

# Package ‘Rcpi’

April 9, 2025

**Type** Package

**Version** 1.43.0

**Title** Molecular Informatics Toolkit for Compound-Protein Interaction  
in Drug Discovery

**Description** A molecular informatics toolkit with an integration of  
bioinformatics and cheminformatics tools for drug discovery.

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**URL** <https://nanx.me/Rcpi/>, <https://github.com/nanxstats/Rcpi>

**BugReports** <https://github.com/nanxstats/Rcpi/issues>

**Encoding** UTF-8

**LazyData** true

**VignetteBuilder** knitr

**Depends** R (>= 3.0.2)

**Imports** Biostrings, GOSemSim, curl, doParallel, foreach, httr2,  
jsonlite, methods, rlang, stats, utils

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

**biocViews** Software, DataImport, DataRepresentation, FeatureExtraction,  
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Rcpi-package                      *Rcpi: Molecular Informatics Toolkit for Compound-Protein Interaction in Drug Discovery*

---

**Description**

A molecular informatics toolkit with an integration of bioinformatics and chemoinformatics tools for drug discovery.

**Author(s)**

**Maintainer:** Nan Xiao <me@nanx.me> ([ORCID](#))

Authors:

- Dong-Sheng Cao
- Qing-Song Xu <qsxu@csu.edu.cn>

**See Also**

Useful links:

- <https://nanx.me/Rcpi/>
- <https://github.com/nanxstats/Rcpi>
- Report bugs at <https://github.com/nanxstats/Rcpi/issues>

---

AA2DACOR	<i>2D Autocorrelations Descriptors for 20 Amino Acids calculated by Dragon</i>
----------	--

---

**Description**

2D Autocorrelations Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the 2D autocorrelations descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AA2DACOR data

**Examples**

```
data(AA2DACOR)
```

---

AA3DMoRSE	<i>3D-MoRSE Descriptors for 20 Amino Acids calculated by Dragon</i>
-----------	---

---

**Description**

3D-MoRSE Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the 3D-MoRSE descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AA3DMoRSE data

**Examples**

```
data(AA3DMoRSE)
```

---

AAACF	<i>Atom-Centred Fragments Descriptors for 20 Amino Acids calculated by Dragon</i>
-------	---

---

**Description**

Atom-Centred Fragments Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the atom-centred fragments descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAACF data

**Examples**

```
data(AAACF)
```

---

AABLOSUM100	<i>BLOSUM100 Matrix for 20 Amino Acids</i>
-------------	--

---

**Description**

BLOSUM100 Matrix for 20 Amino Acids

**Details**

BLOSUM100 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AABLOSUM100 data

**Examples**

```
data(AABLOSUM100)
```

---

AABLOSUM45

*BLOSUM45 Matrix for 20 Amino Acids*

---

**Description**

BLOSUM45 Matrix for 20 Amino Acids

**Details**

BLOSUM45 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AABLOSUM45 data

**Examples**

```
data(AABLOSUM45)
```

---

AABLOSUM50

*BLOSUM50 Matrix for 20 Amino Acids*

---

**Description**

BLOSUM50 Matrix for 20 Amino Acids

**Details**

BLOSUM50 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AABLOSUM50 data

**Examples**

```
data(AABLOSUM50)
```



---

AABLOSUM62

*BLOSUM62 Matrix for 20 Amino Acids*

---

**Description**

BLOSUM62 Matrix for 20 Amino Acids

**Details**

BLOSUM62 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AABLOSUM62 data

**Examples**

```
data(AABLOSUM62)
```

---

AABLOSUM80

*BLOSUM80 Matrix for 20 Amino Acids*

---

**Description**

BLOSUM80 Matrix for 20 Amino Acids

**Details**

BLOSUM80 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AABLOSUM80 data

**Examples**

```
data(AABLOSUM80)
```

---

AABurden	<i>Burden Eigenvalues Descriptors for 20 Amino Acids calculated by Dragon</i>
----------	---

---

**Description**

Burden Eigenvalues Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the Burden eigenvalues descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AABurden data

**Examples**

```
data(AABurden)
```

---

AAConn	<i>Connectivity Indices Descriptors for 20 Amino Acids calculated by Dragon</i>
--------	---

---

**Description**

Connectivity Indices Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the connectivity indices descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAConn data

**Examples**

```
data(AAConn)
```

---

AAConst

*Constitutional Descriptors for 20 Amino Acids calculated by Dragon*

---

**Description**

Constitutional Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the constitutional descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAConst data

**Examples**

```
data(AAConst)
```

---

AACPSA

*CPSA Descriptors for 20 Amino Acids calculated by Discovery Studio*

---

**Description**

CPSA Descriptors for 20 Amino Acids calculated by Discovery Studio

**Details**

This dataset includes the CPSA descriptors of the 20 amino acids calculated by Discovery Studio (version 2.5) used for scales extraction in this package. All amino acid molecules had also been optimized with MOE 2011.10 (semiempirical AM1) before calculating these CPSA descriptors. The SDF file containing the information of the optimized amino acid molecules is included in this package. See [OptAA3d](#) for more information.

**Value**

AACPSA data

**Examples**

```
data(AACPSA)
```

---

`AADescAll`*All 2D Descriptors for 20 Amino Acids calculated by Dragon*

---

**Description**

All 2D Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes all the 2D descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AADescAll data

**Examples**

```
data(AADescAll)
```

---

`AAEdgeAdj`*Edge Adjacency Indices Descriptors for 20 Amino Acids calculated by Dragon*

---

**Description**

Edge Adjacency Indices Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the edge adjacency indices descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAEdgeAdj data

**Examples**

```
data(AAEdgeAdj)
```

---

AAEigIdx	<i>Eigenvalue-Based Indices Descriptors for 20 Amino Acids calculated by Dragon</i>
----------	---

---

**Description**

Eigenvalue-Based Indices Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the eigenvalue-based indices descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAEigIdx data

**Examples**

```
data(AAEigIdx)
```

---

AAFGC	<i>Functional Group Counts Descriptors for 20 Amino Acids calculated by Dragon</i>
-------	--

---

**Description**

Functional Group Counts Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the functional group counts descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAFGC data

**Examples**

```
data(AAFGC)
```

---

AAGeom

*Geometrical Descriptors for 20 Amino Acids calculated by Dragon*

---

**Description**

Geometrical Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the geometrical descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAGeom data

**Examples**

```
data(AAGeom)
```

---

AAGETAWAY

*GETAWAY Descriptors for 20 Amino Acids calculated by Dragon*

---

**Description**

GETAWAY Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the GETAWAY descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAGETAWAY data

**Examples**

```
data(AAGETAWAY)
```

---

AAindex	<i>AAindex Data of 544 Physicochemical and Biological Properties for 20 Amino Acids</i>
---------	---

---

**Description**

AAindex Data of 544 Physicochemical and Biological Properties for 20 Amino Acids

**Details**

The data was extracted from the AAindex1 database ver 9.1 (<ftp://ftp.genome.jp/pub/db/community/aaindex/aaindex1>) as of November 2012 (Data Last Modified 2006-08-14).

With this data, users could investigate each property's accession number and other details. Visit <https://www.genome.jp/dbget/aaindex.html> for more information.

**Value**

AAindex data

**Examples**

```
data(AAindex)
```

---

AAInfo	<i>Information Indices Descriptors for 20 Amino Acids calculated by Dragon</i>
--------	--

---

**Description**

Information Indices Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the information indices descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAInfo data

**Examples**

```
data(AAInfo)
```

---

AAMetaInfo

*Meta Information for the 20 Amino Acids*

---

**Description**

Meta Information for the 20 Amino Acids

**Details**

This dataset includes the meta information of the 20 amino acids used for the 2D and 3D descriptor calculation in this package. Each column represents:

AAName Amino acid name

Short One-letter representation

Abbreviation Three-letter representation

mol SMILES representation

PUBCHEM\_COMPOUND\_CID PubChem CID for the amino acid

PUBCHEM\_LINK PubChem link for the amino acid

**Value**

AAMetaInfo data

**Examples**

```
data(AAMetaInfo)
```

---

AAMOE2D

*2D Descriptors for 20 Amino Acids calculated by MOE 2011.10*

---

**Description**

2D Descriptors for 20 Amino Acids calculated by MOE 2011.10

**Details**

This dataset includes the 2D descriptors of the 20 amino acids calculated by MOE 2011.10 used for scales extraction in this package.

**Value**

AAMOE2D data

**Examples**

```
data(AAMOE2D)
```



---

AAMOE3D

*3D Descriptors for 20 Amino Acids calculated by MOE 2011.10*

---

**Description**

3D Descriptors for 20 Amino Acids calculated by MOE 2011.10

**Details**

This dataset includes the 3D descriptors of the 20 amino acids calculated by MOE 2011.10 used for scales extraction in this package. All amino acid molecules had also been optimized with MOE (semiempirical AM1) before calculating these 3D descriptors. The SDF file containing the information of the optimized amino acid molecules is included in this package. See [OptAA3d](#) for more information.

**Value**

AAMOE3D data

**Examples**

```
data(AAMOE3D)
```

---

AAMolProp

*Molecular Properties Descriptors for 20 Amino Acids calculated by Dragon*

---

**Description**

Molecular Properties Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the molecular properties descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAMolProp data

**Examples**

```
data(AAMolProp)
```

---

AAPAM120

*PAM120 Matrix for 20 Amino Acids*

---

**Description**

PAM120 Matrix for 20 Amino Acids

**Details**

PAM120 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AAPAM120 data

**Examples**

```
data(AAPAM120)
```

---

AAPAM250

*PAM250 Matrix for 20 Amino Acids*

---

**Description**

PAM250 Matrix for 20 Amino Acids

**Details**

PAM250 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AAPAM250 data

**Examples**

```
data(AAPAM250)
```

---

AAPAM30

*PAM30 Matrix for 20 Amino Acids*

---

**Description**

PAM30 Matrix for 20 Amino Acids

**Details**

PAM30 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AAPAM30 data

**Examples**

```
data(AAPAM30)
```

---

AAPAM40

*PAM40 Matrix for 20 Amino Acids*

---

**Description**

PAM40 Matrix for 20 Amino Acids

**Details**

PAM40 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AAPAM40 data

**Examples**

```
data(AAPAM40)
```

---

AAPAM70

*PAM70 Matrix for 20 Amino Acids*

---

**Description**

PAM70 Matrix for 20 Amino Acids

**Details**

PAM70 Matrix for the 20 amino acids. The matrix was extracted from the Biostrings package of Bioconductor.

**Value**

AAPAM70 data

**Examples**

```
data(AAPAM70)
```

---

AARandic

*Randic Molecular Profiles Descriptors for 20 Amino Acids calculated by Dragon*

---

**Description**

Randic Molecular Profiles Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the Randic molecular profiles descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AARandic data

**Examples**

```
data(AARandic)
```

---

AARDF

*RDF Descriptors for 20 Amino Acids calculated by Dragon*

---

**Description**

RDF Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the RDF descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AARDF data

**Examples**

```
data(AARDF)
```

---

AATopo

*Topological Descriptors for 20 Amino Acids calculated by Dragon*

---

**Description**

Topological Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the topological descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AATopo data

**Examples**

```
data(AATopo)
```

---

AATopoChg	<i>Topological Charge Indices Descriptors for 20 Amino Acids calculated by Dragon</i>
-----------	---

---

**Description**

Topological Charge Indices Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the topological charge indices descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AATopoChg data

**Examples**

```
data(AATopoChg)
```

---

AAWalk	<i>Walk and Path Counts Descriptors for 20 Amino Acids calculated by Dragon</i>
--------	---

---

**Description**

Walk and Path Counts Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the walk and path counts descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAWalk data

**Examples**

```
data(AAWalk)
```

AAWHIM

*WHIM Descriptors for 20 Amino Acids calculated by Dragon***Description**

WHIM Descriptors for 20 Amino Acids calculated by Dragon

**Details**

This dataset includes the WHIM descriptors of the 20 amino acids calculated by Dragon (version 5.4) used for scales extraction in this package.

**Value**

AAWHIM data

**Examples**

```
data(AAWHIM)
```

acc

*Auto Cross Covariance (ACC) for Generating Scales-Based Descriptors of the Same Length***Description**

Calculates auto covariance and auto cross covariance for generating scale-based descriptors of the same length.

**Usage**

```
acc(mat, lag)
```

**Arguments**

**mat** A  $p \times n$  matrix. Each row represents one scale (total  $p$  scales), each column represents one amino acid position (total  $n$  amino acids).

**lag** The lag parameter. Must be less than the amino acids.

**Value**

A length  $lag \times p^2$  named vector, the element names are constructed by: the scales index (crossed scales index) and lag index.

**Note**

To see more details about auto cross covariance, check the references.

**References**

Wold, S., Jonsson, J., Sjöström, M., Sandberg, M., & Rännar, S. (1993). DNA and peptide sequences and chemical processes multivariately modelled by principal component analysis and partial least-squares projections to latent structures. *Analytica chimica acta*, 277(2), 239–253.

Sjöström, M., Rännar, S., & Wieslander, Å. (1995). Polypeptide sequence property relationships in *Escherichia coli* based on auto cross covariances. *Chemometrics and intelligent laboratory systems*, 29(2), 295–305.

**See Also**

See [extractPCMScales](#) for generalized scales-based descriptors. For more details, see [extractPCMDescScales](#) and [extractPCMPPropScales](#).

**Examples**

```
p = 8 # p is the scales number
n = 200 # n is the amino acid number
lag = 7 # lag parameter
mat = matrix(rnorm(p * n), nrow = p, ncol = n)
acc(mat, lag)
```

---

calcDrugFPSim

*Calculate Drug Molecule Similarity Derived by Molecular Fingerprints*

---

**Description**

Calculate Drug Molecule Similarity Derived by Molecular Fingerprints

**Usage**

```
calcDrugFPSim(
  fp1,
  fp2,
  fptype = c("compact", "complete"),
  metric = c("tanimoto", "euclidean", "cosine", "dice", "hamming")
)
```



## Arguments

fp1	The first molecule's fingerprints, could be extracted by extractDrugMACCS(), extractDrugMACCSComplete() etc.
fp2	The second molecule's fingerprints.
fptype	The fingerprint type, must be one of "compact" or "complete".
metric	The similarity metric, one of "tanimoto", "euclidean", "cosine", "dice" and "hamming".

## Details

This function calculate drug molecule fingerprints similarity. Define a as the features of object A, b is the features of object B, c is the number of common features to A and B:

- Tanimoto: aka Jaccard -  $c/a + b + c$
- Euclidean:  $\sqrt{(a + b)}$
- Dice: aka Sorensen, Czekanowski, Hodgkin-Richards -  $c/0.5[(a + c) + (b + c)]$
- Cosine: aka Ochiai, Carbo -  $c/\sqrt{(a + c)(b + c)}$
- Hamming: aka Manhattan, taxi-cab, city-block distance -  $(a + b)$

## Value

The numeric similarity value.

## References

Gasteiger, Johann, and Thomas Engel, eds. Chemoinformatics. Wiley.com, 2006.

## Examples

```
mols = readMolFromSDF(system.file('compseq/tyrphostin.sdf', package = 'Rcpi'))

fp1 = extractDrugEstate(mols[[1]])
fp2 = extractDrugEstate(mols[[2]])
calcDrugFPSim(fp1, fp2, fptype = 'compact', metric = 'tanimoto')
calcDrugFPSim(fp1, fp2, fptype = 'compact', metric = 'euclidean')
calcDrugFPSim(fp1, fp2, fptype = 'compact', metric = 'cosine')
calcDrugFPSim(fp1, fp2, fptype = 'compact', metric = 'dice')
calcDrugFPSim(fp1, fp2, fptype = 'compact', metric = 'hamming')

fp3 = extractDrugEstateComplete(mols[[1]])
fp4 = extractDrugEstateComplete(mols[[2]])
calcDrugFPSim(fp3, fp4, fptype = 'complete', metric = 'tanimoto')
calcDrugFPSim(fp3, fp4, fptype = 'complete', metric = 'euclidean')
calcDrugFPSim(fp3, fp4, fptype = 'complete', metric = 'cosine')
calcDrugFPSim(fp3, fp4, fptype = 'complete', metric = 'dice')
calcDrugFPSim(fp3, fp4, fptype = 'complete', metric = 'hamming')
```

---

calcDrugMCSSim	<i>Calculate Drug Molecule Similarity Derived by Maximum Common Substructure Search</i>
----------------	---

---

### Description

Calculate Drug Molecule Similarity Derived by Maximum Common Substructure Search

### Usage

```
calcDrugMCSSim(  
  mol1,  
  mol2,  
  type = c("smile", "sdf"),  
  plot = FALSE,  
  al = 0,  
  au = 0,  
  bl = 0,  
  bu = 0,  
  matching.mode = "static",  
  ...  
)
```

### Arguments

mol1	The first molecule. R character string object containing the molecule. See examples.
mol2	The second molecule. R character string object containing the molecule. See examples.
type	The input molecule format, 'smile' or 'sdf'.
plot	Logical. Should we plot the two molecules and their maximum common substructure?
al	Lower bound for the number of atom mismatches. Default is 0.
au	Upper bound for the number of atom mismatches. Default is 0.
bl	Lower bound for the number of bond mismatches. Default is 0.
bu	Upper bound for the number of bond mismatches. Default is 0.
matching.mode	Three modes for bond matching are supported: 'static', 'aromatic', and 'ring'.
...	Other graphical parameters

### Details

This function calculate drug molecule similarity derived by maximum common substructure search. The maximum common substructure search algorithm is provided by the `fmcsR` package.

**Value**

A list containing the detail MCS information and similarity values. The numeric similarity value includes Tanimoto coefficient and overlap coefficient.

**References**

Wang, Y., Backman, T. W., Horan, K., & Girke, T. (2013). fmcsR: mismatch tolerant maximum common substructure searching in R. *Bioinformatics*, 29(21), 2792–2794.

**Examples**

```
mol1 = 'CC(C)CCCCC(=O)NCC1=CC(=C(C=C1)O)OC'
mol2 = 'O=C(NCc1cc(OC)c(O)cc1)CCCC/C=C/C(C)C'
mol3 = readChar(system.file('compseq/DB00859.sdf', package = 'Rcpi'), nchars = 1e+6)
mol4 = readChar(system.file('compseq/DB00860.sdf', package = 'Rcpi'), nchars = 1e+6)
## Not run:
sim1 = calcDrugMCSSim(mol1, mol2, type = 'smile')
sim2 = calcDrugMCSSim(mol3, mol4, type = 'sdf', plot = TRUE)
print(sim1[[2]]) # Tanimoto Coefficient
print(sim2[[3]]) # Overlap Coefficient

## End(Not run)
```

---

calcParProtGOSim	<i>Protein Sequence Similarity Calculation based on Gene Ontology (GO) Similarity</i>
------------------	---

---

**Description**

Protein Sequence Similarity Calculation based on Gene Ontology (GO) Similarity

**Usage**

```
calcParProtGOSim(
  golist,
  type = c("go", "gene"),
  ont = c("MF", "BP", "CC"),
  organism = "human",
  measure = "Resnik",
  combine = "BMA"
)
```

**Arguments**

golist	A character vector, each component contains a character vector of GO terms or one Entrez Gene ID.
type	Input type of golist, 'go' for GO Terms, 'gene' for gene ID.

ont	Default is 'MF', could be one of 'MF', 'BP', or 'CC' subontologies.
organism	Default is 'human', could be one of 'anopheles', 'arabidopsis', 'bovine', 'canine', 'chicken', 'chimp', 'coelicolor', 'ecolik12', 'ecsakai', 'fly', 'human', 'malaria', 'mouse', 'pig', 'rat', 'rhesus', 'worm', 'xenopus', 'yeast' or 'zebrafish'.
measure	Default is 'Resnik', could be one of 'Resnik', 'Lin', 'Rel', 'Jiang' or 'Wang'.
combine	Default is 'BMA', could be one of 'max', 'average', 'rcmax' or 'BMA' for combining semantic similarity scores of multiple GO terms associated with protein.

### Details

This function calculates protein sequence similarity based on Gene Ontology (GO) similarity.

### Value

A n x n similarity matrix.

### See Also

See [calcTwoProtGOSim](#) for calculating the GO semantic similarity between two groups of GO terms or two Entrez gene IDs. See [calcParProtSeqSim](#) for paralleled protein similarity calculation based on sequence alignment.

### Examples

```
# By GO Terms
go1 = c('GO:0005215', 'GO:0005488', 'GO:0005515', 'GO:0005625', 'GO:0005802', 'GO:0005905') # AP4B1
go2 = c('GO:0005515', 'GO:0005634', 'GO:0005681', 'GO:0008380', 'GO:0031202') # BCAS2
go3 = c('GO:0003735', 'GO:0005622', 'GO:0005840', 'GO:0006412') # PDE4DIP
glist = list(go1, go2, go3)
calcParProtSeqSim(glist, type = 'go', ont = 'CC', measure = 'Wang')

# By Entrez gene id
genelist = list(c('150', '151', '152', '1814', '1815', '1816'))
calcParProtSeqSim(genelist, type = 'gene', ont = 'BP', measure = 'Wang')
```

---

calcParProtSeqSim	<i>Parallellized Protein Sequence Similarity Calculation based on Sequence Alignment</i>
-------------------	--

---

### Description

Parallellized Protein Sequence Similarity Calculation based on Sequence Alignment



---

calcTwoProtGOSim      *Protein Similarity Calculation based on Gene Ontology (GO) Similarity*

---

### Description

Protein Similarity Calculation based on Gene Ontology (GO) Similarity

### Usage

```
calcTwoProtGOSim(
  id1,
  id2,
  type = c("go", "gene"),
  ont = c("MF", "BP", "CC"),
  organism = "human",
  measure = "Resnik",
  combine = "BMA"
)
```

### Arguments

id1	A character vector. length > 1: each element is a GO term; length = 1: the Entrez Gene ID.
id2	A character vector. length > 1: each element is a GO term; length = 1: the Entrez Gene ID.
type	Input type of id1 and id2, 'go' for GO Terms, 'gene' for gene ID.
ont	Default is 'MF', could be one of 'MF', 'BP', or 'CC' subontologies.
organism	Default is 'human', could be one of 'anopheles', 'arabidopsis', 'bovine', 'canine', 'chicken', 'chimp', 'coelicolor', 'ecolik12', 'ecsakai', 'fly', 'human', 'malaria', 'mouse', 'pig', 'rat', 'rhesus', 'worm', 'xenopus', 'yeast' or 'zebrafish'.
measure	Default is 'Resnik', could be one of 'Resnik', 'Lin', 'Rel', 'Jiang' or 'Wang'.
combine	Default is 'BMA', could be one of 'max', 'average', 'rcmax' or 'BMA' for combining semantic similarity scores of multiple GO terms associated with protein.

### Details

This function calculates the Gene Ontology (GO) similarity between two groups of GO terms or two Entrez gene IDs.

### Value

A n x n matrix.

**See Also**

See [calcParProtGOSim](#) for protein similarity calculation based on Gene Ontology (GO) semantic similarity. See [calcParProtSeqSim](#) for paralleled protein similarity calculation based on sequence alignment.

**Examples**

```
# By GO terms
go1 = c("GO:0004022", "GO:0004024", "GO:0004023")
go2 = c("GO:0009055", "GO:0020037")
calcTwoProtGOSim(go1, go2, type = 'go', ont = 'MF', measure = 'Wang')

# By Entrez gene id
gene1 = '241'
gene2 = '251'
calcTwoProtGOSim(gene1, gene2, type = 'gene', ont = 'CC', measure = 'Lin')
```

---

calcTwoProtSeqSim      *Protein Sequence Alignment for Two Protein Sequences*

---

**Description**

Protein Sequence Alignment for Two Protein Sequences

**Usage**

```
calcTwoProtSeqSim(seq1, seq2, type = "local", submat = "BLOSUM62")
```

**Arguments**

seq1	A character string, containing one protein sequence.
seq2	A character string, containing another protein sequence.
type	Type of alignment, default is 'local', could be 'global' or 'local', where 'global' represents Needleman-Wunsch global alignment; 'local' represents Smith-Waterman local alignment.
submat	Substitution matrix, default is 'BLOSUM62', could be one of 'BLOSUM45', 'BLOSUM50', 'BLOSUM62', 'BLOSUM80', 'BLOSUM100', 'PAM30', 'PAM40', 'PAM70', 'PAM120', 'PAM250'.

**Details**

This function implements the sequence alignment between two protein sequences.

**Value**

An Biostrings object containing the scores and other alignment information.

**See Also**

See [calcParProtSeqSim](#) for paralleled pairwise protein similarity calculation based on sequence alignment. See [calcTwoProtGOSim](#) for calculating the GO semantic similarity between two groups of GO terms or two Entrez gene IDs.

**Examples**

```
s1 = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
s2 = readFASTA(system.file('protseq/P10323.fasta', package = 'Rcpi'))[[1]]

seqalign = calcTwoProtSeqSim(s1, s2)
seqalign
slot(seqalign, "score")
```

---

checkProt	<i>Check if the protein sequence's amino acid types are the 20 default types</i>
-----------	--

---

**Description**

Check if the protein sequence's amino acid types are the 20 default types

**Usage**

```
checkProt(x)
```

**Arguments**

x                    A character vector, as the input protein sequence.

**Details**

This function checks if the protein sequence's amino acid types are the 20 default types.

**Value**

Logical. TRUE if all of the amino acid types of the sequence are within the 20 default types.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
checkProt(x) # TRUE
checkProt(paste(x, 'Z', sep = '')) # FALSE
```



---

convMolFormat	<i>Chemical File Formats Conversion</i>
---------------	---

---

**Description**

Chemical File Formats Conversion

**Usage**

```
convMolFormat(infile, outfile, from, to)
```

**Arguments**

infile	A character string. Indicating the input file location.
outfile	A character string. Indicating the output file location.
from	The format of infile. A character string supported by OpenBabel. See the note section for the supported formats.
to	The desired format of outfile. A character string supported by OpenBabel. See the note section for the supported formats.

**Details**

This function converts between various chemical file formats via OpenBabel. The complete supported file format list could be found at <https://openbabel.org/docs/FileFormats/Overview.html>.

**Value**

NULL

**Note**

The supported formats include:

- abinit – ABINIT Output Format [Read-only]
- acr – ACR format [Read-only]
- adf – ADF cartesian input format [Write-only]
- adfout – ADF output format [Read-only]
- alc – Alchemy format
- arc – Accelrys/MSI Biosym/Insight II CAR format [Read-only]
- axsf – XCrySDen Structure Format [Read-only]
- bgf – MSI BGF format
- box – Dock 3.5 Box format
- bs – Ball and Stick format

- c3d1 – Chem3D Cartesian 1 format
- c3d2 – Chem3D Cartesian 2 format
- cac – CAChe MolStruct format [Write-only]
- cacert – Cacao Cartesian format
- cache – CAChe MolStruct format [Write-only]
- cacint – Cacao Internal format [Write-only]
- can – Canonical SMILES format
- car – Accelrys/MSI Biosym/Insight II CAR format [Read-only]
- castep – CASTEP format [Read-only]
- ccc – CCC format [Read-only]
- cdx – ChemDraw binary format [Read-only]
- cdxml – ChemDraw CDXML format
- cht – Chemtool format [Write-only]
- cif – Crystallographic Information File
- ck – ChemKin format
- cml – Chemical Markup Language
- cmlr – CML Reaction format
- com – Gaussian 98/03 Input [Write-only]
- CONFIG – DL-POLY CONFIG
- CONTCAR – VASP format [Read-only]
- copy – Copy raw text [Write-only]
- crk2d – Chemical Resource Kit diagram(2D)
- crk3d – Chemical Resource Kit 3D format
- csr – Accelrys/MSI Quanta CSR format [Write-only]
- cssr – CSD CSSR format [Write-only]
- ct – ChemDraw Connection Table format
- cub – Gaussian cube format
- cube – Gaussian cube format
- dat – Generic Output file format [Read-only]
- dmol – DMol3 coordinates format
- dx – OpenDX cube format for APBS
- ent – Protein Data Bank format
- fa – FASTA format
- fasta – FASTA format
- fch – Gaussian formatted checkpoint file format [Read-only]
- fchk – Gaussian formatted checkpoint file format [Read-only]
- fck – Gaussian formatted checkpoint file format [Read-only]

- feat – Feature format
- fh – Fenske-Hall Z-Matrix format [Write-only]
- fhiaims – FHIaims XYZ format
- fix – SMILES FIX format [Write-only]
- fpt – Fingerprint format [Write-only]
- fract – Free Form Fractional format
- fs – Fastsearch format
- fsa – FASTA format
- g03 – Gaussian Output [Read-only]
- g09 – Gaussian Output [Read-only]
- g92 – Gaussian Output [Read-only]
- g94 – Gaussian Output [Read-only]
- g98 – Gaussian Output [Read-only]
- gal – Gaussian Output [Read-only]
- gam – GAMESS Output [Read-only]
- gamess – GAMESS Output [Read-only]
- gamin – GAMESS Input
- gamout – GAMESS Output [Read-only]
- gau – Gaussian 98/03 Input [Write-only]
- gjc – Gaussian 98/03 Input [Write-only]
- gjf – Gaussian 98/03 Input [Write-only]
- got – GULP format [Read-only]
- gpr – Ghemical format
- gr96 – GROMOS96 format [Write-only]
- gro – GRO format
- gukin – GAMESS-UK Input
- gukout – GAMESS-UK Output
- gzmat – Gaussian Z-Matrix Input
- hin – HyperChem HIN format
- HISTORY – DL-POLY HISTORY [Read-only]
- inchi – InChI format
- inchikey – InChIKey [Write-only]
- inp – GAMESS Input
- ins – ShelX format [Read-only]
- jin – Jaguar input format [Write-only]
- jout – Jaguar output format [Read-only]
- k – Compare molecules using InChI [Write-only]

- log – Generic Output file format [Read-only]
- mcdl – MCDL format
- mcif – Macromolecular Crystallographic Info
- mdl – MDL MOL format
- ml2 – Sybyl Mol2 format
- mmcif – Macromolecular Crystallographic Info
- mmd – MacroModel format
- mmod – MacroModel format
- mna – Multilevel Neighborhoods of Atoms (MNA) [Write-only]
- mol – MDL MOL format
- mol2 – Sybyl Mol2 format
- mold – Molden format
- molden – Molden format
- molf – Molden format
- molreport – Open Babel molecule report [Write-only]
- moo – MOPAC Output format [Read-only]
- mop – MOPAC Cartesian format
- mopcart – MOPAC Cartesian format
- mopin – MOPAC Internal
- mopout – MOPAC Output format [Read-only]
- mp – Molpro input format [Write-only]
- mpc – MOPAC Cartesian format
- mpd – MolPrint2D format [Write-only]
- mpo – Molpro output format [Read-only]
- mpqc – MPQC output format [Read-only]
- mpqcin – MPQC simplified input format [Write-only]
- mrv – Chemical Markup Language
- msi – Accelrys/MSI Cerius II MSI format [Read-only]
- msms – M.F. Sanner's MSMS input format [Write-only]
- nul – Outputs nothing [Write-only]
- nw – NWChem input format [Write-only]
- nwo – NWChem output format [Read-only]
- out – Generic Output file format [Read-only]
- outmol – DMol3 coordinates format
- output – Generic Output file format [Read-only]
- pc – PubChem format [Read-only]
- pcm – PCModel Format

- pdb – Protein Data Bank format
- pdbqt – AutoDock PDQBT format
- png – PNG 2D depiction
- POSCAR – VASP format [Read-only]
- pov – POV-Ray input format [Write-only]
- pqr – PQR format
- pqs – Parallel Quantum Solutions format
- prep – Amber Prep format [Read-only]
- pwscf – PWscf format [Read-only]
- qcin – Q-Chem input format [Write-only]
- qcout – Q-Chem output format [Read-only]
- report – Open Babel report format [Write-only]
- res – ShelX format [Read-only]
- rsmi – Reaction SMILES format
- rxn – MDL RXN format
- sd – MDL MOL format
- sdf – MDL MOL format
- smi – SMILES format
- smiles – SMILES format
- svg – SVG 2D depiction [Write-only]
- sy2 – Sybyl Mol2 format
- t41 – ADF TAPE41 format [Read-only]
- tdd – Thermo format
- text – Read and write raw text
- therm – Thermo format
- tmol – TurboMole Coordinate format
- txt – Title format
- txyz – Tinker XYZ format
- unixyz – UniChem XYZ format
- vmol – ViewMol format
- xed – XED format [Write-only]
- xml – General XML format [Read-only]
- xsf – XCrySDen Structure Format [Read-only]
- xyz – XYZ cartesian coordinates format
- yob – YASARA.org YOB format
- zin – ZINDO input format [Write-only]

## Examples

```
sdf = system.file('sysdata/OptAA3d.sdf', package = 'Rcpi')
# SDF to SMILES
## Not run:
convMolFormat(infile = sdf, outfile = 'aa.smi',
              from = 'sdf', to = 'smiles')
## End(Not run)
# SMILES to MOPAC Cartesian format
## Not run:
convMolFormat(infile = 'aa.smi', outfile = 'aa.mop',
              from = 'smiles', to = 'mop')
## End(Not run)
```

---

extractDrugAIO

*Calculate All Molecular Descriptors in Rcpi at Once*

---

## Description

Calculate All Molecular Descriptors in Rcpi at Once

## Usage

```
extractDrugAIO(molecules, silent = TRUE, warn = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.
warn	Logical. Whether the warning about some descriptors need the 3D coordinates should be shown or not after the calculation, default is TRUE.

## Details

This function calculates all the molecular descriptors in the Rcpi package at once.

## Value

A data frame, each row represents one of the molecules, each column represents one descriptor. Currently, this function returns total 293 descriptors composed of 48 descriptor types.

## Note

Note that we need 3-D coordinates of the molecules to calculate some of the descriptors, if not provided, these descriptors values will be NA.

## Examples

```
# Load 20 small molecules that have 3D coordinates
sdf = system.file('sysdata/0ptAA3d.sdf', package = 'Rcpi')

mol = readMolFromSDF(sdf)
dat = extractDrugAIO(mol, warn = FALSE)
```

---

extractDrugALOGP	<i>Calculate Atom Additive logP and Molar Refractivity Values Descriptor</i>
------------------	--

---

## Description

Calculate Atom Additive logP and Molar Refractivity Values Descriptor

## Usage

```
extractDrugALOGP(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

Calculates ALOGP (Ghose-Crippen LogKow) and the Ghose-Crippen molar refractivity as described by Ghose, A.K. and Crippen, G.M. Note the underlying code in CDK assumes that aromaticity has been detected before evaluating this descriptor. The code also expects that the molecule will have hydrogens explicitly set. For SD files, this is usually not a problem since hydrogens are explicit. But for the case of molecules obtained from SMILES, hydrogens must be made explicit.

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns three columns named ALogP, ALogp2 and AMR.

## References

- Ghose, A.K. and Crippen, G.M. , Atomic physicochemical parameters for three-dimensional structure-directed quantitative structure-activity relationships. I. Partition coefficients as a measure of hydrophobicity, *Journal of Computational Chemistry*, 1986, 7:565-577.
- Ghose, A.K. and Crippen, G.M. , Atomic physicochemical parameters for three-dimensional-structure-directed quantitative structure-activity relationships. 2. Modeling dispersive and hydrophobic interactions, *Journal of Chemical Information and Computer Science*, 1987, 27:21-35.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugALOGP(mol)
head(dat)
```

---

extractDrugAminoAcidCount

*Calculate the Number of Amino Acids Descriptor*

---

## Description

Calculate the Number of Amino Acids Descriptor

## Usage

```
extractDrugAminoAcidCount(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

Calculates the number of each amino acids (total 20 types) found in the molecules.

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 20 columns named nA, nR, nN, nD, nC, nF, nQ, nE, nG, nH, nI, nP, nL, nK, nM, nS, nT, nY, nV, nW.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugAminoAcidCount(mol)
head(dat)
```



---

extractDrugApol	<i>Calculate the Sum of the Atomic Polarizabilities Descriptor</i>
-----------------	--

---

**Description**

Calculate the Sum of the Atomic Polarizabilities Descriptor

**Usage**

```
extractDrugApol(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculates the sum of the atomic polarizabilities (including implicit hydrogens) descriptor. Polarizabilities are taken from <https://bit.ly/3PvNbhe>.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named apol.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugApol(mol)  
head(dat)
```

---

extractDrugAromaticAtomsCount	<i>Calculate the Number of Aromatic Atoms Descriptor</i>
-------------------------------	--

---

**Description**

Calculate the Number of Aromatic Atoms Descriptor

**Usage**

```
extractDrugAromaticAtomsCount(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculates the number of aromatic atoms of a molecule.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nAromAtom.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugAromaticAtomsCount(mol)  
head(dat)
```

---

extractDrugAromaticBondsCount

*Calculate the Number of Aromatic Bonds Descriptor*

---

**Description**

Calculate the Number of Aromatic Bonds Descriptor

**Usage**

```
extractDrugAromaticBondsCount(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculates the number of aromatic bonds of a molecule.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nAromBond.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugAromaticBondsCount(mol)
head(dat)
```

---

extractDrugAtomCount *Calculate the Number of Atom Descriptor*

---

**Description**

Calculate the Number of Atom Descriptor

**Usage**

```
extractDrugAtomCount(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculates the number of atoms of a certain element type in a molecule. By default it returns the count of all atoms.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nAtom.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugAtomCount(mol)
head(dat)
```

---

extractDrugAutocorrelationCharge

*Calculate the Moreau-Broto Autocorrelation Descriptors using Partial Charges*

---

### Description

Calculate the Moreau-Broto Autocorrelation Descriptors using Partial Charges

### Usage

```
extractDrugAutocorrelationCharge(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Calculates the ATS autocorrelation descriptor, where the weight equal to the charges.

### Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 5 columns named ATSc1, ATSc2, ATSc3, ATSc4, ATSc5.

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugAutocorrelationCharge(mol)  
head(dat)
```

---

extractDrugAutocorrelationMass

*Calculate the Moreau-Broto Autocorrelation Descriptors using Atomic Weight*

---

### Description

Calculate the Moreau-Broto Autocorrelation Descriptors using Atomic Weight

**Usage**

```
extractDrugAutocorrelationMass(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculates the ATS autocorrelation descriptor, where the weight equal to the scaled atomic mass.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 5 columns named ATSm1, ATSm2, ATSm3, ATSm4, ATSm5.

**References**

Moreau, Gilles, and Pierre Broto. The autocorrelation of a topological structure: a new molecular descriptor. *Nouv. J. Chim* 4 (1980): 359-360.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugAutocorrelationMass(mol)  
head(dat)
```

---

extractDrugAutocorrelationPolarizability

*Calculate the Moreau-Broto Autocorrelation Descriptors using Polarizability*

---

**Description**

Calculate the Moreau-Broto Autocorrelation Descriptors using Polarizability

**Usage**

```
extractDrugAutocorrelationPolarizability(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculates the ATS autocorrelation descriptor using polarizability.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 5 columns named ATSp1, ATSp2, ATSp3, ATSp4, ATSp5.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugAutocorrelationPolarizability(mol)  
head(dat)
```

---

extractDrugBCUT

*BCUT – Eigenvalue Based Descriptor*

---

**Description**

BCUT – Eigenvalue Based Descriptor

**Usage**

```
extractDrugBCUT(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Eigenvalue based descriptor noted for its utility in chemical diversity. Described by Pearlman et al. The descriptor is based on a weighted version of the Burden matrix which takes into account both the connectivity as well as atomic properties of a molecule. The weights are a variety of atom properties placed along the diagonal of the Burden matrix. Currently three weighting schemes are employed:

- Atomic Weight
- Partial Charge (Gasteiger Marsilli)
- Polarizability (Kang et al.)

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 6 columns:

- BCUTw-1l, BCUTw-2l . . . - n high lowest atom weighted BCUTS
- BCUTw-1h, BCUTw-2h . . . - n low highest atom weighted BCUTS
- BCUTc-1l, BCUTc-2l . . . - n high lowest partial charge weighted BCUTS
- BCUTc-1h, BCUTc-2h . . . - n low highest partial charge weighted BCUTS
- BCUTp-1l, BCUTp-2l . . . - n high lowest polarizability weighted BCUTS
- BCUTp-1h, BCUTp-2h . . . - n low highest polarizability weighted BCUTS

**Note**

By default, the descriptor will return the highest and lowest eigenvalues for the three classes of descriptor in a single ArrayList (in the order shown above). However it is also possible to supply a parameter list indicating how many of the highest and lowest eigenvalues (for each class of descriptor) are required. The descriptor works with the hydrogen depleted molecule.

A side effect of specifying the number of highest and lowest eigenvalues is that it is possible to get two copies of all the eigenvalues. That is, if a molecule has 5 heavy atoms, then specifying the 5 highest eigenvalues returns all of them, and specifying the 5 lowest eigenvalues returns all of them, resulting in two copies of all the eigenvalues.

Note that it is possible to specify an arbitrarily large number of eigenvalues to be returned. However if the number (i.e., nhigh or nlow) is larger than the number of heavy atoms, the remaining eigenvalues will be NaN.

Given the above description, if the aim is to get all the eigenvalues for a molecule, you should set nlow to 0 and specify the number of heavy atoms (or some large number) for nhigh (or vice versa).

**References**

Pearlman, R.S. and Smith, K.M., Metric Validation and the Receptor-Relevant Subspace Concept, *J. Chem. Inf. Comput. Sci.*, 1999, 39:28-35.

Burden, F.R., Molecular identification number for substructure searches, *J. Chem. Inf. Comput. Sci.*, 1989, 29:225-227.

Burden, F.R., Chemically Intuitive Molecular Index, *Quant. Struct. -Act. Relat.*, 1997, 16:309-314

Kang, Y.K. and Jhon, M.S., Additivity of Atomic Static Polarizabilities and Dispersion Coefficients, *Theoretica Chimica Acta*, 1982, 61:41-48

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugBCUT(mol)
head(dat)
```

---

extractDrugBondCount     *Calculate the Descriptor Based on the Number of Bonds of a Certain Bond Order*

---

### Description

Calculate the Descriptor Based on the Number of Bonds of a Certain Bond Order

### Usage

```
extractDrugBondCount(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Calculates the descriptor based on the number of bonds of a certain bond order.

### Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nB.

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugBondCount(mol)  
head(dat)
```

---

extractDrugBPol     *Calculate the Descriptor that Describes the Sum of the Absolute Value of the Difference between Atomic Polarizabilities of All Bonded Atoms in the Molecule*

---

### Description

Calculates the Descriptor that Describes the Sum of the Absolute Value of the Difference between Atomic Polarizabilities of All Bonded Atoms in the Molecule



**Usage**

```
extractDrugBPol(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

This descriptor calculates the sum of the absolute value of the difference between atomic polarizabilities of all bonded atoms in the molecule (including implicit hydrogens) with polarizabilities taken from <https://bit.ly/3PvNbhe>. This descriptor assumes 2-centered bonds.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named bpol.

**Examples**

```
smi = system.file('vignettedata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugBPol(mol)  
head(dat)
```

---

extractDrugCarbonTypes

*Topological Descriptor Characterizing the Carbon Connectivity in Terms of Hybridization*

---

**Description**

Topological Descriptor Characterizing the Carbon Connectivity in Terms of Hybridization

**Usage**

```
extractDrugCarbonTypes(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

Calculates the carbon connectivity in terms of hybridization. The function calculates 9 descriptors in the following order:

- C1SP1 - triply bound carbon bound to one other carbon
- C2SP1 - triply bound carbon bound to two other carbons
- C1SP2 - doubly bound carbon bound to one other carbon
- C2SP2 - doubly bound carbon bound to two other carbons
- C3SP2 - doubly bound carbon bound to three other carbons
- C1SP3 - singly bound carbon bound to one other carbon
- C2SP3 - singly bound carbon bound to two other carbons
- C3SP3 - singly bound carbon bound to three other carbons
- C4SP3 - singly bound carbon bound to four other carbons

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 9 columns named C1SP1, C2SP1, C1SP2, C2SP2, C3SP2, C1SP3, C2SP3, C3SP3 and C4SP3.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugCarbonTypes(mol)  
head(dat)
```

---

extractDrugChiChain	<i>Calculate the Kier and Hall Chi Chain Indices of Orders 3, 4, 5, 6 and 7</i>
---------------------	---

---

## Description

Calculate the Kier and Hall Chi Chain Indices of Orders 3, 4, 5, 6 and 7

## Usage

```
extractDrugChiChain(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

Evaluates chi chain descriptors. The code currently evaluates the simple and valence chi chain descriptors of orders 3, 4, 5, 6 and 7. It utilizes the graph isomorphism code of the CDK to find fragments matching SMILES strings representing the fragments corresponding to each type of chain.

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 10 columns, in the following order:

- SCH.3 - Simple chain, order 3
- SCH.4 - Simple chain, order 4
- SCH.5 - Simple chain, order 5
- SCH.6 - Simple chain, order 6
- SCH.7 - Simple chain, order 7
- VCH.3 - Valence chain, order 3
- VCH.4 - Valence chain, order 4
- VCH.5 - Valence chain, order 5
- VCH.6 - Valence chain, order 6
- VCH.7 - Valence chain, order 7

## Note

These descriptors are calculated using graph isomorphism to identify the various fragments. As a result calculations may be slow. In addition, recent versions of Molconn-Z use simplified fragment definitions (i.e., rings without branches etc.) whereas these descriptors use the older more complex fragment definitions.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugChiChain(mol)  
head(dat)
```

---

extractDrugChiCluster *Evaluates the Kier and Hall Chi cluster indices of orders 3, 4, 5 and 6*

---

## Description

Evaluates the Kier and Hall Chi cluster indices of orders 3, 4, 5 and 6

## Usage

```
extractDrugChiCluster(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Evaluates chi cluster descriptors. It utilizes the graph isomorphism code of the CDK to find fragments matching SMILES strings representing the fragments corresponding to each type of chain.

### Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 8 columns, the order and names of the columns returned is:

- SC.3 - Simple cluster, order 3
- SC.4 - Simple cluster, order 4
- SC.5 - Simple cluster, order 5
- SC.6 - Simple cluster, order 6
- VC.3 - Valence cluster, order 3
- VC.4 - Valence cluster, order 4
- VC.5 - Valence cluster, order 5
- VC.6 - Valence cluster, order 6

### Note

These descriptors are calculated using graph isomorphism to identify the various fragments. As a result calculations may be slow. In addition, recent versions of Molconn-Z use simplified fragment definitions (i.e., rings without branches etc.) whereas these descriptors use the older more complex fragment definitions.

### Examples

```
smi = system.file('vignettedata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugChiCluster(mol)  
head(dat)
```

---

extractDrugChiPath     *Calculate the Kier and Hall Chi Path Indices of Orders 0 to 7*

---

### Description

Calculate the Kier and Hall Chi Path Indices of Orders 0 to 7

### Usage

```
extractDrugChiPath(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Evaluates chi path descriptors. This function utilizes the graph isomorphism code of the CDK to find fragments matching SMILES strings representing the fragments corresponding to each type of chain.

### Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 16 columns, The order and names of the columns returned is:

- SP.0, SP.1, . . . , SP.7 - Simple path, orders 0 to 7
- VP.0, VP.1, . . . , VP.7 - Valence path, orders 0 to 7

### Note

These descriptors are calculated using graph isomorphism to identify the various fragments. As a result calculations may be slow. In addition, recent versions of Molconn-Z use simplified fragment definitions (i.e., rings without branches etc.) whereas these descriptors use the older more complex fragment definitions.

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugChiPath(mol)  
head(dat)
```

---

`extractDrugChiPathCluster`*Calculate the Kier and Hall Chi Path Cluster Indices of Orders 4, 5 and 6*

---

**Description**

Calculate the Kier and Hall Chi Path Cluster Indices of Orders 4, 5 and 6

**Usage**

```
extractDrugChiPathCluster(molecules, silent = TRUE)
```

**Arguments**

<code>molecules</code>	Parsed molecule object.
<code>silent</code>	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Evaluates chi path cluster descriptors. The code currently evaluates the simple and valence chi chain descriptors of orders 4, 5 and 6. It utilizes the graph isomorphism code of the CDK to find fragments matching SMILES strings representing the fragments corresponding to each type of chain.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 6 columns named `SPC.4`, `SPC.5`, `SPC.6`, `VPC.4`, `VPC.5`, `VPC.6`:

- `SPC.4` - Simple path cluster, order 4
- `SPC.5` - Simple path cluster, order 5
- `SPC.6` - Simple path cluster, order 6
- `VPC.4` - Valence path cluster, order 4
- `VPC.5` - Valence path cluster, order 5
- `VPC.6` - Valence path cluster, order 6

**Note**

These descriptors are calculated using graph isomorphism to identify the various fragments. As a result calculations may be slow. In addition, recent versions of Molconn-Z use simplified fragment definitions (i.e., rings without branches etc.) whereas these descriptors use the older more complex fragment definitions.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugChiPathCluster(mol)
head(dat)
```

---

extractDrugCPSA	<i>A Variety of Descriptors Combining Surface Area and Partial Charge Information</i>
-----------------	---

---

## Description

A Variety of Descriptors Combining Surface Area and Partial Charge Information

## Usage

```
extractDrugCPSA(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

Calculates 29 Charged Partial Surface Area (CPSA) descriptors. The CPSA's were developed by Stanton et al.

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 29 columns:

- PPSA.1 - partial positive surface area – sum of surface area on positive parts of molecule
- PPSA.2 - partial positive surface area \* total positive charge on the molecule
- PPSA.3 - charge weighted partial positive surface area
- PNSA.1 - partial negative surface area – sum of surface area on negative parts of molecule
- PNSA.2 - partial negative surface area \* total negative charge on the molecule
- PNSA.3 - charge weighted partial negative surface area
- DPSA.1 - difference of PPSA.1 and PNSA.1
- DPSA.2 - difference of PPSA.2 and PNSA.2
- DPSA.3 - difference of PPSA.3 and PNSA.3
- FPSA.1 - PPSA.1 / total molecular surface area

- FFSA. 2 - PPSA.2 / total molecular surface area
- FPSA. 3 - PPSA.3 / total molecular surface area
- FNSA. 1 - PNSA.1 / total molecular surface area
- FNSA. 2 - PNSA.2 / total molecular surface area
- FNSA. 3 - PNSA.3 / total molecular surface area
- WPSA. 1 - PPSA.1 \* total molecular surface area / 1000
- WPSA. 2 - PPSA.2 \* total molecular surface area /1000
- WPSA. 3 - PPSA.3 \* total molecular surface area / 1000
- WNSA. 1 - PNSA.1 \* total molecular surface area /1000
- WNSA. 2 - PNSA.2 \* total molecular surface area / 1000
- WNSA. 3 - PNSA.3 \* total molecular surface area / 1000
- RPCG - relative positive charge – most positive charge / total positive charge
- RNCG - relative negative charge – most negative charge / total negative charge
- RPCS - relative positive charge surface area – most positive surface area \* RPCG
- RNCS - relative negative charge surface area – most negative surface area \* RNCG
- THSA - sum of solvent accessible surface areas of atoms with absolute value of partial charges less than 0.2
- TPSA - sum of solvent accessible surface areas of atoms with absolute value of partial charges greater than or equal 0.2
- RHSA - THSA / total molecular surface area
- RPSA - TPSA / total molecular surface area

## References

Stanton, D.T. and Jurs, P.C. , Development and Use of Charged Partial Surface Area Structural Descriptors in Computer Assisted Quantitative Structure Property Relationship Studies, Analytical Chemistry, 1990, 62:2323.2329.

## Examples

```
sdf = system.file('sysdata/OptAA3d.sdf', package = 'Rcpi')  
  
mol = readMolFromSDF(sdf)  
dat = extractDrugCPSA(mol)  
head(dat)
```



---

extractDrugDescOB      *Calculate Molecular Descriptors Provided by OpenBabel*

---

**Description**

Calculate Molecular Descriptors Provided by OpenBabel

**Usage**

```
extractDrugDescOB(molecules, type = c("smile", "sdf"))
```

**Arguments**

molecules	R character string object containing the molecules. See the example section for details.
type	'smile' or 'sdf'.

**Details**

This function calculates 14 types of the *numerical* molecular descriptors provided in OpenBabel.

**Value**

A data frame, each row represents one of the molecules, each column represents one descriptor. This function returns 14 columns named abonds, atoms, bonds, dbonds, HBA1, HBA2, HBD, logP, MR, MW, nF, sbonds, tbonds, TPSA:

- abonds - Number of aromatic bonds
- atoms - Number of atoms
- bonds - Number of bonds
- dbonds - Number of double bonds
- HBA1 - Number of Hydrogen Bond Acceptors 1
- HBA2 - Number of Hydrogen Bond Acceptors 2
- HBD - Number of Hydrogen Bond Donors
- logP - Octanol/Water Partition Coefficient
- MR - Molar Refractivity
- MW - Molecular Weight Filter
- nF - Number of Fluorine Atoms
- sbonds - Number of single bonds
- tbonds - Number of triple bonds
- TPSA - Topological Polar Surface Area

**Examples**

```

mol1 = 'CC(=O)NCCC1=CNc2c1cc(OC)cc2' # one molecule SMILE in a vector
mol2 = c('OCCc1c(C)[n+](=cs1)Cc2cnc(C)nc(N)2',
        'CCc(c1)ccc2[n+]1ccc3c2Nc4c3cccc4',
        '[Cu+2].[O-]S(=O)(=O)[O-]') # multiple SMILES in a vector
mol3 = readChar(system.file('compseq/DB00860.sdf', package = 'Rcpi'),
               nchars = 1e+6) # single molecule in a sdf file
mol4 = readChar(system.file('sysdata/OptAA3d.sdf', package = 'Rcpi'),
               nchars = 1e+6) # multiple molecules in a sdf file

## Not run:
smidesc0 = extractDrugDescOB(mol1, type = 'smile')
smidesc1 = extractDrugDescOB(mol2, type = 'smile')
sdfdesc0 = extractDrugDescOB(mol3, type = 'sdf')
sdfdesc1 = extractDrugDescOB(mol4, type = 'sdf')
## End(Not run)

```

---

 extractDrugECI

*Calculate the Eccentric Connectivity Index Descriptor*


---

**Description**

Calculate the Eccentric Connectivity Index Descriptor

**Usage**

```
extractDrugECI(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Eccentric Connectivity Index (ECI) is a topological descriptor combining distance and adjacency information. This descriptor is described by Sharma et al. and has been shown to correlate well with a number of physical properties. The descriptor is also reported to have good discriminatory ability. The eccentric connectivity index for a hydrogen suppressed molecular graph is given by

$$x_i^c = \sum_{i=1}^n E(i)V(i)$$

where E(i) is the eccentricity of the i-th atom (path length from the i-th atom to the atom farthest from it) and V(i) is the vertex degree of the i-th atom.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named ECCEN.

**References**

Sharma, V. and Goswami, R. and Madan, A.K. (1997), Eccentric Connectivity Index: A Novel Highly Discriminating Topological Descriptor for Structure-Property and Structure-Activity Studies, *Journal of Chemical Information and Computer Sciences*, 37:273-282

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugECI(mol)  
head(dat)
```

---

extractDrugEstate	<i>Calculate the E-State Molecular Fingerprints (in Compact Format)</i>
-------------------	---

---

**Description**

Calculate the E-State Molecular Fingerprints (in Compact Format)

**Usage**

```
extractDrugEstate(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

79 bit fingerprints corresponding to the E-State atom types described by Hall and Kier.

**Value**

A list, each component represents one of the molecules, each element in the component represents the index of which element in the fingerprint is 1. Each component's name is the length of the fingerprints.

**See Also**

[extractDrugEstateComplete](#)

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
fp = extractDrugEstate(mol)
head(fp)
```

---

extractDrugEstateComplete

*Calculate the E-State Molecular Fingerprints (in Complete Format)*

---

### Description

Calculate the E-State Molecular Fingerprints (in Complete Format)

### Usage

```
extractDrugEstateComplete(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

79 bit fingerprints corresponding to the E-State atom types described by Hall and Kier.

### Value

An integer vector or a matrix. Each row represents one molecule, the columns represent the fingerprints.

### See Also

[extractDrugEstate](#)

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
fp = extractDrugEstateComplete(mol)
dim(fp)
```

---

extractDrugExtended     *Calculate the Extended Molecular Fingerprints (in Compact Format)*

---

### Description

Calculate the Extended Molecular Fingerprints (in Compact Format)

### Usage

```
extractDrugExtended(molecules, depth = 6, size = 1024, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
depth	The search depth. Default is 6.
size	The length of the fingerprint bit string. Default is 1024.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Calculate the extended molecular fingerprints. Considers paths of a given length, similar to the standard type, but takes rings and atomic properties into account. This is hashed fingerprints, with a default length of 1024.

### Value

A list, each component represents one of the molecules, each element in the component represents the index of which element in the fingerprint is 1. Each component's name is the length of the fingerprints.

### See Also

[extractDrugExtendedComplete](#)

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugExtended(mol)  
head(fp)
```

---

`extractDrugExtendedComplete`*Calculate the Extended Molecular Fingerprints (in Complete Format)*

---

### Description

Calculate the Extended Molecular Fingerprints (in Complete Format)

### Usage

```
extractDrugExtendedComplete(molecules, depth = 6, size = 1024, silent = TRUE)
```

### Arguments

<code>molecules</code>	Parsed molecule object.
<code>depth</code>	The search depth. Default is 6.
<code>size</code>	The length of the fingerprint bit string. Default is 1024.
<code>silent</code>	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Calculate the extended molecular fingerprints. Considers paths of a given length, similar to the standard type, but takes rings and atomic properties into account. This is hashed fingerprints, with a default length of 1024.

### Value

An integer vector or a matrix. Each row represents one molecule, the columns represent the fingerprints.

### See Also

[extractDrugExtended](#)

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugExtendedComplete(mol)  
dim(fp)
```

---

extractDrugFMF      *Calculate the FMF Descriptor*

---

### Description

Calculate the FMF Descriptor

### Usage

```
extractDrugFMF(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Calculates the FMF descriptor characterizing molecular complexity in terms of its Murcko framework. This descriptor is the ratio of heavy atoms in the framework to the total number of heavy atoms in the molecule. By definition, acyclic molecules which have no frameworks, will have a value of 0. Note that the authors consider an isolated ring system to be a framework (even though there is no linker).

### Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named FMF.

### References

Yang, Y., Chen, H., Nilsson, I., Muresan, S., & Engkvist, O. (2010). Investigation of the relationship between topology and selectivity for druglike molecules. *Journal of medicinal chemistry*, 53(21), 7709-7714.

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugFMF(mol)  
head(dat)
```

---

extractDrugFragmentComplexity  
*Calculate Complexity of a System*

---

## Description

Calculate Complexity of a System

## Usage

```
extractDrugFragmentComplexity(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

This descriptor calculates the complexity of a system. The complexity is defined in Nilakantan, R. et al. as:

$$C = abs(B^2 - A^2 + A) + \frac{H}{100}$$

where C is complexity, A is the number of non-hydrogen atoms, B is the number of bonds and H is the number of heteroatoms.

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named fragC.

## References

Nilakantan, R. and Nunn, D.S. and Greenblatt, L. and Walker, G. and Haraki, K. and Mobilio, D., A family of ring system-based structural fragments for use in structure-activity studies: database mining and recursive partitioning., Journal of chemical information and modeling, 2006, 46:1069-1077

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugFragmentComplexity(mol)  
head(dat)
```



---

extractDrugGraph      *Calculate the Graph Molecular Fingerprints (in Compact Format)*

---

### Description

Calculate the Graph Molecular Fingerprints (in Compact Format)

### Usage

```
extractDrugGraph(molecules, depth = 6, size = 1024, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
depth	The search depth. Default is 6.
size	The length of the fingerprint bit string. Default is 1024.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Calculate the graph molecular fingerprints. Similar to the standard type by simply considers connectivity. This is hashed fingerprints, with a default length of 1024.

### Value

A list, each component represents one of the molecules, each element in the component represents the index of which element in the fingerprint is 1. Each component's name is the length of the fingerprints.

### See Also

[extractDrugGraphComplete](#)

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugGraph(mol)  
head(fp)
```

---

extractDrugGraphComplete

*Calculate the Graph Molecular Fingerprints (in Complete Format)*

---

### Description

Calculate the Graph Molecular Fingerprints (in Complete Format)

### Usage

```
extractDrugGraphComplete(molecules, depth = 6, size = 1024, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
depth	The search depth. Default is 6.
size	The length of the fingerprint bit string. Default is 1024.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Calculate the graph molecular fingerprints. Similar to the standard type by simply considers connectivity. This is hashed fingerprints, with a default length of 1024.

### Value

An integer vector or a matrix. Each row represents one molecule, the columns represent the fingerprints.

### See Also

[extractDrugGraph](#)

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugGraphComplete(mol)  
dim(fp)
```

---

`extractDrugGravitationalIndex`*Descriptor Characterizing the Mass Distribution of the Molecule.*

---

### Description

Descriptor Characterizing the Mass Distribution of the Molecule.

### Usage

```
extractDrugGravitationalIndex(molecules, silent = TRUE)
```

### Arguments

<code>molecules</code>	Parsed molecule object.
<code>silent</code>	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Descriptor characterizing the mass distribution of the molecule described by Katritzky et al. For modelling purposes the value of the descriptor is calculated both with and without H atoms. Furthermore the square and cube roots of the descriptor are also generated as described by Wessel et al.

### Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 9 columns:

- `GRAV.1` - gravitational index of heavy atoms
- `GRAV.2` - square root of gravitational index of heavy atoms
- `GRAV.3` - cube root of gravitational index of heavy atoms
- `GRAVH.1` - gravitational index - hydrogens included
- `GRAVH.2` - square root of hydrogen-included gravitational index
- `GRAVH.3` - cube root of hydrogen-included gravitational index
- `GRAV.4` - `grav1` for all pairs of atoms (not just bonded pairs)
- `GRAV.5` - `grav2` for all pairs of atoms (not just bonded pairs)
- `GRAV.6` - `grav3` for all pairs of atoms (not just bonded pairs)

## References

Katritzky, A.R. and Mu, L. and Lobanov, V.S. and Karelson, M., Correlation of Boiling Points With Molecular Structure. 1. A Training Set of 298 Diverse Organics and a Test Set of 9 Simple Inorganics, *J. Phys. Chem.*, 1996, 100:10400-10407.

Wessel, M.D. and Jurs, P.C. and Tolan, J.W. and Muskal, S.M. , Prediction of Human Intestinal Absorption of Drug Compounds From Molecular Structure, *Journal of Chemical Information and Computer Sciences*, 1998, 38:726-735.

## Examples

```
sdf = system.file('sysdata/0ptAA3d.sdf', package = 'Rcpi')  
  
mol = readMolFromSDF(sdf)  
dat = extractDrugGravitationalIndex(mol)  
head(dat)
```

---

```
extractDrugHBondAcceptorCount  
      Number of Hydrogen Bond Acceptors
```

---

## Description

Number of Hydrogen Bond Acceptors

## Usage

```
extractDrugHBondAcceptorCount(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

This descriptor calculates the number of hydrogen bond acceptors using a slightly simplified version of the PHACIR atom types. The following groups are counted as hydrogen bond acceptors: any oxygen where the formal charge of the oxygen is non-positive (i.e. formal charge  $\leq 0$ ) except

1. an aromatic ether oxygen (i.e. an ether oxygen that is adjacent to at least one aromatic carbon)
2. an oxygen that is adjacent to a nitrogen

and any nitrogen where the formal charge of the nitrogen is non-positive (i.e. formal charge  $\leq 0$ ) except a nitrogen that is adjacent to an oxygen.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nHBacc.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugHBondAcceptorCount(mol)  
head(dat)
```

---

extractDrugHBondDonorCount

*Number of Hydrogen Bond Donors*

---

**Description**

Number of Hydrogen Bond Donors

**Usage**

```
extractDrugHBondDonorCount(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

This descriptor calculates the number of hydrogen bond donors using a slightly simplified version of the PHACIR atom types (<https://bit.ly/3qXQELf>). The following groups are counted as hydrogen bond donors:

- Any-OH where the formal charge of the oxygen is non-negative (i.e. formal charge  $\geq 0$ )
- Any-NH where the formal charge of the nitrogen is non-negative (i.e. formal charge  $\geq 0$ )

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nHBDon.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugHBondDonorCount(mol)
head(dat)
```

---

extractDrugHybridization

*Calculate the Hybridization Molecular Fingerprints (in Compact Format)*

---

## Description

Calculate the Hybridization Molecular Fingerprints (in Compact Format)

## Usage

```
extractDrugHybridization(molecules, depth = 6, size = 1024, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
depth	The search depth. Default is 6.
size	The length of the fingerprint bit string. Default is 1024.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

Calculate the hybridization molecular fingerprints. Similar to the standard type, but only consider hybridization state. This is hashed fingerprints, with a default length of 1024.

## Value

A list, each component represents one of the molecules, each element in the component represents the index of which element in the fingerprint is 1. Each component's name is the length of the fingerprints.

## See Also

[extractDrugHybridizationComplete](#)

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
fp = extractDrugHybridization(mol)
head(fp)
```

---

extractDrugHybridizationComplete

*Calculate the Hybridization Molecular Fingerprints (in Complete Format)*

---

## Description

Calculate the Hybridization Molecular Fingerprints (in Complete Format)

## Usage

```
extractDrugHybridizationComplete(
  molecules,
  depth = 6,
  size = 1024,
  silent = TRUE
)
```

## Arguments

molecules	Parsed molecule object.
depth	The search depth. Default is 6.
size	The length of the fingerprint bit string. Default is 1024.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

Calculate the hybridization molecular fingerprints. Similar to the standard type, but only consider hybridization state. This is hashed fingerprints, with a default length of 1024.

## Value

An integer vector or a matrix. Each row represents one molecule, the columns represent the fingerprints.

## See Also

[extractDrugHybridization](#)

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
fp = extractDrugHybridizationComplete(mol)
dim(fp)
```

---

extractDrugHybridizationRatio

*Descriptor that Characterizing Molecular Complexity in Terms of Carbon Hybridization States*

---

## Description

Descriptor that Characterizing Molecular Complexity in Terms of Carbon Hybridization States

## Usage

```
extractDrugHybridizationRatio(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

This descriptor calculates the fraction of sp<sup>3</sup> carbons to sp<sup>2</sup> carbons. Note that it only considers carbon atoms and rather than use a simple ratio it reports the value of  $N_{sp3}/(N_{sp3} + N_{sp2})$ . The original form of the descriptor (i.e., simple ratio) has been used to characterize molecular complexity, especially in the are of natural products, which usually have a high value of the sp<sup>3</sup> to sp<sup>2</sup> ratio.

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named HybRatio.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugHybridizationRatio(mol)
head(dat)
```



---

`extractDrugIPMolecularLearning`*Calculate the Descriptor that Evaluates the Ionization Potential*

---

**Description**

Calculate the Descriptor that Evaluates the Ionization Potential

**Usage**

```
extractDrugIPMolecularLearning(molecules, silent = TRUE)
```

**Arguments**

<code>molecules</code>	Parsed molecule object.
<code>silent</code>	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculate the ionization potential of a molecule. The descriptor assumes that explicit hydrogens have been added to the molecules.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named MolIP.

**Examples**

```
smi = system.file('vignettedata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugIPMolecularLearning(mol)  
head(dat)
```

---

`extractDrugKappaShapeIndices`*Descriptor that Calculates Kier and Hall Kappa Molecular Shape Indices*

---

**Description**

Descriptor that Calculates Kier and Hall Kappa Molecular Shape Indices

**Usage**

```
extractDrugKappaShapeIndices(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Kier and Hall Kappa molecular shape indices compare the molecular graph with minimal and maximal molecular graphs; see <https://bit.ly/3ramdBy> for details: "they are intended to capture different aspects of molecular shape. Note that hydrogens are ignored. In the following description, n denotes the number of atoms in the hydrogen suppressed graph, m is the number of bonds in the hydrogen suppressed graph. Also, let p2 denote the number of paths of length 2 and let p3 denote the number of paths of length 3".

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 3 columns named Kier1, Kier2 and Kier3:

- Kier1 - First kappa shape index
- Kier2 - Second kappa shape index
- Kier3 - Third kappa shape index

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugKappaShapeIndices(mol)  
head(dat)
```

---

extractDrugKierHallSmarts

*Descriptor that Counts the Number of Occurrences of the E-State Fragments*

---

**Description**

Descriptor that Counts the Number of Occurrences of the E-State Fragments

**Usage**

```
extractDrugKierHallSmarts(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

A fragment count descriptor that uses e-state fragments. Traditionally the e-state descriptors identify the relevant fragments and then evaluate the actual e-state value. However it has been shown in Butina et al. that simply using the counts of the e-state fragments can lead to QSAR models that exhibit similar performance to those built using the actual e-state indices.

Atom typing and aromaticity perception should be performed prior to calling this descriptor. The atom type definitions are taken from Hall et al. The SMARTS definitions were obtained from RDKit.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 79 columns:

ID	Name	Pattern
0	khs.sLi	[LiD1]-*
1	khs.ssBe	[BeD2](-*)-*
2	khs.ssssBe	[BeD4](-*)(-*)(-*)-*
3	khs.ssBH	[BD2H](-*)-*
4	khs.sssB	[BD3](-*)(-*)-*
5	khs.ssssB	[BD4](-*)(-*)(-*)-*
6	khs.sCH3	[CD1H3]-*
7	khs.dCH2	[CD1H2]=*
8	khs.ssCH2	[CD2H2](-*)-*
9	khs.tCH	[CD1H]#*
10	khs.dsCH	[CD2H](=*)-*
11	khs.aaCH	[C,c;D2H](:*):*
12	khs.sssCH	[CD3H](-*)(-*)-*
13	khs.ddC	[CD2H0](=*)=*
14	khs.tsC	[CD2H0]#*-*
15	khs.dssC	[CD3H0](=*)(-*)-*
16	khs.aasC	[C,c;D3H0](:*)(:*)-*
17	khs.aaaC	[C,c;D3H0](:*)(:*)(:*)-*
18	khs.ssssC	[CD4H0](-*)(-*)(-*)-*
19	khs.sNH3	[ND1H3]-*
20	khs.sNH2	[ND1H2]-*
21	khs.ssNH2	[ND2H2](-*)-*
22	khs.dNH	[ND1H]=*
23	khs.ssNH	[ND2H](-*)-*
24	khs.aaNH	[N,nD2H](:*)(:*)-*
25	khs.tN	[ND1H0]#*
26	khs.sssNH	[ND3H](-*)(-*)-*

27	khs.dsN	[ND2H0](=*)-*
28	khs.aaN	[N,nD2H0](:*):*
29	khs.sssN	[ND3H0](-*)(-*)-*
30	khs.ddsN	[ND3H0](~[OD1H0])(~[OD1H0])-,:*
31	khs.aasN	[N,nD3H0](:*)(:*)-,:*
32	khs.ssssN	[ND4H0](-*)(-*)(-*)-*
33	khs.sOH	[OD1H]-*
34	khs.dO	[OD1H0]=*
35	khs.ssO	[OD2H0](-*)-*
36	khs.aaO	[O,oD2H0](:*):*
37	khs.sF	[FD1]-*
38	khs.sSiH3	[SiD1H3]-*
39	khs.ssSiH2	[SiD2H2](-*)-*
40	khs.sssSiH	[SiD3H1](-*)(-*)-*
41	khs.ssssSi	[SiD4H0](-*)(-*)(-*)-*
42	khs.sPH2	[PD1H2]-*
43	khs.ssPH	[PD2H1](-*)-*
44	khs.sssP	[PD3H0](-*)(-*)-*
45	khs.dsssP	[PD4H0](=*)(-*)(-*)-*
46	khs.sssssP	[PD5H0](-*)(-*)(-*)(-*)-*
47	khs.sSH	[SD1H1]-*
48	khs.dS	[SD1H0]=*
49	khs.ssS	[SD2H0](-*)-*
50	khs.aaS	[S,sD2H0](:*):*
51	khs.dssS	[SD3H0](=*)(-*)-*
52	khs.ddssS	[SD4H0](~[OD1H0])(~[OD1H0])(-*)-*
53	khs.sCl	[ClD1]-*
54	khs.sGeH3	[GeD1H3](-*)
55	khs.ssGeH2	[GeD2H2](-*)-*
56	khs.sssGeH	[GeD3H1](-*)(-*)-*
57	khs.ssssGe	[GeD4H0](-*)(-*)(-*)-*
58	khs.sAsH2	[AsD1H2]-*
59	khs.ssAsH	[AsD2H1](-*)-*
60	khs.sssAs	[AsD3H0](-*)(-*)-*
61	khs.sssdAs	[AsD4H0](=*)(-*)(-*)-*
62	khs.sssssAs	[AsD5H0](-*)(-*)(-*)(-*)-*
63	khs.sSeH	[SeD1H1]-*
64	khs.dSe	[SeD1H0]=*
65	khs.ssSe	[SeD2H0](-*)-*
66	khs.aaSe	[SeD2H0](:*):*
67	khs.dssSe	[SeD3H0](=*)(-*)-*
68	khs.ddssSe	[SeD4H0](=*)(=*)(-*)-*
69	khs.sBr	[BrD1]-*
70	khs.sSnH3	[SnD1H3]-*
71	khs.ssSnH2	[SnD2H2](-*)-*
72	khs.sssSnH	[SnD3H1](-*)(-*)-*
73	khs.ssssSn	[SnD4H0](-*)(-*)(-*)-*
74	khs.sI	[ID1]-*

75	khs.sPbH3	[PbD1H3]-*
76	khs.ssPbH2	[PbD2H2](-*)-*
77	khs.sssPbH	[PbD3H1](-*)(-*)-*
78	khs.ssssPb	[PbD4H0](-*)(-*)(-*)-*

## References

Butina, D. , Performance of Kier-Hall E-state Descriptors in Quantitative Structure Activity Relationship (QSAR) Studies of Multifunctional Molecules, *Molecules*, 2004, 9:1004-1009.

Hall, L.H. and Kier, L.B. , Electrotological State Indices for Atom Types: A Novel Combination of Electronic, Topological, and Valence State Information, *Journal of Chemical Information and Computer Science*, 1995, 35:1039-1045.

## Examples

```
smi = system.file('vignettedata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugKierHallSmarts(mol)
head(dat)
```

---

extractDrugKR	<i>Calculate the KR (Klekota and Roth) Molecular Fingerprints (in Compact Format)</i>
---------------	---

---

## Description

Calculate the KR (Klekota and Roth) Molecular Fingerprints (in Compact Format)

## Usage

```
extractDrugKR(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

Calculate the 4860 bit fingerprint defined by Klekota and Roth.

## Value

A list, each component represents one of the molecules, each element in the component represents the index of which element in the fingerprint is 1. Each component's name is the length of the fingerprints.

**See Also**

[extractDrugKRComplete](#)

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugKR(mol)  
head(fp)
```

---

extractDrugKRComplete *Calculate the KR (Klekota and Roth) Molecular Fingerprints (in Complete Format)*

---

**Description**

Calculate the KR (Klekota and Roth) Molecular Fingerprints (in Complete Format)

**Usage**

```
extractDrugKRComplete(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculate the 4860 bit fingerprint defined by Klekota and Roth.

**Value**

An integer vector or a matrix. Each row represents one molecule, the columns represent the fingerprints.

**See Also**

[extractDrugKR](#)

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugKRComplete(mol)  
dim(fp)
```

---

`extractDrugLargestChain`*Descriptor that Calculates the Number of Atoms in the Largest Chain*

---

**Description**

Descriptor that Calculates the Number of Atoms in the Largest Chain

**Usage**

```
extractDrugLargestChain(molecules, silent = TRUE)
```

**Arguments**

<code>molecules</code>	Parsed molecule object.
<code>silent</code>	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

This descriptor calculates the number of atoms in the largest chain. Note that a chain exists if there are two or more atoms. Thus single atom molecules will return 0.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nAtomLC.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugLargestChain(mol)  
head(dat)
```

---

`extractDrugLargestPiSystem`*Descriptor that Calculates the Number of Atoms in the Largest Pi Chain*

---

**Description**

Descriptor that Calculates the Number of Atoms in the Largest Pi Chain

**Usage**

```
extractDrugLargestPiSystem(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

This descriptor calculates the number of atoms in the largest pi chain.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nAtomP.

**Examples**

```
smi = system.file('vignettedata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugLargestPiSystem(mol)  
head(dat)
```

---

extractDrugLengthOverBreadth

*Calculate the Ratio of Length to Breadth Descriptor*

---

**Description**

Calculate the Ratio of Length to Breadth Descriptor

**Usage**

```
extractDrugLengthOverBreadth(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculates the Ratio of Length to Breadth, as a result it does not perform any orientation and only considers the X & Y extents for a series of rotations about the Z axis (in 10 degree increments).



**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns two columns named LOBMAX and LOBMIN:

- LOBMAX - The maximum L/B ratio;
- LOBMIN - The L/B ratio for the rotation that results in the minimum area (defined by the product of the X & Y extents for that orientation).

**Note**

The descriptor assumes that the atoms have been configured.

**Examples**

```
sdf = system.file('sysdata/OptAA3d.sdf', package = 'Rcpi')  
  
mol = readMolFromSDF(sdf)  
dat = extractDrugLengthOverBreadth(mol)  
head(dat)
```

---

extractDrugLongestAliphaticChain

*Descriptor that Calculates the Number of Atoms in the Longest Aliphatic Chain*

---

**Description**

Descriptor that Calculates the Number of Atoms in the Longest Aliphatic Chain

**Usage**

```
extractDrugLongestAliphaticChain(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

This descriptor calculates the number of atoms in the longest aliphatic chain.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nAtomLAC.

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugLongestAliphaticChain(mol)
head(dat)
```

---

extractDrugMACCS	<i>Calculate the MACCS Molecular Fingerprints (in Compact Format)</i>
------------------	---

---

### Description

Calculate the MACCS Molecular Fingerprints (in Compact Format)

### Usage

```
extractDrugMACCS(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

The popular 166 bit MACCS keys described by MDL.

### Value

A list, each component represents one of the molecules, each element in the component represents the index of which element in the fingerprint is 1. Each component's name is the length of the fingerprints.

### See Also

[extractDrugMACCSComplete](#)

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
fp = extractDrugMACCS(mol)
head(fp)
```

---

`extractDrugMACCSComplete`*Calculate the MACCS Molecular Fingerprints (in Complete Format)*

---

**Description**

Calculate the MACCS Molecular Fingerprints (in Complete Format)

**Usage**

```
extractDrugMACCSComplete(molecules, silent = TRUE)
```

**Arguments**

<code>molecules</code>	Parsed molecule object.
<code>silent</code>	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

The popular 166 bit MACCS keys described by MDL.

**Value**

An integer vector or a matrix. Each row represents one molecule, the columns represent the fingerprints.

**See Also**

[extractDrugMACCS](#)

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugMACCSComplete(mol)  
dim(fp)
```

---

extractDrugMannholdLogP

*Descriptor that Calculates the LogP Based on a Simple Equation Using the Number of Carbons and Hetero Atoms*

---

## Description

Descriptor that Calculates the LogP Based on a Simple Equation Using the Number of Carbons and Hetero Atoms

## Usage

```
extractDrugMannholdLogP(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

This descriptor calculates the LogP based on a simple equation using the number of carbons and hetero atoms. The implemented equation was proposed in Mannhold et al.

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named MLogP.

## References

Mannhold, R., Poda, G. I., Ostermann, C., & Tetko, I. V. (2009). Calculation of molecular lipophilicity: State-of-the-art and comparison of log P methods on more than 96,000 compounds. *Journal of pharmaceutical sciences*, 98(3), 861-893.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugMannholdLogP(mol)  
head(dat)
```

---

extractDrugMDE	<i>Calculate Molecular Distance Edge (MDE) Descriptors for C, N and O</i>
----------------	---

---

### Description

Calculate Molecular Distance Edge (MDE) Descriptors for C, N and O

### Usage

```
extractDrugMDE(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

This descriptor calculates the 10 molecular distance edge (MDE) descriptor described in Liu, S., Cao, C., & Li, Z, and in addition it calculates variants where O and N are considered.

### Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nAtomLAC.

### References

Liu, S., Cao, C., & Li, Z. (1998). Approach to estimation and prediction for normal boiling point (NBP) of alkanes based on a novel molecular distance-edge (MDE) vector, lambda. *Journal of chemical information and computer sciences*, 38(3), 387-394.

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugMDE(mol)  
head(dat)
```

---

extractDrugMomentOfInertia

*Descriptor that Calculates the Principal Moments of Inertia and Ratios of the Principal Moments*

---

## Description

Descriptor that Calculates the Principal Moments of Inertia and Ratios of the Principal Moments

## Usage

```
extractDrugMomentOfInertia(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

A descriptor that calculates the moment of inertia and radius of gyration. Moment of inertia (MI) values characterize the mass distribution of a molecule. Related to the MI values, ratios of the MI values along the three principal axes are also well know modeling variables. This descriptor calculates the MI values along the X, Y and Z axes as well as the ratio's X/Y, X/Z and Y/Z. Finally it also calculates the radius of gyration of the molecule.

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 7 columns named MOMI.X, MOMI.Y, MOMI.Z, MOMI.XY, MOMI.XZ, MOMI.YZ, MOMI.R:

- MOMI.X - MI along X axis
- MOMI.Y - MI along Y axis
- MOMI.Z - MI along Z axis
- MOMI.XY - X/Y
- MOMI.XZ - X/Z
- MOMI.YZ - Y/Z
- MOMI.R - Radius of gyration

One important aspect of the algorithm is that if the eigenvalues of the MI tensor are below  $1e-3$ , then the ratio's are set to a default of 1000.

**Examples**

```
sdf = system.file('sysdata/OptAA3d.sdf', package = 'Rcpi')

mol = readMolFromSDF(sdf)
dat = extractDrugMomentOfInertia(mol)
head(dat)
```

---

extractDrugOBFP2	<i>Calculate the FP2 Molecular Fingerprints</i>
------------------	---

---

**Description**

Calculate the FP2 Molecular Fingerprints

**Usage**

```
extractDrugOBFP2(molecules, type = c("smile", "sdf"))
```

**Arguments**

molecules	R character string object containing the molecules. See the example section for details.
type	'smile' or 'sdf'.

**Details**

Calculate the 1024 bit FP2 fingerprints provided by OpenBabel.

**Value**

A matrix. Each row represents one molecule, the columns represent the fingerprints.

**Examples**

```
mol1 = 'C1CCC1CC(CN(C)(C))CC(=O)CC' # one molecule SMILE in a vector
mol2 = c('CCC', 'CCN', 'CCN(C)(C)', 'c1ccccc1Cc1ccccc1',
        'C1CCC1CC(CN(C)(C))CC(=O)CC') # multiple SMILES in a vector
mol3 = readChar(system.file('compseq/DB00860.sdf', package = 'Rcpi'),
                nchars = 1e+6) # single molecule in a sdf file
mol4 = readChar(system.file('sysdata/OptAA3d.sdf', package = 'Rcpi'),
                nchars = 1e+6) # multiple molecules in a sdf file

## Not run:
smifp0 = extractDrugOBFP2(mol1, type = 'smile')
smifp1 = extractDrugOBFP2(mol2, type = 'smile')
sdfp0 = extractDrugOBFP2(mol3, type = 'sdf')
sdfp1 = extractDrugOBFP2(mol4, type = 'sdf')
## End(Not run)
```

---

extractDrugOBFP3      *Calculate the FP3 Molecular Fingerprints*

---

### Description

Calculate the FP3 Molecular Fingerprints

### Usage

```
extractDrugOBFP3(molecules, type = c("smile", "sdf"))
```

### Arguments

molecules	R character string object containing the molecules. See the example section for details.
type	'smile' or 'sdf'.

### Details

Calculate the 64 bit FP3 fingerprints provided by OpenBabel.

### Value

A matrix. Each row represents one molecule, the columns represent the fingerprints.

### Examples

```
mol1 = 'C1CCC1CC(CN(C)(C))CC(=O)CC' # one molecule SMILE in a vector
mol2 = c('CCC', 'CCN', 'CCN(C)(C)', 'c1ccccc1Cc1ccccc1',
        'C1CCC1CC(CN(C)(C))CC(=O)CC') # multiple SMILES in a vector
mol3 = readChar(system.file('compseq/DB00860.sdf', package = 'Rcpi'),
                nchars = 1e+6) # single molecule in a sdf file
mol4 = readChar(system.file('sysdata/OptAA3d.sdf', package = 'Rcpi'),
                nchars = 1e+6) # multiple molecules in a sdf file

## Not run:
smifp0 = extractDrugOBFP3(mol1, type = 'smile')
smifp1 = extractDrugOBFP3(mol2, type = 'smile')
sdffp0 = extractDrugOBFP3(mol3, type = 'sdf')
sdffp1 = extractDrugOBFP3(mol4, type = 'sdf')
## End(Not run)
```



---

extractDrugOBFP4      *Calculate the FP4 Molecular Fingerprints*

---

## Description

Calculate the FP4 Molecular Fingerprints

## Usage

```
extractDrugOBFP4(molecules, type = c("smile", "sdf"))
```

## Arguments

molecules	R character string object containing the molecules. See the example section for details.
type	'smile' or 'sdf'.

## Details

Calculate the 512 bit FP4 fingerprints provided by OpenBabel.

## Value

A matrix. Each row represents one molecule, the columns represent the fingerprints.

## Examples

```
mol1 = 'C1CCC1CC(CN(C)(C))CC(=O)CC' # one molecule SMILE in a vector
mol2 = c('CCC', 'CCN', 'CCN(C)(C)', 'c1ccccc1Cc1ccccc1',
        'C1CCC1CC(CN(C)(C))CC(=O)CC') # multiple SMILES in a vector
mol3 = readChar(system.file('compseq/DB00860.sdf', package = 'Rcpi'),
                nchars = 1e+6) # single molecule in a sdf file
mol4 = readChar(system.file('sysdata/OptAA3d.sdf', package = 'Rcpi'),
                nchars = 1e+6) # multiple molecules in a sdf file

## Not run:
smifp0 = extractDrugOBFP4(mol1, type = 'smile')
smifp1 = extractDrugOBFP4(mol2, type = 'smile')
sdfp0 = extractDrugOBFP4(mol3, type = 'sdf')
sdfp1 = extractDrugOBFP4(mol4, type = 'sdf')
## End(Not run)
```

---

extractDrugOBMACCS      *Calculate the MACCS Molecular Fingerprints*

---

### Description

Calculate the MACCS Molecular Fingerprints

### Usage

```
extractDrugOBMACCS(molecules, type = c("smile", "sdf"))
```

### Arguments

molecules	R character string object containing the molecules. See the example section for details.
type	'smile' or 'sdf'.

### Details

Calculate the 256 bit MACCS fingerprints provided by OpenBabel.

### Value

A matrix. Each row represents one molecule, the columns represent the fingerprints.

### Examples

```
mol1 = 'C1CCC1CC(CN(C)(C))CC(=O)CC' # one molecule SMILE in a vector
mol2 = c('CCC', 'CCN', 'CCN(C)(C)', 'c1ccccc1Cc1ccccc1',
        'C1CCC1CC(CN(C)(C))CC(=O)CC') # multiple SMILES in a vector
mol3 = readChar(system.file('compseq/DB00860.sdf', package = 'Rcpi'),
               nchars = 1e+6) # single molecule in a sdf file
mol4 = readChar(system.file('sysdata/OptAA3d.sdf', package = 'Rcpi'),
               nchars = 1e+6) # multiple molecules in a sdf file

## Not run:
# MACCS may not be available in current version of ChemmineOB
smifp0 = extractDrugOBMACCS(mol1, type = 'smile')
smifp1 = extractDrugOBMACCS(mol2, type = 'smile')
sdffp0 = extractDrugOBMACCS(mol3, type = 'sdf')
sdffp1 = extractDrugOBMACCS(mol4, type = 'sdf')
## End(Not run)
```

---

`extractDrugPetitjeanNumber`*Descriptor that Calculates the Petitjean Number of a Molecule*

---

## Description

Descriptor that Calculates the Petitjean Number of a Molecule

## Usage

```
extractDrugPetitjeanNumber(molecules, silent = TRUE)
```

## Arguments

<code>molecules</code>	Parsed molecule object.
<code>silent</code>	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

This descriptor calculates the Petitjean number of a molecule. According to the Petitjean definition, the eccentricity of a vertex corresponds to the distance from that vertex to the most remote vertex in the graph.

The distance is obtained from the distance matrix as the count of edges between the two vertices. If  $r(i)$  is the largest matrix entry in row  $i$  of the distance matrix  $D$ , then the radius is defined as the smallest of the  $r(i)$ . The graph diameter  $D$  is defined as the largest vertex eccentricity in the graph. (<http://www.edusoft-lc.com/molconn/manuals/400/chaptwo.html>)

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named `PetitjeanNumber`.

## Examples

```
smi = system.file('vignettedata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugPetitjeanNumber(mol)  
head(dat)
```

---

`extractDrugPetitjeanShapeIndex`*Descriptor that Calculates the Petitjean Shape Indices*

---

**Description**

Descriptor that Calculates the Petitjean Shape Indices

**Usage**

```
extractDrugPetitjeanShapeIndex(molecules, silent = TRUE)
```

**Arguments**

<code>molecules</code>	Parsed molecule object.
<code>silent</code>	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

The topological and geometric shape indices described Petitjean and Bath et al. respectively. Both measure the anisotropy in a molecule.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns two columns named `topoShape` (Topological Shape Index) and `geomShape` (Geometric Shape Index).

**References**

Petitjean, M., Applications of the radius-diameter diagram to the classification of topological and geometrical shapes of chemical compounds, *Journal of Chemical Information and Computer Science*, 1992, 32:331-337

Bath, P.A. and Poirette, A.R. and Willet, P. and Allen, F.H. , The Extent of the Relationship between the Graph-Theoretical and the Geometrical Shape Coefficients of Chemical Compounds, *Journal of Chemical Information and Computer Science*, 1995, 35:714-716.

**Examples**

```
sdf = system.file('sysdata/OptAA3d.sdf', package = 'Rcpi')  
  
mol = readMolFromSDF(sdf)  
dat = extractDrugPetitjeanShapeIndex(mol)  
head(dat)
```

---

extractDrugPubChem     *Calculate the PubChem Molecular Fingerprints (in Compact Format)*

---

### Description

Calculate the PubChem Molecular Fingerprints (in Compact Format)

### Usage

```
extractDrugPubChem(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Calculate the 881 bit fingerprints defined by PubChem.

### Value

A list, each component represents one of the molecules, each element in the component represents the index of which element in the fingerprint is 1. Each component's name is the length of the fingerprints.

### See Also

[extractDrugPubChemComplete](#)

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugPubChem(mol)  
head(fp)
```

---

`extractDrugPubChemComplete`*Calculate the PubChem Molecular Fingerprints (in Complete Format)*

---

### Description

Calculate the PubChem Molecular Fingerprints (in Complete Format)

### Usage

```
extractDrugPubChemComplete(molecules, silent = TRUE)
```

### Arguments

<code>molecules</code>	Parsed molecule object.
<code>silent</code>	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

Calculate the 881 bit fingerprints defined by PubChem.

### Value

An integer vector or a matrix. Each row represents one molecule, the columns represent the fingerprints.

### See Also

[extractDrugPubChem](#)

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugPubChemComplete(mol)  
dim(fp)
```

---

extractDrugRotatableBondsCount

*Descriptor that Calculates the Number of Nonrotatable Bonds on A Molecule*

---

### Description

Descriptor that Calculates the Number of Nonrotatable Bonds on A Molecule

### Usage

```
extractDrugRotatableBondsCount(molecules, silent = TRUE)
```

### Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

### Details

The number of rotatable bonds is given by the SMARTS specified by Daylight on SMARTS tutorial ([https://www.daylight.com/dayhtml\\_tutorials/languages/smarts/smarts\\_examples.html](https://www.daylight.com/dayhtml_tutorials/languages/smarts/smarts_examples.html))

### Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named nRotB.

### Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugRotatableBondsCount(mol)  
head(dat)
```

---

extractDrugRuleOfFive *Descriptor that Calculates the Number Failures of the Lipinski's Rule Of Five*

---

### Description

Descriptor that Calculates the Number Failures of the Lipinski's Rule Of Five

**Usage**

```
extractDrugRuleOfFive(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

This descriptor calculates the number failures of the Lipinski's Rule Of Five: [http://en.wikipedia.org/wiki/Lipinski%27s\\_Rule\\_of\\_Five](http://en.wikipedia.org/wiki/Lipinski%27s_Rule_of_Five).

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named LipinskiFailures.

**Examples**

```
smi = system.file('vignettedata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugRuleOfFive(mol)  
head(dat)
```

---

extractDrugShortestPath

*Calculate the Shortest Path Molecular Fingerprints (in Compact Format)*

---

**Description**

Calculate the Shortest Path Molecular Fingerprints (in Compact Format)

**Usage**

```
extractDrugShortestPath(molecules, depth = 6, size = 1024, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
depth	The search depth. Default is 6.
size	The length of the fingerprint bit string. Default is 1024.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.



**Details**

Calculate the fingerprint based on the shortest paths between pairs of atoms and takes into account ring systems, charges etc.

**Value**

A list, each component represents one of the molecules, each element in the component represents the index of which element in the fingerprint is 1. Each component's name is the length of the fingerprints.

**See Also**

[extractDrugShortestPathComplete](#)

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugShortestPath(mol)  
head(fp)
```

---

extractDrugShortestPathComplete

*Calculate the Shortest Path Molecular Fingerprints (in Complete Format)*

---

**Description**

Calculate the Shortest Path Molecular Fingerprints (in Complete Format)

**Usage**

```
extractDrugShortestPathComplete(  
  molecules,  
  depth = 6,  
  size = 1024,  
  silent = TRUE  
)
```

**Arguments**

molecules	Parsed molecule object.
depth	The search depth. Default is 6.
size	The length of the fingerprint bit string. Default is 1024.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculate the fingerprint based on the shortest paths between pairs of atoms and takes into account ring systems, charges etc.

**Value**

An integer vector or a matrix. Each row represents one molecule, the columns represent the fingerprints.

**See Also**

[extractDrugShortestPath](#)

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugShortestPathComplete(mol)  
dim(fp)
```

---

extractDrugStandard     *Calculate the Standard Molecular Fingerprints (in Compact Format)*

---

**Description**

Calculate the Standard Molecular Fingerprints (in Compact Format)

**Usage**

```
extractDrugStandard(molecules, depth = 6, size = 1024, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
depth	The search depth. Default is 6.
size	The length of the fingerprint bit string. Default is 1024.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculate the standard molecular fingerprints. Considers paths of a given length. This is hashed fingerprints, with a default length of 1024.

**Value**

A list, each component represents one of the molecules, each element in the component represents the index of which element in the fingerprint is 1. Each component's name is the length of the fingerprints.

**See Also**

[extractDrugStandardComplete](#)

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
fp = extractDrugStandard(mol)  
head(fp)
```

---

extractDrugStandardComplete

*Calculate the Standard Molecular Fingerprints (in Complete Format)*

---

**Description**

Calculate the Standard Molecular Fingerprints (in Complete Format)

**Usage**

```
extractDrugStandardComplete(molecules, depth = 6, size = 1024, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
depth	The search depth. Default is 6.
size	The length of the fingerprint bit string. Default is 1024.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculate the standard molecular fingerprints. Considers paths of a given length. This is hashed fingerprints, with a default length of 1024.

**Value**

An integer vector or a matrix. Each row represents one molecule, the columns represent the fingerprints.

**See Also**[extractDrugStandard](#)**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
fp = extractDrugStandardComplete(mol)
dim(fp)
```

---

extractDrugTPSA	<i>Descriptor of Topological Polar Surface Area Based on Fragment Contributions (TPSA)</i>
-----------------	--

---

**Description**

Descriptor of Topological Polar Surface Area Based on Fragment Contributions (TPSA)

**Usage**

```
extractDrugTPSA(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Calculate the descriptor of topological polar surface area based on fragment contributions (TPSA).

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named TopoPSA.

**References**

Ertl, P., Rohde, B., & Selzer, P. (2000). Fast calculation of molecular polar surface area as a sum of fragment-based contributions and its application to the prediction of drug transport properties. *Journal of medicinal chemistry*, 43(20), 3714-3717.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugTPSA(mol)
head(dat)
```

---

extractDrugVABC	<i>Descriptor that Calculates the Volume of A Molecule</i>
-----------------	--

---

**Description**

Descriptor that Calculates the Volume of A Molecule

**Usage**

```
extractDrugVABC(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

This descriptor calculates the volume of a molecule.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named VABC.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugVABC(mol)
head(dat)
```

---

extractDrugVAdjMa	<i>Descriptor that Calculates the Vertex Adjacency Information of A Molecule</i>
-------------------	--

---

**Description**

Descriptor that Calculates the Vertex Adjacency Information of A Molecule

**Usage**

```
extractDrugVAdjMa(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Vertex adjacency information (magnitude):  $1 + \log_2^m$  where  $m$  is the number of heavy-heavy bonds. If  $m$  is zero, then  $\emptyset$  is returned.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named VAdjMat.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugVAdjMa(mol)  
head(dat)
```

---

extractDrugWeight	<i>Descriptor that Calculates the Total Weight of Atoms</i>
-------------------	---

---

**Description**

Descriptor that Calculates the Total Weight of Atoms

**Usage**

```
extractDrugWeight(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

This descriptor calculates the molecular weight.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named MW.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugWeight(mol)  
head(dat)
```

---

extractDrugWeightedPath

*Descriptor that Calculates the Weighted Path (Molecular ID)*

---

**Description**

Descriptor that Calculates the Weighted Path (Molecular ID)

**Usage**

```
extractDrugWeightedPath(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

This descriptor calculates the weighted path (molecular ID) described by Randic, characterizing molecular branching. Five descriptors are calculated, based on the implementation in the ADAPT software package. Note that the descriptor is based on identifying all paths between pairs of atoms and so is NP-hard. This means that it can take some time for large, complex molecules.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 5 columns named WTPT.1, WTPT.2, WTPT.3, WTPT.4, WTPT.5:

- WTPT.1 - molecular ID
- WTPT.2 - molecular ID / number of atoms
- WTPT.3 - sum of path lengths starting from heteroatoms
- WTPT.4 - sum of path lengths starting from oxygens
- WTPT.5 - sum of path lengths starting from nitrogens

**References**

Randic, M., On molecular identification numbers (1984). *Journal of Chemical Information and Computer Science*, 24:164-175.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugWeightedPath(mol)  
head(dat)
```

---

extractDrugWHIM

*Calculate Holistic Descriptors Described by Todeschini et al.*

---

**Description**

Calculate Holistic Descriptors Described by Todeschini et al.

**Usage**

```
extractDrugWHIM(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.



## Details

Holistic descriptors described by Todeschini et al, the descriptors are based on a number of atom weightings. There are six different possible weightings:

- unit weights
- atomic masses
- van der Waals volumes
- Mulliken atomic electronegativities
- atomic polarizabilities
- E-state values described by Kier and Hall

Currently weighting schemes 1, 2, 3, 4 and 5 are implemented. The weight values are taken from Todeschini et al. and as a result 19 elements are considered. For each weighting scheme we can obtain

- 11 directional WHIM descriptors ( $\lambda_1 \dots \lambda_3$ ,  $\nu_1 \dots \nu_2$ ,  $\gamma_1 \dots \gamma_3$ ,  $\epsilon_1 \dots \epsilon_3$ )
- 6 non-directional WHIM descriptors (T, A, V, K, G, D)

Though Todeschini et al. mentions that for planar molecules only 8 directional WHIM descriptors are required the current code will return all 11.

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns 17 columns:

- Wlambda1
- Wlambda2
- wlambda3
- Wnu1
- Wnu2
- Wgamma1
- Wgamma2
- Wgamma3
- Weta1
- Weta2
- Weta3
- WT
- WA
- WV
- WK
- WG
- WD

Each name will have a suffix of the form .X where X indicates the weighting scheme used. Possible values of X are

- unity
- mass
- volume
- eneg
- polar

## References

Todeschini, R. and Gramatica, P., New 3D Molecular Descriptors: The WHIM theory and QAR Applications, *Persepectives in Drug Discovery and Design*, 1998, ?:355-380.

## Examples

```
sdf = system.file('sysdata/0ptAA3d.sdf', package = 'Rcpi')  
  
mol = readMolFromSDF(sdf)  
dat = extractDrugWHIM(mol)  
head(dat)
```

---

extractDrugWienerNumbers

*Descriptor that Calculates Wiener Path Number and Wiener Polarity Number*

---

## Description

Descriptor that Calculates Wiener Path Number and Wiener Polarity Number

## Usage

```
extractDrugWienerNumbers(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

This descriptor calculates the Wiener numbers, including the Wiener Path number and the Wiener Polarity Number. Wiener path number: half the sum of all the distance matrix entries; Wiener polarity number: half the sum of all the distance matrix entries with a value of 3.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns two columns named WPATH (weiner path number) and WPOL (weiner polarity number).

**References**

Wiener, H. (1947). Structural determination of paraffin boiling points. Journal of the American Chemical Society, 69(1), 17-20.

**Examples**

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol = readMolFromSmi(smi, type = 'mol')  
dat = extractDrugWienerNumbers(mol)  
head(dat)
```

---

extractDrugXLogP	<i>Descriptor that Calculates the Prediction of logP Based on the Atom-Type Method Called XLogP</i>
------------------	---

---

**Description**

Descriptor that Calculates the Prediction of logP Based on the Atom-Type Method Called XLogP

**Usage**

```
extractDrugXLogP(molecules, silent = TRUE)
```

**Arguments**

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

**Details**

Prediction of logP based on the atom-type method called XLogP.

**Value**

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named XLogP.

## References

Wang, R., Fu, Y., and Lai, L., A New Atom-Additive Method for Calculating Partition Coefficients, Journal of Chemical Information and Computer Sciences, 1997, 37:615-621.

Wang, R., Gao, Y., and Lai, L., Calculating partition coefficient by atom-additive method, Perspectives in Drug Discovery and Design, 2000, 19:47-66.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugXLogP(mol)
head(dat)
```

---

extractDrugZagrebIndex

*Descriptor that Calculates the Sum of the Squared Atom Degrees of All Heavy Atoms*

---

## Description

Descriptor that Calculates the Sum of the Squared Atom Degrees of All Heavy Atoms

## Usage

```
extractDrugZagrebIndex(molecules, silent = TRUE)
```

## Arguments

molecules	Parsed molecule object.
silent	Logical. Whether the calculating process should be shown or not, default is TRUE.

## Details

Zagreb index: the sum of the squares of atom degree over all heavy atoms  $i$ .

## Value

A data frame, each row represents one of the molecules, each column represents one feature. This function returns one column named Zagreb.

## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')

mol = readMolFromSmi(smi, type = 'mol')
dat = extractDrugZagrebIndex(mol)
head(dat)
```

---

extractPCMBLOSUM      *Generalized BLOSUM and PAM Matrix-Derived Descriptors*

---

**Description**

Generalized BLOSUM and PAM Matrix-Derived Descriptors

**Usage**

```
extractPCMBLOSUM(x, submat = "AABLOSUM62", k, lag, scale = TRUE, silent = TRUE)
```

**Arguments**

x	A character vector, as the input protein sequence.
submat	Substitution matrix for the 20 amino acids. Should be one of AABLOSUM45, AABLOSUM50, AABLOSUM62, AABLOSUM80, AABLOSUM100, AAPAM30, AAPAM40, AAPAM70, AAPAM120, AAPAM250. Default is 'AABLOSUM62'.
k	Integer. The number of selected scales (i.e. the first k scales) derived by the substitution matrix. This could be selected according to the printed relative importance values.
lag	The lag parameter. Must be less than the amino acids.
scale	Logical. Should we auto-scale the substitution matrix (submat) before doing eigen decomposition? Default is TRUE.
silent	Logical. Whether we print the relative importance of each scales (diagonal value of the eigen decomposition result matrix B) or not. Default is TRUE.

**Details**

This function calculates the generalized BLOSUM matrix-derived descriptors. For users' convenience, Rcp*i* provides the BLOSUM45, BLOSUM50, BLOSUM62, BLOSUM80, BLOSUM100, PAM30, PAM40, PAM70, PAM120, and PAM250 matrices for the 20 amino acids to select.

**Value**

A length  $\text{lag} * p^2$  named vector, p is the number of scales selected.

**References**

Georgiev, A. G. (2009). Interpretable numerical descriptors of amino acid space. *Journal of Computational Biology*, 16(5), 703–723.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
blosum = extractPCMBLOSUM(x, submat = 'AABLOSUM62', k = 5, lag = 7, scale = TRUE, silent = FALSE)
```

---

extractPCMDescScales *Scales-Based Descriptors with 20+ classes of Molecular Descriptors*

---

## Description

Scales-Based Descriptors with 20+ classes of Molecular Descriptors

## Usage

```
extractPCMDescScales(
  x,
  propmat,
  index = NULL,
  pc,
  lag,
  scale = TRUE,
  silent = TRUE
)
```

## Arguments

x	A character vector, as the input protein sequence.
propmat	The matrix containing the descriptor set for the amino acids, which could be chosen from AAMOE2D, AAMOE3D, AACPSA, AADescAll, AA2DACOR, AA3DMORSE, AAACF, AABurden, AACConn, AACConst, AAEdgeAdj, AAeigIdx, AAFGC, AAGeom, AAGETAWAY, AAInfo, AAMolProp, AARandic, AARDF, AATopo, AATopoChg, AAWalk, AAWHIM.
index	Integer vector or character vector. Specify which molecular descriptors to select from one of these descriptor sets by specify the numerical or character index of the molecular descriptors in the descriptor set. Default is NULL, means selecting all the molecular descriptors in this descriptor set.
pc	Integer. The maximum dimension of the space which the data are to be represented in. Must be no greater than the number of AA properties provided.
lag	The lag parameter. Must be less than the amino acids.
scale	Logical. Should we auto-scale the property matrix (propmat) before doing MDS? Default is TRUE.
silent	Logical. Whether we print the standard deviation, proportion of variance and the cumulative proportion of the selected principal components or not. Default is TRUE.

## Details

This function calculates the scales-based descriptors with molecular descriptors sets calculated by Dragon, Discovery Studio and MOE. Users could specify which molecular descriptors to select from one of these descriptor sets by specify the numerical or character index of the molecular descriptors in the descriptor set.

**Value**

A length  $\text{lag} * p^2$  named vector,  $p$  is the number of scales selected.

**See Also**

See [extractPCMScales](#) for generalized AA-descriptor based scales descriptors.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
descscales = extractPCMDescScales(x, propmat = 'AATopo', index = c(37:41, 43:47),
                                  pc = 5, lag = 7, silent = FALSE)
```

---

extractPCMFAScales      *Generalized Scales-Based Descriptors derived by Factor Analysis*

---

**Description**

Generalized Scales-Based Descriptors derived by Factor Analysis

**Usage**

```
extractPCMFAScales(
  x,
  propmat,
  factors,
  scores = "regression",
  lag,
  scale = TRUE,
  silent = TRUE
)
```

**Arguments**

x	A character vector, as the input protein sequence.
propmat	A matrix containing the properties for the amino acids. Each row represent one amino acid type, each column represents one property. Note that the one-letter row names must be provided for we need them to seek the properties for each AA type.
factors	Integer. The number of factors to be fitted. Must be no greater than the number of AA properties provided.
scores	Type of scores to produce. The default is "regression", which gives Thompson's scores, "Bartlett" given Bartlett's weighted least-squares scores.
lag	The lag parameter. Must be less than the amino acids number in the protein sequence.

scale	Logical. Should we auto-scale the property matrix (propmat) before doing Factor Analysis? Default is TRUE.
silent	Logical. Whether we print the SS loadings, proportion of variance and the cumulative proportion of the selected factors or not. Default is TRUE.

### Details

This function calculates the generalized scales-based descriptors derived by Factor Analysis (FA). Users could provide customized amino acid property matrices.

### Value

A length  $\text{lag} * p^2$  named vector,  $p$  is the number of scales (factors) selected.

### References

Atchley, W. R., Zhao, J., Fernandes, A. D., & Druke, T. (2005). Solving the protein sequence metric problem. *Proceedings of the National Academy of Sciences of the United States of America*, 102(18), 6395-6400.

### Examples

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
data(AATopo)
tprops = AATopo[, c(37:41, 43:47)] # select a set of topological descriptors
fa = extractPCMFAScales(x, propmat = tprops, factors = 5, lag = 7, silent = FALSE)
```

---

extractPCMMDScales	<i>Generalized Scales-Based Descriptors derived by Multidimensional Scaling</i>
--------------------	---

---

### Description

Generalized Scales-Based Descriptors derived by Multidimensional Scaling

### Usage

```
extractPCMMDScales(x, propmat, k, lag, scale = TRUE, silent = TRUE)
```

### Arguments

x	A character vector, as the input protein sequence.
propmat	A matrix containing the properties for the amino acids. Each row represent one amino acid type, each column represents one property. Note that the one-letter row names must be provided for we need them to seek the properties for each AA type.



k	Integer. The maximum dimension of the space which the data are to be represented in. Must be no greater than the number of AA properties provided.
lag	The lag parameter. Must be less than the amino acids.
scale	Logical. Should we auto-scale the property matrix (propmat) before doing MDS? Default is TRUE.
silent	Logical. Whether we print the k eigenvalues computed during the scaling process or not. Default is TRUE.

### Details

This function calculates the generalized scales-based descriptors derived by Multidimensional Scaling (MDS). Users could provide customized amino acid property matrices.

### Value

A length  $lag * p^2$  named vector, p is the number of scales (dimensionality) selected.

### References

Venkatarajan, M. S., & Braun, W. (2001). New quantitative descriptors of amino acids based on multidimensional scaling of a large number of physical-chemical properties. *Molecular modeling annual*, 7(12), 445–453.

### See Also

See [extractPCMScales](#) for generalized scales-based descriptors derived by Principal Components Analysis.

### Examples

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
data(AATopo)
tprops = AATopo[, c(37:41, 43:47)] # select a set of topological descriptors
mds = extractPCMMDScales(x, propmat = tprops, k = 5, lag = 7, silent = FALSE)
```

---

extractPCMPPropScales *Generalized AA-Properties Based Scales Descriptors*

---

### Description

Generalized AA-Properties Based Scales Descriptors

### Usage

```
extractPCMPPropScales(x, index = NULL, pc, lag, scale = TRUE, silent = TRUE)
```

**Arguments**

x	A character vector, as the input protein sequence.
index	Integer vector or character vector. Specify which AAindex properties to select from the AAindex database by specify the numerical or character index of the properties in the AAindex database. Default is NULL, means selecting all the AA properties in the AAindex database.
pc	Integer. Use the first pc principal components as the scales. Must be no greater than the number of AA properties provided.
lag	The lag parameter. Must be less than the amino acids.
scale	Logical. Should we auto-scale the property matrix before PCA? Default is TRUE.
silent	Logical. Whether we print the standard deviation, proportion of variance and the cumulative proportion of the selected principal components or not. Default is TRUE.

**Details**

This function calculates the generalized amino acid properties based scales descriptors. Users could specify which AAindex properties to select from the AAindex database by specify the numerical or character index of the properties in the AAindex database.

**Value**

A length  $\text{lag} * p^2$  named vector, p is the number of scales (principal components) selected.

**See Also**

See [extractPCMScales](#) for generalized scales-based descriptors.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
propscales = extractPCMPPropScales(x, index = c(160:165, 258:296), pc = 5, lag = 7, silent = FALSE)
```

---

extractPCMScales	<i>Generalized Scales-Based Descriptors derived by Principal Components Analysis</i>
------------------	--

---

**Description**

Generalized Scales-Based Descriptors derived by Principal Components Analysis

**Usage**

```
extractPCMScales(x, propmat, pc, lag, scale = TRUE, silent = TRUE)
```

## Arguments

x	A character vector, as the input protein sequence.
propmat	A matrix containing the properties for the amino acids. Each row represent one amino acid type, each column represents one property. Note that the one-letter row names must be provided for we need them to seek the properties for each AA type.
pc	Integer. Use the first pc principal components as the scales. Must be no greater than the number of AA properties provided.
lag	The lag parameter. Must be less than the amino acids.
scale	Logical. Should we auto-scale the property matrix (propmat) before PCA? Default is TRUE.
silent	Logical. Whether we print the standard deviation, proportion of variance and the cumulative proportion of the selected principal components or not. Default is TRUE.

## Details

This function calculates the generalized scales-based descriptors derived by Principal Components Analysis (PCA). Users could provide customized amino acid property matrices. This function implements the core computation procedure needed for the generalized scales-based descriptors derived by AA-Properties (AAindex) and generalized scales-based descriptors derived by 20+ classes of 2D and 3D molecular descriptors (Topological, WHIM, VHSE, etc.).

## Value

A length  $\text{lag} * p^2$  named vector, p is the number of scales (principal components) selected.

## See Also

See [extractPCMDescScales](#) for generalized AA property based scales descriptors, and [extractPCMPPropScales](#) for (19 classes) AA descriptor based scales descriptors.

## Examples

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
data(AAindex)
AAidxmat = t(na.omit(as.matrix(AAindex[, 7:26])))
scales = extractPCMScales(x, propmat = AAidxmat, pc = 5, lag = 7, silent = FALSE)
```

---

extractProtAAC	<i>Amino Acid Composition Descriptor</i>
----------------	--

---

**Description**

Amino Acid Composition Descriptor

**Usage**

```
extractProtAAC(x)
```

**Arguments**

x                    A character vector, as the input protein sequence.

**Details**

This function calculates the Amino Acid Composition descriptor (Dim: 20).

**Value**

A length 20 named vector

**References**

M. Bhasin, G. P. S. Raghava. Classification of Nuclear Receptors Based on Amino Acid Composition and Dipeptide Composition. *Journal of Biological Chemistry*, 2004, 279, 23262.

**See Also**

See [extractProtDC](#) and [extractProtTC](#) for Dipeptide Composition and Tripeptide Composition descriptors.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtAAC(x)
```

---

extractProtAPAAC      *Amphiphilic Pseudo Amino Acid Composition Descriptor*

---

## Description

Amphiphilic Pseudo Amino Acid Composition Descriptor

## Usage

```
extractProtAPAAC(
  x,
  props = c("Hydrophobicity", "Hydrophilicity"),
  lambda = 30,
  w = 0.05,
  customprops = NULL
)
```

## Arguments

x	A character vector, as the input protein sequence.
props	A character vector, specifying the properties used. 2 properties are used by default, as listed below: 'Hydrophobicity' Hydrophobicity value of the 20 amino acids 'Hydrophilicity' Hydrophilicity value of the 20 amino acids
lambda	The lambda parameter for the APAAC descriptors, default is 30.
w	The weighting factor, default is 0.05.
customprops	A n x 21 named data frame contains n customize property. Each row contains one property. The column order for different amino acid types is 'AccNo', 'A', 'R', 'N', 'D', 'C', 'E', 'Q', 'G', 'H', 'I', 'L', 'K', 'M', 'F', 'P', 'S', 'T', 'W', 'Y', 'V', and the columns should also be <i>exactly</i> named like this. The AccNo column contains the properties' names. Then users should explicitly specify these properties with these names in the argument props. See the examples below for a demonstration. The default value for customprops is NULL.

## Details

This function calculates the Amphiphilic Pseudo Amino Acid Composition (APAAC) descriptor (Dim:  $20 + (n * \text{lambda})$ , n is the number of properties selected, default is 80).

## Value

A length  $20 + n * \text{lambda}$  named vector, n is the number of properties selected.



---

extractProtCTDC	<i>CTD Descriptors - Composition</i>
-----------------	--------------------------------------

---

**Description**

CTD Descriptors - Composition

**Usage**

```
extractProtCTDC(x)
```

**Arguments**

x                    A character vector, as the input protein sequence.

**Details**

This function calculates the Composition descriptor of the CTD descriptors (Dim: 21).

**Value**

A length 21 named vector

**References**

Inna Dubchak, Ilya Muchink, Stephen R. Holbrook and Sung-Hou Kim. Prediction of protein folding class using global description of amino acid sequence. *Proceedings of the National Academy of Sciences*. USA, 1995, 92, 8700-8704.

Inna Dubchak, Ilya Muchink, Christopher Mayor, Igor Dralyuk and Sung-Hou Kim. Recognition of a Protein Fold in the Context of the SCOP classification. *Proteins: Structure, Function and Genetics*, 1999, 35, 401-407.

**See Also**

See [extractProtCTDT](#) and [extractProtCTDD](#) for the Transition and Distribution descriptors.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtCTDC(x)
```

---

extractProtCTDD      *CTD Descriptors - Distribution*

---

### Description

CTD Descriptors - Distribution

### Usage

```
extractProtCTDD(x)
```

### Arguments

x                      A character vector, as the input protein sequence.

### Details

This function calculates the Distribution descriptor of the CTD descriptors (Dim: 105).

### Value

A length 105 named vector

### References

Inna Dubchak, Ilya Muchink, Stephen R. Holbrook and Sung-Hou Kim. Prediction of protein folding class using global description of amino acid sequence. *Proceedings of the National Academy of Sciences*. USA, 1995, 92, 8700-8704.

Inna Dubchak, Ilya Muchink, Christopher Mayor, Igor Dralyuk and Sung-Hou Kim. Recognition of a Protein Fold in the Context of the SCOP classification. *Proteins: Structure, Function and Genetics*, 1999, 35, 401-407.

### See Also

See [extractProtCTDC](#) and [extractProtCTDT](#) for the Composition and Transition descriptors.

### Examples

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtCTDD(x)
```



---

extractProtCTDT	<i>CTD Descriptors - Transition</i>
-----------------	-------------------------------------

---

**Description**

CTD Descriptors - Transition

**Usage**

```
extractProtCTDT(x)
```

**Arguments**

x                    A character vector, as the input protein sequence.

**Details**

This function calculates the Transition descriptor of the CTD descriptors (Dim: 21).

**Value**

A length 21 named vector

**References**

Inna Dubchak, Ilya Muchink, Stephen R. Holbrook and Sung-Hou Kim. Prediction of protein folding class using global description of amino acid sequence. *Proceedings of the National Academy of Sciences*. USA, 1995, 92, 8700-8704.

Inna Dubchak, Ilya Muchink, Christopher Mayor, Igor Dralyuk and Sung-Hou Kim. Recognition of a Protein Fold in the Context of the SCOP classification. *Proteins: Structure, Function and Genetics*, 1999, 35, 401-407.

**See Also**

See [extractProtCTDC](#) and [extractProtCTDD](#) for the Composition and Distribution descriptors.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtCTDT(x)
```

---

extractProtCTriad      *Conjoint Triad Descriptor*

---

**Description**

Conjoint Triad Descriptor

**Usage**

```
extractProtCTriad(x)
```

**Arguments**

x                      A character vector, as the input protein sequence.

**Details**

This function calculates the Conjoint Triad descriptor (Dim: 343).

**Value**

A length 343 named vector

**References**

J.W. Shen, J. Zhang, X.M. Luo, W.L. Zhu, K.Q. Yu, K.X. Chen, Y.X. Li, H.L. Jiang. Predicting Protein-protein Interactions Based Only on Sequences Information. *Proceedings of the National Academy of Sciences*. 007, 104, 4337–4341.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtCTriad(x)
```

---

extractProtDC              *Dipeptide Composition Descriptor*

---

**Description**

Dipeptide Composition Descriptor

**Usage**

```
extractProtDC(x)
```

**Arguments**

x                    A character vector, as the input protein sequence.

**Details**

This function calculates the Dipeptide Composition descriptor (Dim: 400).

**Value**

A length 400 named vector

**References**

M. Bhasin, G. P. S. Raghava. Classification of Nuclear Receptors Based on Amino Acid Composition and Dipeptide Composition. *Journal of Biological Chemistry*, 2004, 279, 23262.

**See Also**

See [extractProtAAC](#) and [extractProtTC](#) for Amino Acid Composition and Tripeptide Composition descriptors.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtDC(x)
```

---

extractProtGeary            *Geary Autocorrelation Descriptor*

---

**Description**

Geary Autocorrelation Descriptor

**Usage**

```
extractProtGeary(  
  x,  
  props = c("CIDH920105", "BHAR880101", "CHAM820101", "CHAM820102", "CHOC760101",  
            "BIGC670101", "CHAM810101", "DAYM780201"),  
  nlag = 30L,  
  customprops = NULL  
)
```

**Arguments**

x	A character vector, as the input protein sequence.
props	A character vector, specifying the Accession Number of the target properties. 8 properties are used by default, as listed below: <b>AccNo. CIDH920105</b> Normalized average hydrophobicity scales (Cid et al., 1992) <b>AccNo. BHAR880101</b> Average flexibility indices (Bhaskaran-Ponnuswamy, 1988) <b>AccNo. CHAM820101</b> Polarizability parameter (Charton-Charton, 1982) <b>AccNo. CHAM820102</b> Free energy of solution in water, kcal/mole (Charton-Charton, 1982) <b>AccNo. CHOC760101</b> Residue accessible surface area in tripeptide (Chothia, 1976) <b>AccNo. BIGC670101</b> Residue volume (Bigelow, 1967) <b>AccNo. CHAM810101</b> Steric parameter (Charton, 1981) <b>AccNo. DAYM780201</b> Relative mutability (Dayhoff et al., 1978b)
nlag	Maximum value of the lag parameter. Default is 30.
customprops	A n x 21 named data frame contains n customize property. Each row contains one property. The column order for different amino acid types is 'AccNo', 'A', 'R', 'N', 'D', 'C', 'E', 'Q', 'G', 'H', 'I', 'L', 'K', 'M', 'F', 'P', 'S', 'T', 'W', 'Y', 'V', and the columns should also be <i>exactly</i> named like this. The AccNo column contains the properties' names. Then users should explicitly specify these properties with these names in the argument props. See the examples below for a demonstration. The default value for customprops is NULL.

**Details**

This function calculates the Geary autocorrelation descriptor (Dim: length(props) \* nlag).

**Value**

A length nlag named vector

**References**

- AAindex: Amino acid index database. <https://www.genome.jp/dbget/aaindex.html>
- Feng, Z.P. and Zhang, C.T. (2000) Prediction of membrane protein types based on the hydrophobic index of amino acids. *Journal of Protein Chemistry*, 19, 269-275.
- Horne, D.S. (1988) Prediction of protein helix content from an autocorrelation analysis of sequence hydrophobicities. *Biopolymers*, 27, 451-477.
- Sokal, R.R. and Thomson, B.A. (2006) Population structure inferred by local spatial autocorrelation: an usage from an Amerindian tribal population. *American Journal of Physical Anthropology*, 129, 121-131.

**See Also**

See [extractProtMoreauBroto](#) and [extractProtMoran](#) for Moreau-Broto autocorrelation descriptors and Moran autocorrelation descriptors.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtGeary(x)

myprops = data.frame(AccNo = c("MyProp1", "MyProp2", "MyProp3"),
  A = c(0.62, -0.5, 15), R = c(-2.53, 3, 101),
  N = c(-0.78, 0.2, 58), D = c(-0.9, 3, 59),
  C = c(0.29, -1, 47), E = c(-0.74, 3, 73),
  Q = c(-0.85, 0.2, 72), G = c(0.48, 0, 1),
  H = c(-0.4, -0.5, 82), I = c(1.38, -1.8, 57),
  L = c(1.06, -1.8, 57), K = c(-1.5, 3, 73),
  M = c(0.64, -1.3, 75), F = c(1.19, -2.5, 91),
  P = c(0.12, 0, 42), S = c(-0.18, 0.3, 31),
  T = c(-0.05, -0.4, 45), W = c(0.81, -3.4, 130),
  Y = c(0.26, -2.3, 107), V = c(1.08, -1.5, 43))

# Use 4 properties in the AAindex database, and 3 customized properties
extractProtGeary(x, customprops = myprops,
  props = c('CIDH920105', 'BHAR880101',
    'CHAM820101', 'CHAM820102',
    'MyProp1', 'MyProp2', 'MyProp3'))
```

---

extractProtMoran      *Moran Autocorrelation Descriptor*

---

**Description**

Moran Autocorrelation Descriptor

**Usage**

```
extractProtMoran(
  x,
  props = c("CIDH920105", "BHAR880101", "CHAM820101", "CHAM820102", "CHOC760101",
    "BIGC670101", "CHAM810101", "DAYM780201"),
  nlag = 30L,
  customprops = NULL
)
```

**Arguments**

**x**                    A character vector, as the input protein sequence.

**props**                A character vector, specifying the Accession Number of the target properties. 8 properties are used by default, as listed below:

**AccNo. CIDH920105** Normalized average hydrophobicity scales (Cid et al., 1992)

**AccNo. BHAR880101** Average flexibility indices (Bhaskaran-Ponnuswamy, 1988)

	<b>AccNo. CHAM820101</b> Polarizability parameter (Charton-Charton, 1982)
	<b>AccNo. CHAM820102</b> Free energy of solution in water, kcal/mole (Charton-Charton, 1982)
	<b>AccNo. CHOC760101</b> Residue accessible surface area in tripeptide (Chothia, 1976)
	<b>AccNo. BIGC670101</b> Residue volume (Bigelow, 1967)
	<b>AccNo. CHAM810101</b> Steric parameter (Charton, 1981)
	<b>AccNo. DAYM780201</b> Relative mutability (Dayhoff et al., 1978b)
nlag	Maximum value of the lag parameter. Default is 30.
customprops	A n x 21 named data frame contains n customize property. Each row contains one property. The column order for different amino acid types is 'AccNo', 'A', 'R', 'N', 'D', 'C', 'E', 'Q', 'G', 'H', 'I', 'L', 'K', 'M', 'F', 'P', 'S', 'T', 'W', 'Y', 'V', and the columns should also be <i>exactly</i> named like this. The AccNo column contains the properties' names. Then users should explicitly specify these properties with these names in the argument props. See the examples below for a demonstration. The default value for customprops is NULL.

### Details

This function calculates the Moran autocorrelation descriptor (Dim: length(props) \* nlag).

### Value

A length nlag named vector

### References

- AAindex: Amino acid index database. <https://www.genome.jp/dbget/aaindex.html>
- Feng, Z.P. and Zhang, C.T. (2000) Prediction of membrane protein types based on the hydrophobic index of amino acids. *Journal of Protein Chemistry*, 19, 269-275.
- Horne, D.S. (1988) Prediction of protein helix content from an autocorrelation analysis of sequence hydrophobicities. *Biopolymers*, 27, 451-477.
- Sokal, R.R. and Thomson, B.A. (2006) Population structure inferred by local spatial autocorrelation: an usage from an Amerindian tribal population. *American Journal of Physical Anthropology*, 129, 121-131.

### See Also

See [extractProtMoreauBroto](#) and [extractProtGeary](#) for Moreau-Broto autocorrelation descriptors and Geary autocorrelation descriptors.

### Examples

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtMoran(x)

myprops = data.frame(AccNo = c("MyProp1", "MyProp2", "MyProp3"),
                     A = c(0.62, -0.5, 15), R = c(-2.53, 3, 101),
```

```

N = c(-0.78, 0.2, 58), D = c(-0.9, 3, 59),
C = c(0.29, -1, 47), E = c(-0.74, 3, 73),
Q = c(-0.85, 0.2, 72), G = c(0.48, 0, 1),
H = c(-0.4, -0.5, 82), I = c(1.38, -1.8, 57),
L = c(1.06, -1.8, 57), K = c(-1.5, 3, 73),
M = c(0.64, -1.3, 75), F = c(1.19, -2.5, 91),
P = c(0.12, 0, 42), S = c(-0.18, 0.3, 31),
T = c(-0.05, -0.4, 45), W = c(0.81, -3.4, 130),
Y = c(0.26, -2.3, 107), V = c(1.08, -1.5, 43))

```

```

# Use 4 properties in the AAindex database, and 3 customized properties
extractProtMoran(x, customprops = myprops,
  props = c('CIDH920105', 'BHAR880101',
            'CHAM820101', 'CHAM820102',
            'MyProp1', 'MyProp2', 'MyProp3'))

```

---

extractProtMoreauBroto

*Normalized Moreau-Broto Autocorrelation Descriptor*

---

## Description

Normalized Moreau-Broto Autocorrelation Descriptor

## Usage

```

extractProtMoreauBroto(
  x,
  props = c("CIDH920105", "BHAR880101", "CHAM820101", "CHAM820102", "CHOC760101",
            "BIGC670101", "CHAM810101", "DAYM780201"),
  nlag = 30L,
  customprops = NULL
)

```

## Arguments

**x** A character vector, as the input protein sequence.

**props** A character vector, specifying the Accession Number of the target properties. 8 properties are used by default, as listed below:

**AccNo. CIDH920105** Normalized average hydrophobicity scales (Cid et al., 1992)

**AccNo. BHAR880101** Average flexibility indices (Bhaskaran-Ponnuswamy, 1988)

**AccNo. CHAM820101** Polarizability parameter (Charton-Charton, 1982)

**AccNo. CHAM820102** Free energy of solution in water, kcal/mole (Charton-Charton, 1982)

	<b>AccNo. CHOC760101</b> Residue accessible surface area in tripeptide (Chothia, 1976)
	<b>AccNo. BIGC670101</b> Residue volume (Bigelow, 1967)
	<b>AccNo. CHAM810101</b> Steric parameter (Charton, 1981)
	<b>AccNo. DAYM780201</b> Relative mutability (Dayhoff et al., 1978b)
nlag	Maximum value of the lag parameter. Default is 30.
customprops	A n x 21 named data frame contains n customize property. Each row contains one property. The column order for different amino acid types is 'AccNo', 'A', 'R', 'N', 'D', 'C', 'E', 'Q', 'G', 'H', 'I', 'L', 'K', 'M', 'F', 'P', 'S', 'T', 'W', 'Y', 'V', and the columns should also be <i>exactly</i> named like this. The AccNo column contains the properties' names. Then users should explicitly specify these properties with these names in the argument props. See the examples below for a demonstration. The default value for customprops is NULL.

### Details

This function calculates the normalized Moreau-Broto autocorrelation descriptor (Dim: length(props) \* nlag).

### Value

A length nlag named vector

### References

- AAindex: Amino acid index database. <https://www.genome.jp/dbget/aaindex.html>
- Feng, Z.P. and Zhang, C.T. (2000) Prediction of membrane protein types based on the hydrophobic index of amino acids. *Journal of Protein Chemistry*, 19, 269-275.
- Horne, D.S. (1988) Prediction of protein helix content from an autocorrelation analysis of sequence hydrophobicities. *Biopolymers*, 27, 451-477.
- Sokal, R.R. and Thomson, B.A. (2006) Population structure inferred by local spatial autocorrelation: an usage from an Amerindian tribal population. *American Journal of Physical Anthropology*, 129, 121-131.

### See Also

See [extractProtMoran](#) and [extractProtGeary](#) for Moran autocorrelation descriptors and Geary autocorrelation descriptors.

### Examples

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtMoreauBroto(x)

myprops = data.frame(AccNo = c("MyProp1", "MyProp2", "MyProp3"),
                     A = c(0.62, -0.5, 15), R = c(-2.53, 3, 101),
                     N = c(-0.78, 0.2, 58), D = c(-0.9, 3, 59),
                     C = c(0.29, -1, 47), E = c(-0.74, 3, 73),
```



```

Q = c(-0.85, 0.2, 72), G = c(0.48, 0, 1),
H = c(-0.4, -0.5, 82), I = c(1.38, -1.8, 57),
L = c(1.06, -1.8, 57), K = c(-1.5, 3, 73),
M = c(0.64, -1.3, 75), F = c(1.19, -2.5, 91),
P = c(0.12, 0, 42), S = c(-0.18, 0.3, 31),
T = c(-0.05, -0.4, 45), W = c(0.81, -3.4, 130),
Y = c(0.26, -2.3, 107), V = c(1.08, -1.5, 43))

```

```

# Use 4 properties in the AAindex database, and 3 customized properties
extractProtMoreauBroto(x, customprops = myprops,
  props = c('CIDH920105', 'BHAR880101',
            'CHAM820101', 'CHAM820102',
            'MyProp1', 'MyProp2', 'MyProp3'))

```

---

 extractProtPAAC

*Pseudo Amino Acid Composition Descriptor*


---

## Description

Pseudo Amino Acid Composition Descriptor

## Usage

```

extractProtPAAC(
  x,
  props = c("Hydrophobicity", "Hydrophilicity", "SideChainMass"),
  lambda = 30,
  w = 0.05,
  customprops = NULL
)

```

## Arguments

x	A character vector, as the input protein sequence.
props	A character vector, specifying the properties used. 3 properties are used by default, as listed below: 'Hydrophobicity' Hydrophobicity value of the 20 amino acids 'Hydrophilicity' Hydrophilicity value of the 20 amino acids 'SideChainMass' Side-chain mass of the 20 amino acids
lambda	The lambda parameter for the PAAC descriptors, default is 30.
w	The weighting factor, default is 0.05.
customprops	A n x 21 named data frame contains n customize property. Each row contains one property. The column order for different amino acid types is 'AccNo', 'A', 'R', 'N', 'D', 'C', 'E', 'Q', 'G', 'H', 'I', 'L', 'K', 'M', 'F', 'P', 'S', 'T', 'W', 'Y', 'V', and the columns should also be <i>exactly</i> named like this. The AccNo column contains the properties' names. Then users should explicitly specify these properties with these names in the argument props. See the examples below for a demonstration. The default value for customprops is NULL.

**Details**

This function calculates the Pseudo Amino Acid Composition (PAAC) descriptor (Dim:  $20 + \lambda$ , default is 50).

**Value**

A length  $20 + \lambda$  named vector

**Note**

Note the default  $20 * 3$  prop values have been already independently given in the function. Users could also specify other (up to 544) properties with the Accession Number in the [AAindex](#) data, with or without the default three properties, which means users should explicitly specify the properties to use.

**References**

Kuo-Chen Chou. Prediction of Protein Cellular Attributes Using Pseudo-Amino Acid Composition. *PROTEINS: Structure, Function, and Genetics*, 2001, 43: 246-255.

Type 1 pseudo amino acid composition. <http://www.csbio.sjtu.edu.cn/bioinf/PseAAC/type1.htm>

Kuo-Chen Chou. Using Amphiphilic Pseudo Amino Acid Composition to Predict Enzyme Subfamily Classes. *Bioinformatics*, 2005, 21, 10-19.

JACS, 1962, 84: 4240-4246. (C. Tanford). (The hydrophobicity data)

PNAS, 1981, 78:3824-3828 (T.P.Hopp & K.R.Woods). (The hydrophilicity data)

CRC Handbook of Chemistry and Physics, 66th ed., CRC Press, Boca Raton, Florida (1985). (The side-chain mass data)

R.M.C. Dawson, D.C. Elliott, W.H. Elliott, K.M. Jones, Data for Biochemical Research 3rd ed., Clarendon Press Oxford (1986). (The side-chain mass data)

**See Also**

See [extractProtAPAAC](#) for amphiphilic pseudo amino acid composition descriptor.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtPAAC(x)
```

```
myprops = data.frame(AccNo = c("MyProp1", "MyProp2", "MyProp3"),
  A = c(0.62, -0.5, 15), R = c(-2.53, 3, 101),
  N = c(-0.78, 0.2, 58), D = c(-0.9, 3, 59),
  C = c(0.29, -1, 47), E = c(-0.74, 3, 73),
  Q = c(-0.85, 0.2, 72), G = c(0.48, 0, 1),
  H = c(-0.4, -0.5, 82), I = c(1.38, -1.8, 57),
  L = c(1.06, -1.8, 57), K = c(-1.5, 3, 73),
  M = c(0.64, -1.3, 75), F = c(1.19, -2.5, 91),
  P = c(0.12, 0, 42), S = c(-0.18, 0.3, 31),
```

```

T = c(-0.05, -0.4, 45), W = c(0.81, -3.4, 130),
Y = c(0.26, -2.3, 107), V = c(1.08, -1.5, 43))

# Use 3 default properties, 4 properties in the AAindex database,
# and 3 customized properties
extractProtPAAC(x, customprops = myprops,
               props = c('Hydrophobicity', 'Hydrophilicity', 'SideChainMass',
                         'CIDH920105', 'BHAR880101',
                         'CHAM820101', 'CHAM820102',
                         'MyProp1', 'MyProp2', 'MyProp3'))

```

---

extractProtPSSM	<i>Compute PSSM (Position-Specific Scoring Matrix) for given protein sequence</i>
-----------------	---

---

### Description

Compute PSSM (Position-Specific Scoring Matrix) for given protein sequence

### Usage

```

extractProtPSSM(
  seq,
  start.pos = 1L,
  end.pos = nchar(seq),
  psiblast.path = NULL,
  makeblastdb.path = NULL,
  database.path = NULL,
  iter = 5,
  silent = TRUE,
  evalue = 10L,
  word.size = NULL,
  gapopen = NULL,
  gapextend = NULL,
  matrix = "BLOSUM62",
  threshold = NULL,
  seg = "no",
  soft.masking = FALSE,
  culling.limit = NULL,
  best.hit.overhang = NULL,
  best.hit.score.edge = NULL,
  xdrop.ungap = NULL,
  xdrop.gap = NULL,
  xdrop.gap.final = NULL,
  window.size = NULL,
  gap.trigger = 22L,
  num.threads = 1L,

```

```

    pseudocount = 0L,
    inclusion.ethresh = 0.002
)

```

### Arguments

<code>seq</code>	Character vector, as the input protein sequence.
<code>start.pos</code>	Optional integer denoting the start position of the fragment window. Default is 1, i.e. the first amino acid of the given sequence.
<code>end.pos</code>	Optional integer denoting the end position of the fragment window. Default is <code>nchar(seq)</code> , i.e. the last amino acid of the given sequence.
<code>psiblast.path</code>	Character string indicating the path of the <code>psiblast</code> program. If NCBI Blast+ was previously installed in the operation system, the path will be automatically detected.
<code>makeblastdb.path</code>	Character string indicating the path of the <code>makeblastdb</code> program. If NCBI Blast+ was previously installed in the system, the path will be automatically detected.
<code>database.path</code>	Character string indicating the path of a reference database (a FASTA file).
<code>iter</code>	Number of iterations to perform for PSI-Blast.
<code>silent</code>	Logical. Whether the PSI-Blast running output should be shown or not (May not work on some Windows versions and PSI-Blast versions), default is TRUE.
<code>evaluate</code>	Expectation value (E) threshold for saving hits. Default is 10.
<code>word.size</code>	Word size for wordfinder algorithm. An integer $\geq 2$ .
<code>gapopen</code>	Integer. Cost to open a gap.
<code>gapextend</code>	Integer. Cost to extend a gap.
<code>matrix</code>	Character string. The scoring matrix name (default is 'BLOSUM62').
<code>threshold</code>	Minimum word score such that the word is added to the BLAST lookup table. A real value $\geq 0$ .
<code>seg</code>	Character string. Filter query sequence with SEG ('yes', 'window locut hicut', or 'no' to disable) Default is 'no'.
<code>soft.masking</code>	Logical. Apply filtering locations as soft masks? Default is FALSE.
<code>culling.limit</code>	An integer $\geq 0$ . If the query range of a hit is enveloped by that of at least this many higher-scoring hits, delete the hit. Incompatible with <code>best.hit.overhang</code> and <code>best.hit.score.edge</code> .
<code>best.hit.overhang</code>	Best Hit algorithm overhang value (A real value $\geq 0$ and $\leq 0.5$ , recommended value: 0.1). Incompatible with <code>culling.limit</code> .
<code>best.hit.score.edge</code>	Best Hit algorithm score edge value (A real value $\geq 0$ and $\leq 0.5$ , recommended value: 0.1). Incompatible with <code>culling.limit</code> .
<code>xdrop.ungap</code>	X-dropoff value (in bits) for ungapped extensions.
<code>xdrop.gap</code>	X-dropoff value (in bits) for preliminary gapped extensions.

<code>xdrop.gap.final</code>	X-dropoff value (in bits) for final gapped alignment.
<code>window.size</code>	An integer $\geq 0$ . Multiple hits window size, To specify 1-hit algorithm, use 0.
<code>gap.trigger</code>	Number of bits to trigger gapping. Default is 22.
<code>num.threads</code>	Integer. Number of threads (CPUs) to use in the BLAST search. Default is 1.
<code>pseudocount</code>	Integer. Pseudo-count value used when constructing PSSM. Default is 0.
<code>inclusion.ethresh</code>	E-value inclusion threshold for pairwise alignments. Default is 0.002.

### Details

This function calculates the PSSM (Position-Specific Scoring Matrix) derived by PSI-Blast for given protein sequence or peptides. For given protein sequences or peptides, PSSM represents the log-likelihood of the substitution of the 20 types of amino acids at that position in the sequence. Note that the output value is not normalized.

### Value

The original PSSM, a numeric matrix which has `end.pos - start.pos + 1` columns and 20 named rows.

### Note

The function requires the `makeblastdb` and `psiblast` programs to be properly installed in the operation system or their paths provided.

The two command-line programs are included in the NCBI-BLAST+ software package. To install NCBI Blast+, just open the NCBI FTP site using web browser or FTP software: <ftp://anonymous@ftp.ncbi.nlm.nih.gov:21/blast/executables/blast+/LATEST/> then download the executable version of BLAST+ according to your operation system, and compile or install the downloaded source code or executable program.

Ubuntu/Debian users can directly use the command `sudo apt-get install ncbi-blast+` to install NCBI Blast+. For OS X users, download `ncbi-blast- ... .dmg` then install. For Windows users, download `ncbi-blast- ... .exe` then install.

### References

Altschul, Stephen F., et al. "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." *Nucleic acids research* 25.17 (1997): 3389–3402.

Ye, Xugang, Guoli Wang, and Stephen F. Altschul. "An assessment of substitution scores for protein profile-profile comparison." *Bioinformatics* 27.24 (2011): 3356–3363.

Rangwala, Huzefa, and George Karypis. "Profile-based direct kernels for remote homology detection and fold recognition." *Bioinformatics* 21.23 (2005): 4239–4247.

### See Also

[extractProtPSSMFeature](#) [extractProtPSSMAcc](#)

## Examples

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]

dbpath = tempfile('tempdb', fileext = '.fasta')
invisible(file.copy(from = system.file('protseq/Plasminogen.fasta', package = 'Rcpi'), to = dbpath))
pssmmat = extractProtPSSM(seq = x, database.path = dbpath)
dim(pssmmat) # 20 x 562 (P00750: length 562, 20 Amino Acids)
```

---

extractProtPSSMAcc	<i>Profile-based protein representation derived by PSSM (Position-Specific Scoring Matrix) and auto cross covariance</i>
--------------------	--

---

## Description

Profile-based protein representation derived by PSSM (Position-Specific Scoring Matrix) and auto cross covariance

## Usage

```
extractProtPSSMAcc(pssmmat, lag)
```

## Arguments

pssmmat	The PSSM computed by <a href="#">extractProtPSSM</a> .
lag	The lag parameter. Must be less than the number of amino acids in the sequence (i.e. the number of columns in the PSSM matrix).

## Details

This function calculates the feature vector based on the PSSM by running PSI-Blast and auto cross covariance transformation.

## Value

A length  $lag * 20^2$  named numeric vector, the element names are derived by the amino acid name abbreviation (crossed amino acid name abbreviation) and lag index.

## References

Wold, S., Jonsson, J., Sjöström, M., Sandberg, M., & Rännar, S. (1993). DNA and peptide sequences and chemical processes multivariately modelled by principal component analysis and partial least-squares projections to latent structures. *Analytica chimica acta*, 277(2), 239–253.

## See Also

[extractProtPSSM](#) [extractProtPSSMFeature](#)

## Examples

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]

dbpath = tempfile('tempdb', fileext = '.fasta')
invisible(file.copy(from = system.file('protseq/Plasminogen.fasta', package = 'Rcpi'), to = dbpath))
pssmmat = extractProtPSSM(seq = x, database.path = dbpath)
pssmacc = extractProtPSSMAcc(pssmmat, lag = 3)
tail(pssmacc)
```

---

extractProtPSSMFeature

*Profile-based protein representation derived by PSSM (Position-Specific Scoring Matrix)*

---

## Description

Profile-based protein representation derived by PSSM (Position-Specific Scoring Matrix)

## Usage

```
extractProtPSSMFeature(pssmmat)
```

## Arguments

pssmmat      The PSSM computed by [extractProtPSSM](#).

## Details

This function calculates the profile-based protein representation derived by PSSM. The feature vector is based on the PSSM computed by [extractProtPSSM](#). For a given sequence, The PSSM feature represents the log-likelihood of the substitution of the 20 types of amino acids at that position in the sequence. Each PSSM feature value in the vector represents the degree of conservation of a given amino acid type. The value is normalized to interval (0, 1) by the transformation  $1/(1+e^{(-x)})$ .

## Value

A numeric vector which has  $20 \times N$  named elements, where N is the size of the window (number of rows of the PSSM).

## References

Ye, Xugang, Guoli Wang, and Stephen F. Altschul. "An assessment of substitution scores for protein profile-profile comparison." *Bioinformatics* 27.24 (2011): 3356–3363.

Rangwala, Huzefa, and George Karypis. "Profile-based direct kernels for remote homology detection and fold recognition." *Bioinformatics* 21.23 (2005): 4239–4247.

**See Also**

[extractProtPSSM](#) [extractProtPSSMAcc](#)

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]

dbpath = tempfile('tempdb', fileext = '.fasta')
invisible(file.copy(from = system.file('protseq/Plasminogen.fasta', package = 'Rcpi'), to = dbpath))
pssmmat = extractProtPSSM(seq = x, database.path = dbpath)
pssmfeature = extractProtPSSMFeature(pssmmat)
head(pssmfeature)
```

---

extractProtQSO

*Quasi-Sequence-Order (QSO) Descriptor*

---

**Description**

Quasi-Sequence-Order (QSO) Descriptor

**Usage**

```
extractProtQSO(x, nlag = 30, w = 0.1)
```

**Arguments**

x	A character vector, as the input protein sequence.
nlag	The maximum lag, default is 30.
w	The weighting factor, default is 0.1.

**Details**

This function calculates the Quasi-Sequence-Order (QSO) descriptor (Dim:  $20 + 20 + (2 * nlag)$ , default is 100).

**Value**

A length  $20 + 20 + (2 * nlag)$  named vector

**References**

Kuo-Chen Chou. Prediction of Protein Subcellar Locations by Incorporating Quasi-Sequence-Order Effect. *Biochemical and Biophysical Research Communications*, 2000, 278, 477-483.

Kuo-Chen Chou and Yu-Dong Cai. Prediction of Protein Sucellular Locations by GO-FunD-PseAA Predictor. *Biochemical and Biophysical Research Communications*, 2004, 320, 1236-1239.

Gisbert Schneider and Paul Wrede. The Rational Design of Amino Acid Sequences by Artificial Neural Networks and Simulated Molecular Evolution: Do Novo Design of an Idealized Leader Cleavage Site. *Biophys Journal*, 1994, 66, 335-344.



**See Also**

See [extractProtSOCN](#) for sequence-order-coupling numbers.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtQSO(x)
```

---

extractProtSOCN	<i>Sequence-Order-Coupling Numbers</i>
-----------------	--

---

**Description**

Sequence-Order-Coupling Numbers

**Usage**

```
extractProtSOCN(x, nlag = 30)
```

**Arguments**

x	A character vector, as the input protein sequence.
nlag	The maximum lag, default is 30.

**Details**

This function calculates the Sequence-Order-Coupling Numbers (Dim: nlag \* 2, default is 60).

**Value**

A length nlag \* 2 named vector

**References**

Kuo-Chen Chou. Prediction of Protein Subcellar Locations by Incorporating Quasi-Sequence-Order Effect. *Biochemical and Biophysical Research Communications*, 2000, 278, 477-483.

Kuo-Chen Chou and Yu-Dong Cai. Prediction of Protein Sucellular Locations by GO-FunD-PseAA Predictor. *Biochemical and Biophysical Research Communications*, 2004, 320, 1236-1239.

Gisbert Schneider and Paul Wrede. The Rational Design of Amino Acid Sequences by Artifical Neural Networks and Simulated Molecular Evolution: Do Novo Design of an Idealized Leader Cleavage Site. *Biophys Journal*, 1994, 66, 335-344.

**See Also**

See [extractProtQSO](#) for quasi-sequence-order descriptors.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtSOCN(x)
```

---

extractProtTC	<i>Tripeptide Composition Descriptor</i>
---------------	--

---

**Description**

Tripeptide Composition Descriptor

**Usage**

```
extractProtTC(x)
```

**Arguments**

x                    A character vector, as the input protein sequence.

**Details**

This function calculates the Tripeptide Composition descriptor (Dim: 8000).

**Value**

A length 8000 named vector

**References**

M. Bhasin, G. P. S. Raghava. Classification of Nuclear Receptors Based on Amino Acid Composition and Dipeptide Composition. *Journal of Biological Chemistry*, 2004, 279, 23262.

**See Also**

See [extractProtAAC](#) and [extractProtDC](#) for Amino Acid Composition and Dipeptide Composition descriptors.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
extractProtTC(x)
```

---

`getCPI`*Generating Compound-Protein Interaction Descriptors*

---

**Description**

Generating Compound-Protein Interaction Descriptors

**Usage**

```
getCPI(drugmat, protmat, type = c("combine", "tensorprod"))
```

**Arguments**

<code>drugmat</code>	The compound descriptor matrix.
<code>protmat</code>	The protein descriptor matrix.
<code>type</code>	The interaction type, one or two of "combine" and "tensorprod".

**Details**

This function calculates the compound-protein interaction descriptors by three types of interaction:

- `combine` - combine the two descriptor matrix, result has  $(p1 + p2)$  columns
- `tensorprod` - calculate column-by-column (pseudo)-tensor product type interactions, result has  $(p1 * p2)$  columns

**Value**

A matrix containing the compound-protein interaction descriptors

**See Also**

See [getPPI](#) for generating protein-protein interaction descriptors.

**Examples**

```
x = matrix(1:10, ncol = 2)
y = matrix(1:15, ncol = 3)

getCPI(x, y, 'combine')
getCPI(x, y, 'tensorprod')
getCPI(x, y, type = c('combine', 'tensorprod'))
getCPI(x, y, type = c('tensorprod', 'combine'))
```

---

getDrug	<i>Retrieve Drug Molecules in MOL and SMILES Format from Databases</i>
---------	--

---

### Description

Retrieve Drug Molecules in MOL and SMILES Format from Databases

### Usage

```
getDrug(  
  id,  
  from = c("pubchem", "chembl", "cas", "kegg", "drugbank"),  
  type = c("mol", "smile"),  
  parallel = 5  
)
```

### Arguments

id	A character vector, as the drug ID(s).
from	The database, one of 'pubchem', 'chembl', 'cas', 'kegg', 'drugbank'.
type	The returned molecule format, mol or smile.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

### Details

This function retrieves drug molecules in MOL and SMILES format from five databases.

### Value

A length of id character vector, each element containing the corresponding drug molecule.

### See Also

See [getProt](#) for retrieving protein sequences from three databases.

### Examples

```
id = c('DB00859', 'DB00860')  
getDrug(id, 'drugbank', 'smile')
```

---

getFASTAFromKEGG	<i>Retrieve Protein Sequence in FASTA Format from the KEGG Database</i>
------------------	---

---

## Description

Retrieve Protein Sequence in FASTA Format from the KEGG Database

## Usage

```
getFASTAFromKEGG(id, parallel = 5)
```

## Arguments

<code>id</code>	A character vector, as the protein ID.
<code>parallel</code>	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

## Details

This function retrieves protein sequences in FASTA format from the KEGG database.

## Value

A list, each component contains one of the protein sequences in FASTA format.

## See Also

See [getSeqFromKEGG](#) for retrieving protein represented by amino acid sequence from the KEGG database. See [readFASTA](#) for reading FASTA format files.

## Examples

```
id = c('hsa:10161', 'hsa:10162')  
  
getFASTAFromKEGG(id)
```

---

getFASTAFromUniProt     *Retrieve Protein Sequence in FASTA Format from the UniProt Database*

---

### Description

Retrieve Protein Sequence in FASTA Format from the UniProt Database

### Usage

```
getFASTAFromUniProt(id, parallel = 5)
```

### Arguments

id	A character vector, as the protein ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

### Details

This function retrieves protein sequences in FASTA format from the UniProt database.

### Value

A list, each component contains one of the protein sequences in FASTA format.

### References

UniProt. <https://www.uniprot.org/>

UniProt REST API Documentation. <https://www.uniprot.org/help/api>

### See Also

See [getSeqFromUniProt](#) for retrieving protein represented by amino acid sequence from the UniProt database. See [readFASTA](#) for reading FASTA format files.

### Examples

```
id = c('P00750', 'P00751', 'P00752')
```

```
getFASTAFromUniProt(id)
```

---

getMolFromCAS	<i>Retrieve Drug Molecules in InChI Format from the CAS Database</i>
---------------	--

---

## Description

Retrieve Drug Molecules in InChI Format from the CAS Database

## Usage

```
getMolFromCAS(id, parallel = 5)
```

## Arguments

id	A character vector, as the CAS drug ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

## Details

This function retrieves drug molecules in InChI format from the CAS database. CAS database only provides InChI data, so here we return the molecule in InChI format, users could convert them to SMILES format using Open Babel or other third-party tools.

## Value

A length of id character vector, each element containing the corresponding drug molecule.

## See Also

See [getDrug](#) for retrieving drug molecules in MOL and SMILES Format from other databases.

## Examples

```
id = '52-67-5' # Penicillamine  
getMolFromCAS(id)
```

---

getMolFromChEMBL	<i>Retrieve Drug Molecules in MOL Format from the ChEMBL Database</i>
------------------	---

---

### Description

Retrieve Drug Molecules in MOL Format from the ChEMBL Database

### Usage

```
getMolFromChEMBL(id, parallel = 5)
```

### Arguments

id	A character vector, as the ChEMBL drug ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

### Details

This function retrieves drug molecules in MOL format from the ChEMBL database.

### Value

A length of id character vector, each element containing the corresponding drug molecule.

### See Also

See [getSmiFromChEMBL](#) for retrieving drug molecules in SMILES format from the ChEMBL database.

### Examples

```
id = 'CHEMBL1430' # Penicillamine  
getMolFromChEMBL(id)
```



---

getMolFromDrugBank	<i>Retrieve Drug Molecules in MOL Format from the DrugBank Database</i>
--------------------	---

---

### Description

Retrieve Drug Molecules in MOL Format from the DrugBank Database

### Usage

```
getMolFromDrugBank(id, parallel = 5)
```

### Arguments

id	A character vector, as the DrugBank drug ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

### Details

This function retrieves drug molecules in MOL format from the DrugBank database.

### Value

A length of id character vector, each element containing the corresponding drug molecule.

### See Also

See [getSmiFromDrugBank](#) for retrieving drug molecules in SMILES format from the DrugBank database.

### Examples

```
id = 'DB00859' # Penicillamine  
  
getMolFromDrugBank(id)
```

---

getMolFromKEGG	<i>Retrieve Drug Molecules in MOL Format from the KEGG Database</i>
----------------	---

---

**Description**

Retrieve Drug Molecules in MOL Format from the KEGG Database

**Usage**

```
getMolFromKEGG(id, parallel = 5)
```

**Arguments**

id	A character vector, as the KEGG drug ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

**Details**

This function retrieves drug molecules in MOL format from the KEGG database.

**Value**

A length of id character vector, each element containing the corresponding drug molecule.

**See Also**

See [getSmiFromKEGG](#) for retrieving drug molecules in SMILES format from the KEGG database.

**Examples**

```
id = 'D00496' # Penicillamine  
  
getMolFromKEGG(id)
```

---

getMolFromPubChem	<i>Retrieve Drug Molecules in MOL Format from the PubChem Database</i>
-------------------	--

---

## Description

Retrieve Drug Molecules in MOL Format from the PubChem Database

## Usage

```
getMolFromPubChem(id, parallel = 5)
```

## Arguments

<code>id</code>	A character vector, as the PubChem drug ID.
<code>parallel</code>	An integer, the parallel parameter, indicates how many processes the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

## Details

This function retrieves drug molecules in MOL format from the PubChem database.

## Value

A length of `id` character vector, each element containing the corresponding drug molecule.

## See Also

See [getSmiFromPubChem](#) for retrieving drug molecules in SMILES format from the PubChem database.

## Examples

```
id = c('7847562', '7847563') # Penicillamine  
  
getMolFromPubChem(id)
```

---

getPDBFromRCSBPDB      *Retrieve Protein Sequence in PDB Format from RCSB PDB*

---

## Description

Retrieve Protein Sequence in PDB Format from RCSB PDB

## Usage

```
getPDBFromRCSBPDB(id, parallel = 5)
```

## Arguments

id	A character vector, as the protein ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

## Details

This function retrieves protein sequences in PDB format from RCSB PDB.

## Value

A list, each component contains one of the protein sequences in PDB format.

## See Also

See [getSeqFromRCSBPDB](#) for retrieving protein represented by amino acid sequence from the RCSB PDB database.

## Examples

```
id = c('4HHB', '4FF9')  
  
getPDBFromRCSBPDB(id)
```

**Description**

Generating Protein-Protein Interaction Descriptors

**Usage**

```
getPPI(protmat1, protmat2, type = c("combine", "tensorprod", "entrywise"))
```

**Arguments**

protmat1	The first protein descriptor matrix, must have the same ncol with protmat2.
protmat2	The second protein descriptor matrix, must have the same ncol with protmat1.
type	The interaction type, one or more of "combine", "tensorprod", and "entrywise".

**Details**

This function calculates the protein-protein interaction descriptors by three types of interaction:

- combine - combine the two descriptor matrix, result has  $(p + p)$  columns
- tensorprod - calculate column-by-column (pseudo)-tensor product type interactions, result has  $(p * p)$  columns
- entrywise - calculate entrywise product and entrywise sum of the two matrices, then combine them, result has  $(p + p)$  columns

**Value**

A matrix containing the protein-protein interaction descriptors

**See Also**

See [getCPI](#) for generating compound-protein interaction descriptors.

**Examples**

```
x = matrix(1:10, ncol = 2)
y = matrix(5:14, ncol = 2)

getPPI(x, y, type = 'combine')
getPPI(x, y, type = 'tensorprod')
getPPI(x, y, type = 'entrywise')
getPPI(x, y, type = c('combine', 'tensorprod'))
getPPI(x, y, type = c('combine', 'entrywise'))
getPPI(x, y, type = c('entrywise', 'tensorprod'))
getPPI(x, y, type = c('combine', 'entrywise', 'tensorprod'))
```

---

`getProt`*Retrieve Protein Sequence in various Formats from Databases*

---

**Description**

Retrieve Protein Sequence in various Formats from Databases

**Usage**

```
getProt(  
  id,  
  from = c("uniprot", "kegg", "pdb"),  
  type = c("fasta", "pdb", "aaseq"),  
  parallel = 5  
)
```

**Arguments**

<code>id</code>	A character vector, as the protein ID(s).
<code>from</code>	The database, one of 'uniprot', 'kegg', or 'pdb'.
<code>type</code>	The returned protein format, one of fasta, pdb, or aaseq.
<code>parallel</code>	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

**Details**

This function retrieves protein sequence in various formats from three databases.

**Value**

A length of `id` character list, each element containing the corresponding protein sequence(s) or file(s).

**See Also**

See [getDrug](#) for retrieving drug molecules from five databases.

**Examples**

```
id = c('P00750', 'P00751', 'P00752')  
  
getProt(id, from = 'uniprot', type = 'aaseq')
```

---

getSeqFromKEGG	<i>Retrieve Protein Sequence from the KEGG Database</i>
----------------	---

---

**Description**

Retrieve Protein Sequence from the KEGG Database

**Usage**

```
getSeqFromKEGG(id, parallel = 5)
```

**Arguments**

id	A character vector, as the protein ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

**Details**

This function retrieves protein represented by amino acid sequence from the KEGG database.

**Value**

A list, each component contains one of the protein represented by amino acid sequence(s).

**See Also**

See [getFASTAFromKEGG](#) for retrieving protein sequence in FASTA format from the KEGG database.

**Examples**

```
id = c('hsa:10161', 'hsa:10162')  
  
getSeqFromKEGG(id)
```

---

getSeqFromRCSBPDB      *Retrieve Protein Sequence from RCSB PDB*

---

### Description

Retrieve Protein Sequence from RCSB PDB

### Usage

```
getSeqFromRCSBPDB(id, parallel = 5)
```

### Arguments

id	A character vector, as the protein ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

### Details

This function retrieves protein sequences from RCSB PDB.

### Value

A list, each component contains one of the protein represented by amino acid sequence(s).

### See Also

See [getPDBFromRCSBPDB](#) for retrieving protein in PDB format from the RCSB PDB database.

### Examples

```
id = c('4HHB', '4FF9')  
  
getSeqFromRCSBPDB(id)
```



---

getSeqFromUniProt      *Retrieve Protein Sequence from the UniProt Database*

---

## Description

Retrieve Protein Sequence from the UniProt Database

## Usage

```
getSeqFromUniProt(id, parallel = 5)
```

## Arguments

id	A character vector, as the protein ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

## Details

This function retrieves protein represented by amino acid sequence from the UniProt database.

## Value

A list, each component contains one of the protein represented by amino acid sequence(s).

## References

UniProt. <https://www.uniprot.org/>

UniProt REST API Documentation. <https://www.uniprot.org/help/api>

## See Also

See [getFASTAFromUniProt](#) for retrieving protein sequences in FASTA format from the UniProt database.

## Examples

```
id = c('P00750', 'P00751', 'P00752')  
  
getSeqFromUniProt(id)
```

---

getSmiFromChEMBL	<i>Retrieve Drug Molecules in SMILES Format from the ChEMBL Database</i>
------------------	--

---

### Description

Retrieve Drug Molecules in SMILES Format from the ChEMBL Database

### Usage

```
getSmiFromChEMBL(id, parallel = 5)
```

### Arguments

id	A character vector, as the ChEMBL drug ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

### Details

This function retrieves drug molecules in SMILES format from the ChEMBL database.

### Value

A length of id character vector, each element containing the corresponding drug molecule.

### See Also

See [getMolFromChEMBL](#) for retrieving drug molecules in MOL format from the ChEMBL database.

### Examples

```
id = 'CHEMBL1430' # Penicillamine  
  
getSmiFromChEMBL(id)
```

---

getSmiFromDrugBank	<i>Retrieve Drug Molecules in SMILES Format from the DrugBank Database</i>
--------------------	--

---

### Description

Retrieve Drug Molecules in SMILES Format from the DrugBank Database

### Usage

```
getSmiFromDrugBank(id, parallel = 5)
```

### Arguments

id	A character vector, as the DrugBank drug ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

### Details

This function retrieves drug molecules in SMILES format from the DrugBank database.

### Value

A length of id character vector, each element containing the corresponding drug molecule.

### See Also

See [getMolFromDrugBank](#) for retrieving drug molecules in MOL format from the DrugBank database.

### Examples

```
id = 'DB00859' # Penicillamine  
getSmiFromDrugBank(id)
```

---

getSmiFromKEGG	<i>Retrieve Drug Molecules in SMILES Format from the KEGG Database</i>
----------------	--

---

### Description

Retrieve Drug Molecules in SMILES Format from the KEGG Database

### Usage

```
getSmiFromKEGG(id, parallel = 5)
```

### Arguments

id	A character vector, as the KEGG drug ID.
parallel	An integer, the parallel parameter, indicates how many process the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

### Details

This function retrieves drug molecules in SMILES format from the KEGG database.

### Value

A length of id character vector, each element containing the corresponding drug molecule.

### See Also

See [getMolFromKEGG](#) for retrieving drug molecules in MOL format from the KEGG database.

### Examples

```
id = 'D00496' # Penicillamine  
getSmiFromKEGG(id)
```

---

getSmiFromPubChem	<i>Retrieve Drug Molecules in SMILES Format from the PubChem Database</i>
-------------------	---

---

### Description

Retrieve Drug Molecules in SMILES Format from the PubChem Database

### Usage

```
getSmiFromPubChem(id, parallel = 5)
```

### Arguments

id	A character vector, as the PubChem drug ID.
parallel	An integer, the parallel parameter, indicates how many processes the user would like to use for retrieving the data (using RCurl), default is 5. For regular cases, we recommend a number less than 20.

### Details

This function retrieves drug molecules in SMILES format from the PubChem database.

### Value

A length of id character vector, each element containing the corresponding drug molecule.

### See Also

See [getMolFromPubChem](#) for retrieving drug molecules in MOL format from the PubChem database.

### Examples

```
id = c('7847562', '7847563') # Penicillamine  
getSmiFromPubChem(id)
```

---

OptAA3d	<i>OptAA3d.sdf - 20 Amino Acids Optimized with MOE 2011.10 (Semiempirical AM1)</i>
---------	--

---

**Description**

OptAA3d.sdf - 20 Amino Acids Optimized with MOE 2011.10 (Semiempirical AM1)

**Details**

OptAA3d.sdf - 20 Amino Acids Optimized with MOE 2011.10 (Semiempirical AM1)

**Value**

OptAA3d data

**Examples**

```
# This example requires the rcdk package
# library('rcdk')
# optaa3d = load.molecules(system.file('sysdata/OptAA3d.sdf', package = 'Rcpi'))
# view.molecule.2d(optaa3d[[1]]) # view the first amino acid
```

---

readFASTA	<i>Read Protein Sequences in FASTA Format</i>
-----------	---

---

**Description**

Reads protein sequences in FASTA format.

**Usage**

```
readFASTA(
  file = system.file("protseq/P00750.fasta", package = "Rcpi"),
  legacy.mode = TRUE,
  seqonly = FALSE
)
```

**Arguments**

file	The name of the file which the sequences in fasta format are to be read from. If it does not contain an absolute or relative path, the file name is relative to the current working directory, <a href="#">getwd</a> . The default here is to read the P00750.fasta file which is present in the protseq directory of the Rcpi package.
legacy.mode	If set to TRUE, lines starting with a semicolon ';' are ignored. Default value is TRUE.

seqonly      If set to TRUE, only sequences as returned without attempt to modify them or to get their names and annotations (execution time is divided approximately by a factor 3). Default value is FALSE.

**Value**

Character vector.

**References**

Pearson, W.R. and Lipman, D.J. (1988) Improved tools for biological sequence comparison. *Proceedings of the National Academy of Sciences of the United States of America*, 85: 2444-2448.

**See Also**

See [readPDB](#) for reading protein sequences in PDB format.

**Examples**

```
P00750 = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))
P00750
```

---

readMolFromSDF	<i>Read Molecules from SDF Files and Return Parsed Java Molecular Object</i>
----------------	--

---

**Description**

Read Molecules from SDF Files and Return Parsed Java Molecular Object

**Usage**

```
readMolFromSDF(sdf file)
```

**Arguments**

sdf file      Character vector, containing SDF file location(s).

**Details**

This function reads molecules from SDF files and return parsed Java molecular object needed by extractDrug... functions.

**Value**

A list, containing parsed Java molecular object.

**See Also**

See [readMolFromSmi](#) for reading molecules by SMILES string and returning parsed Java molecular object.

**Examples**

```
sdf = system.file('compseq/DB00859.sdf', package = 'Rcpi')
sdfs = c(system.file('compseq/DB00859.sdf', package = 'Rcpi'),
         system.file('compseq/DB00860.sdf', package = 'Rcpi'))

mol = readMolFromSDF(sdf)
mols = readMolFromSDF(sdfs)
```

---

readMolFromSmi	<i>Read Molecules from SMILES Files and Return Parsed Java Molecular Object or Plain Text List</i>
----------------	--

---

**Description**

Read Molecules from SMILES Files and Return Parsed Java Molecular Object or Plain Text List

**Usage**

```
readMolFromSmi(smifile, type = c("mol", "text"))
```

**Arguments**

smifile	Character vector, containing SMILES file location(s).
type	'mol' or 'text'. 'mol' returns parsed Java molecular object, used for 'text' returns (plain-text) character string list. For common molecular descriptors and fingerprints, use 'mol'. For descriptors and fingerprints calculated by OpenBabel, i.e. functions named <code>extractDrugOB...()</code> , use 'text'.

**Details**

This function reads molecules from SMILES strings and return parsed Java molecular object or plain text list needed by `extractDrug...()` functions.

**Value**

A list, containing parsed Java molecular object or character strings.

**See Also**

See [readMolFromSDF](#) for reading molecules from SDF files and returning parsed Java molecular object.



## Examples

```
smi = system.file('vignettesdata/FDAMDD.smi', package = 'Rcpi')  
  
mol1 = readMolFromSmi(smi, type = 'mol')  
mol2 = readMolFromSmi(smi, type = 'text')
```

---

readPDB

*Read Protein Sequences in PDB Format*

---

## Description

Read Protein Sequences in PDB Format

## Usage

```
readPDB(file = system.file("protseq/4HHB.pdb", package = "Rcpi"))
```

## Arguments

file	The name of the file which the sequences in PDB format are to be read from. If it does not contain an absolute or relative path, the file name is relative to the current working directory, <code>getwd</code> . The default here is to read the 4HHB.PDB file which is present in the protseq directory of the Rcpi package.
------	--

## Details

This function reads protein sequences in PDB (Protein Data Bank) format, and return the amino acid sequences represented by single-letter code.

## Value

A character vector, representing the amino acid sequence of the single-letter code.

## References

Protein Data Bank Contents Guide: Atomic Coordinate Entry Format Description, Version 3.30. Accessed 2013-06-26. [https://files.wwpdb.org/pub/pdb/doc/format\\_descriptions/Format\\_v33\\_Letter.pdf](https://files.wwpdb.org/pub/pdb/doc/format_descriptions/Format_v33_Letter.pdf)

## See Also

See [readFASTA](#) for reading protein sequences in FASTA format.

## Examples

```
Seq4HHB = readPDB(system.file('protseq/4HHB.pdb', package = 'Rcpi'))  
Seq4HHB
```

searchDrug

*Parallelized Drug Molecule Similarity Search by Molecular Fingerprints Similarity or Maximum Common Substructure Search***Description**

Parallelized Drug Molecule Similarity Search by Molecular Fingerprints Similarity or Maximum Common Substructure Search

**Usage**

```
searchDrug(
  mol,
  molddb,
  cores = 2,
  method = c("fp", "mcs"),
  fptype = c("standard", "extended", "graph", "hybrid", "maccs", "estate", "pubchem",
            "kr", "shortestpath", "fp2", "fp3", "fp4", "obmaccs"),
  fpsim = c("tanimoto", "euclidean", "cosine", "dice", "hamming"),
  mcssid = c("tanimoto", "overlap"),
  ...
)
```

**Arguments**

mol	The query molecule. The location of a sdf file containing one molecule.
molddb	The molecule database. The location of a sdf file containing all the molecules to be searched with.
cores	Integer. The number of CPU cores to use for parallel search, default is 2. Users could use the detectCores() function in the parallel package to see how many cores they could use.
method	'fp' or 'mcs'. Search by molecular fingerprints or by maximum common substructure searching.
fptype	The fingerprint type, only available when method = 'fp'. Rcpis supports 13 types of fingerprints, including 'standard', 'extended', 'graph', 'hybrid', 'maccs', 'estate', 'pubchem', 'kr', 'shortestpath', 'fp2', 'fp3', 'fp4', 'obmaccs'.
fpsim	Similarity measure type for fingerprint, only available when method = 'fp'. Including 'tanimoto', 'euclidean', 'cosine', 'dice' and 'hamming'. See calcDrugFPSim for details.
mcssid	Similarity measure type for maximum common substructure search, only available when method = 'mcs'. Including 'tanimoto' and 'overlap'.
...	Other possible parameter for maximum common substructure search, see calcDrugMCSSim for available options.

## Details

This function does compound similarity search derived by various molecular fingerprints with various similarity measures or derived by maximum common substructure search. This function runs for a query compound against a set of molecules.

## Value

Named numerical vector. With the decreasing similarity value of the molecules in the database.

## Examples

```
mol = system.file('compseq/DB00530.sdf', package = 'Rcpi')
# DrugBank ID DB00530: Erlotinib
molddb = system.file('compseq/tyrphostin.sdf', package = 'Rcpi')
# Database composed by searching 'tyrphostin' in PubChem and filtered by Lipinski's Rule of Five

searchDrug(mol, molddb, cores = 4, method = 'fp', fptype = 'maccs', fpsim = 'hamming')
searchDrug(mol, molddb, cores = 4, method = 'fp', fptype = 'fp2', fpsim = 'tanimoto')
searchDrug(mol, molddb, cores = 4, method = 'mcs', mcssim = 'tanimoto')
```

---

segProt

*Protein Sequence Segmentation*

---

## Description

Protein Sequence Segmentation

## Usage

```
segProt(
  x,
  aa = c("A", "R", "N", "D", "C", "E", "Q", "G", "H", "I", "L", "K", "M", "F", "P", "S",
        "T", "W", "Y", "V"),
  k = 7
)
```

## Arguments

x	A character vector, as the input protein sequence.
aa	A character, the amino acid type. one of 'A', 'R', 'N', 'D', 'C', 'E', 'Q', 'G', 'H', 'I', 'L', 'K', 'M', 'F', 'P', 'S', 'T', 'W', 'Y', 'V'.
k	A positive integer, specifies the window size (half of the window), default is 7.

## Details

This function extracts the segmentations from the protein sequence.

**Value**

A named list, each component contains one of the segmentations (a character string), names of the list components are the positions of the specified amino acid in the sequence.

**Examples**

```
x = readFASTA(system.file('protseq/P00750.fasta', package = 'Rcpi'))[[1]]
segProt(x, aa = 'R', k = 5)
```

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