
NAME

PDBFileUtil

SYNOPSIS

```
use PDBFileUtil ;

use PDBFileUtil qw(:all);
```

DESCRIPTION

PDBFileUtil module provides the following functions:

GenerateAtomOrHetatmRecordLine, GenerateAtomRecordLine, GenerateConectRecordLine,
 GenerateEndRecordLine, GenerateHeaderRecordLine, GenerateHeaderRecordTimeStamp,
 GenerateHetatmRecordLine, GenerateTerRecordLine, GetAllResidues, GetChainsAndResidues,
 GetConectRecordLines, GetExperimentalTechnique, GetExperimentalTechniqueResolution, GetMinMaxCoords,
 GetPDBRecordType, GetRecordTypesCount, IsAtomRecordType, IsConectRecordType, IsEndmdlRecordType,
 IsHeaderRecordType, IsHetatmRecordType, IsMasterRecordType, IsModelRecordType, IsPDBFile,
 IsSeqresRecordType, IsTerRecordType, ParseAtomOrHetatmRecordLine, ParseAtomRecordLine,
 ParseConectRecordLine, ParseExpdtaRecordLine, ParseHeaderRecordLine, ParseHetatmRecordLine,
 ParseMasterRecordLine, ParseRemark2ResolutionRecordLine, ParseSeqresRecordLine, ParseTerRecordLine,
 ReadPDBFile

METHODS**GenerateAtomOrHetatmRecordLine**

```
$RecordLine = GenerateAtomOrHetatmRecordLine($RecordType,
  $AtomNumber, $AtomName, $AlternateLocation, $ResidueName,
  $ChainID, $ResidueNumber, $InsertionCode, $X, $Y, $Z,
  $Occupancy, $TemperatureFactor, $SegmentID,
  $ElementSymbol, $AtomCharge);
```

Returns ATOM or HETATM record line.

GenerateAtomRecordLine

```
$RecordLine = GenerateAtomRecordLine($AtomNumber,
  $AtomName, $AlternateLocation, $ResidueName, $ChainID,
  $ResidueNumber, $InsertionCode, $X, $Y, $Z, $Occupancy,
  $TemperatureFactor, $SegmentID, $ElementSymbol, $AtomCharge);
```

Returns ATOM record line.

GenerateConectRecordLine

```
$RecordLine = GenerateConectRecordLine($AtomNum, $BondedAtomNum1,
  $BondedAtomNum2, $BondedAtomNum3, $BondedAtomNum4,
  $HBondedAtomNum1, $HBondedAtomNum2, $SaltBridgedAtomNum1,
  $HBondedAtomNum3, $HBondedAtomNum4, $SaltBridgedAtomNum2);
```

Returns CONNECT record line.

GenerateHeaderRecordLine

```
$RecordLine = GenerateHeaderRecordLine($IDCode, [$Classification,
  $Date]);
```

Returns HEADER record line.

GenerateHeaderRecordTimeStamp

```
$Date = GenerateHeaderRecordTimeStamp();
```

Returns PDB header time stamp.

GenerateHetatmRecordLine

```
$RecordLine = GenerateHetatmRecordLine($AtomNumber, $AtomName,
```

```
$AlternateLocation, $ResidueName, $ChainID, $ResidueNumber,
$InsertionCode, $X, $Y, $Z, $Occupancy, $TemperatureFactor,
$SegmentID, $ElementSymbol, $AtomCharge);
```

Returns HETATM record line.

GenerateEndRecordLine

```
$RecordLine = GenerateEndRecordLine();
```

Returns END record line.

GenerateTerRecordLine

```
$RecordLine = GenerateTerRecordLine($SerialNumber, [$ResidueName,
$ChainID, $ResidueNumber, $InsertionCode]);
```

Returns TER record line.

GetAllResidues

```
$ResiduesDataRef = GetAllResidues($PDBRecordLinesRef);
```

Gets residue information using ATOM/HETATM records and returns a reference to a hash with following key/value pairs:

```
$ResiduesDataRef->{ResidueNames} - Array of all the residues
$ResiduesDataRef->{ResidueCount}{$ResidueName} - Count of residues
$ResiduesDataRef->{AtomResidueNames} - Array of all ATOM residues
$ResiduesDataRef->{AtomResidueCount}{$ResidueName} - Count of
residues in ATOM records
$ResiduesDataRef->{HetatomResidueNames} - List of all HETATM
residues
$ResiduesDataRef->{HetatmResidueCount}{$ResidueName} - Count of
residues HETATM records
```

ATOM/HETATM records after the first ENDMDL records are simply ignored.

GetChainsAndResidues

```
$ChainsDataRef = GetChainsAndResidues($PDBRecordLinesRef,
[$RecordsSource, $GetChainResiduesBeyondTERFlag,
$GetRecordLinesFlag]);
```

Gets chains and residue information using ATOM/HETATM or SEQRES records and returns a reference to a hash with these keys:

```
$ChainsDataRef->{ChainIDs} - List of chain IDs with 'None' for
no IDs
$ChainsDataRef->{Residues}{$ChainID} - List of residues in order
of their appearance in a chain
$ChainsDataRef->{ResidueCount}{$ChainID}{$ResidueName} - Count of
residues in a chain
```

Chains and residue data can be extracted using either ATOM/HETATM records or SEQRES records. ATOM/HETATM records after the first ENDMDL records are simply ignored.

GetConectRecordLines

```
$ConectRecordLinesRef = GetConectRecordLines($PDBRecordLinesRef,
$AtomNumbersMapRef);
```

Collects CONECT record lines for specific atom number, modified specified data to exclude any atom number not present in the list of specified atom numbers and returns a reference to list of CONECT record lines.

GetExperimentalTechnique

```
$ExperimentalTechnique = GetExperimentalTechnique($PDBRecordLinesRef);
```

Returns *ExperimentalTechnique* value retrieved from EXPDATA record line.

GetExperimentalTechniqueResolution

```
($Resolution, $ResolutionUnits) = GetExperimentalTechniqueResolution(  
    $PDBRecordLinesRef);
```

Returns *Resolution* and *ResolutionUnits* values from REMARK 2 RESOLUTION record line.

GetMinMaxCoords

```
($XMin, $YMin, $ZMin, $XMax, $YMax, $ZMax) =  
    GetMinMaxCoords($PDBRecordLinesRef);
```

Returns minimum and maximum XYZ coordinates for ATOM/HETATM records.

GetPDBRecordType

```
$RecordType = GetPDBRecordType($RecordLine);
```

Returns type of *RecordLine*.

GetRecordTypesCount

```
$RecordTypeDataRef = GetRecordTypesCount($PDBRecordLinesRef,  
    [$SpecifiedRecordType, $GetRecordLinesFlag]);
```

Counts the number of each record type or a \$SpecifiedRecordType and returns a reference to data type with following key/value pairs:

```
$RecordTypeDataRef->{RecordTypes} - An array of unique record types  
    in order of their presence in the file  
$RecordTypeDataRef->{Count}{$RecordType} - Count of each record type  
$RecordTypeDataRef->{Lines}{$RecordType} - Optional lines data for a  
    specific record type.
```

IsAtomRecordType

```
$Status = IsAtomRecordType($RecordLine);
```

Returns 1 or 0 based on whether it's a ATOM record line.

IsConectRecordType

```
$Status = IsAtomConectType($RecordLine);
```

Returns 1 or 0 based on whether it's a CONECT record line.

IsEndmdlRecordType

```
$Status = IsEndmdlRecordType($RecordLine);
```

Returns 1 or 0 based on whether it's a ENDMDL a record line.

IsHeaderRecordType

```
$Status = IsHeaderRecordType($RecordLine);
```

Returns 1 or 0 based on whether it's a HEADER a record line.

IsHetatmRecordType

```
$Status = IsHetatmRecordType($RecordLine);
```

Returns 1 or 0 based on whether it's a HETATM a record line.

IsMasterRecordType

```
$Status = IsMasterRecordType($RecordLine);
```

Returns 1 or 0 based on whether it's a MASTER a record line.

IsModelRecordType

```
$Status = IsModelRecordType($RecordLine);
```

Returns 1 or 0 based on whether it's a MODEL record line.

IsPDBFile

```
$Status = IsPDBFile($PDBFile);
```

Returns 1 or 0 based on whether it's a PDB file.

IsSeqresRecordType

```
$Status = IsSeqresRecordType($RecordLine);
```

Returns 1 or 0 based on whether it's SEQRES a record line.

IsTerRecordType

```
$Status = IsTerRecordType($RecordLine);
```

Returns 1 or 0 based on whether it's a TER record line.

ParseAtomOrHetatmRecordLine

```
( $AtomNumber, $AtomName, $AlternateLocation, $ResidueName, $ChainID,  
  $ResidueNumber, $InsertionCode, $X, $Y, $Z, $Occupancy,  
  $TemperatureFactor, $SegmentID, $ElementSymbol, $AtomCharge ) =  
  ParseAtomOrHetatmRecordLine($RecordLine);
```

Parses ATOM or HETATM record line.

ParseAtomRecordLine

```
( $AtomNumber, $AtomName, $AlternateLocation, $ResidueName, $ChainID,  
  $ResidueNumber, $InsertionCode, $X, $Y, $Z, $Occupancy,  
  $TemperatureFactor, $SegmentID, $ElementSymbol, $AtomCharge ) =  
  ParseAtomRecordLine($RecordLine);
```

Parses ATOM record line.

ParseConectRecordLine

```
( $AtomNum, $BondedAtomNum1, $BondedAtomNum2, $BondedAtomNum3,  
  $BondedAtomNum4, $HBondedAtomNum1, $HBondedAtomNum2,  
  $SaltBridgedAtomNum1, $HBondedAtomNum3, $HBondedAtomNum4,  
  $SaltBridgedAtomNum2 ) = ParseConectRecordLine($RecordLine);
```

Parses CONECT record line.

ParseExpdtaRecordLine

```
( $ContinuationNum, $ExperimentalTechnique ) = ParseExpdtaRecordLine($Line);
```

Parses EXPDTA record line.

ParseHeaderRecordLine

```
( $Classification, $DepositionDate, $IDCode ) = ParseHeaderRecordLine($RecordLine);
```

Parses HEADER record line

ParseHetatmRecordLine

```
( $AtomNumber, $AtomName, $AlternateLocation, $ResidueName, $ChainID,  
  $ResidueNumber, $InsertionCode, $X, $Y, $Z, $Occupancy,  
  $TemperatureFactor, $SegmentID, $ElementSymbol, $AtomCharge ) =  
  ParseHetatmRecordLine($RecordLine);
```

Parses HETATM record line.

ParseMasterRecordLine

```
( $NumOfRemarkRecords, $NumOfHetRecords, $NumOfHelixRecords,  
  $NumOfSheetRecords, $NumOfTurnRecords, $NumOfSiteRecords,  
  $NumOfTransformationsRecords, $NumOfAtomAndHetatmRecords,  
  $NumOfTerRecords, $NumOfConectRecords, $NumOfSeqresRecords ) =  
  ParseMasterRecordLine($RecordLine);
```

Parses MASTER record line.

ParseRemark2ResolutionRecordLine

```
( $Resolution, $ResolutionUnits ) = ParseRemark2ResolutionRecordLine(  
  $RecordLine);
```

Parses REMARK 2 RESOLUTION record line.

ParseSeqresRecordLine

```
( $RecordSerialNumber, $ChainID, $NumOfResidues, $ResidueNames ) =  
  ParseSeqresRecordLine($RecordLine);
```

Parses SEQRES record line.

ParseTerRecordLine

```
( $SerialNumber, $ResidueName, $ChainID, $ResidueNumber, $InsertionCode ) =  
  ParseTerRecordLine($RecordLine);
```

Parses TER record line.

ReadPDBFile

```
$PDBRecordLinesRef = ReadPDBFile($PDBFile);
```

Reads PDB file and returns reference to record lines.

AUTHOR

Manish Sud <msud@san.rr.com>

SEE ALSO

FileUtil.pm, SequenceFileUtil.pm, TextUtil.pm

COPYRIGHT

Copyright (C) 2017 Manish Sud. All rights reserved.

This file is part of MayaChemTools.

MayaChemTools is free software; you can redistribute it and/or modify it under the terms of the GNU Lesser General Public License as published by the Free Software Foundation; either version 3 of the License, or (at your option) any later version.