgfParProtocol object.

### Methods (by generic)

- show: Short summary of msgfParProtocol object
- length: Report the length of an msgfParProtocol object
- getMSGFpar: Get [system](#) compliant function call

### Slots

protocol An integer specifying a specific protocol type

**See Also**

Other msgfParClasses: `[[,msgfParModificationList,numeric,missing-method,[<-,msgfParModificationList,nu  
 getMSGFpar,msgfParModificationList-method,length,msgfParModificationList-method,  
 msgfParModificationList,msgfParModificationList-class,show,msgfParModificationList-method;  
 getMSGFpar,msgfPar-method,length,msgfPar-method,msgfPar-class,runMSGF,msgfPar-method,  
 show,msgfPar-method;getMSGFpar,msgfParChargeRange-method,length,msgfParChargeRange-method,  
 msgfParChargeRange,msgfParChargeRange-class,show,msgfParChargeRange-method;getMSGFpar,msgfParEnzyme-  
 length,msgfParEnzyme-method,msgfParEnzyme,msgfParEnzyme-class,show,msgfParEnzyme-method;  
 getMSGFpar,msgfParFragmentation-method,length,msgfParFragmentation-method,msgfParFragmentation,  
 msgfParFragmentation-class,show,msgfParFragmentation-method;getMSGFpar,msgfParInstrument-method,  
 length,msgfParInstrument-method,msgfParInstrument,msgfParInstrument-class,show,msgfParInstrument-me  
 getMSGFpar,msgfParIsotopeError-method,length,msgfParIsotopeError-method,msgfParIsotopeError,  
 msgfParIsotopeError-class,show,msgfParIsotopeError-method;getMSGFpar,msgfParLengthRange-method,  
 length,msgfParLengthRange-method,msgfParLengthRange,msgfParLengthRange-class,show,msgfParLengthRang  
 getMSGFpar,msgfParMatches-method,length,msgfParMatches-method,msgfParMatches,msgfParMatches-class,  
 show,msgfParMatches-method;getMSGFpar,msgfParModification-method,msgfParModification,  
 msgfParModification-class,show,msgfParModification-method;getMSGFpar,msgfParNtt-method,  
 length,msgfParNtt-method,msgfParNtt,msgfParNtt-class,show,msgfParNtt-method;getMSGFpar,msgfParTda-me  
 length,msgfParTda-method,msgfParTda,msgfParTda-class,show,msgfParTda-method;getMSGFpar,msgfParTolera  
 length,msgfParTolerance-method,msgfParTolerance,msgfParTolerance-class,show,msgfParTolerance-method;  
 msgfPar`

**Examples**

```
protocol <- msgfParProtocol(0)
protocol <- msgfParProtocol(No protocol)
```

---

msgfParTda-class

*A class handling use of target-decoy approach for FDR estimation*

---

**Description**

This class defines whether to use target-decoy approach and provides methods to get correct system call parameters.

**Usage**

```
## S4 method for signature msgfParTda
show(object)
```

```
## S4 method for signature msgfParTda
length(x)
```

```
## S4 method for signature msgfParTda
getMSGFpar(object)
```

```
msgfParTda(value)
```

**Arguments**

object	An msgfParTda object
x	An msgfParTda object
value	A boolean defining whether to use tda or not

**Value**

For length() An integer.

For getMSGFpar() A string.

For msgfParTda() An msgfParTda object.

**Methods (by generic)**

- show: Short summary of msgfParTda object
- length: Report the length of an msgfParTda object
- getMSGFpar: Get [system](#) compliant function call

**Slots**

tda A boolean defining whether to use tda or not

**See Also**

Other msgfParClasses: `[[,msgfParModificationList,numeric,missing-method,[<- ,msgfParModificationList,n  
getMSGFpar,msgfParModificationList-method,length,msgfParModificationList-method,  
msgfParModificationList,msgfParModificationList-class,show,msgfParModificationList-method;  
getMSGFpar,msgfPar-method,length,msgfPar-method,msgfPar-class,runMSGF,msgfPar-method,  
show,msgfPar-method;getMSGFpar,msgfParChargeRange-method,length,msgfParChargeRange-method,  
msgfParChargeRange,msgfParChargeRange-class,show,msgfParChargeRange-method;getMSGFpar,msgfParEnzyme-  
length,msgfParEnzyme-method,msgfParEnzyme,msgfParEnzyme-class,show,msgfParEnzyme-method;  
getMSGFpar,msgfParFragmentation-method,length,msgfParFragmentation-method,msgfParFragmentation,  
msgfParFragmentation-class,show,msgfParFragmentation-method;getMSGFpar,msgfParInstrument-method,  
length,msgfParInstrument-method,msgfParInstrument,msgfParInstrument-class,show,msgfParInstrument-me  
getMSGFpar,msgfParIsotopeError-method,length,msgfParIsotopeError-method,msgfParIsotopeError,  
msgfParIsotopeError-class,show,msgfParIsotopeError-method;getMSGFpar,msgfParLengthRange-method,  
length,msgfParLengthRange-method,msgfParLengthRange,msgfParLengthRange-class,show,msgfParLengthRang  
getMSGFpar,msgfParMatches-method,length,msgfParMatches-method,msgfParMatches,msgfParMatches-class,  
show,msgfParMatches-method;getMSGFpar,msgfParModification-method,msgfParModification,  
msgfParModification-class,show,msgfParModification-method;getMSGFpar,msgfParNtt-method,  
length,msgfParNtt-method,msgfParNtt,msgfParNtt-class,show,msgfParNtt-method;getMSGFpar,msgfParProto  
length,msgfParProtocol-method,msgfParProtocol,msgfParProtocol-class,show,msgfParProtocol-method;  
getMSGFpar,msgfParTolerance-method,length,msgfParTolerance-method,msgfParTolerance,  
msgfParTolerance-class,show,msgfParTolerance-method;msgfPar`

**Examples**

```
tda <- msgfParTda(TRUE)
```

---

msgfParTolerance-class

*A class handling parent ion tolerance*

---

## Description

This class defines a parent ion tolerance and provides methods to get correct system call parameters.

## Usage

```
## S4 method for signature msgfParTolerance
show(object)
```

```
## S4 method for signature msgfParTolerance
length(x)
```

```
## S4 method for signature msgfParTolerance
getMSGFpar(object)
```

```
msgfParTolerance(value, low, high, unit)
```

## Arguments

object	An msgfParTolerance object
x	An msgfParTolerance object
value	A numeric giving the upper and lower bounds of the tolerance
low	A numeric giving the lower bounds of the tolerance
high	A numeric giving the higher bounds of the tolerance
unit	The unit used. Either 'ppm' or 'Da'

## Value

For length() An integer.

For getMSGFpar() A string.

For msgfParTolerance() An msgfParTolerance object.

## Methods (by generic)

- show: Short summary of msgfParTolerance object
- length: Report the length of an msgfParTolerance object
- getMSGFpar: Get [system](#) compliant function call

**Slots**

`unit` The unit used to define the tolerance

`low` The lower bound of the tolerance

`high` The higher bound of the tolerance

**See Also**

Other `msgfParClasses`: `[[], msgfParModificationList, numeric, missing-method, [[<- , msgfParModificationList, n`  
`getMSGFpar, msgfParModificationList-method, length, msgfParModificationList-method,`  
`msgfParModificationList, msgfParModificationList-class, show, msgfParModificationList-method;`  
`getMSGFpar, msgfPar-method, length, msgfPar-method, msgfPar-class, runMSGF, msgfPar-method,`  
`show, msgfPar-method; getMSGFpar, msgfParChargeRange-method, length, msgfParChargeRange-method,`  
`msgfParChargeRange, msgfParChargeRange-class, show, msgfParChargeRange-method; getMSGFpar, msgfParEnzyme-`  
`length, msgfParEnzyme-method, msgfParEnzyme, msgfParEnzyme-class, show, msgfParEnzyme-method;`  
`getMSGFpar, msgfParFragmentation-method, length, msgfParFragmentation-method, msgfParFragmentation,`  
`msgfParFragmentation-class, show, msgfParFragmentation-method; getMSGFpar, msgfParInstrument-method,`  
`length, msgfParInstrument-method, msgfParInstrument, msgfParInstrument-class, show, msgfParInstrument-me`  
`getMSGFpar, msgfParIsotopeError-method, length, msgfParIsotopeError-method, msgfParIsotopeError,`  
`msgfParIsotopeError-class, show, msgfParIsotopeError-method; getMSGFpar, msgfParLengthRange-method,`  
`length, msgfParLengthRange-method, msgfParLengthRange, msgfParLengthRange-class, show, msgfParLengthRang`  
`getMSGFpar, msgfParMatches-method, length, msgfParMatches-method, msgfParMatches, msgfParMatches-class,`  
`show, msgfParMatches-method; getMSGFpar, msgfParModification-method, msgfParModification,`  
`msgfParModification-class, show, msgfParModification-method; getMSGFpar, msgfParNtt-method,`  
`length, msgfParNtt-method, msgfParNtt, msgfParNtt-class, show, msgfParNtt-method; getMSGFpar, msgfParProto`  
`length, msgfParProtocol-method, msgfParProtocol, msgfParProtocol-class, show, msgfParProtocol-method;`  
`getMSGFpar, msgfParTda-method, length, msgfParTda-method, msgfParTda, msgfParTda-class,`  
`show, msgfParTda-method; msgfPar`

**Examples**

```
# Symmetric
tolerance <- msgfParTolerance(20, unit=ppm)

# Asymmetric
tolerance <- msgfParTolerance(low=0.5, high=1.5, unit=Da)
```

---

ntt

*Get and set cleavage specificity in msgfPar objects*


---

**Description**

These functions allow you to retrieve and set the quality of cleavage allowed during search in MS-GF+ (number of tolerable termini - `ntt`)

**Usage**

```
ntt(object)

ntt(object) <- value

## S4 method for signature msgfPar
ntt(object)

## S4 replacement method for signature msgfPar,numeric
ntt(object) <- value

## S4 replacement method for signature msgfPar,msgfParNtt
ntt(object) <- value
```

**Arguments**

object	An msgfPar object
value	An integer or an msgfParNtt object

**Value**

In case of the getter an integer between 0 and 2

**Methods (by class)**

- msgfPar: Get the number of tolerable termini
- object = msgfPar, value = numeric: Set the ntt using an integer
- object = msgfPar, value = msgfParNtt: Set the ntt using an msgfParNtt object

**See Also**

Other msgfPar-getter\_setter: [chargeRange](#), [chargeRange](#), [msgfPar-method](#), [chargeRange<-](#), [chargeRange<-](#), [msgfPar, numeric-method](#); [db](#), [db](#), [msgfPar-method](#), [db<-](#), [db<-](#), [msgfPar, character-method](#); [enzyme](#), [enzyme](#), [msgfPar-method](#), [enzyme<-](#), [enzyme<-](#), [msgfPar, character-method](#), [enzyme<-](#), [msgfPar, msgfParEnzyme-method](#); [fragmentation](#), [fragmentation](#), [msgfPar-method](#), [fragmentation<-](#), [fragmentation<-](#), [msgfPar, character-method](#), [fragmentation<-](#), [msgfPar, msgfParFragmentation-method](#); [instrument](#), [instrument](#), [msgfPar-method](#), [instrument<-](#), [instrument<-](#), [msgfPar, character-method](#), [instrument<-](#), [msgfPar, msgfParInstrument-method](#); [isotopeError](#), [isotopeError](#), [msgfPar-method](#), [isotopeError<-](#), [isotopeError<-](#), [msgfPar, msgfParIsotopeError-method](#); [lengthRange](#), [lengthRange](#), [msgfPar-method](#), [lengthRange<-](#), [lengthRange<-](#), [msgfPar, msgfParLengthRange-method](#); [matches](#), [matches](#), [msgfPar-method](#), [matches<-](#), [matches<-](#), [msgfPar, msgfParMatches-method](#); [mods](#), [mods](#), [msgfPar-method](#), [mods<-](#), [mods<-](#), [msgfPar, msgfParModificationList-method](#); [nMod](#), [nMod](#), [msgfPar-method](#), [nMod<-](#), [nMod<-](#), [msgfPar, numeric-method](#); [protocol](#), [protocol](#), [msgfPar-method](#), [protocol<-](#), [protocol<-](#), [msgfPar, character-method](#); [tda](#), [tda](#), [msgfPar-method](#), [tda<-](#), [tda<-](#), [msgfPar, logical-method](#), [tda<-](#), [msgfPar, msgfParTda-method](#); [tolerance](#), [tolerance](#), [msgfPar-method](#), [tolerance<-](#), [tolerance<-](#), [msgfPar, character-method](#),

```
tolerance<-,msgfPar,msgfParTolerance-method,toleranceRange,toleranceRange,msgfPar-method,
toleranceRange<-,toleranceRange<-,msgfPar,numeric-method,toleranceUnit,toleranceUnit,msgfPar-method,
toleranceUnit<-,toleranceUnit<-,msgfPar,character-method
```

## Examples

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
ntt(parameters) <- 2
ntt(parameters)
```

---

protocol	<i>Get and set protocol in msgfPar objects</i>
----------	--

---

## Description

These functions allow you to retrieve and set the protocol used during MS-GF+ analysis. This allows you to fine tune the analysis in case of labelled or phosphoproteomic analysis

## Usage

```
protocol(object)

protocol(object) <- value

## S4 method for signature msgfPar
protocol(object)

## S4 replacement method for signature msgfPar,numeric
protocol(object) <- value

## S4 replacement method for signature msgfPar,character
protocol(object) <- value

## S4 replacement method for signature msgfPar,msgfParProtocol
protocol(object) <- value
```

## Arguments

object	An msgfPar object
value	Either an integer, a string or an msgfParProtocol object

## Value

In case of the getter a named integer

**Methods (by class)**

- msgfPar: Get the protocol currently used
- object = msgfPar, value = numeric: Set the protocol using the key for the protocol
- object = msgfPar, value = character: Set the protocol using the name of the protocol
- object = msgfPar, value = msgfParProtocol: Set the protocol using an msgfParProtocol object

**See Also**

Other msgfPar-getter\_setter: [chargeRange](#), [chargeRange](#), [msgfPar-method](#), [chargeRange<-](#), [chargeRange<-](#), [msgfPar](#), [m](#), [chargeRange<-](#), [msgfPar](#), [numeric-method](#); [db](#), [db](#), [msgfPar-method](#), [db<-](#), [db<-](#), [msgfPar](#), [character-method](#); [enzyme](#), [enzyme](#), [msgfPar-method](#), [enzyme<-](#), [enzyme<-](#), [msgfPar](#), [character-method](#), [enzyme<-](#), [msgfPar](#), [msgfParEnzy](#), [enzyme<-](#), [msgfPar](#), [numeric-method](#); [fragmentation](#), [fragmentation](#), [msgfPar-method](#), [fragmentation<-](#), [fragmentation<-](#), [msgfPar](#), [character-method](#), [fragmentation<-](#), [msgfPar](#), [msgfParFragmentation-method](#), [fragmentation<-](#), [msgfPar](#), [numeric-method](#); [instrument](#), [instrument](#), [msgfPar-method](#), [instrument<-](#), [instrument<-](#), [msgfPar](#), [character-method](#), [instrument<-](#), [msgfPar](#), [msgfParInstrument-method](#), [instrument<-](#), [msgfPar](#), [numeric-method](#); [isotopeError](#), [isotopeError](#), [msgfPar-method](#), [isotopeError<-](#), [isotopeError<-](#), [msgfPar](#), [msgfParIsotopeError-method](#), [isotopeError<-](#), [msgfPar](#), [numeric-method](#); [lengthRange](#), [lengthRange](#), [msgfPar-method](#), [lengthRange<-](#), [lengthRange<-](#), [msgfPar](#), [msgfParLengthRange-method](#), [lengthRange<-](#), [msgfPar](#), [numeric-method](#); [matches](#), [matches](#), [msgfPar-method](#), [matches<-](#), [matches<-](#), [msgfPar](#), [msgfParMatches-method](#), [matches<-](#), [msgfPar](#), [numeric-method](#); [mods](#), [mods](#), [msgfPar-method](#), [mods<-](#), [mods<-](#), [msgfPar](#), [msgfParModificationList-method](#), [nMod](#), [nMod](#), [msgfPar-method](#), [nMod<-](#), [nMod<-](#), [msgfPar](#), [numeric-method](#); [ntt](#), [ntt](#), [msgfPar-method](#), [ntt<-](#), [ntt<-](#), [msgfPar](#), [msgfParNtt-method](#), [ntt<-](#), [msgfPar](#), [numeric-method](#); [tda](#), [tda](#), [msgfPar-method](#), [tda<-](#), [tda<-](#), [msgfPar](#), [logical-method](#), [tda<-](#), [msgfPar](#), [msgfParTda-method](#); [tolerance](#), [tolerance](#), [msgfPar-method](#), [tolerance<-](#), [tolerance<-](#), [msgfPar](#), [character-method](#), [tolerance<-](#), [msgfPar](#), [msgfParTolerance-method](#), [toleranceRange](#), [toleranceRange](#), [msgfPar-method](#), [toleranceRange<-](#), [toleranceRange<-](#), [msgfPar](#), [numeric-method](#); [toleranceUnit](#), [toleranceUnit](#), [msgfPar-method](#), [toleranceUnit<-](#), [toleranceUnit<-](#), [msgfPar](#), [character-method](#)

**Examples**

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
protocol(parameters) <- Phosphorylation
protocol(parameters) <- 0
protocol(parameters)
```

---

runMSGF

*Runs MS-GF+ based on the given msgfPar object*


---

**Description**

This function assembles a system call based on the parameters specified in the object and the arguments given in the function call. By default the function uses the MS-GF+ jar file bundled with this package, but it is possible to specify an alternative location using the msgfPar argument. Version compatibility can not be assured in this case though.

**Usage**

```
runMSGF(object, rawfiles, savenames, import, memory, async, msgfPath)
```

**Arguments**

object	An msgfPar object
rawfiles	A character vector holding the filepath to the spectrum files to be analysed (currently supported formats: *.mzML, *.mzXML, *.mgf, *.ms2, *.pkl or *_dta.txt)
savenames	An optional vector of same length as rawfiles. Specifies the name used to save the results. If omitted the results will be saved with the same name as the rawfile, but with an .mzid extension.
import	Logical (default=TRUE). Should the results be imported in to R after the analysis is finished.
memory	An integer (default=10000). How much memory should be allocated to the java virtual machine during execution (in mb)
async	An Logical (default=FALSE). Should MS-GF+ be run asynchronously?
msgfPath	The path to an alternative MSGFPlus.jar file if the bundled one is not desired

**Value**

If import=TRUE a list of mzID object otherwise NULL

**See Also**

[mzID](#)

**Examples**

```
## Not run:
parameters <- msgfPar(
  database=system.file(package=MSGFplus, extdata, milk-proteins.fasta),
  tolerance=20 ppm,
  instrument=TOF,
  enzyme=Lys-C
)
runMSGF(parameters, c(file1.mzML, file2.mzML))

## End(Not run)
```

---

 running

*A class referencing an asynchronous execution of MS-GF+*


---

### Description

Objects of this class contains a reference to an asynchronous running MS-GF+ process and can be used to query the state of the process, and import the results if the process has finished. Instances of this class are created when the runMSGF() method is called with async=TRUE on an msgfPar object.

Unlike regular runMSGF() calls, this does not support batch mode, meaning that if a more than one raw file is supplied, all but the first are ignored with a warning.

In order to insulate instances of this class from being corrupted (thus loosing the reference to the process), all slots are functions and should be queried as such if needed.

### Usage

```
running(object)
```

```
finished(object)
```

```
import(object)
```

```
## S4 method for signature msgfAsync
running(object)
```

```
## S4 method for signature msgfAsync
finished(object)
```

```
## S4 method for signature msgfAsync
import(object)
```

### Arguments

object            An msgfAsync object

### Value

running(object) Returns a logical indicating if the process is running

finished(object) Returns a logical indicating if the process is finished

import(object) Returns an mzID object or NULL if the process is still running. Throws an error if the process is finished but the result file doesn't exist.

### Methods (by generic)

- running: Check whether the MS-GF+ process is still running
- finished: Check whether the MS-GF+ process is finished
- import: Import the result of the asynchronous MS-GF+ process

**Slots**

`status` Returns the status of the MS-GF+ process; either 'Running' or 'Done'.

`resultFile` Returns the location of the result file from the MS-GF+ analysis. **WARNING:** Checking for the existence of this file is not a safe way to determine the status of the process, as the file gets written to continuously.

**Examples**

```
## Not run:
parameters <- msgfPar(
  database=system.file(package=MSGFplus, extdata, milk-proteins.fasta),
  tolerance=20 ppm,
  instrument=TOF,
  enzyme=Lys-C
)
asyncMSGF <- runMSGF(parameters, file1.mzML, async=TRUE)
while(!running(asyncMSGF)){
  Sys.sleep(1)
}
results <- import(asyncMSGF)

## End(Not run)
```

---

tda

*Get and set use of target-decoy approach in msgfPar objects*


---

**Description**

These functions allow you to retrieve and set whether the target-decoy approach should be used to estimate q-values.

**Usage**

```
tda(object)
```

```
tda(object) <- value
```

```
## S4 method for signature msgfPar
```

```
tda(object)
```

```
## S4 replacement method for signature msgfPar,logical
```

```
tda(object) <- value
```

```
## S4 replacement method for signature msgfPar,msgfParTda
```

```
tda(object) <- value
```

**Arguments**

object	An msgfPar object
value	Either a boolean or msgfParTda object

**Value**

In case of the getter a boolean indicating whether tda is used or not

**Methods (by class)**

- msgfPar: Get whether tda is currently used for FDR estimation
- object = msgfPar, value = logical: Set the use of tda using a boolean (TRUE/FALSE)
- object = msgfPar, value = msgfParTda: Set the use of tda using an msgfParTda object

**See Also**

Other msgfPar-getter\_setter: chargeRange, chargeRange, msgfPar-method, chargeRange<-, chargeRange<-, msgfPar, msgfParChargeRange-method, chargeRange<-, msgfPar, numeric-method; db, db, msgfPar-method, db<-, db<-, msgfPar, character-method; enzyme, enzyme, msgfPar-method, enzyme<-, enzyme<-, msgfPar, character-method, enzyme<-, msgfPar, msgfParEnzyme-method, enzyme<-, msgfPar, numeric-method; fragmentation, fragmentation, msgfPar-method, fragmentation<-, fragmentation<-, msgfPar, character-method, fragmentation<-, msgfPar, msgfParFragmentation-method, fragmentation<-, msgfPar, numeric-method; instrument, instrument, msgfPar-method, instrument<-, instrument<-, msgfPar, character-method, instrument<-, msgfPar, msgfParInstrument-method, instrument<-, msgfPar, numeric-method; isotopeError, isotopeError, msgfPar-method, isotopeError<-, isotopeError<-, msgfPar, msgfParIsotopeError-method, isotopeError<-, msgfPar, numeric-method; lengthRange, lengthRange, msgfPar-method, lengthRange<-, lengthRange<-, msgfPar, msgfParLengthRange-method, lengthRange<-, msgfPar, numeric-method; matches, matches, msgfPar-method, matches<-, matches<-, msgfPar, numeric-method; mods, mods, msgfPar-method, mods<-, mods<-, msgfPar, msgfParModificationList-method, nMod, nMod, msgfPar-method, nMod<-, nMod<-, msgfPar, numeric-method; ntt, ntt, msgfPar-method, ntt<-, ntt<-, msgfPar, msgfParNtt-method, ntt<-, msgfPar, numeric-method; protocol, protocol, msgfPar-method, protocol<-, protocol<-, msgfPar, character-method, protocol<-, msgfPar, msgfParProtocol-method, protocol<-, msgfPar, numeric-method; tolerance, tolerance, msgfPar-method, tolerance<-, tolerance<-, msgfPar, character-method, tolerance<-, msgfPar, msgfParTolerance-method, toleranceRange, toleranceRange, msgfPar-method, toleranceRange<-, toleranceRange<-, msgfPar, numeric-method; toleranceUnit, toleranceUnit, msgfPar-method, toleranceUnit<-, toleranceUnit<-, msgfPar, character-method

**Examples**

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
tda(parameters) <- TRUE
tda(parameters)
```

---

tolerance	<i>Get and set the parent tolerance in msgfPar objects</i>
-----------	--

---

**Description**

These functions allow you to retrieve and set the tolerance used for matching parent ions to peptides in the database

**Usage**

```
tolerance(object)

tolerance(object) <- value

toleranceRange(object)

toleranceRange(object) <- value

toleranceUnit(object)

toleranceUnit(object) <- value

## S4 method for signature msgfPar
tolerance(object)

## S4 method for signature msgfPar
toleranceRange(object)

## S4 method for signature msgfPar
toleranceUnit(object)

## S4 replacement method for signature msgfPar,numeric
toleranceRange(object) <- value

## S4 replacement method for signature msgfPar,character
toleranceUnit(object) <- value

## S4 replacement method for signature msgfPar,character
tolerance(object) <- value

## S4 replacement method for signature msgfPar,msgfParTolerance
tolerance(object) <- value
```

**Arguments**

object            An msgfPar object

value For tolerance a character vector of length 2, each element of the form '<value> <unit>'. For toleranceUnit a string. For toleranceRange a numeric vector of length 2.

### Value

For tolerance a character vector with the lower and upper tolerance limit with unit. For toleranceUnit a string with the unit used. For toleranceRange a numeric vector with lower and upper tolerance limit.

### Methods (by class)

- msgfPar: Get the lower and upper bounds of the tolerance
- msgfPar: Get the lower and upper bounds of the tolerance
- msgfPar: Get the unit the tolerance is measured in
- object = msgfPar, value = numeric: Set the lower and upper bounds of the tolerance using a numeric vector of length 2
- object = msgfPar, value = character: Set the unit the tolerance is measured in
- object = msgfPar, value = character: Set the lower and upper bounds of the tolerance using a character vector of length 2, where each element is of the form '<value> <unit>'
- object = msgfPar, value = msgfParTolerance: Set the lower and upper bounds of the tolerance using an msgfParTolerance object

### See Also

Other msgfPar-getter\_setter: [chargeRange](#), [chargeRange](#), [msgfPar-method](#), [chargeRange<-](#), [chargeRange<-](#), [msgfPar](#), [msgfPar-method](#), [chargeRange<-](#), [msgfPar](#), [numeric-method](#); [db](#), [db](#), [msgfPar-method](#), [db<-](#), [db<-](#), [msgfPar](#), [character-method](#); [enzyme](#), [enzyme](#), [msgfPar-method](#), [enzyme<-](#), [enzyme<-](#), [msgfPar](#), [character-method](#), [enzyme<-](#), [msgfPar](#), [msgfParEnzyme-method](#), [enzyme<-](#), [msgfPar](#), [numeric-method](#); [fragmentation](#), [fragmentation](#), [msgfPar-method](#), [fragmentation<-](#), [fragmentation<-](#), [msgfPar](#), [character-method](#), [fragmentation<-](#), [msgfPar](#), [msgfParFragmentation-method](#), [fragmentation<-](#), [msgfPar](#), [numeric-method](#); [instrument](#), [instrument](#), [msgfPar-method](#), [instrument<-](#), [instrument<-](#), [msgfPar](#), [character-method](#), [instrument<-](#), [msgfPar](#), [msgfParInstrument-method](#), [instrument<-](#), [msgfPar](#), [numeric-method](#); [isotopeError](#), [isotopeError](#), [msgfPar-method](#), [isotopeError<-](#), [isotopeError<-](#), [msgfPar](#), [msgfParIsotopeError-method](#), [isotopeError<-](#), [msgfPar](#), [numeric-method](#); [lengthRange](#), [lengthRange](#), [msgfPar-method](#), [lengthRange<-](#), [lengthRange<-](#), [msgfPar](#), [msgfParLengthRange-method](#), [lengthRange<-](#), [msgfPar](#), [numeric-method](#); [matches](#), [matches](#), [msgfPar-method](#), [matches<-](#), [matches<-](#), [msgfPar](#), [msgfParMatches-method](#), [matches<-](#), [msgfPar](#), [numeric-method](#); [mods](#), [mods](#), [msgfPar-method](#), [mods<-](#), [mods<-](#), [msgfPar](#), [msgfParModificationList-method](#), [nMod](#), [nMod](#), [msgfPar-method](#), [nMod<-](#), [nMod<-](#), [msgfPar](#), [numeric-method](#); [ntt](#), [ntt](#), [msgfPar-method](#), [ntt<-](#), [ntt<-](#), [msgfPar](#), [msgfParNtt-method](#), [ntt<-](#), [msgfPar](#), [numeric-method](#); [protocol](#), [protocol](#), [msgfPar-method](#), [protocol<-](#), [protocol<-](#), [msgfPar](#), [character-method](#), [protocol<-](#), [msgfPar](#), [msgfParProtocol-method](#), [protocol<-](#), [msgfPar](#), [numeric-method](#); [tda](#), [tda](#), [msgfPar-method](#), [tda<-](#), [tda<-](#), [msgfPar](#), [logical-method](#), [tda<-](#), [msgfPar](#), [msgfParTda-method](#)

### Examples

```
parameters <- msgfPar(system.file(package=MSGFplus, extdata, milk-proteins.fasta))
tolerance(parameters) <- c(20 ppm, 20 ppm)
toleranceUnit(parameters) <- Da
```

```
toleranceRange(parameters) <- c(1.5, 1.5)  
tolerance(parameters)
```

# Index

[[,msgfParModificationList,numeric,missing-method  
(msgfParModificationList-class),  
37

[[<- ,msgfParModificationList,numeric,missing,  
(msgfParModificationList-class),  
37

chargeRange, 3, 5, 6, 8, 10, 11, 13, 14, 16, 46,  
48, 52, 54

chargeRange,msgfPar-method  
(chargeRange), 3

chargeRange<- (chargeRange), 3

chargeRange<- ,msgfPar ,msgfParChargeRange-method  
(chargeRange), 3

chargeRange<- ,msgfPar ,numeric-method  
(chargeRange), 3

db, 3, 4, 6, 8, 10, 11, 13, 14, 16, 46, 48, 52, 54

db,msgfPar-method (db), 4

db<- (db), 4

db<- ,msgfPar ,character-method (db), 4

enzyme, 3, 5, 5, 8, 10, 11, 13, 14, 16, 46, 48,  
52, 54

enzyme,msgfPar-method (enzyme), 5

enzyme<- (enzyme), 5

enzyme<- ,msgfPar ,character-method  
(enzyme), 5

enzyme<- ,msgfPar ,msgfParEnzyme-method  
(enzyme), 5

enzyme<- ,msgfPar ,numeric-method  
(enzyme), 5

finished (running), 50

finished,msgfAsync-method (running), 50

fragmentation, 3, 5, 6, 7, 10, 11, 13, 14, 16,  
46, 48, 52, 54

fragmentation,msgfPar-method  
(fragmentation), 7

fragmentation<- (fragmentation), 7

fragmentation<- ,msgfPar ,character-method  
(fragmentation), 7

fragmentation<- ,msgfPar ,msgfParFragmentation-method  
(fragmentation), 7

fragmentation<- ,msgfPar ,numeric-method  
(fragmentation), 7

getMSGFpar, 8

getMSGFpar ,msgfPar-method  
(msgfPar-class), 20

getMSGFpar ,msgfParChargeRange-method  
(msgfParChargeRange-class), 23

getMSGFpar ,msgfParEnzyme-method  
(msgfParEnzyme-class), 24

getMSGFpar ,msgfParFragmentation-method  
(msgfParFragmentation-class),  
26

getMSGFpar ,msgfParInstrument-method  
(msgfParInstrument-class), 29

getMSGFpar ,msgfParIsotopeError-method  
(msgfParIsotopeError-class), 30

getMSGFpar ,msgfParLengthRange-method  
(msgfParLengthRange-class), 32

getMSGFpar ,msgfParMatches-method  
(msgfParMatches-class), 33

getMSGFpar ,msgfParModification-method  
(msgfParModification-class), 35

getMSGFpar ,msgfParModificationList-method  
(msgfParModificationList-class),  
37

getMSGFpar ,msgfParNtt-method  
(msgfParNtt-class), 39

getMSGFpar ,msgfParProtocol-method  
(msgfParProtocol-class), 41

getMSGFpar ,msgfParTda-method  
(msgfParTda-class), 42

getMSGFpar ,msgfParTolerance-method  
(msgfParTolerance-class), 44

import (running), 50

- import,msgfAsync-method (running), 50
- instrument, 3, 5, 6, 8, 9, 11, 13, 14, 16, 46, 48, 52, 54
- instrument,msgfPar-method (instrument), 9
- instrument<- (instrument), 9
- instrument<- ,msgfPar, character-method (instrument), 9
- instrument<- ,msgfPar,msgfParInstrument-method (instrument), 9
- instrument<- ,msgfPar, numeric-method (instrument), 9
- isotopeError, 3, 5, 6, 8, 10, 11, 13, 14, 16, 46, 48, 52, 54
- isotopeError,msgfPar-method (isotopeError), 11
- isotopeError<- (isotopeError), 11
- isotopeError<- ,msgfPar,msgfParIsotopeError-method (isotopeError), 11
- isotopeError<- ,msgfPar, numeric-method (isotopeError), 11
  
- length,msgfPar-method (msgfPar-class), 20
- length,msgfParChargeRange-method (msgfParChargeRange-class), 23
- length,msgfParEnzyme-method (msgfParEnzyme-class), 24
- length,msgfParFragmentation-method (msgfParFragmentation-class), 26
- length,msgfParInstrument-method (msgfParInstrument-class), 29
- length,msgfParIsotopeError-method (msgfParIsotopeError-class), 30
- length,msgfParLengthRange-method (msgfParLengthRange-class), 32
- length,msgfParMatches-method (msgfParMatches-class), 33
- length,msgfParModificationList-method (msgfParModificationList-class), 37
- length,msgfParNtt-method (msgfParNtt-class), 39
- length,msgfParProtocol-method (msgfParProtocol-class), 41
- length,msgfParTda-method (msgfParTda-class), 42
  
- length,msgfParTolerance-method (msgfParTolerance-class), 44
- lengthRange, 4–6, 8, 10, 12, 12, 14, 16, 46, 48, 52, 54
- lengthRange,msgfPar-method (lengthRange), 12
- lengthRange<- (lengthRange), 12
- lengthRange<- ,msgfPar,msgfParLengthRange-method (lengthRange), 12
- lengthRange<- ,msgfPar, numeric-method (lengthRange), 12
  
- matches, 4–6, 8, 10, 12, 13, 13, 16, 46, 48, 52, 54
- matches,msgfPar-method (matches), 13
- matches<- (matches), 13
- matches<- ,msgfPar,msgfParMatches-method (matches), 13
- matches<- ,msgfPar, numeric-method (matches), 13
- mods, 4–6, 8, 10, 12–14, 15, 46, 48, 52, 54
- mods,msgfPar-method (mods), 15
- mods<- (mods), 15
- mods<- ,msgfPar,msgfParModificationList-method (mods), 15
- msgfAsync-class (running), 50
- msgfPar, 17, 22, 24, 25, 27, 28, 30, 31, 33–36, 38, 40, 42, 43, 45
- msgfPar-class, 20
- msgfParChargeRange, 19, 22, 25, 27, 30, 31, 33, 34, 36, 38, 40, 42, 43, 45
- msgfParChargeRange (msgfParChargeRange-class), 23
- msgfParChargeRange-class, 23
- msgfParEnzyme, 19, 22, 24, 27, 30, 31, 33, 34, 36, 38, 40, 42, 43, 45
- msgfParEnzyme (msgfParEnzyme-class), 24
- msgfParEnzyme-class, 24
- msgfParFragmentation, 19, 22, 24, 25, 30, 31, 33, 34, 36, 38, 40, 42, 43, 45
- msgfParFragmentation (msgfParFragmentation-class), 26
- msgfParFragmentation-class, 26
- msgfParFromID, 27
- msgfParGUI, 22, 28
- msgfParInstrument, 19, 22, 24, 25, 27, 31, 33, 34, 36, 38, 40, 42, 43, 45

- msgfParInstrument
  - (msgfParInstrument-class), 29
- msgfParInstrument-class, 29
- msgfParIsotopeError, 19, 22, 24, 25, 27, 30, 33, 34, 36, 38, 40, 42, 43, 45
- msgfParIsotopeError
  - (msgfParIsotopeError-class), 30
- msgfParIsotopeError-class, 30
- msgfParLengthRange, 19, 22, 24, 25, 27, 30, 31, 34, 36, 38, 40, 42, 43, 45
- msgfParLengthRange
  - (msgfParLengthRange-class), 32
- msgfParLengthRange-class, 32
- msgfParMatches, 19, 22, 24, 25, 27, 30, 31, 33, 36, 38, 40, 42, 43, 45
- msgfParMatches (msgfParMatches-class), 33
- msgfParMatches-class, 33
- msgfParModification, 19, 22, 24, 25, 27, 30, 31, 33, 34, 37, 38, 40, 42, 43, 45
- msgfParModification
  - (msgfParModification-class), 35
- msgfParModification-class, 35
- msgfParModificationList, 19, 22, 24, 25, 27, 30, 31, 33–36, 40, 42, 43, 45
- msgfParModificationList
  - (msgfParModificationList-class), 37
- msgfParModificationList-class, 37
- msgfParNtt, 19, 22, 24, 25, 27, 30, 31, 33, 34, 36, 38, 42, 43, 45
- msgfParNtt (msgfParNtt-class), 39
- msgfParNtt-class, 39
- msgfParProtocol, 19, 22, 24, 25, 27, 30, 31, 33, 34, 36, 38, 40, 43, 45
- msgfParProtocol
  - (msgfParProtocol-class), 41
- msgfParProtocol-class, 41
- msgfParTda, 19, 22, 24, 25, 27, 30, 31, 33, 34, 36, 38, 40, 42, 45
- msgfParTda (msgfParTda-class), 42
- msgfParTda-class, 42
- msgfParTolerance, 19, 22, 24, 25, 27, 30, 31, 33, 34, 36, 38, 40, 42, 43
- msgfParTolerance
  - (msgfParTolerance-class), 44
- msgfParTolerance-class, 44
- MSGFplus-package, 2
- mzID, 49
- nMod, 4–6, 8, 10, 12–14, 46, 48, 52, 54
- nMod (mods), 15
- nMod, msgfPar-method (mods), 15
- nMod<- (mods), 15
- nMod<- , msgfPar , numeric-method (mods), 15
- ntt, 4–6, 8, 10, 12–14, 16, 45, 48, 52, 54
- ntt, msgfPar-method (ntt), 45
- ntt<- (ntt), 45
- ntt<- , msgfPar , msgfParNtt-method (ntt), 45
- ntt<- , msgfPar , numeric-method (ntt), 45
- protocol, 4–6, 8, 10, 12–14, 16, 46, 47, 52, 54
- protocol, msgfPar-method (protocol), 47
- protocol<- (protocol), 47
- protocol<- , msgfPar , character-method (protocol), 47
- protocol<- , msgfPar , msgfParProtocol-method (protocol), 47
- protocol<- , msgfPar , numeric-method (protocol), 47
- runMSGF, 48
- runMSGF, msgfPar-method (msgfPar-class), 20
- running, 50
- running, msgfAsync-method (running), 50
- show, msgfPar-method (msgfPar-class), 20
- show, msgfParChargeRange-method (msgfParChargeRange-class), 23
- show, msgfParEnzyme-method (msgfParEnzyme-class), 24
- show, msgfParFragmentation-method (msgfParFragmentation-class), 26
- show, msgfParInstrument-method (msgfParInstrument-class), 29
- show, msgfParIsotopeError-method (msgfParIsotopeError-class), 30
- show, msgfParLengthRange-method (msgfParLengthRange-class), 32
- show, msgfParMatches-method (msgfParMatches-class), 33
- show, msgfParModification-method (msgfParModification-class), 35

show,msgfParModificationList-method  
(msgfParModificationList-class),  
37

show,msgfParNtt-method  
(msgfParNtt-class), 39

show,msgfParProtocol-method  
(msgfParProtocol-class), 41

show,msgfParTda-method  
(msgfParTda-class), 42

show,msgfParTolerance-method  
(msgfParTolerance-class), 44

system, 21, 23, 25, 26, 29, 31, 32, 34, 35, 38,  
40, 41, 43, 44

tda, 4–6, 8, 10, 12–14, 16, 46, 48, 51, 54

tda,msgfPar-method (tda), 51

tda<- (tda), 51

tda<- ,msgfPar ,logical-method (tda), 51

tda<- ,msgfPar ,msgfParTda-method (tda),  
51

tolerance, 4–6, 8, 10, 12, 13, 15, 16, 46, 48,  
52, 53

tolerance,msgfPar-method (tolerance), 53

tolerance<- (tolerance), 53

tolerance<- ,msgfPar ,character-method  
(tolerance), 53

tolerance<- ,msgfPar ,msgfParTolerance-method  
(tolerance), 53

toleranceRange, 4, 5, 7, 8, 10, 12, 13, 15, 16,  
47, 48, 52

toleranceRange (tolerance), 53

toleranceRange,msgfPar-method  
(tolerance), 53

toleranceRange<- (tolerance), 53

toleranceRange<- ,msgfPar ,numeric-method  
(tolerance), 53

toleranceUnit, 4, 5, 7, 8, 10, 12, 13, 15, 16,  
47, 48, 52

toleranceUnit (tolerance), 53

toleranceUnit,msgfPar-method  
(tolerance), 53

toleranceUnit<- (tolerance), 53

toleranceUnit<- ,msgfPar ,character-method  
(tolerance), 53