the chemmacros bundle

v4.0 2013/07/06

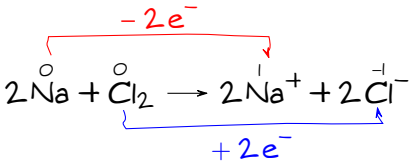
packages chemmacros (v4.0), chemformula (v4.0), ghsystem (v4.0) and chemgreek (v0.1a)

documentation for the chemmacros package

Clemens Niederberger

https://bitbucket.org/cgnieder/chemmacros/
contact@mychemistry.eu

English documentation



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Part I.
Preliminaries

1. Licence, Requirements and README

Permission is granted to copy, distribute and/or modify this software under the terms of the LaTeX project public license (lppl) version 1.3 or later (`http://www.latex-project.org/lppl.txt`). The package has the status "maintained."

The CHEMMACROS bundle needs the bundles l3kernel[1] and l3packages.[2] It also needs the packages siunitx,[3] mathtools,[4] bm,[5] nicefrac[6] and environ[7] as well as tikz[8] and the Ti*k*Z libraries `calc` and `arrows`. Language support is done with the help of the translations package from the exsheets[9] bundle. The CHEMMACROS package also loads the other packages of this bundle.

The package option `xspace` also loads the package xspace.[10]

The CHEMMACROS bundle bundles four packages: CHEMMACROS, CHEMFORMULA, GHSYSTEM and CHEMGREEK. The package dependencies of the other packages are described in the respective manuals.

[1] on CTAN: l3kernel [2] on CTAN: l3packages [3] on CTAN: siunitx [4] on CTAN: mathtools [5] on CTAN: bm [6] on CTAN: nicefrac [7] on CTAN: environ [8] on CTAN: pgf [9] on CTAN: exsheets [10] on CTAN: xspace

2. Motivation and Background

CHEMMACROS started some years ago as a growing list of custom macros that I frequently used. I cannot completely recall when and why I decided to release them as a package. Well – here we go and you might find it useful, too, I hope.

Both the macros and their functionality have changed over time and quite a lot have been added. Many things have been unified and what's probably most important: many possibilities to customize have been added, too.

Probably every chemist using LaTeX 2_ε is aware of the great mhchem[11] package by Martin Hensel. There have always been some difficulties intertwining it with CHEMMACROS, though. Also, some other minor points in mhchem always bothered me, but they hardly seemed enough for a new package. They weren't even enough for a feature request to the mhchem author. The challenge and the fun of creating a new package and the wish for a highly customizable alternative led to CHEMFORMULA after all.

CHEMFORMULA works very similar to mhchem but is more strict as to how compounds, stoichiometric factors and arrows are input. In the same time CHEMFORMULA offers possibilities to customize the output that mhchem does not. Although CHEMFORMULA is meant as an *alternative* to mhchem CHEMMACROS only loads CHEMFORMULA and uses it at various places internally, too.

As a chemist you are probably aware of the fact that the United Nations have developed the Globally Harmonized System of Classification and Labelling of Chemicals (GHS) as a global replacement for the various different systems in different countries. While it has not been implemented by all countries yet [Eur12], it is only a matter of time.

The package GHSYSTEM enables you to typeset all the hazard and precautionary statements and pictograms in a very easy way. The statements are taken from EU regulation 1272/2008 [Theo8].

There are four points I hope I have achieved with this bundle:

- intuitive usage as far as the syntax of the commands is concerned
- the commands shall not only make typesetting easier and faster but also the document source more readable with respect to semantics (`\ortho-dichlorobenzene` is easier to read and understand than `\textsl{o}-dichlorobenzene`)
- as much customizability as I could think of so every user can adapt the commands to his or her own wishes
- default settings compliant with the recommendations of the International Union of Pure and Applied Chemistry (IUPAC).

Especially the last point needed some pushing from users to get things right in many places. If you find anything not compliant with IUPAC recommendations[12] I would welcome an email very much!

3. News

With version 4.0 some changes have been made:

[11] on CTAN: mhchem [12] This does not concern the `\ox` command. The IUPAC version is `\ox*`.

- first of all the packages CHEMFORMULA and GHSYSTEM do not load CHEMMACROS any more which means they can be used independently.
- the option `bpchem` has been dropped.
- the commands `\mch` and `\pch` now match CHEMFORMULA's charges.
- the option `method` has been dropped.

charges

- the option `append` has deprecated.
- the option `greek` has been extended to support other uppercase greek letters, for example those provided by kpfonts.[13] This is handled internally by the new package in the family: CHEMGREEK. This package is not really a package for usage at a user-level but could in principle be used to extend the `greek` option.
- language support is now done with the help of the translations package from the exsheets bundle. This means that with version 4.0 the document language is recognized automatically.
- the status of the commands `\Lfi` and `\Dfi` has been changed from *deprecated* to *dropped*.
- various other changes like bug fixes and improvements on the typographical appearance of CHEMFORMULA's inline formulae with `\ch`.

4. Package Options

CHEMMACROS has several package options. They all are used as key/value pairs like

```
\usepackage[option1 = <value1>, option2 = <value2>]{chemmacros}
```

Some also can be used without value (`\usepackage[option1]{chemmacros}`), which means that the underlined value is used.

Both CHEMFORMULA and GHSYSTEM don't have package options of their own. If you load them explicitly any given option will silently fail. Options can then only be set using the setup command.

`option circled = formal|all|none` Default: `formal`

CHEMMACROS uses two different kinds of charges which indicate the usage of real (+/−) and formal (⊕/⊖) charges. The option `formal` distinguishes between them, option `none` displays them all without circle, option `all` circles all.

`option circletype = chem|mathchem` This option switches between two kinds of circled charge symbols: `\fplus` ⊕ and `$\oplus$` ⊕.

`option cmversion = 1|2|3|4|newest` Default: `newest`

This option restores the old definitions of some commands and tries to ensure backwards compatibility as much as possible (default = 4). Actually 2 and 3 are aliases, as are – for now – 4 and `newest`. *This option can only be chosen in the preamble.*

option ghsystem = true|false Default: true
Disable the automatic loading of the GHSYSTEM package.

option greek = auto|kpfonts|math|newtx|textgreek|upgreek Default: auto
This option determines how the letters \Chemalpha and friends are typeset. See page 8 for more information. Please note that this option *does not load either upgreek,*[14] *kpfonts, newtxmath*[15] *nor textgreek*[16]*!* It only determines which one to choose if available. The option auto will detect if either (in order of priority) upgreek, textgreek, kpfonts or newtxmath have been loaded and use them if available. If you explicitly choose upgreek, textgreek, kpfonts or newtxmath you also have to load the corresponding package. *This option can only be chosen in the preamble.*

option iupac = auto|restricted|strict Default: auto
Take care of how IUPAC naming commands are defined, see page 10.

option language = american|british|english|french|german|italian|ngerman (initially empty)
Load the language used by CHEMMACROS. *This option can only be chosen in the preamble.*

option Nu = chemmacros|mathspec Default: chemmacros
The package mathspec[17] also defines a macro \Nu. This option chooses which definition holds, see page 8. *This option can only be chosen in the preamble.*

option strict = true|false Default: false
Setting strict = true will turn all warning messages into erros messages.

option synchronize = true|false Default: false
The setting true will tell CHEMMACROS to adapt the font settings of CHEMFORMULA.

option xspace = true|false Default: true
With this option most commands are defined with a \xspace.

5. Setup

Various of CHEMMACROS', CHEMFORMULA's and GHSYSTEM's commands have key/value pairs with which they can be customized. Most times they can be used as (optional) argument of the commands themselves. They also can most times be used with the \chemsetup command.

```
\chemsetup[<module>]{<key> = <value>} or

\chemsetup{<module>/<key> = <value>}
```

The keys each belong to a module, which defines for which commands they are intended for. If a key is presented, you'll see the module to which it belongs in the left margin. You have two ways to use keys with the \chemsetup, as you can see above.

The package options can also be seen as keys belonging to the module option. This means they
option can also be used with the \chemsetup command (except for the option version = 1/2/3).

[13] on CTAN: kpfonts [14] on CTAN: upgreek [15] on CTAN: newtxmath [16] on CTAN: textgreek [17] on CTAN: mathspec

```
\chemsetup[option]{circled=none}\mch\ \pch\ \fmch\ \fpch\ \el\ \prt \\
\chemsetup[option]{circled=formal}\mch\ \pch\ \fmch\ \fpch\ \el\ \prt \\
\chemsetup[option]{circletype=math}\mch\ \pch\ \fmch\ \fpch\ \el\ \prt \\
\chemsetup{option/circletype=chem,option/circled=all}\mch\ \pch\ \fmch\ \fpch\ \
 el\ \prt \\
\chemsetup{option/circletype=math}\mch\ \pch\ \fmch\ \fpch\ \el\ \prt
```

$^{-}$ $^{+}$ $^{\ominus}$ $^{\oplus}$ e^{-} p^{+}
$^{-}$ $^{+}$ $^{\ominus}$ $^{\oplus}$ e^{-} p^{+}
$^{-}$ $^{+}$ $^{\ominus}$ $^{\oplus}$ e^{-} p^{+}
$^{-}$ $^{+}$ $^{\ominus}$ $^{\oplus}$ e^{-} p^{+}
$^{-}$ $^{+}$ $^{\ominus}$ $^{\oplus}$ e^{-} p^{+}

Keys *not* belonging to a module *cannot* be used with `\chemsetup`!

All options of CHEMFORMULA belong to the module `chemformula` and all of GHSYSTEM's options belong to the module `ghsystem`.

6. Language Settings

6.1. Supported Languages

By choosing the option

```
\chemsetup[option]{language=<language>}
```

you can set the language that is used by CHEMMACROS if you want that to be a different language than your main document language.

These translate (if the translations are available)

- The header of the list of reactions.
- The beginning of the entries in the list of reactions.
- The H- and P-statements of the GHS.

Currently the following translations are provided:

```
% subscript used in \Ka:
\DeclareTranslation{German}{K-acid}{S}
% the phases \sld and \lqd:
\DeclareTranslation{German}{phase-sld}{f}
\DeclareTranslation{German}{phase-lqd}{f{}l}
% heading of the list of reactions:
\DeclareTranslation{English}{list-of-reactions}{List of reactions}
\DeclareTranslation{German} {list-of-reactions}{Reaktionsverzeichnis}
\DeclareTranslation{Italian}{list-of-reactions}{Elenco delle reazioni}
\DeclareTranslation{French} {list-of-reactions}{Table des r\'eactions}
% name at the beginning of each entry in the list of reactions:
\DeclareTranslation{English}{lor-reaction}{Reaction }
```

```
\DeclareTranslation{German} {lor-reaction}{Reaktion }
\DeclareTranslation{Italian}{lor-reaction}{Reazione }
\DeclareTranslation{French} {lor-reaction}{R\'eaction }
```

All other languages will fall back to English. However, you can always add the translation you want. If you send me an email with translations you'd like to have added to CHEMMACROS I'll gladly add them.

6.2. Specialties

6.2.1. German

If you choose `german/ngerman` the phase commands `\sld` and `\lqd` and the command `\pKa` are translated.

6.2.2. Italian

Choosing the language `italian` defines two additional IUPAC commands:

`\ter` *ter*

`\sin` *sin*

Part II.
chemmacros

7. Particles, Ions and Symbols

7.1. Predefined

CHEMMACROS defines some simple macros for displaying often needed particles and symbols. Please note, that they're displayed differently depending on the package options used, see section 4. These commands can be used in text as well as in math mode. Note that they are not meant to be used in CHEMFORMULA's `\ch`.

`\Hpl` H^+ (proton)

`\Hyd` OH^- (hydroxide)

`\HtO` H_3O^+ (oxonium ion) (**H** three **O**)

`\water` H_2O

`\el` e^- (electron)

`\prt` p^+ (proton)

`\ntr` n^0 (neutron)

`\Nu` Nu^- (nucleophile).
The package mathspec also defines a macro `\Nu`. If you chose package option `Nu = mathspec` CHEMMACROS defines `\Nuc` instead.

`\El` E^+ (electrophile)

`\ba` ba^- (base)

`\fplus` ⊕

`\fminus` ⊖

`\transitionstatesymbol` ‡

`\standardstate` ⦵.
This symbol is only provided by CHEMMACROS, if the package chemstyle[18] is not loaded; the idea is borrowed from there.[19]

`\Chemalpha` α, `\ChemAlpha` A
For each of the 24 greek letters a lowercase and uppercase `\Chem...` command is defined that maps to the upright greek letter as set with the option `greek`. More details on this can be found in the manual of the CHEMGREEK package.

The two particles `\Nu` and `\ba` can be modified. To do that you use the option

`particle elpair = false|dots|dash` Default: `false`
Set how the electron pair of the particles `\Nu` and `\ba` are set.

It only has any effect, if the package chemfig[20] is loaded, since it uses it's command `\Lewis`.

```
% needs package `chemfig'
\ba[elpair] \Nu[elpair=dash]

\chemsetup[particle]{elpair}
\ba \Nu
```

ba:⁻ Nu|⁻
ba:⁻ Nu:⁻

The greek letters aren't newly defined symbols but are defined differently depending on the packages you've loaded. The default definition is the corresponding math letter. If you have loaded the textgreek package the letters are taken from there, and if you have loaded the package upgreek the macros of that package are used. This is also described in the description of the package option `greek`, other details can be found in the documentation of the CHEMGREEK package. This documentation uses newtxmath and the setting `greek = newtx` for instance.

The reason why CHEMMACROS uses these macros in the first place is IUPAC compliance. IUPAC recommends to use upright greek letters in nomenclature.

> Greek letters are used in systematic organic, inorganic, macromolecular and biochemical nomenclature. These should be roman (upright), since they are not symbols for physical quantities. *IUPAC Green Book* [*Coh+08, p. 9*]

CHEMMACROS uses these commands now to define nomenclature commands, see page 11.

[18] on CTAN: chemstyle [19] many thanks to the package author Joseph Wright. [20] on CTAN: chemfig

7.2. Own Particles

Surely sometimes it can be handy to have other particle macros defined such as `\positron` or `\photon`. This can easily be done with this command:

`\DeclareChemParticle{<cmd>}{<definition>}`

`\RenewChemParticle{<cmd>}{<definition>}`

The particle defined this way behaves uses CHEMFORMULA's `\ch` to typeset the particle which means that the `<definition>` should be a vaild CHEMFORMULA compound. Please have a look at the CHEMFORMULA manual for details. The particle will obey the `circled` option.

```
\DeclareChemParticle{\positron}{\Chembeta+}
\DeclareChemParticle{\photon}{\Chemgamma}
\RenewChemParticle{\el}{\Chembeta-}
\positron\ \photon\ \el
```

$\beta^+ \gamma \beta^-$

`\DeclareChemParticle` only defines a particle if `<cmd>` is not already used by any other command. If it *is* already used CHEMMACROS will either give a warning or an error, depending on the option `strict`. `\RenewChemParticle` *only* defines a particle if `<cmd>` *is* already used and issues a warning/error otherwise.

8. Nomenclature, Stereo Descriptors, Latin Phrases

8.1. IUPAC Names

Similar to the bpchem[21] package CHEMMACROS provides a command[22] to typeset IUPAC names. Why is that useful? IUPAC names can get very long. So long indeed that they span over more than two lines, especially in two-column documents. This means they must be allowed to be broken more than one time. This is what the following command does.

`\iupac{<IUPAC name>}`

Inside this command use `\|` and `\-` to indicate a breaking point or a breaking dash. Use `\^` as a shortcut for `\textsuperscript`. (These commands are similar to the shorthands provided by babel[23] for certain languages.)

```
\begin{minipage}{.4\linewidth}
 \iupac{Tetra\|cyclo[2.2.2.1\^{1,4}]\-un\|decane-2\-dodecyl\-5\-(hepta\|decyl\|
iso\|dodecyl\|thio\|ester)}
\end{minipage}
```

Tetracyclo[2.2.2.1^{1,4}]-undecane-2-dodecyl-5-(heptadecylisododecylthioester)

[21] on CTAN: bpchem [22] The idea and the implementation is shamelessly borrowed from bpchem by Bjørn Pedersen.
[23] on CTAN: babel

The \iupac command is more of a semantic command. Most times you can achieve (nearly) the same thing by using \- instead of \|, - instead of \- and \textsuperscript instead of \^.

There are some subtleties: \- inserts a small space before the hyphen and removes a small space after it. The command \| not only prevents ligatures but also inserts a small space.

```
\huge\iupac{2,4\-Di\|chlor\|pentan} \\
2,4-Dichlorpentan
```

2,4-Dichlorpentan
2,4-Dichlorpentan

The spaces inserted by these commands can be customized.

`iupac hyphen-pre-space = <dim>` Default: `.01em`

Set the space that is inserted before the hyphen set with \-.

`iupac hyphen-post-space = <dim>` Default: `-.03em`

Set the space that is inserted after the hyphen set with \-.

`iupac break-space = <dim>` Default: `.01em`

Set the space inserted by \|.

The command \iupac serves another purpose, too, however. Regardless of the setting of the iupac option all the commands presented in this section are always defined *inside* \iupac. Quite a number of the naming commands have very general names: \meta, \D, \E, \L, \R, \S, \trans and so forth. This means they either are predefined already (\L Ł) or are easily defined by another package or class (the cool[24] package defines both \D and \E, for example). In order to give you control which commands are defined in which way, there is the package option iupac. It has three modes:

- iupac = auto: if the commands are *not* defined by any package or class you're using they are available generally, otherwise only *inside* \iupac.
- iupac = restricted: all naming commands are *only* defined inside \iupac. If the commands are defined by another package they of course have that meaning outside. They're not defined outside otherwise.
- iupac = strict: CHEMMACROS overwrites any other definition and makes the commands available throughout the document. Of course the commands can be redefined (but only in the document body). They will still be available inside \iupac then.

Table 1 demonstrates the different modes.

8.1.1. Predefined Commands

The macros in this section are intended to make the writing of IUPAC names more convenient.

[24] on CTAN: cool

	auto	restricted	strict
\L	Ł	Ł	L
\iupac{\L}	L	L	L
\D	D	–	D
\iupac{\D}	D	D	D

Table 1: Demonstration of iupac's modes.

Greek Letters Greek letters in compound names are typeset upright. For this there are for example the packages upgreek and textgreek. If you have loaded one of them[25] CHEMMACROS typesets the following commands upright:

\a α

\b β

\g γ

\d δ

\k κ

\m μ

\n η

\w ω

```
\iupac{5\a\-androstan\-3\b\-ol} \\
\iupac{\a\-(tri\|chloro\|methyl)\-\w\-chloro\|poly(1,4\-phenylene\|methylene)}
```

5α-androstan-3β-ol
α-(trichloromethyl)-ω-chloropoly(1,4-phenylenemethylene)

Hetero Atoms and added Hydrogen Attachments to hetero atoms and added hydrogen atoms are indicated by italic letters [Coh+08]. CHEMMACROS defines a few shortcuts for the most common ones.

\H *H*

\O *O*

\N *N*

\Sf *S*

\P *P*

[25] There are other options, see the description of the greek option.

```
\iupac{\N\-methyl\|benz\|amide} \\
\iupac{3\H\-pyrrole} \\
\iupac{\O\-ethyl hexanethioate}
```

N-methylbenzamide
3*H*-pyrrole
O-ethyl hexanethioate

Cahn-Ingold-Prelog

`\cip{<conf>}` e.g.: `\cip{R,S}` (*R*,*S*)

`\R` (*R*)

`\S` (*S*)

Since the command `\S` has another meaning already (§) it is only available inside `\iupac` in the default setting.

Both these commands and the entgegen/zusammen descriptors get a small additional amount of kerning after the closing parenthesis. This amount can be changed through the following option:

`iupac cip-kern = <dim>` Default: `.075em`

Set the amount of kerning after the closing parenthesis.

Fischer

`\D` D

`\L` L

Since the command `\L` has another meaning already (Ł) it is only available inside `\iupac` in the default setting.

cis/trans, zusammen/entgegen, syn/anti & tert

`\cis` *cis*

`\trans` *trans*

`\Z` (*Z*)

`\E` (*E*)

`\syn` *syn*

`\anti` *anti*

`\tert` *tert*

The package cool defines the commands `\E` and `\D`, too. If you load it, the CHEMMACROS version will only be available inside `\iupac` in the default setting.

ortho/meta/para

`\ortho` *o*

`\meta` *m*

`\para` *p*

Absolute Configuration (uses Ti*k*Z)

`\Rconf[<letter>]` `\Rconf`: (R) `\Rconf[]`: ( )

`\Sconf[<letter>]` `\Sconf`: (S) `\Sconf[]`: ( )

Examples:

```
\iupac{\D\-Wein\|s\"aure} = \\
\iupac{\cip{2S,3S}\-Wein\|s\"aure} \\
\iupac{\D\-($-$)\-Threose} = \\
\iupac{\cip{2S,3R}\-($-$)\-2,3,4\-Tri\|hydroxy\|butanal} \\
\iupac{\cis\-2\-Butene} = \\
\iupac{\Z\-2\-Butene}, \\
\iupac{\cip{2E,4Z}\-Hexa\|diene} \\
\iupac{\meta\-Xylol} = \\
\iupac{1,3\-Di\|methyl\|benzene}
```

D-Weinsäure =
(*2S,3S*)-Weinsäure
D-(−)-Threose =
(*2S,3R*)-(−)-2,3,4-Trihydroxybutanal
cis-2-Butene =
(*Z*)-2-Butene,
(*2E,4Z*)-Hexadiene
m-Xylol =
1,3-Dimethylbenzene

Coordination Chemistry

CHEMMACROS provides two commands useful with coordination chemistry:

`\bridge{<num>}` μ_3-

`\hapto{<num>}` η^5-

```
Ferrocene = \iupac{bis(\hapto{5}cyclo\|penta\|dienyl)iron} \\
\iupac{tetra\-\bridge{3}iodido\-tetrakis[tri\|methyl\|platinum(IV)]}
```

Ferrocene = bis(η^5-cyclopentadienyl)iron
tetra-μ_3-iodido-tetrakis[trimethylplatinum(IV)]

Two options allow customization:

`iupac bridge-number = sub|super` Default: `sub`

Appends the number as a subscript or superscript. IUPAC recommendation is the subscript [Con+05].

`iupac coord-use-hyphen = true|false` Default: `true`

Append a hyphen to `\hapto` and `\bridge` or don't.

8.1.2. Own Naming Commands

If you find any commands missing you can define them using

`\DeclareChemIUPAC{<cmd>}{<declaration>}`

`\RenewChemIUPAC{<cmd>}{<declaration>}`

A command defined in this way will obey the setting of the option `iupac`. This means any existing command is only overwritten with `iupac = strict`. However, `\DeclareChemIUPAC` will *not* change the definition of an existing IUPAC naming command but issue a warning/an error (depending on the package option `strict`) if the IUPAC naming command already exists.

```
\DeclareChemIUPAC\endo{\textit{endo}}
\RenewChemIUPAC\anti{\textit{anti}}
\iupac{(2\-\endo,7\-\anti)\-2\-bromo\-7\-fluoro\|bicyclo[2.2.1]heptane}
```

(2-*endo*,7-*anti*)-2-bromo-7-fluorobicyclo[2.2.1]heptane

`\RenewChemIUPAC` allows you to redefine the existing IUPAC naming commands.

```
\iupac{\meta\-Xylol} \\
\RenewChemIUPAC\meta{\textit{m}}
\iupac{\meta\-Xylol}
```

m-Xylol
m-Xylol

8.2. Latin Phrases

The package chemstyle provides the command `\latin` to typeset common latin phrases in a consistent way. CHEMMACROS defines a similar `\latin` only if chemstyle has *not* been loaded and additionally provides these commands:

`\insitu` *in situ*

`\abinitio` *ab initio*

`\invacuo` *in vacuo*

If the package chemstyle has been loaded they are defined using chemstyle's `\latin` command. This means that then the appearance depends on chemstyle's option `abbremph`.

The commands are defined through

`\DeclareChemLatin{<cmd>}{<phrase>}`

`\RenewChemLatin{<cmd>}{<phrase>}`

```
\DeclareChemLatin\ltn{latin text}
\ltn
```

latin text

If you have *not* loaded chemstyle you can change the appearance with this option:

`latin format = <definition>` Default: `\itshape`

Set the format of the latin phrases.

9. Units for the Usage With siunitx

In chemistry some non-SI units are very common. siunitx provides the command `\DeclareSIUnit{<command>}{<unit>}` to add arbitrary units. CHEMMACROS uses that command to provide some units. Like all siunitx units they're only valid inside `\SI{<num>}{<unit>}` and `\si{<unit>}`.

`\atmosphere` atm

`\atm` atm

`\calory` cal

`\cal` cal

`\cmc` cm^3

The units `\cmc`, `\molar`, and `\Molar` are defined by the package chemstyle as well. CHEMMACROS only defines them, if chemstyle is not loaded.

`\molar` $\mathrm{mol\,dm}^{-3}$

`\moLar` $\mathrm{mol\,L}^{-1}$

`\Molar` M

`\MolMass` $\mathrm{g\,mol}^{-1}$

`\normal` N

`\torr` torr

By the way: `\mmHg` mmHg already is defined by siunitx and chemstyle.

10. Acid/Base

Easy representation of pH, pK_A ... (the command `\pKa` depends on the package option `language`).

`\pH` pH

`\pOH` pOH

`\Ka` K_A

`\Kb` K_B

`\Kw` K_W

`\pKa[<num>]` `\pKa`: $\mathrm{p}K_A$, `\pKa[1]`: $\mathrm{p}K_{A1}$

`\pKb[<num>]` `\pKb`: $\mathrm{p}K_B$, `\pKb[1]`: $\mathrm{p}K_{B1}$

`\p{<anything>}` e.g. `\p{\Kw}` $\mathrm{p}K_W$

```
\Ka \Kb \pKa \pKa[1] \pKb \pKb[1]
```

K_A K_B $\mathrm{p}K_A$ $\mathrm{p}K_{A1}$ $\mathrm{p}K_B$ $\mathrm{p}K_{B1}$

The default appearance of the p-commands has changed to follow IUPAC recommendations.

> The operator p [...] shall be printed in Roman type. — *IUPAC Green Book* [*Coh+08, p. 103*]

There is one option which changes the style the p is typeset:

`acid-base p-style = italics|slanted|upright` Default: `upright`

Set the style of the p operator.

```
\pH, \pKa

\chemsetup[acid-base]{p-style=slanted} \pH, \pKa

\chemsetup[acid-base]{p-style=italics} \pH, \pKa
```

pH, $\mathrm{p}K_A$
pH, $\mathrm{p}K_A$
pH, $\mathrm{p}K_A$

11. Oxidation Numbers, Real and Formal Charges

CHEMMACROS distinguishes between real (+/−) and formal (⊕/⊖) charge symbols, also see section 4. All commands using formal charge symbols start with a `f`.

11.1. Ion Charges

Simple displaying of (real) charges. It is worth noting that these commands really are relicts from a time when CHEMMACROS tried hard to be compliant with mhchem and CHEMFORMULA didn't exist, yet. They are still provided for backwards compatibility but *my recommendation is to use* `\ch` (see the documentation of the CHEMFORMULA package) *and forget about these commands:*

`\pch[<number>]` positive charge (**p**lus + **ch**arge)

`\mch[<number>]` negative charge (**m**inus + **ch**arge)

```
\pch, Na\pch, Ca\pch[2]\\
\mch, F\mch, S\mch[2]
```
$^{+}$, Na^{+}, Ca^{2+}
$^{-}$, F^{-}, S^{2-}

The same for formal charges:

`\fpch[<number>]` positive charge

`\fmch[<number>]` negative charge

```
\fpch\ \fmch\ \fpch[3] \fmch[3]
```
$\oplus$ $\ominus$ $3\oplus$ $3\ominus$

11.2. Oxidation Numbers

Typesetting oxidation numbers:

`\ox[<keyval>]{<number>,<atom>}`
Places `<number>` above `<atom>`; `<number>` has to be a (rational) number!

```
\ox{+1,Na}, \ox{2,Ca}, \ox{-2,S}, \ox{-1,F}
```
$\overset{\mathrm{I}}{\mathrm{Na}}$, $\overset{\mathrm{II}}{\mathrm{Ca}}$, $\overset{-\mathrm{II}}{\mathrm{S}}$, $\overset{-\mathrm{I}}{\mathrm{F}}$

There are a number of keys, that can be used to modify the `\ox` command.

`ox parse = true|false` Default: `true`
When `false` an arbitrary entry can be used for `<number>`.

`ox roman = true|false` Default: `false`
Switches from roman to arabic numbers.

`ox pos = top|super|side` Default: `top`
`top` places `<number>` above `<atom>`, `super` to the upper right as superscript and `side` to the right and inside brackets.

`ox explicit-sign = true|false` Default: `false`
Shows the $+$ for positiv numbers and the $\pm$ for 0.

`ox decimal-marker = comma|point` Default: `point`
Choice for the decimal marker for formal oxidation numbers like $\overset{1.2}{\mathrm{X}}$.

`ox align = center|right` Default: `center`
Center the oxidation number relative to the atom or right-align it.

```
\ox[roman=false]{2,Ca} \ox{2,Ca} \\
\ox[pos=super]{3,Fe}-Oxide \\
\ox[pos=side]{3,Fe}-Oxide \\
\ox[parse=false]{?,Mn} \\
\ox[align=right]{2,Ca}
```

$\overset{2}{\mathrm{Ca}}\ \overset{\mathrm{II}}{\mathrm{Ca}}$
$\mathrm{Fe}^{\mathrm{III}}$-Oxide
Fe(III)-Oxide
$\overset{?}{\mathrm{Mn}}$
$\overset{\mathrm{II}}{\mathrm{Ca}}$

The `pos = super` variant also can be set with the shortcut `\ox*`:

```
\ox{3,Fe} \ox*{3,Fe}
```

$\overset{\mathrm{III}}{\mathrm{Fe}}\ \mathrm{Fe}^{\mathrm{III}}$

Using the `explicit-sign` key will always show the sign of the oxidation number:

```
\chemsetup[ox]{explicit-sign = true}
\ox{+1,Na}, \ox{2,Ca}, \ox{-2,S}, \ch{"\ox{0,F}" {}2}
```

$\overset{+\mathrm{I}}{\mathrm{Na}},\ \overset{+\mathrm{II}}{\mathrm{Ca}},\ \overset{-\mathrm{II}}{\mathrm{S}},\ \overset{\pm 0}{\mathrm{F}_2}$

```
Compare \ox{-1,\ch{O2^2-}} to \ch{"\ox{-1,O}" {}2^2-}
```

Compare $\overset{-\mathrm{I}}{\mathrm{O}_2}^{2-}$ to $\overset{-\mathrm{I}}{\mathrm{O}_2}^{2-}$

Sometimes one might want to use formal oxidation numbers like 0.5 or $\frac{1}{3}$:

```
\ox{.5,\ch{Br2}} \ch{"\ox{1/3,I}" {}3+}
```

$\overset{0.5}{\mathrm{Br}_2}\ \overset{1/3}{\mathrm{I}_3}^{+}$

The fraction uses the `\sfrac` command of the xfrac[26] package. For this purpose the instance `chemmacros-ox-frac` is defined.

```
\DeclareInstance{xfrac}{chemmacros-ox-frac}{text}
  {
    scale-factor        = 1.2 ,
    denominator-bot-sep = -.5ex ,
    numerator-top-sep   = -.3ex ,
    slash-left-kern     = -.2em ,
    slash-right-kern    = -.2em ,
    slash-symbol-font   = lmr
  }
```

Of course you can redefine it so that it suits your needs as the output often strongly depends on the used font.

11.3. Partial Charges and Similar Stuff

The next ones probably are seldomly needed but nevertheless useful:

[26] on CTAN: xfrac

`\delp` $\delta+$ (**del**ta + **p**lus)

`\delm` $\delta-$ (**del**ta + **m**inus)

`\fdelp` $\delta\oplus$

`\fdelm` $\delta\ominus$

These macros for example can be used with the `\ox` command or with the chemfig package:

```
\chemsetup{
  option/circled = all,
  ox/parse       = false
}
\ce{\ox{\delp,H}-\ox{\delm,Cl}} \hspace*{1cm}
\chemfig{\chemabove[3pt]{\lewis{246,Br}}{\delm}-\chemabove[3pt]{H}{\delp}}
```

The following macros are useful together with chemfig, too.

`\scrp` $+$ (**scr**iptstyle + **p**lus)

`\scrm` $-$ (**scr**iptstyle + **m**inus)

`\fscrp` $\oplus$

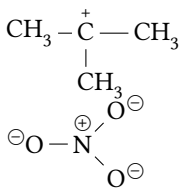
`\fscrm` $\ominus$

`\fsscrp` $\oplus$ (using `\scriptscriptstyle`)

`\fsscrm` $\ominus$

```
\setatomsep{1.8em}\chemfig{CH_3-\chemabove{C}{\scrp}(-[6]C|H_3)-\vphantom{H_3}CH
 _3}

\chemfig{\fmch{}|O-\chemabove{N}{\fscrp}(-[1]O|\fmch)-[7]O|\fmch}
```



12. Reaction Mechanisms

With the command

`\mech[<type>]`

one can specify the most common reaction mechanisms. <type> can have one of the following values:

`\mech`
(empty, no opt. argument) nucleophilic substitution S_N

`\mech[1]`
unimolecular nucleophilic substitution S_N1

`\mech[2]`
bimolecular nucleophilic substitution S_N2

`\mech[se]`
electrophilic substitution S_E

`\mech[1e]`
unimolecular electrophilic substitution S_E1

`\mech[2e]`
bimolecular electrophilic substitution S_E2

`\mech[ar]`
electrophilic aromatic substitution Ar-S_E

`\mech[e]`
elimination E

`\mech[e1]`
unimolecular elimination $E1$

`\mech[e2]`
bimolecular elimination $E2$

`\mech[cb]`
unimolecular elimination "conjugated base", i.e. via carbanion $E1_{cb}$

13. Redox Reactions

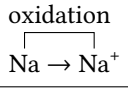
CHEMMACROS provides two commands to visualize the transfer of electrons in redox reactions. Both commands are using Ti*k*Z.

`\OX{<name>,<atom>}`

`\redox(<name1>,<name2>)[<tikz>][<num>]<text>`
Only the first argument `(<name1>,<name2>)` is required, the others are all optional.

`\OX` places `<atom>` into a node, which is named with `<name>`. If you have set two `\OX`, they can be connected with a line using `\redox`. To do so the names of the two nodes that are to be connected are written in the round braces. Since `\redox` draws a tikzpicture with options `remember picture,overlay`, the document needs to be *compiled at least two times.*

```
\OX{a,Na} $\rightarrow$ \OX{b,Na}\pch\redox(a,b){oxidation}
```

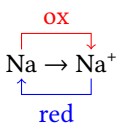


This line can be customized using Ti*k*Z keys in `[<tikz>]`:

```
\OX{a,Na} $\rightarrow$ \OX{b,Na}\pch\redox(a,b)[->,red]{ox}
```

With the argument `[<num>]` the length of the vertical parts of the line can be adjusted. The default length is `.6em`. This length is multiplied with `<num>`. If you use a negative value the line is placed *below* the text.

```
\OX{a,Na} $\rightarrow$ \OX{b,Na}\pch
\redox(a,b)[->,red]{ox}
\redox(a,b)[<-,blue][-1]{red}
\vspace{7mm}
```

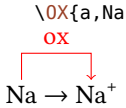


The default length of the vertical lines can be customized with the option

`redox dist = <dim>` Default: `.6em`

A TEX dimension.

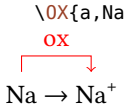
```
\chemsetup{redox/dist=1em}
\OX{a,Na} $\rightarrow$ \OX{b,Na}\pch\redox(a,b)[->,red]{ox}
```



`redox sep = <dim>` Default: `.2em`

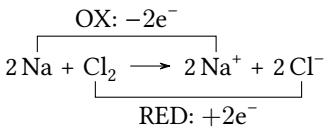
The option can be used to change the distance between the atom and the beginning of the line.

```
\chemsetup{redox/sep=.5em}
\OX{a,Na} $\rightarrow$ \OX{b,Na}\pch\redox(a,b)[->,red]{ox}
```

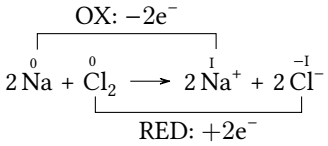


Examples:

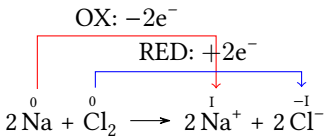
```
\ch{ 2 "\OX{o1,Na}" + "\OX{r1,Cl}" {}2 -> 2 "\OX{o2,Na}" \pch{} + 2
"\OX{r2,Cl}" \mch }
\redox(o1,o2){\small OX: $- 2\el$}
\redox(r1,r2)[][-1]{\small RED: $+ 2\el$}
\vspace{7mm}
```



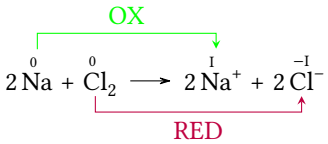

```
\ch{ 2 "\OX{o1,\ox{0,Na}}" + "\OX{r1,\ox{0,Cl}}" {}2 -> 2 "\OX{o2,\ox{+1,Na}}"
\pch{} + 2 "\OX{r2,\ox{-1,Cl}}" \mch }
\redox(o1,o2){\small OX: $- 2\el$}
\redox(r1,r2)[][-1]{\small RED: $+ 2\el$}
\vspace{7mm}
```




```
\ch{ 2 "\OX{o1,\ox{0,Na}}" + "\OX{r1,\ox{0,Cl}}" {}2 -> 2 "\OX{o2,\ox{+1,Na}}"
\pch{} + 2 "\OX{r2,\ox{-1,Cl}}" \mch }
\redox(o1,o2)[draw=red,->][3.33]{\small OX: $- 2\el$}
\redox(r1,r2)[draw=blue,->]{\small RED: $+ 2\el$}
```




```
\ch{ 2 "\OX{o1,\ox{0,Na}}" + "\OX{r1,\ox{0,Cl}}" {}2 -> 2 "\OX{o2,\ox{+1,Na}}"
\pch{} + 2 "\OX{r2,\ox{-1,Cl}}" \mch }
\redox(o1,o2)[green,-stealth]{\small OX}
\redox(r1,r2)[purple,-stealth][-1]{\small RED}
\vspace{7mm}
```



14. (Standard) State, Thermodynamics

14.1. Thermodynamic Variables

The following commands use siunitx:

`\Enthalpy[<keyval>](<subscript>){<value>}`

`\Entropy[<keyval>](<subscript>){<value>}`

`\Gibbs[<keyval>](<subscript>){<value>}`

Their usage is pretty much self-explaining:

```
\Enthalpy{123} \\
\Entropy{123} \\
\Gibbs{123}
```

$\Delta H^\ominus = 123\,\mathrm{kJ\,mol^{-1}}$
$S^\ominus = 123\,\mathrm{J\,K^{-1}\,mol^{-1}}$
$\Delta G^\ominus = 123\,\mathrm{kJ\,mol^{-1}}$

The argument `(<subscript>)` adds a subscript for specification: `\Enthalpy(r){123}` $\Delta_\mathrm{r} H^\ominus = 123\,\mathrm{kJ\,mol^{-1}}$.

There are several keys to customize the commands.

−none− `exponent = <anything>`

−none− `delta = <anything>|false`

−none− `subscript = left|right`

−none− `unit = <unit>`

The default values depend on the command.

```
\Enthalpy[unit=\kilo\joule]{-285} \\
\Gibbs[delta=false]{0} \\
\Entropy[delta=\Delta,exponent=]{56.7}
```

$\Delta H^\ominus = -285\,\mathrm{kJ}$
$G^\ominus = 0\,\mathrm{kJ\,mol^{-1}}$
$\Delta S = 56.7\,\mathrm{J\,K^{-1}\,mol^{-1}}$

The unit is set corresponding to the rules of siunitx and depends on its settings:

```
\Enthalpy{-1234.56e3} \\
\sisetup{per-mode=symbol,exponent-product=\cdot,output-decimal-marker={,},group-
 four-digits=true}
\Enthalpy{-1234.56e3}
```

$\Delta H^\ominus = -1234.56 \times 10^3\,\mathrm{kJ\,mol^{-1}}$
$\Delta H^\ominus = -1\,234{,}56 \cdot 10^3\,\mathrm{kJ/mol}$

14.1.1. Create New Variables

You can use the command

`\DeclareChemState[<keyval>]{<name>}{<symbol>}{<unit>}`

to create new corresponding commands:

```
\DeclareChemState{Helmholtz}{A}{\kilo\joule\per\mole}
\DeclareChemState[subscript-left=false,exponent=]{ElPot}{E}{\volt}
\Helmholtz{123.4} \\
\ElPot{-1.1} \\
\ElPot[exponent=0]($\ch{Sn}|\ch{Sn^2+}||\ch{Pb^2+}|\ch{Pb}$){0.01}
```

$\Delta A^{\ominus} = 123.4\,\mathrm{kJ\,mol^{-1}}$
$\Delta E = -1.1\,\mathrm{V}$
$\Delta E^{0}_{\mathrm{Sn|Sn^{2+}||Pb^{2+}|Pb}} = 0.01\,\mathrm{V}$

The command has some keys with which the default behaviour of the new command can be set.

`exponent = <anything>`

`delta = <anything>|false`

–none– `subscript-left = true|false`

`subscript = <anything>`

14.1.2. Redefine Variables

With

`\RenewChemState[<keyval>]{<name>}{<symbol>}{<unit>}`

you can redefine the already existing commands:

```
\RenewChemState{Enthalpy}{h}{\joule}
\Enthalpy(f){12.5}
```

$\Delta_f h^{\ominus} = 12.5\,\mathrm{J}$

The command is analogous to `\DeclareChemState`, i.e. it has the same keys.

So – for following thermodynamic conventions – one could define a molar and an absolute variable:

```
\DeclareChemState[exponent=]{enthalpy}{h}{\kilo\joule\per\mole}% molar
\RenewChemState[exponent=]{Enthalpy}{H}{\kilo\joule}% absolute
\enthalpy{-12.3} \Enthalpy{-12.3}
```

$\Delta h = -12.3\,\mathrm{kJ\,mol^{-1}}$ $\Delta H = -12.3\,\mathrm{kJ}$

14.2. State

The commands presented in section 14.1 internally all use the command[27]

`\State[<keyval>]{<symbol>}{<subscript>}`

It can be used to write the thermodynamic variables without value and unit.

Examples:

[27] Please note that `{<subscript>}` is an *optional* argument.

```
\State{A}, \State{G}{f}, \State[subscript-left=false]{E}{\ch{Na}}, \State[
 exponent=\SI{1000}{\celsius}]{H}
```

$\Delta A^{\ominus}$, $\Delta_{\mathrm{f}} G^{\ominus}$, $\Delta E^{\ominus}_{\mathrm{Na}}$, $\Delta H^{1000\,^{\circ}\mathrm{C}}$

Again there are some keys to customize the command:

```
state exponent = <anything>

state subscript-left = true|false

state delta = <anything>|false
```

15. Spectroscopy and Experimental Data

15.1. The \NMR Command

When you're trying to find out if a compound is the one you think it is often NMR spectroscopy is used. The experimental data are typeset similar to this:

^{1}H-NMR (400 MHz, $CDCl_3$): δ = 1.59

CHEMMACROS provides a command which simplifies the input (uses siunitx).

```
\NMR*{<num>,<elem>}(<num>,<unit>)[<solvent>]
```

All Argument are optional! Without arguments we get:

```
\NMR \\
\NMR*
```

^{1}H-NMR: δ
^{1}H-NMR

The first argument specifies the kind of NMR:

```
\NMR{13,C}
```

^{13}C-NMR: δ

The second argument sets the frequency (in MHz):

```
\NMR(400)
```

^{1}H-NMR (400 MHz): δ

You can choose another unit:

```
\NMR(4e8,\hertz)
```

^{1}H-NMR (4×10^{8} Hz): δ

Please note that the setup of siunitx also affects this command:

```
\sisetup{exponent-product=\cdot}\NMR(4e8,\hertz)
```

^{1}H-NMR ($4 \cdot 10^{8}$ Hz): δ

The third argument specifies the solvent:

```
\NMR[CDCl3]
```

^{1}H-NMR ($CDCl_3$): δ

15.2. Short Cuts

It is possible to define short cut commands for specific nuclei.

`\DeclareChemNMR{<csname>}{<num>,<atom>}`

`\RenewChemNMR{<csname>}{<num>,<atom>}`

This defines a command with the same arguments as `\NMR` *except* for `{<num>,<atom>}`.

```
\DeclareChemNMR\HNMR{1,H}%
\DeclareChemNMR\CNMR{13,C}%
\CNMR*(100) \\
\HNMR*(400)
```

^{13}C-NMR (100 MHz)
^{1}H-NMR (400 MHz)

15.3. An Environment to Typeset Experimental Data

CHEMMACROS provides an environment to ease the input of experimental data.

`\begin{experimental}` data `\end{experimental}`
Environment for the output of experimental data. Inside the environment the following commands are defined.

`\data{<type>}[<specification>]`
Type of data, e.g. IR, MS… The optional argument takes further specifications which are output in parentheses.

`\data*{<type>}[<specification>]`
Like `\data` but changes the `=` into a `:`, given that `use-equal = true` is used.

`\NMR{<num>,<elem>[<coupling core>]}(<num>,<unit>)[<solvent>]`
This command gets an additional argument: `\NMR{13,C[^1H]}` ^{13}C{^{1}H}-NMR: δ

`\J(<bonds>;<nuclei>)[<unit>]{<list of nums>}`
Coupling constant, values are input separated by `;` (NMR). The argument `(<bonds>;<nuclei>)` is optional and enables further specifications of the coupling.

`\#{<num>}`
Number of nuclei (NMR).

`\pos{<num>}`
Position of nuclues (NMR).

`\val{<num>}`
A number, an alias of siunitx' `\num{<num>}`.

`\val{<num1>--<num2>}`
An alias of siunitx' `\numrange{<num1>}{<num2>}`.

```
\begin{experimental}
 \data{type1} Data.
 \data{type2}[specifications] More data.
 \data*{type3} Even more data.
\end{experimental}
```

type1 Data. type2 (specifications) More data. type3 Even more data.

15.4. Customization

The output of the environment and of the NMR commands can be customized be a number of options. For historical reasons they all belong to the module `nmr`.

`nmr unit = <unit>` Default: `\mega\hertz`
The used default unit.

`nmr nucleus = {<num>,<atom>}` Default: `{1,H}`
The used default nucleus.

`nmr format = <commands>` (initially empty)
For example `\bfseries`.

`nmr pos-number = side|sub` Default: `side`
Position of the number next to the atom.

`nmr coupling-unit = <unit>` Default: `\hertz`
A siunitx unit.

`nmr parse = true|false` Default: `true`
Treat the solvent as CHEMFORMULA formula or not.

`nmr delta = <tokens>` (initially empty)
The `<tokens>` are added after δ.

`nmr list = true|false` Default: `false`
The environment `\begin{nmr}[<optionen>] \end{nmr}` is formatted as a list

`nmr list-setup = <setup>`
Setup of the list. See below for the default settings.

`nmr use-equal = true|false` Default: `false`
Add egual sign after `\NMR` and `\data`.

The default setup of the list:

```
    \topsep\z@skip \partopsep\z@skip
    \itemsep\z@ \parsep\z@ \itemindent\z@
    \leftmargin\z@
```

```
\begin{experimental}[format=\bfseries]
 \data{type1} Data.
 \data{type2}[specifications] More data.
 \data*{type3} Even more data.
\end{experimental}
```

type1 Data. **type2 (specifications)** More data. **type3** Even more data.

The command \NMR and all commands defined through \DeclareChemNMR can be used like \data for the NMR data.

```
\begin{experimental}[format=\bfseries,use-equal]
 \data{type1} Data.
 \data{type2}[specifications] More data.
 \NMR Even more data.
\end{experimental}
```

type1 = Data. **type2 (specifications)** = More data. **^{1}H-NMR:** δ = Even more data.

15.5. An Example

The code below is shown with different specifications for <optionen>. Of course options can also be chosen with \chemsetup.

```
\sisetup{separate-uncertainty,per-mode=symbol,detect-all,range-phrase=--}
\begin{experimental}[<optionen>]
 \data*{yield} \SI{17}{\milli\gram} yellow needles (\SI{0.04}{\milli\mole},
  \SI{13}{\percent}).
 %
 \data{mp.} \SI{277}{\celsius} (DSC).
 %
 \NMR(600)[CDCl3] \val{2.01} (s, \#{24}, \pos{5}), \val{2.31} (s, \#{12},
 \pos{1}), \val{6.72--6.74} (m, \#{2}, \pos{11}), \val{6.82} (s, \#{8},
 \pos{3}), \val{7.05--7.07} (m, \#{2}, \pos{12}), \val{7.39--7.41} (m,
  \#{4},
 \pos{9}), \val{7.48--7.49} (m, \#{4}, \pos{8}).
 %
 \NMR{13,C}(150)[CDCl3] \val{21.2} ($+$, \#{4}, \pos{1}), \val{23.4} ($+$,
 \#{8}, \pos{5}), \val{126.0} ($+$, \#{4}, \pos{9}), \val{128.2} ($+$,
  \#{8},
 \pos{3}), \val{130.8} ($+$, \#{2}, \pos{12}), \val{133.6} ($+$, \#{2},
 \pos{11}), \val{137.0} ($+$, \#{4}, \pos{8}), \val{138.6} (q, \#{4},
 \pos{2}), \val{140.6} (q, \#{2}, \pos{10}), \val{140.8} (q, \#{8}, \pos{4})
  ,
 \val{141.8} (q, \#{4}, \pos{6}), \val{145.6} (q, \#{2}, \pos{7}).
 %
 \data{MS}[DCP, EI, \SI{60}{\electronvolt}] \val{703} (2, \ch{M+}), \val
```

```
    {582}
(1), \val{462} (1), \val{249} (13), \val{120} (41), \val{105} (100).
%
\data{MS}[\ch{MeOH + H2O + KI}, ESI, \SI{10}{\electronvolt}] \val{720}
 (100,
\ch{M+ + OH-}), \val{368} (\ch{M+ + 2 OH-}).
%
\data{IR}[KBr] \val{3443} (w), \val{3061} (w), \val{2957} (m), \val{2918}
(m), \val{2856} (w), \val{2729} (w), \val{1725} (w), \val{1606} (s),
\val{1592} (s), \val{1545} (w), \val{1446} (m), \val{1421} (m), \val{1402}
(m), \val{1357} (w), \val{1278} (w), \val{1238} (s), \val{1214} (s),
\val{1172} (s), \val{1154} (m), \val{1101} (w), \val{1030} (w), \val{979}
(m), \val{874} (m), \val{846} (s), \val{818} (w), \val{798} (m), \val{744}
(w), \val{724} (m), \val{663} (w), \val{586} (w), \val{562} (w), \val{515}
(w).
%
\data*{UV-Vis} \SI{386}{\nano\metre} ($\varepsilon = \val{65984}$),
\SI{406}{\nano\metre} ($\varepsilon = \val{65378}$).
%
\data*{quantum yield} $\Phi = \val{0.74+-0.1}$\,.
\end{experimental}
```

15.5.1. Nearly Standard

Output with these options: `<optionen>: delta=(ppm),pos-number=sub,use-equal`

yield: 17 mg yellow needles (0.04 mmol, 13 %). mp. = 277 °C (DSC). ^{1}H-NMR (600 MHz, $CDCl_3$): δ (ppm) = 2.01 (s, 24 H, H_5), 2.31 (s, 12 H, H_1), 6.72–6.74 (m, 2 H, H_{11}), 6.82 (s, 8 H, H_3), 7.05–7.07 (m, 2 H, H_{12}), 7.39–7.41 (m, 4 H, H_9), 7.48–7.49 (m, 4 H, H_8). ^{13}C-NMR (150 MHz, $CDCl_3$): δ (ppm) = 21.2 (+, 4 C, C_1), 23.4 (+, 8 C, C_5), 126.0 (+, 4 C, C_9), 128.2 (+, 8 C, C_3), 130.8 (+, 2 C, C_{12}), 133.6 (+, 2 C, C_{11}), 137.0 (+, 4 C, C_8), 138.6 (q, 4 C, C_2), 140.6 (q, 2 C, C_{10}), 140.8 (q, 8 C, C_4), 141.8 (q, 4 C, C_6), 145.6 (q, 2 C, C_7). MS (DCP, EI, 60 eV) = 703 (2, M^+), 582 (1), 462 (1), 249 (13), 120 (41), 105 (100). MS (MeOH + H_2O + KI, ESI, 10 eV) = 720 (100, $M^+ + OH^-$), 368 ($M^+ + 2\,OH^-$). IR (KBr) = 3443 (w), 3061 (w), 2957 (m), 2918 (m), 2856 (w), 2729 (w), 1725 (w), 1606 (s), 1592 (s), 1545 (w), 1446 (m), 1421 (m), 1402 (m), 1357 (w), 1278 (w), 1238 (s), 1214 (s), 1172 (s), 1154 (m), 1101 (w), 1030 (w), 979 (m), 874 (m), 846 (s), 818 (w), 798 (m), 744 (w), 724 (m), 663 (w), 586 (w), 562 (w), 515 (w). UV-Vis: 386 nm (ε = 65 984), 406 nm (ε = 65 378). quantum yield: $\Phi = 0.74 \pm 0.10$.

15.5.2. Formatted List

Output with these options: `<optionen>: format=\bfseries,delta=(ppm),list=true,use-equal`

yield: 17 mg yellow needles (0.04 mmol, 13 %).
mp. = 277 °C (DSC).
^{1}H-NMR (600 MHz, $CDCl_3$): δ (ppm) = 2.01 (s, 24 H, H-5), 2.31 (s, 12 H, H-1), 6.72–6.74 (m, 2 H, H-11), 6.82 (s, 8 H, H-3), 7.05–7.07 (m, 2 H, H-12), 7.39–7.41 (m, 4 H, H-9), 7.48–7.49 (m, 4 H, H-8).
^{13}C-NMR (150 MHz, $CDCl_3$): δ (ppm) = 21.2 (+, 4 C, C-1), 23.4 (+, 8 C, C-5), 126.0 (+, 4 C, C-9), 128.2 (+, 8 C, C-3), 130.8 (+, 2 C, C-12), 133.6 (+, 2 C, C-11), 137.0 (+, 4 C, C-8), 138.6 (q, 4 C, C-2), 140.6 (q, 2 C, C-10), 140.8 (q, 8 C, C-4), 141.8 (q, 4 C, C-6), 145.6 (q, 2 C, C-7).
MS (DCP, EI, 60 eV) = 703 (2, M^+), 582 (1), 462 (1), 249 (13), 120 (41), 105 (100).

MS (MeOH + H_2O + KI, ESI, 10 eV) = 720 (100, $M^+ + OH^-$), 368 ($M^+ + 2\,OH^-$).
IR (KBr) = 3443 (w), 3061 (w), 2957 (m), 2918 (m), 2856 (w), 2729 (w), 1725 (w), 1606 (s), 1592 (s), 1545 (w), 1446 (m), 1421 (m), 1402 (m), 1357 (w), 1278 (w), 1238 (s), 1214 (s), 1172 (s), 1154 (m), 1101 (w), 1030 (w), 979 (m), 874 (m), 846 (s), 818 (w), 798 (m), 744 (w), 724 (m), 663 (w), 586 (w), 562 (w), 515 (w).
UV-Vis: 386 nm (ε = 65 984), 406 nm (ε = 65 378).
quantum yield: $\Phi = 0.74 \pm 0.10$.

15.5.3. Crazy

Output for these options: <optionen>:

```
format=\color{red}\itshape,
list=true,
delta=\textcolor{green}{\ch{M+ + H2O}},
pos-number=side,
coupling-unit=\mega\gram\per\square\second,
list-setup=,
use-equal
```

yield: 17 mg yellow needles (0.04 mmol, 13 %).

mp. = 277 °C (DSC).

^{1}H-NMR (600 MHz, $CDCl_3$): δ $M^+ + H_2O$ = 2.01 (s, 24 H, H-5), 2.31 (s, 12 H, H-1), 6.72–6.74 (m, 2 H, H-11), 6.82 (s, 8 H, H-3), 7.05–7.07 (m, 2 H, H-12), 7.39–7.41 (m, 4 H, H-9), 7.48–7.49 (m, 4 H, H-8).

^{13}C-NMR (150 MHz, $CDCl_3$): δ $M^+ + H_2O$ = 21.2 (+, 4 C, C-1), 23.4 (+, 8 C, C-5), 126.0 (+, 4 C, C-9), 128.2 (+, 8 C, C-3), 130.8 (+, 2 C, C-12), 133.6 (+, 2 C, C-11), 137.0 (+, 4 C, C-8), 138.6 (q, 4 C, C-2), 140.6 (q, 2 C, C-10), 140.8 (q, 8 C, C-4), 141.8 (q, 4 C, C-6), 145.6 (q, 2 C, C-7).

MS (DCP, EI, 60 eV) = 703 (2, M^+), 582 (1), 462 (1), 249 (13), 120 (41), 105 (100).

MS (MeOH + H_2O + KI, ESI, 10 eV) = 720 (100, $M^+ + OH^-$), 368 ($M^+ + 2\,OH^-$).

IR (KBr) = 3443 (w), 3061 (w), 2957 (m), 2918 (m), 2856 (w), 2729 (w), 1725 (w), 1606 (s), 1592 (s), 1545 (w), 1446 (m), 1421 (m), 1402 (m), 1357 (w), 1278 (w), 1238 (s), 1214 (s), 1172 (s), 1154 (m), 1101 (w), 1030 (w), 979 (m), 874 (m), 846 (s), 818 (w), 798 (m), 744 (w), 724 (m), 663 (w), 586 (w), 562 (w), 515 (w).

UV-Vis: 386 nm (ε = 65 984), 406 nm (ε = 65 378).

quantum yield: $\Phi = 0.74 \pm 0.10$.

16. Commands for mhchem

mhchem is not officially supported by CHEMMACROS as it used CHEMFORMULA instead. However, for historical reasons the following command is still provided.

`\mhName[<keyval>]{<formula>}{<text>}`

For example:

```
\ce{4 C2H5Cl + Pb{/}Na -> \mhName{Pb(C2H5)4}{former antiknock additive} + NaCl}
```

There are several keys to customize `\mhName`.

`mhName align = <alignment command>` Default: `\centering`

The alignment of the text in the box it is placed in.

`mhName format = <anything>` (initially empty)

The format of the text.

`mhName fontsize = <font size command>` Default: `\tiny`

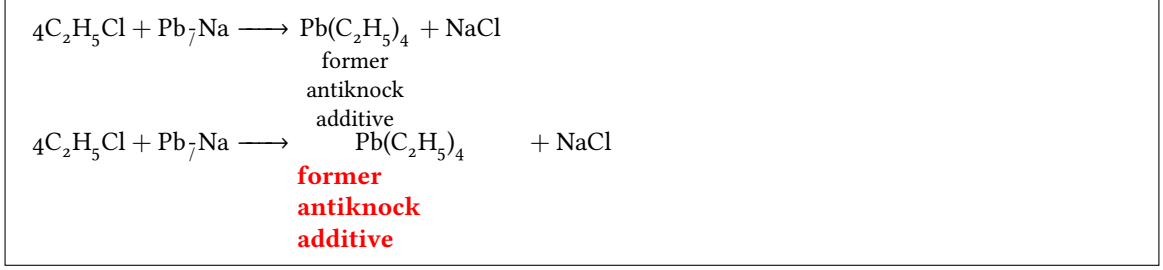
The fontsize of the text.

`mhName width = <dim>|auto` Default: `auto`

The width of the box the text is placed in.

Since version 3.13 of mhchem you need to hide the command in braces if you want to use the optional argument,

```
\ce{4 C2H5Cl + Pb / Na -> {\mhName[fontsize=\footnotesize]{Pb(C2H5)4}{former
 antiknock additive}} + NaCl}\\
\chemsetup[mhName]{align=\raggedright,fontsize=\small,format=\bfseries\color{red
 },width=3cm}
\ce{4 C2H5Cl + Pb / Na -> \mhName{Pb(C2H5)4}{former antiknock additive} + NaCl}
```



17. Reaction Environments

17.1. Defined by CHEMMACROS

You can use these environments for numbered...

`\begin{reaction}` <formula or mhchem code> `\end{reaction}`

`\begin{reactions}` <formula or mhchem code> `\end{reactions}`

...and their starred versions for unnumbered reactions.

`\begin{reaction*}` <formula or mhchem code> `\end{reaction*}`

`\begin{reactions*}` <formula or mhchem code> `\end{reactions*}`

With them you can create (un)numbered reaction equations similar to mathematical equations. Theses environments use the `equation`/`equation*` environments or the `align`/`align*` environments, respectively, to display the reactions.

```
Reaction with counter:
\begin{reaction}
 A -> B
\end{reaction}
```

Reaction with counter:

$$\mathrm{A} \longrightarrow \mathrm{B} \qquad \{1\}$$

```
Reaction without counter:
\begin{reaction*}
 C -> D
\end{reaction*}
```

Reaction without counter:

$$\mathrm{C} \longrightarrow \mathrm{D}$$

```
Several aligned reactions with counter:
\begin{reactions}
 A     &-> B + C \\
 D + E &-> F
\end{reactions}
```

Several aligned reactions with counter:

$$\begin{aligned} \mathrm{A} &\longrightarrow \mathrm{B + C} && \{2\} \\ \mathrm{D + E} &\longrightarrow \mathrm{F} && \{3\} \end{aligned}$$

```
Several aligned reactions without counter:
\begin{reactions*}
 G     &-> H + I \\
 J + K &-> L
\end{reactions*}
```

Several aligned reactions without counter:

$$\begin{aligned} \mathrm{G} &\longrightarrow \mathrm{H + I} \\ \mathrm{J + K} &\longrightarrow \mathrm{L} \end{aligned}$$

If you want to change the layout of the counter tags, you can use `\renewtagform{<tagname>}[<format>]{<right delim>}{<left delim>}`.[28]

```
\renewtagform{reaction}[R \textbf]{[}{]}
\begin{reaction}
 H2O + CO2 <=> H2CO3
\end{reaction}
```

$$\mathrm{H_2O + CO_2} \rightleftharpoons \mathrm{H_2CO_3} \qquad [\mathrm{R}\ \mathbf{4}]$$

With version 3.3 referencing and the use of AMSmath's `\intertext` also function properly:

[28] Provided by the mathtools package

```
\begin{reactions}
 A + 2 B &-> 3 C + D \label{rxn:test}
 \intertext{Some text in between aligned reactions}
 3 E + F &<=> G + 1/2 H
\end{reactions}
See reaction~\ref{rxn:test}.
```

$$\mathrm{A} + 2\,\mathrm{B} \longrightarrow 3\,\mathrm{C} + \mathrm{D} \tag{5}$$

Some text in between aligned reactions

$$3\,\mathrm{E} + \mathrm{F} \rightleftharpoons \mathrm{G} + \frac{1}{2}\,\mathrm{H} \tag{6}$$

See reaction 5.

You should not use `\mch` and its relatives inside the `reaction` environments.

17.2. Own Reactions

You can create new types of reactions with the command:

`\DeclareChemReaction[<keyval>]{<name>}{<math name>}`

`<name>` will be the name of the new environment. `<math name>` is the used math environment.

The command has two options.

−none− star = true|false

−none− arg = true|false

There is `star`, which will also define a starred version of the new environment, if the starred math environment exists. If it doesn't exist, this will cause an error.

Then there is `arg`, which is used to define an environment with a mandatory argument. Of course this only works, if the used math environment has a mandatory argument.

The predefined environments are defined via

`\DeclareChemReaction[star]{reaction}{equation}` and

`\DeclareChemReaction[star]{reactions}{align}`.

Let's suppose, you'd like to have the alignment behaviour of the `alignat` environment for chemformula/mhchem reactions. You could do the following:

`\DeclareChemReaction[star,arg]{reactionsat}{alignat}`

With this the `reactionsat` environment is defined.

```
\DeclareChemReaction[star,arg]{reactionsat}{alignat}
\begin{reactionsat}{3}
 A     &-> B     &&-> C     &&-> D \\
 aaaaa &-> bbbbb &&-> ccccc &&-> ddddd
\end{reactionsat}
\begin{reactionsat*}{2}
 A     &-> B     & C            &-> D  \\
 aaaaa &-> bbbbb &\quad{} ccccc &-> ddddd
\end{reactionsat*}
```

$$\begin{aligned} A &\longrightarrow B &&\longrightarrow C &&\longrightarrow D && \{7\}\\ aaaaa &\longrightarrow bbbbb &&\longrightarrow ccccc &&\longrightarrow ddddd && \{8\} \end{aligned}$$

$$\begin{aligned} A &\longrightarrow B & C &\longrightarrow D\\ aaaaa &\longrightarrow bbbbb & ccccc &\longrightarrow ddddd \end{aligned}$$

17.3. List of Reactions

CHEMMACROS also provides a command to display a list of the reactions created with the `reaction` environment.

`\listofreactions`

```
\listofreactions
```

List of reactions

The Output of this list can be modified by two options:

`reaction list-name = <name of the list>` Default: `List of reactions`

Let's you set the name of the list manually. The default name is language dependent, see section 6.

`reaction list-entry = <prefix to each entry>` Default: `Reaction`

Let's you set a prefix to each list entry. The default name is language dependent, see section 6.

Instead of using the option `list-name` you also could redefine `\reactionlistname`.

The list lists all reactions with a number and disregards reactions without number. All reaction environments without star have an optional argument which let's you add a description (or caption) for the entry in the list.

```
\begin{reaction}[Autoprotolyse]
 2 H2O <<=> H3O+ + OH-
\end{reaction}
```

$$2\,H_2O \rightleftharpoons H_3O^+ + OH^- \qquad \{9\}$$

If you use the `reactions` environment this will not work, though. In this case you can use

`\AddRxnDesc{<description>}`

```
\begin{reactions}
 Cl "\Lewis{0.,\vphantom{Cl}}" + CH4  &
   -> HCl + "\Lewis{4.,\vphantom{CH}}" CH3 \AddRxnDesc{first~step~of~chain} \\
 "\Lewis{4.,\vphantom{CH}}" CH3 + Cl2 &
   -> CH3Cl + Cl "\Lewis{0.,\vphantom{Cl}}" \AddRxnDesc{second~step~of~chain}
\end{reactions}
```

$$Cl\cdot + CH_4 \longrightarrow HCl + \cdot CH_3 \qquad \{10\}$$

$$\cdot CH_3 + Cl_2 \longrightarrow CH_3Cl + Cl\cdot \qquad \{11\}$$

Note: you don't have to use the phantom commands if you haven't changed the format of the atoms (see the documentation of the CHEMFORMULA package for information on how to do this).

18. Phases

18.1. Basics

These commands are intended to indicate the phase of a compound.

`\sld` (s)

`\lqd` (lc)

`\gas` (g)

`\aq` (aq)

The default behaviour of the phases commands has changed to be consistent with IUPAC recommendations. Both `\sld` and `\lqd` have lost their optional argument.

```
\ch{C\sld{} + 2 H2O\lqd{} -> CO2\gas{} + 2 H2\gas}\\
To make it complete: NaCl\aq.
```

$\mathrm{C(s) + 2\,H_2O(lc) \longrightarrow CO_2(g) + 2\,H_2(g)}$
To make it complete: $\mathrm{NaCl(aq)}$.

The IUPAC recommendation to indicate the state of aggregation is to put it in parentheses after the compound [Coh+08]. However, you might want to put it as a subscript which is also very common.

> The [...] symbols are used to represent the states of aggregation of chemical species. The letters are appended to the formula in parentheses and should be printed in Roman (upright) type without a full stop (period). *IUPAC Green Book* [*Coh+08, p. 54*]

There are two options to customize the output:

`phases pos = side|sub` Default: `side`

Switch the position of the phase indicator.

`phases space = <dim>` Default: `.1333em`

Change the default spacing between compound a phase indicator if `pos = side`. A TEX dimension.

```
\chemsetup[phases]{pos=sub}
\ch{C\sld{} + 2 H2O\lqd{} -> CO2\gas{} + 2 H2\gas}\\
To make it complete: NaCl\aq.
```

$\mathrm{C_{(s)} + 2\,H_2O_{(lc)} \longrightarrow CO_{2(g)} + 2\,H_{2(g)}}$
To make it complete: $\mathrm{NaCl_{(aq)}}$.

18.2. Define Own Phases

Depending on the subject of your document you might need to indicate other states of aggregation. You can easily define them.

`\DeclareChemPhase{<cmd>}[<german>]{<english>}`

`\RenewChemPhase{<cmd>}[<german>]{<english>}`

`\phase{<phase>}`

If you need a phase indicator just once or twice.

`\DeclareChemPhase` only defines a phase if `<cmd>` is not already used by any other command. If it *is* already used CHEMMACROS will either give a warning or an error, depending on the option `strict`. `\RenewChemPhase` *only* defines a phase if `<cmd>` *is* already used and issues a warning/error otherwise. Unlike the other declaration commands of CHEMMACROS `\DeclareChemPhase` and `\RenewChemPhase` *can only be used in the preamble.*

```
% preamble:
% \DeclareChemPhase{\aqi}{aq,$\infty$}% aqueous solution at infinite dilution
% \DeclareChemPhase{\cd}{cd}% condensed phase
% \RenewChemPhase{\lqd}{lc}% liquid crystal
NaOH\aqi\ \ch{H2O\cd} U\phase{cr} A\lqd \\
\chemsetup[phases]{pos=sub}
NaOH\aqi\ \ch{H2O\cd} U\phase{cr} A\lqd
```

NaOH (aq,∞) H_2O (cd) U (cr) A (lc)
$NaOH_{(aq,\infty)}$ $H_2O_{(cd)}$ $U_{(cr)}$ $A_{(lc)}$

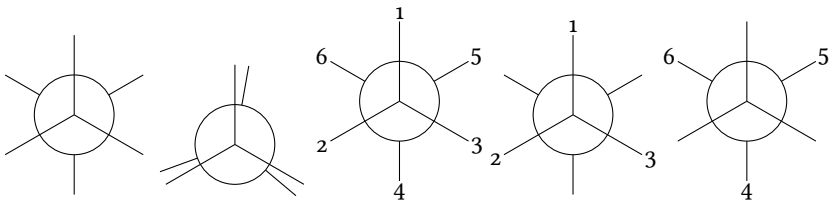
19. Newman Projections

CHEMMACROS provides the command

`\newman[<keyval>](<angle>){<1>,<2>,<3>,<4>,<5>,<6>}`

which allows you to create newman projections (uses Ti*k*Z). With `<angle>` the back atoms are rotated counter clockwise with respect to the front atoms.

```
\newman{} \newman(170){}
\newman{1,2,3,4,5,6} \newman{1,2,3} \newman{,,,4,5,6}
```



Several options allow customization:

`newman angle = <angle>` Default: `0`
Default angle.

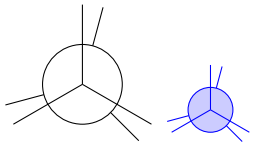
`newman scale = <factor>` Default: `1`
Scale the whole projection.

`newman ring = <tikz>` (initially empty)
Customize the ring with Ti*k*Z keys.

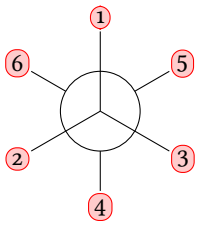
`newman atoms = <tikz>` (initially empty)
Customize the nodes within which the atoms are set.

`newman back-atoms = <tikz>` (initially empty)
Explicitly customize the back atoms.

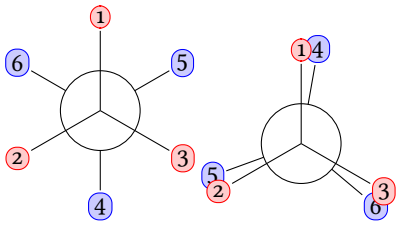
```
\chemsetup[newman]{angle=45} \newman{}
\newman[scale=.75,ring={draw=blue,fill=blue!20}]{}
```



```
\chemsetup[newman]{atoms={draw=red,fill=red!20,inner sep=2pt,rounded corners}}
\newman{1,2,3,4,5,6}
```




```
\chemsetup[newman]{
  atoms = {draw=red,fill=red!20,inner sep=2pt,rounded corners},
  back-atoms = {draw=blue,fill=blue!20,inner sep=2pt,rounded corners}
}
\newman{1,2,3,4,5,6} \newman(170){1,2,3,4,5,6}
```



20. s, p, and Hybrid Orbitals

CHEMMACROS provides the following command to create orbitals:

`\orbital[<keyval>]{<type}`

There are the following types available for `<type>`:

`s`

`p`

`sp`

`sp2`

sp3

```
\orbital{s} \orbital{p} \orbital{sp} \orbital{sp2} \orbital{sp3}
```

Depending on the type you have different options to modify the orbitals:

`orbital phase = +|-`
changes the phase of the orbital (all types)

`orbital scale = <factor>`
changes the size of the orbital (all types)

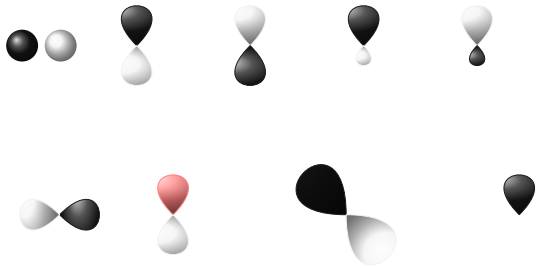
`orbital color = <color>`
changes the color of the orbital (all types)

`orbital angle = <angle>`
rotates the orbitals with a p contribution counter clockwise (all types except `s`)

`orbital half = true|false`
displays only half an orbital (only `p`)

```
\orbital{s} \orbital[phase=-]{s}
\orbital{p} \orbital[phase=-]{p}
\orbital{sp3} \orbital[phase=-]{sp3}

\orbital[angle=0]{p} \orbital[color=red!50]{p}
\orbital[angle=135,scale=1.5]{p} \orbital[half]{p}
```

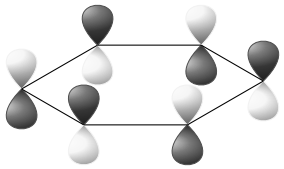


Additionally there are two options, with which the Ti*k*Z behaviour can be changed.

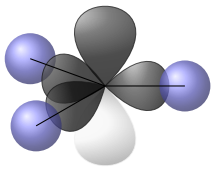
`orbital overlay = true|false`
The orbital "doesn't need space"; it is displayed with the Ti*k*Z option `overlay`.

`orbital opacity = <num>`
The orbital becomes transparent; `<value>` can have values between `1` (fully opaque) to `0` (invisible).

```
\hspace{1cm}
\chemsetup[orbital]{
  overlay,
  p/color = black!70
}
\setbondoffset{0pt}
\chemfig{
  ?\orbital{p}
  -[,1.3]{\orbital[phase=-]{p}}
  -[:30,1.1]\orbital{p}
  -[:150,.9]{\orbital[phase=-]{p}}
  -[4,1.3]\orbital{p}
  -[:-150,1.1]{\orbital[phase=-]{p}}?
}
\vspace{7mm}
```



```
\hspace{2cm}
\setbondoffset{0pt}
\chemsetup[orbital]{
  overlay ,
  opacity = .75 ,
  p/scale = 1.6 ,
  s/color = blue!50 ,
  s/scale = 1.6
}
\chemfig{
  \orbital{s}
  -[:-20]{\orbital[scale=2]{p}}{\orbital[half,angle=0]{p}}{\orbital[angle=170,
 half]{p}}{\orbital[angle=-150,half]{p}}
  (-[:-150]\orbital{s})-\orbital{s}
}
\vspace{1cm}
```



Part III.
Other Packages of the Bundle

The other three package, chemformula, ghsystem and chemgreek, all have their own documentation:

- `chemformula_en.pdf`
- `ghsystem_en.pdf`
- `chemgreek_en.pdf`

Introduced in version 4.0

This change has been made with version 4.0 since with this version every of those packages can be used independently from the chemmacros package. It made sense to give each of them an own documentation file. You should be able to find them in the same folder as this document as well as via the `texdoc` program. You can also try and click on the names in the list above. They are links and *should* open the respective file.

Part IV.
Appendix

Suggestions and Bug Reports

Feedback on chemmacros, chemformula and ghsystem is highly appreciated and welcome!

If you have suggestions for macros, missing features etc., please don't hesitate to contact me. If you recognize any errors, be it chemical ones, wrong documentation and the like, I'd be grateful about a short email.[29]

If you find any bugs, it would be best, if you'd send me a minimal example, with which I can reproduce the bug. You can also submit an issue on `https://bitbucket.org/cgnieder/chemmacros/` instead.

Many thanks to all the people who already provided me with feedback, especially (in alphabetical order):

- Peter Cao
- Christina Lüdigk
- Dr. Paul King
- Jonas Rivetti (Special thanks for his translation of the hazard and precautionary statements into Italian!)
- Christoph Schäfer
- Timo Stein

[29] contact@mychemistry.eu

References

[Coh+08] E. Richard Cohan, Tomislav Cvitaš, Jeremy G. Frey, Bertil Holmström, Kozo Kuchitsu, Roberto Marquardt, Ian Mills, Franco Pavese, Martin Quack, Jürgen Stohner, Herbert L. Strauss, Michio Takami, and Anders J Thor. *"Quantities, Symbols and Units in Physical Chemistry", IUPAC Green Book*. 3rd Edition. 2nd Printing. IUPAC & RSC Publishing, Cambridge, 2008.

[Con+05] Neil G. Connelly, Ture Damhus, Richard M. Hartshorn, and Alan T. Hutton. *"Nomenclature of Inorganic Chemistry", IUPAC Red Book*. IUPAC & RSC Publishing, Cambridge, 2005. ISBN: 0-85404-438-8.

[Eur12] United Nations Economic Commission for Europe. *GHS Implementation*. Mar. 20, 2012. URL: `http://www.unece.org/trans/danger/publi/ghs/implementation_e.html` (visited on 03/20/2012).

[The08] The European Parliament and The Council of the European Union. *Regulation (EC) No 1272/2008 of the European Parliament and of the Council. on classification, labelling and packaging of substances and mixtures, amending and repealing Directives 67/548/EEC and 1999/45/EC, and amending Regulation (EC) No 1907/2006*. Dec. 16, 2008.

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Section titles are indicated **bold**, packages sans serif, commands \brown, options yellow and modules (only CHEMMACROS) blue.