

# the chemmacros bundle

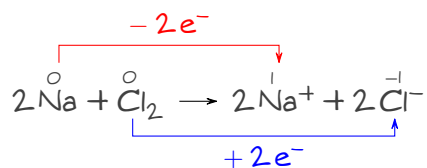
v3.3a      2012/05/13

packages `chemmacros`, `chemformula` and `ghsystem`

Clemens NIEDERBERGER

<https://bitbucket.org/cgnieder/chemmacros/>  
[contact@mychemistry.eu](mailto:contact@mychemistry.eu)

English documentation



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# Part I.

## Preliminaries

### 1. Licence, Requirements and README

The CHEMMACROS bundle underlies the L<sup>A</sup>T<sub>E</sub>X project public license (lppl) version 1.3 or later (<http://www.latex-project.org/lppl.txt>) and has the status “maintained”.

The CHEMMACROS bundle needs the bundles l3kernel<sup>1</sup> and l3packages<sup>2</sup>. It also needs the packages siunitx<sup>3</sup>, mathtools<sup>4</sup>, bm<sup>5</sup>, nicefrac<sup>6</sup> and environ<sup>7</sup> as well as tikz<sup>8</sup> and the TikZ libraries calc and arrows.

Package option bpchem (section 4) needs the package bpchem<sup>9</sup>, package option xspace needs the package xspace<sup>10</sup> and package option method = mhchem needs the package mhchem<sup>11</sup>.

With v3.0 the CHEMMACROS package has been bundled with the new packages CHEMFORMULA and GHSYSTEM. CHEMFORMULA provides an alternative to mhchem. This leads to some internal changes in CHEMMACROS. On the same time the documentation has been redesigned.

You might remember that CHEMMACROS’ options all belong to different modules, see section 5 for further information. These are typeset in the left margin when the option is first mentioned. In section V all options and the module they belong to are listed. Throughout the document options are typeset green and modules red.

The package GHSYSTEM needs the packages CHEMMACROS, tabu<sup>12</sup>, longtable<sup>13</sup>, ifpdf<sup>14</sup> and graphicx<sup>15</sup>. GHSYSTEM has no own package options but passes all options on to CHEMMACROS.

There are some deprecated commands and options which are not explained in the manual any more but still exist to ensure backwards compatibility. These commands issue a warning. They may be dropped some time in the future.

### 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.

<sup>1</sup> CTAN: l3kernel   <sup>2</sup> CTAN: l3packages   <sup>3</sup> CTAN: siunitx   <sup>4</sup> CTAN: mathtools   <sup>5</sup> CTAN: bm   <sup>6</sup> CTAN: nicefrac  
<sup>7</sup> CTAN: environ   <sup>8</sup> CTAN: pgf   <sup>9</sup> CTAN: bpchem   <sup>10</sup> CTAN: xspace   <sup>11</sup> CTAN: mhchem   <sup>12</sup> CTAN: tabu  
<sup>13</sup> CTAN: longtable   <sup>14</sup> CTAN: ifpdf   <sup>15</sup> CTAN: graphicx

Probably every chemist using  $\LaTeX$  2<sub>ε</sub> is aware of the great mhchem 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. Since CHEMFORMULA is meant as an *alternative* to mhchem CHEMMACROS offers a package option allowing you to choose which one of the two is used. The default however is CHEMMACROS own way: CHEMFORMULA.

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 now 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 [The08].

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
- IUPAC compliant default settings

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<sup>16</sup> I would welcome an email very much!

In a package this large with older parts and rather new parts (which have to be considered being in beta state) it is unavoidable that there are flaws and bugs. I am very keen on correcting and improving this package so please: if you find anything that bothers you and may it be just so small please send me a short email and I'll see what I can do. I would especially like feedback on CHEMFORMULA (see part III) and GHSYSTEM (see part IV) but also welcome feedback on every other part of this bundle.

### 3. Installation, Loading the Bundle

The bundle comes with three style files<sup>17</sup>, a directory called language/ containing the language-definition files for GHS (ending def), and a directory pictures/ containing eps, jpg and png files

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<sup>16</sup> This does not concern the `\ox` command. The IUPAC version is `\ox*`. <sup>17</sup> Those ending sty.

(the GHS pictograms). If you install the bundle manually *please make sure to place the directories language/ and pictures/ in the same directory as the style files.*

Loading CHEMMACROS with

```
1 \usepackage{chemmacros} % 'chemmacros', 'chemformula' and 'ghsystem' are
   loaded
```

will also load CHEMFORMULA and GHSYSTEM. However, you can prevent CHEMMACROS from loading GHSYSTEM:

```
1 \usepackage[ghsystem=false]{chemmacros} % 'chemmacros' and 'chemformula' are
   loaded
```

Loading CHEMFORMULA or GHSYSTEM explicitly is possible and will also load CHEMMACROS if it hasn't been loaded yet, and will therefore implicitly load the other package, too.

```
1 \usepackage{chemformula} % 'chemmacros', 'chemformula' and 'ghsystem' are
   loaded
2 or
3 \usepackage[ghsystem=false]{chemformula} % 'chemmacros' and 'chemformula'
   are loaded
```

However, it is recommended to simply use `\usepackage{chemmacros}` and setup the required options with `\chemsetup` (also see section 5).

## 4. Package Options

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

```
1 \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 you can give them CHEMMACROS' options instead and they will pass them on to CHEMMACROS.

**option ▶ bpchem** = true/false → This option loads the package bpchem and adjusts the layout of the `\NMR` command to the bpchem commands `\HNMR` and `\CNMR`. (default = false)

**option ▶ circled** = formal/all/none → CHEMMACROS uses two different kinds of charges which indicate the usage of real (+/-) and formal ( $\oplus/\ominus$ ) charges. The option formal distinguishes between them, option none displays them all without circle, option all circles all (default = formal)

- option** ▶ **circletype** = chem/math → This option switches between two kinds of circled charge symbols: `\fplus`  $\oplus$  and `\oplus`  $\oplus$ . (default = chem)
- option** ▶ **cmversion** = 1/2/bundle → This option restores the old definitions of some commands, so documents set with v1.\* will still compile correctly. (default = bundle). Actually 2 and bundle are only aliases. *This option can only be chosen in the preamble.*
- option** ▶ **ghsystem** = true/false → Disable the use of the **GHSYSTEM** package. Setting **ghs** = false will prevent **CHEMMACROS** from loading **GHSYSTEM**. (default = true)
- option** ▶ **greek** = math/textgreek/upgreek → This Options determines how the letters `\Chemalpha` and friends are typeset. See page 10 for more information. *This option can only be chosen in the preamble.* (default = upgreek)
- option** ▶ **iupac** = auto/restricted/strict → Take care of how iupac naming commands are defined, see page 12 (default = auto)
- option** ▶ **language** = american/british/english/french/german/italian/ngerman → Load language specific options. english, american and british are aliases, as are german and ngerman. *This option can only be chosen in the preamble.* (default = english).
- option** ▶ **method** = chemformula/mhchem → You can choose the method which **CHEMMACROS** will use for the reaction environments (see section 18) and the typesetting of the particles (see section 8). (default = chemformula). *This option can only be chosen in the preamble.*
- option** ▶ **Nu** = chemmacros/mathspec → The package mathspec<sup>18</sup> also defines a macro `\Nu`. This option chooses which definition holds, see page 9. (default = chemmacros). *This option can only be chosen in the preamble.*
- option** ▶ **strict** = true/false → Setting **strict** = true will turn all warning messages into errors messages. (default = false)
- option** ▶ **synchronize** = true/false → The setting true will tell **CHEMMACROS** the adapt the font settings of **CHEMFORMULA** if that method has been chosen (default = false). In order to demonstrate this feature this document is set with **synchronize** = true and the **CHEMFORMULA** setting `\chemsetup [chemformula]{font-spec={[[Color=darkgray]Latin Modern Sans}}`.
- option** ▶ **xspace** = true/false → With this option most commands are defined with a `\xspace`. (default = true)

## 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

---

<sup>18</sup> CTAN: mathspec

► `\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 can also be used with the `\chemsetup` command (except for the option `version = 1/2/3`).

```
1 \chemsetup[option]{circled=none}\mch\ \pch\ \fmch\ \fpch\ \el\ \prt \\  
2 \chemsetup[option]{circled=formal}\mch\ \pch\ \fmch\ \fpch\ \el\ \prt \\  
3 \chemsetup[option]{circletype=math}\mch\ \pch\ \fmch\ \fpch\ \el\ \prt \\  
4 \chemsetup{option/circletype=chem,option/circled=all}\mch\ \pch\ \fmch\ \fpch\ \  
   el\ \prt \\  
5 \chemsetup{option/circletype=math}\mch\ \pch\ \fmch\ \fpch\ \el\ \prt  
  
- + - + e- p+  
- + ⊖ ⊕ e- p+  
- + ⊖ ⊕ e- p+  
⊖ ⊕ ⊖ ⊕ e⊖ p⊕  
⊖ ⊕ ⊖ ⊕ 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 `ghs`.

## 6. Language Settings

### 6.1. Supported Languages

By choosing the option

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

you can set one of these languages: american/british/english/french/german/italian/ngerman. The languages american/british/english are aliases, as are german/ngerman.

These translate

- 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.

Please note, that the GHS statements are not provided in all languages, see also section 36.

## 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*

## 7. News

### 7.1. Version 3.3

- With v3.3 there is the environment `\begin{experimental} \end{experimental}`, see section 16. It can be used together with some new options and commands for the consistent typesetting of experimental data.
- The environment `\begin{reaction} \end{reaction}` and its kin can now cope with `\label`, `\ref` and `\intertext`, see section 18.
- The package options `german` and `ngerman` are deprecated, the replacement is `language`, see page 6 and section 6 from page 7.
- The package option `upgreek` got renamed into `greek`.
- Some additional `\Chem<greekletter>`-commands are provided, see section 8.

### 7.2. Version 3.3a

- The IUPAC commands `\hapto` and `\bridge` are new.
- The H and P statements now are available in Italian.

## Part II.

# chemmacros

## 8. Particles, Ions and Symbols

### 8.1. 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.

- ▶ `\Hp1` →  $\text{H}^+$  (proton)
- ▶ `\Hyd` →  $\text{OH}^-$  (hydroxide)
- ▶ `\HtO` →  $\text{H}_3\text{O}^+$  (oxonium ion) (H three O)
- ▶ `\water` →  $\text{H}_2\text{O}$
- ▶ `\e1` →  $\text{e}^-$  (electron)
- ▶ `\prt` →  $\text{p}^+$  (proton)
- ▶ `\ntr` →  $\text{n}^0$  (neutron)
- ▶ `\Nu` →  $\text{Nu}^-$  (nucleophile). The package `mathspec` also defines a macro `\Nu`. If you chose package option `Nu = mathspec` `CHEMMACROS` defines `\Nuc` instead.
- ▶ `\El` →  $\text{E}^+$  (electrophile)
- ▶ `\ba` →  $\text{ba}^-$  (base)
- ▶ `\fplus` →  $\oplus$
- ▶ `\fminus` →  $\ominus$
- ▶ `\transitionstatesymbol` →  $\ddagger$
- ▶ `\standardstate` →  $\ominus$ . This symbol is only provided by `CHEMMACROS`, if the package `chemstyle`<sup>19</sup> is not loaded; the idea is borrowed from there<sup>20</sup>.
- ▶ `\Chemalpha` →  $\alpha$
- ▶ `\Chembeta` →  $\beta$
- ▶ `\Chemgamma` →  $\gamma$
- ▶ `\Chemdelta` →  $\delta$
- ▶ `\Chemepsilon` →  $\varepsilon$
- ▶ `\Chemeta` →  $\eta$
- ▶ `\Chemkappa` →  $\kappa$
- ▶ `\Chemmu` →  $\mu$
- ▶ `\Chemnu` →  $\nu$
- ▶ `\Chemrho` →  $\rho$
- ▶ `\Chempi` →  $\pi$

---

<sup>19</sup> CTAN: `chemstyle`    <sup>20</sup> many thanks to the package author [Joseph Wright](#).

► `\Chemsigma` →  $\sigma$

► `\Chemomega` →  $\omega$

► `\ChemDelta` →  $\Delta$

The command `\Rad` has been dropped!

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

`particle` ► `elpair` = `false/dots/dash`.

It only has any effect, if the package `chemfig`<sup>21</sup> is loaded, since it uses its command `\Lewis`.

```
1 % needs package 'chemfig'
2 \ba[elpair] \Nu[elpair=dash]          ba:~ Nu|~
3                                     ba:~ Nu:~
4 \chemsetup[particle]{elpair}
5 \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`<sup>22</sup> package the letters are taken from there, and if you have loaded the package `upgreek`<sup>23</sup> the macros of that package are used. This documentation uses `upgreek` for instance. If you load both `upgreek` and `textgreek` the letters from `upgreek` are used.

If you don't want `CHEMMACROS` to use a package automatically but want to decide for yourself, there is the option `greek`. Table 1 shows the different styles for some of the letters.

Table 1: The greek letters

	math	upgreek	textgreek
<code>\Chemalpha</code>	$\alpha$	$\alpha$	$\alpha$
<code>\Chembeta</code>	$\beta$	$\beta$	$\beta$
<code>\ChemDelta</code>	$\Delta$	$\Delta$	$\Delta$

The reason why `CHEMMACROS` defines 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 defined nomenclature commands, see page 13.

<sup>21</sup> CTAN: `chemfig`    <sup>22</sup> CTAN: `textgreek`    <sup>23</sup> CTAN: `upgreek`

## 8.2. 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>}`

Depending on the `method` you chose as option the `<definition>` will either be a formula defined with `mhchem` or with `CHEMFORMULA`. The particle defined this way behaves like the predefined ones with one exception: if you chose `method = mhchem` the particle *will not* obey the option `circled`. If you want formal charges with this method you need to use `CHEMMACROS`' commands (see section 12) explicitly. If you chose `method = chemformula` the particle *will* obey the `circled` option.

```
1 % uses the 'upgreek' package
2 \DeclareChemParticle{\positron}{${\upbeta}^{+}}
3 \DeclareChemParticle{\photon}{${\upgamma}}
4 \RenewChemParticle{\el}{${\upbeta}^{-}}
5 \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.

## 9. Nomenclature, Stereo Descriptors, Latin Phrases

### 9.1. IUPAC Names

Similar to the `bpchem` package `CHEMMACROS` provides a command<sup>24</sup> 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`<sup>25</sup>.

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

<sup>24</sup> The idea and the implementation is shamelessly borrowed from `bpchem` by Bjørn Pedersen. <sup>25</sup> Actually another mechanism is used, but the effect is essentially the same.

Tetracyclo[2.2.2.1<sup>1,4</sup>]-undecane-2-decyl-5-(heptadecylisododecylthioester)

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.

1	<code>\huge\iupac{2,4-Di\ chlor\ pentan} \\\</code>	2,4-Dichlorpentan
2	<code>2,4-Dichlorpentan</code>	2,4-Dichlorpentan

The spaces inserted by these commands can be customized.

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

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

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

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 L`) or are easily defined by another package or class (the `cool`<sup>26</sup> 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 2 demonstrates the different modes.

### 9.1.1. Predefined Commands

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

<sup>26</sup> CTAN: `cool`

Table 2: Demonstration of `iupac`'s modes.

	auto	restricted	strict
<code>\L</code>	L̸	L̸	L
<code>\iupac{\L}</code>	L	L	L
<code>\D</code>	D	–	D
<code>\iupac{\D}</code>	D	D	D

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

- `\a` → α
- `\b` → β
- `\g` → γ
- `\d` → δ
- `\k` → κ
- `\m` → μ
- `\n` → η
- `\w` → ω

```

1 \iupac{5\a\androstano-3\b-ol} \
2 \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*

1	<code>\iupac{\N\methyl\benz\amide} \</code>	<i>N</i> -methylbenzamide
2	<code>\iupac{3\H\pyrrole} \</code>	3 <i>H</i> -pyrrole
3	<code>\iupac{\O\ethyl hexanethioate}</code>	<i>O</i> -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 ( $\S$ ) it is only available inside `\iupac` in the default setting.

### Fischer

- `\D` → *D*
- `\L` → *L*

Since the command `\L` has another meaning already ( $\mathbb{L}$ ) 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 TikZ)

- `\Rconf[<letter>]` → `\Rconf:`  `\Rconf[]:` 
- `\Sconf[<letter>]` → `\Sconf:`  `\Sconf[]:` 

Examples:

```
1 \iupac{\D\Wein\|s\"aure} = \\
2 \iupac{\cip{2S,3S}\Wein\|s\"aure} \\
3 \iupac{\D\-(\$-)\Threose} = \\
4 \iupac{\cip{2S,3R}\-(\$-)\-2,3,4-Tri\|hydroxy\|butanal} \\
5 \iupac{\cis\2\Butene} = \\
6 \iupac{\Z\2\Butene}, \\
7 \iupac{\cip{2E,4Z}\Hexa\|diene} \\
8 \iupac{\meta\Xylol} = \\
9 \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>}` →  $\mu_3$ -
- `\hapto{<num>}` →  $\eta^5$ -

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

Ferrocene = bis( $\eta^5$ -cyclopentadienyl)iron  
tetra- $\mu_3$ -iodido-tetrakis[trimethylplatinum(IV)]

Two options allow customization:

iupac ► bridge-number = sub/super → appends the number as a superscript or superscript. IUPAC recommendation is the subscript [[Con+05](#)]. Default = sub

iupac ► coord-use-hyphen = true/false → append a hyphen to `\hapto` and `\bridge` or don't. Default = true

### 9.1.2. 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.

```
1 \DeclareChemIUPAC\endo{\textit{endo}}
2 \DeclareChemIUPAC\anti{\textit{anti}}
3 \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.

```
1 \iupac{\meta{-Xylol}} \ \ \ \ \ \ m-Xylol
2 \RenewChemIUPAC\meta{\textit{m}} \ \ \ \ \ m-Xylol
3 \iupac{\meta{-Xylol}}
```

### 9.2. 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`:

```
1 \insitu, \abinitio \ \ \ \ \ \ in situ, ab initio
2 \cstsetup{abbremph=false} \ \ \ \ \ in situ, ab initio
3 \insitu, \abinitio
```

The commands are defined through

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

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



1	<code>\DeclareChemLatin\ltn{latin text}</code>	<i>latin text</i> latin text
2	<code>\ltn \cstsetup{abbremph=false} \ltn</code>	

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

`latin` ▶ `format` = <definition> → Default = `\itshape`

## 10. 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<sup>3</sup> The units `\cmc`, `\molar`, and `\Molar` are defined by the package chemstyle as well. CHEMMACROS only defines them, if chemstyle is not loaded.
- ▶ `\molar` → mol dm<sup>-3</sup>
- ▶ `\moLar` → mol L<sup>-1</sup>
- ▶ `\Molar` → M
- ▶ `\MolMass` → g mol<sup>-1</sup>
- ▶ `\normal` → N
- ▶ `\torr` → torr

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

## 11. Acid/Base

Easy representation of pH, p*K*<sub>A</sub> ... (the command `\pKa` depends on the package option `language`).

- ▶ `\pH` → pH
- ▶ `\pOH` → pOH
- ▶ `\Ka` → *K*<sub>A</sub>
- ▶ `\Kb` → *K*<sub>B</sub>
- ▶ `\Kw` → *K*<sub>W</sub>

- `\pKa[<num>]` → `\pKa`:  $pK_A$ , `\pKa[1]`:  $pK_{A1}$
- `\pKb[<num>]` → `\pKb`:  $pK_B$ , `\pKb[1]`:  $pK_{B1}$
- `\p{<anything>}` → e.g. `\p{\Kw}`  $pK_W$

<pre>1 \Ka \Kb \pKa \pKa[1] \pKb \pKb[1]</pre>	$K_A K_B pK_A pK_{A1} pK_B pK_{B1}$
--	-------------------------------------

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

<pre>1 \pH, \pKa 2 3 \chemsetup[acid-base]{p-style=slanted} \pH, \pKa 4 5 \chemsetup[acid-base]{p-style=italics} \pH, \pKa</pre>	$pH, pK_A$ $pH, pK_A$ $pH, pK_A$
--	--

## 12. Oxidation Numbers, Real and Formal Charges

**CHEMMACROS** distinguishes between real (+/−) and formal ( $\oplus/\ominus$ ) charge symbols, also see section 4. All commands using formal charge symbols start with a f.

### 12.1. Ion Charges

Simple displaying of (real) charges:

- `\pch[<number>]` → positive charge (plus + charge)
- `\mch[<number>]` → negative charge (minus + charge)

<pre>1 \pch, Na\pch, Ca\pch[2]\ 2 \mch, F\mch, S\mch[2]</pre>	$^+, Na^+, Ca^{2+}$ $^-, F^-, S^{2-}$
---	--

The same for formal charges:

- `\fpch[<number>]` → positive charge

► `\fmch[<number>]` → negative charge

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

There is a key which influences the behaviour of the charges.

`charges` ► `append` = `true/false` → if set true, the charge is appended together with an empty group.

This is how the key influences the behaviour:

```
1 % uses package 'mhchem'
2 \chemsetup{charges/append=false,phases/pos=sub}
3 \ce{H\pch\aq} \ce{H\aq\pch}
4
5 \chemsetup{charges}{append=true}
6 \ce{H\pch\aq} \ce{H\aq\pch}
```

$$\begin{array}{cc} \text{H}_{(\text{aq})}^+ & \text{H}_{(\text{aq})}^+ \\ \text{H}_{(\text{aq})}^+ & \text{H}_{(\text{aq})}^+ \end{array}$$

In most cases this behaviour will be unwanted. However, in some cases it might be useful, for example together with the `\ox` command (see next section):

```
1 \chemsetup{charges/append=false,phases/pos=sub}
2 \ce{\ox{1,H}\pch\aq}
3
4 \chemsetup{charges}{append=true}
5 \ce{\ox{1,H}\pch\aq}
```

$$\begin{array}{c} \text{I}^+ \\ \text{H}_{(\text{aq})} \\ \text{I}^+ \\ \text{H}_{(\text{aq})} \end{array}$$

## 12.2. Oxidation Numbers

Typesetting oxidation numbers:

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

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

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

`ox` ► `parse` = `true/false` → when false an arbitrary entry can be used for <number>. Default = true

`ox` ► `roman` = `true/false` → switches from roman to arabic numbers. Default = true

- ox** ► **pos** = top/super/side →; top places <number> above <atom>, super to the upper right as superscript and side to the right and inside brackets. Default = top
- ox** ► **explicit-sign** = true/false → shows the + for positiv numbers and the ± for 0. Default = false
- ox** ► **decimal-marker** = comma/point → choice for the decimal marker for formal oxidation numbers like <sup>1,2</sup>X. Default = point

1	<code>\ox[roman=false]{2,Ca} \ox{2,Ca} \</code>	$\overset{2}{\text{Ca}} \overset{\text{II}}{\text{Ca}}$
2	<code>\ox[pos=super]{3,Fe}-Oxide \</code>	$\text{Fe}^{\text{III}}\text{-Oxide}$
3	<code>\ox[pos=side]{3,Fe}-Oxide \</code>	$\text{Fe}(\text{III})\text{-Oxide}$
4	<code>\ox[parse=false]{?,Mn}</code>	$\overset{?}{\text{Mn}}$

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

1	<code>\ox{3,Fe} \ox*{3,Fe}</code>	$\overset{\text{III}}{\text{Fe}} \text{Fe}^{\text{III}}$
---	-----------------------------------	--

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

1	<code>\chemsetup{ox}{explicit-sign = true}</code>	
2	<code>\ox{+1,Na}, \ox{2,Ca}, \ox{-2,S}, \ch{"\ox{0,F}" }{2}</code>	
		$\overset{+1}{\text{Na}}, \overset{+2}{\text{Ca}}, \overset{-2}{\text{S}}, \overset{-II \pm 0}{\text{F}_2}$

1	Compare <code>\ox{-1,\ch{O2^2-}}</code> to <code>\ch{"\ox{-1,O}" }{2^2-}</code>	
		Compare $\overset{-1}{\text{O}_2^{2-}}$ to $\overset{-1}{\text{O}_2^{2-}}$

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

1	<code>\ox{.5,\ch{Br2}} \ch{"\ox{1/3,I}" }{3+}</code>	$\overset{0.5}{\text{Br}_2} \overset{\frac{1}{3}}{\text{I}}^+$
---	--	--

The fraction uses the **\sfrac** command of the xfrac<sup>27</sup> package. For this purpose the instance chemmacros-ox-frac is defined.

1	<code>\DeclareInstance{xfrac}{chemmacros-ox-frac}{text}</code>	
2	<code>{</code>	
3	<code>scale-factor = 1.2 ,</code>	
4	<code>denominator-bot-sep = -.5ex ,</code>	
5	<code>numerator-top-sep = -.3ex ,</code>	
6	<code>slash-left-kern = -.2em ,</code>	
7	<code>slash-right-kern = -.2em ,</code>	
8	<code>slash-symbol-font = lmr</code>	
9	<code>}</code>	

<sup>27</sup> CTAN: xfrac

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

### 12.3. Partial Charges and Similar Stuff

The next ones probably are seldomly needed but nevertheless useful:

- ▶ `\delp` →  $\delta+$  (delta + plus)
- ▶ `\delm` →  $\delta-$  (delta + minus)
- ▶ `\fdelp` →  $\delta\oplus$
- ▶ `\fdelm` →  $\delta\ominus$

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

```
1 \chemsetup{
2   option/circled = all,
3   ox/parse = false
4 }
5 \ce{\ox{\delp,H}-\ox{\delm,Cl}} \hspace*{1cm}
6 \chemfig{\chemabove[3pt]{\lewis{246,Br}}{\delm}-\chemabove[3pt]{H}{\delp}}
```

$$\delta\oplus \quad \delta\ominus \quad \delta\ominus \quad \delta\oplus$$

$$\text{H} - \text{Cl} \quad | \text{Br} - \text{H}$$

The following macros are useful together with `chemfig`, too.

- ▶ `\scrp` → + (scriptstyle + plus)
- ▶ `\scrm` → − (scriptstyle + minus)
- ▶ `\fscrp` →  $\oplus$
- ▶ `\fscrm` →  $\ominus$
- ▶ `\fsscrp` →  $\oplus$  (using `\scriptscriptstyle`)
- ▶ `\fsscrm` →  $\ominus$

```
1 \setatomsep{1.8em}\chemfig{CH_3-\chemabove{C}{\scrp}(-[6]C|H_3)-\vphantom{H_3}CH
2   _3}
3 \chemfig{\fmch{}}|O-\chemabove{N}{\fscrp}(-[1]O|\fmch)-[7]O|\fmch}
```

$$\text{CH}_3 - \overset{+}{\text{C}} - \text{CH}_3$$

$$\quad |$$

$$\quad \text{CH}_3$$

$$\quad \ominus \text{O} - \overset{\oplus}{\text{N}} \begin{matrix} \nearrow \text{O}^\ominus \\ \searrow \text{O}^\ominus \end{matrix}$$

## 13. 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  $E1_{cb}$

## 14. Redox Reactions

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

► `\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*.

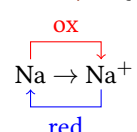
```
1 \OX{a,Na} $\rightarrow$ \OX{b,Na}\pch\redox(a,b){oxidation}
oxidation
┌───┐
Na → Na+
```

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

```
1 \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.

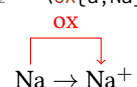
```
1 \OX{a,Na} $\rightarrow$ \OX{b,Na}\pch
2 \redox(a,b)[->,red]{ox}
3 \redox(a,b)[->,blue][-1]{red}
4 \vspace{7mm}
```



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

**redox** ► **dist** = `<dim>` → A  $\text{\TeX}$  dimension. Default = .6em

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

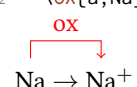


Additionally the option

**redox** ► **sep** = `<dim>` → Default = .2em

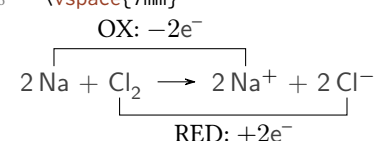
can be used to change the distance between the atom and the beginning of the line.

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



Examples:

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



```

1 \ch{ 2 "\OX{o1,\ox{\0,Na}}"} + "\OX{r1,\ox{\0,C1}}"} {}2 -> 2 "\OX{o2,\ox{+1,Na}}"}
2 \pch{} + 2 "\OX{r2,\ox{-1,C1}}"} \mch {}
3 \redox{o1,o2}{\small OX: $- 2\el$}
4 \redox{r1,r2}[][[-1]{\small RED: $+ 2\el$}
5 \vspace{7mm}

```

```

1 \ch{ 2 "\OX{o1,\ox{0,Na}}" + "\OX{r1,\ox{0,C1}}" {j2 -> 2 "\OX{o2,\ox{+1,Na}}"}
2 \pch{ + 2 "\OX{r2,\ox{-1,C1}}"} \mch }
3 \redox{o1,o2}[draw=red,->][3.33]{\small OX: $- 2\text{e1}$}
4 \redox{r1,r2}[draw=blue,->]{\small RED: $+ 2\text{e1}$}

```

```

1 \ch{ 2 "\OX{o1,\ox{0,Na}}" + "\OX{r1,\ox{0,C1}}" }{2 -> 2 "\OX{o2,\ox{+1,Na}}"}
2 \pch{} + 2 "\OX{r2,\ox{-1,C1}}" \mch }
3 \redox{o1,o2}[green,-stealth]{\small OX}
4 \redox{r1,r2}[purple,-stealth][-1]{\small RED}
5 \vspace{7mm}

```



1	<code>\Enthalpy{123} \\\</code>	$\Delta H^\ominus = 123 \text{ kJ mol}^{-1}$
2	<code>\Entropy{123} \\\</code>	$S^\ominus = 123 \text{ J K}^{-1} \text{ mol}^{-1}$
3	<code>\Gibbs{123}</code>	$\Delta G^\ominus = 123 \text{ kJ mol}^{-1}$

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

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.

1	<code>\Enthalpy[unit=kilo\joule]{-285} \\\</code>	$\Delta H^\ominus = -285 \text{ kJ}$
2	<code>\Gibbs[delta=false]{0} \\\</code>	$G^\ominus = 0 \text{ kJ mol}^{-1}$
3	<code>\Entropy[delta=Delta,exponent=]{56.7}</code>	$\Delta S = 56.7 \text{ J K}^{-1} \text{ mol}^{-1}$

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

1	<code>\Enthalpy{-1234.56e3} \\\</code>
2	<code>\sisetup{per-mode=symbol,exponent-product=\cdot,output-decimal-marker={,},group-four-digits=true}</code>
3	<code>\Enthalpy{-1234.56e3}</code>
$\Delta H^\ominus = -1234.56 \times 10^3 \text{ kJ mol}^{-1}$	
$\Delta H^\ominus = -1\,234,56 \cdot 10^3 \text{ kJ/mol}$	

### 15.1.1. Create New Variables

You can use the command

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

to create new corresponding commands:

1	<code>\DeclareChemState{Helmholtz}{A}{\kilo\joule\per\mole}</code>
2	<code>\DeclareChemState[subscript-left=false,exponent=]{ElPot}{E}{\volt}</code>
3	<code>\Helmholtz{123.4} \\\</code>
4	<code>\ElPot{-1.1} \\\</code>
5	<code>\ElPot[exponent=0]{\$\ch{Sn} \ch{Sn^2+}  \ch{Pb^2+} \ch{Pb}}{0.01}</code>
$\Delta A^\ominus = 123.4 \text{ kJ mol}^{-1}$	
$\Delta E = -1.1 \text{ V}$	
$\Delta E_{\text{Sn} \text{Sn}^{2+}  \text{Pb}^{2+} \text{Pb}}^0 = 0.01 \text{ V}$	

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

- ▶ `exponent` = <anything>
- ▶ `delta` = <anything>/false
- ~~▶ `subscript-left` = true/false~~
- ▶ `subscript` = <anything>

### 15.1.2. Redefine Variables

With

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

you can redefine the already existing commands:

<pre>1 \RenewChemState{Enthalpy}{h}{\joule} 2 \Enthalpy{f}{12.5}</pre>	$\Delta_f h^\ominus = 12.5 \text{ J}$
--	---------------------------------------

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:

<pre>1 \DeclareChemState[exponent=]{enthalpy}{h}{\kilo\joule\per\mole}% molar 2 \RenewChemState[exponent=]{Enthalpy}{H}{\kilo\joule}% absolute 3 \enthalpy{-12.3} \Enthalpy{-12.3}</pre>	$\Delta h = -12.3 \text{ kJ mol}^{-1} \quad \Delta H = -12.3 \text{ kJ}$
--	--

## 15.2. State

The commands presented in section 15.1 internally all use the command<sup>28</sup>

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

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

Examples:

<pre>1 \State{A}, \State{G}{f}, \State[subscript-left=false]{E}{\ch{Na}}, \State[   exponent=\SI{1000}{\celsius}]{H}</pre>	$\Delta A^\ominus, \Delta_f G^\ominus, \Delta E_{\text{Na}}^\ominus, \Delta H^{1000\text{ }^\circ\text{C}}$
--	---

Again there are some keys to customize the command:

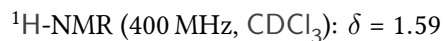
- `state` ▶ `exponent` = <anything>
- `state` ▶ `subscript-left` = true/false
- `state` ▶ `delta` = <anything>/false

<sup>28</sup> Please note that {<subscript>} is an *optional* argument.

## 16. Spectroscopy and Experimental Data

### 16.1. 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:



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

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

All Argument are optional! Without arguments we get:

1	<code>\NMR \</code>	$^1\text{H-NMR: } \delta$
2	<code>\NMR*</code>	$^1\text{H-NMR}$

The first argument specifies the kind of NMR:

1	<code>\NMR{13,C}</code>	$^{13}\text{C-NMR: } \delta$
---	-------------------------	------------------------------

The second argument sets the frequency (in MHz):

1	<code>\NMR(400)</code>	$^1\text{H-NMR (400 MHz): } \delta$
---	------------------------	-------------------------------------

You can choose another unit:

1	<code>\NMR(4e8,\hertz)</code>	$^1\text{H-NMR (4} \times 10^8 \text{ Hz): } \delta$
---	-------------------------------	--

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

1	<code>\sisetup{exponent-product=\cdot}\NMR(4e8,\hertz)</code>	$^1\text{H-NMR (4} \cdot 10^8 \text{ Hz): } \delta$
---	---	---

The third argument specifies the solvent:

1	<code>\NMR[CDCl3]</code>	$^1\text{H-NMR (CDCl}_3\text{): } \delta$
---	--------------------------	---

### 16.2. 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>}`.

1	<code>\DeclareChemNMR\HNMR{1,H}%</code>	$^{13}\text{C}$ -NMR (100 MHz)
2	<code>\DeclareChemNMR\CNMR{13,C}%</code>	$^1\text{H}$ -NMR (400 MHz)
3	<code>\CNMR*(100) \\\</code>	
4	<code>\HNMR*(400)</code>	

### 16.3. 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 this 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.
- ▶ `\J[<unit>]{<list of nums>}` → Coupling constant, values are input separated by ; (NMR).
- ▶ `\#{<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>}`

1	<code>\begin{experimental}</code>	
2	<code>\data{type1} Data.</code>	type1 Data. type2 (specifications) More data. type3
3	<code>\data{type2}[specifications] More data.</code>	Even more data.
4	<code>\data*{type3} Even more data.</code>	
5	<code>\end{experimental}</code>	

### 16.4. Customization

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

`nmr` ▶ `unit = <unit>` → Default = `\mega\hertz`

`nmr` ▶ `nucleus = {<num>, <atom>}` → Default = `{1,H}`

`nmr` ▶ `format = <commands>` → for example `\bfseries`

`nmr` ▶ `pos-number = side/sub` → Position of the number next to the atom. Default = side

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

**nmr** ► **parse** = true/false → Treat the solvent as mhchem/**CHEMFORMULA** formula or not. Default = true

**nmr** ► **delta** = <tokens> → The <tokens> are added after  $\delta$ .

**nmr** ► **list** = true/false → The environment `\begin{nmr}[<optionen>] \end{nmr}` is formatted as a list.  
Default = false

**nmr** ► **list-setup** = <setup> → Setup of the list. Default = see below.

**nmr** ► **use-equal** = true/false → Add equal sign after `\NMR` and `\data`. Default = false

The default setup of the list:

```
1 \topsep\z@skip \partopsep\z@skip
2 \itemsep\z@ \parsep\z@ \itemindent\z@
3 \leftmargin\z@
```

```
1 \begin{experimental}[format=\bfseries]
2 \data{type1} Data.
3 \data{type2}[specifications] More data.
4 \data*{type3} Even more data.
5 \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.

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

**type1** = Data. **type2 (specifications)** = More data. <sup>1</sup>H-NMR:  $\delta$  = Even more data.

## 16.5. An Example

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

```
1 \sisetup{separate-uncertainty,per-mode=symbol,detect-all,range-phrase=--}
2 \begin{experimental}[<optionen>]
3 \data*{yield} \SI{17}{\milli\gram} yellow needles (\SI{0.04}{\milli\mole}, \SI
  {13}{\percent}).
4 %
5 \data{mp.} \SI{277}{\celsius} (DSC).
6 %
```

```

7 \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}).
8 %
9 \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}).
10 %
11 \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).
12 %
13 \data{MS}[\ch{MeOH + H2O + KI}, ESI, \SI{10}{\electronvolt}] \val{720} (100, \
  ch{M+ + OH-}), \val{368} (\ch{M+ + 2 OH-}).
14 %
15 \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).
16 %
17 \data*{UV-Vis} \SI{386}{\nano\metre} ($\varepsilon = \val{65984}$), \SI{406}{\
  nano\metre} ($\varepsilon = \val{65378}$).
18 %
19 \data*{quantum yield} $\Phi = \val{0.74+-0.1}$\,.
20 \end{experimental}

```

### 16.5.1. 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). <sup>1</sup>H-NMR (600 MHz, CDCl<sub>3</sub>): δ (ppm) = 2.01 (s, 24 H, H<sub>5</sub>), 2.31 (s, 12 H, H<sub>1</sub>), 6.72–6.74 (m, 2 H, H<sub>11</sub>), 6.82 (s, 8 H, H<sub>3</sub>), 7.05–7.07 (m, 2 H, H<sub>12</sub>), 7.39–7.41 (m, 4 H, H<sub>9</sub>), 7.48–7.49 (m, 4 H, H<sub>8</sub>). <sup>13</sup>C-NMR (150 MHz, CDCl<sub>3</sub>): δ (ppm) = 21.2 (+, 4 C, C<sub>1</sub>), 23.4 (+, 8 C, C<sub>5</sub>), 126.0 (+, 4 C, C<sub>9</sub>), 128.2 (+, 8 C, C<sub>3</sub>), 130.8 (+, 2 C, C<sub>12</sub>), 133.6 (+, 2 C, C<sub>11</sub>), 137.0 (+, 4 C, C<sub>8</sub>), 138.6 (q, 4 C, C<sub>2</sub>), 140.6 (q, 2 C, C<sub>10</sub>), 140.8 (q, 8 C, C<sub>4</sub>), 141.8 (q, 4 C, C<sub>6</sub>), 145.6 (q, 2 C, C<sub>7</sub>). MS (DCP, EI, 60 eV) = 703 (2, M<sup>+</sup>), 582 (1), 462 (1), 249 (13), 120 (41), 105 (100). MS (MeOH + H<sub>2</sub>O + KI, ESI, 10 eV) = 720 (100, M<sup>+</sup> + OH<sup>-</sup>), 368 (M<sup>+</sup> + 2 OH<sup>-</sup>). 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 ( $\varepsilon = 65\,984$ ), 406 nm ( $\varepsilon = 65\,378$ ). quantum yield:  $\Phi = 0.74 \pm 0.10$ .

### 16.5.2. 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).

**<sup>1</sup>H-NMR (600 MHz, CDCl<sub>3</sub>):**  $\delta$  (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).

**<sup>13</sup>C-NMR (150 MHz, CDCl<sub>3</sub>):**  $\delta$  (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<sup>+</sup>), 582 (1), 462 (1), 249 (13), 120 (41), 105 (100).

**MS (MeOH + H<sub>2</sub>O + KI, ESI, 10 eV)** = 720 (100, M<sup>+</sup> + OH<sup>-</sup>), 368 (M<sup>+</sup> + 2 OH<sup>-</sup>).

**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 ( $\varepsilon = 65\,984$ ), 406 nm ( $\varepsilon = 65\,378$ ).

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

### 16.5.3. Crazy

Output for these options: <optionen>:

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

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

**mp.** = 277 °C (DSC).

**<sup>1</sup>H-NMR (600 MHz, CDCl<sub>3</sub>):**  $\delta$  **M<sup>+</sup> + H<sub>2</sub>O** = 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).

**<sup>13</sup>C-NMR (150 MHz, CDCl<sub>3</sub>):**  $\delta$  **M<sup>+</sup> + H<sub>2</sub>O** = 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<sup>+</sup>), 582 (1), 462 (1), 249 (13), 120 (41), 105 (100).

*MS (MeOH + H<sub>2</sub>O + KI, ESI, 10 eV) = 720 (100, M<sup>+</sup> + OH<sup>-</sup>), 368 (M<sup>+</sup> + 2 OH<sup>-</sup>).*

*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 ( $\epsilon = 65\,984$ ), 406 nm ( $\epsilon = 65\,378$ ).*

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

## 17. Commands for mhchem

mhchem isn't loaded automatically any more but only if you've specified `method = mhchem` in the preamble. In the default settings `CHEMMACROS` uses `CHEMFORMULA` instead.

`CHEMMACROS` provides only one command specifically for mhchem<sup>29</sup>. It is meant to place text below of compounds.

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

For example:

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

4 C2H5Cl + Pb/Na → Pb(C2H5)4 + NaCl
                        former antiknock
                        additive
```

There are several keys to customize `\mhName`.

`mhName` ► `align = <alignment command>` → the alignment of the text in the box it is placed in, default = `\centering`

`mhName` ► `format = <anything>` → the format of the text

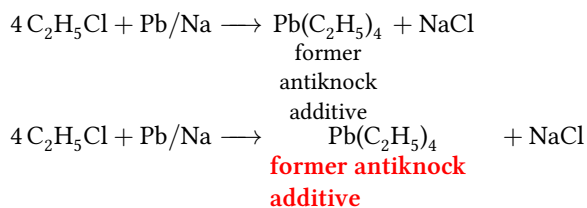
`mhName` ► `fontsize = <font size command>` → the fontsize of the text, default = `\tiny`

`mhName` ► `width = <dim>/auto` → the width of the box the text is placed in, default = auto

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

<sup>29</sup> `CHEMFORMULA` provides its own possibility.





## 18. Reaction Environments

### 18.1. 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}`

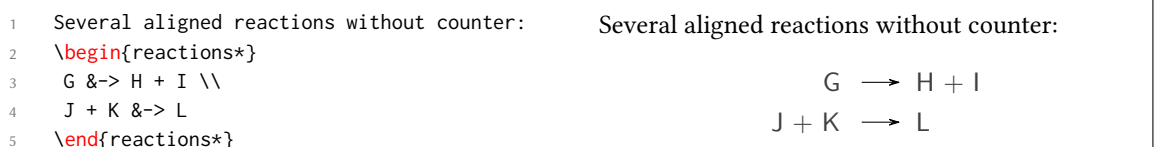
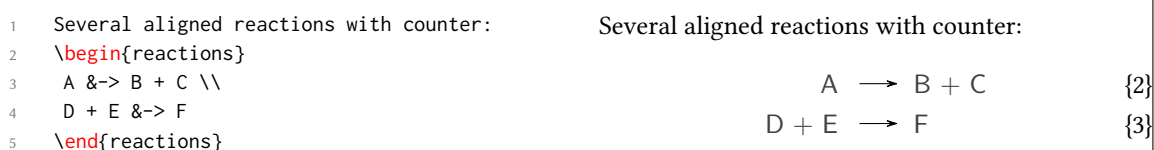
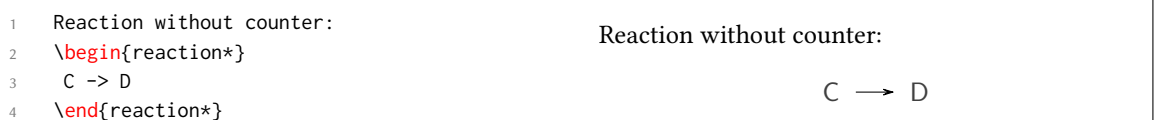
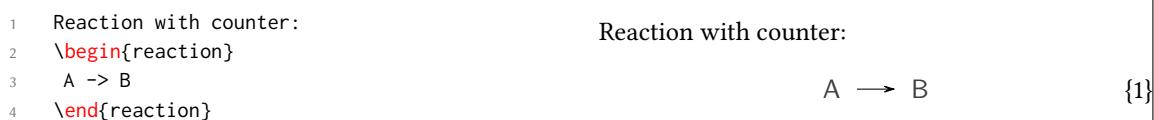
...and their starred versions for unnumbered reactions.

► `\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.

These environments use the `equation/equation*` environments or the `align/align*` environments, respectively, to display the reactions.



If you want to change the layout of the counter tags, you can use

`\renewtagform{<tagname>}[<format>]{<right delim>}{<left delim>}`<sup>30</sup>.

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

$$\text{H}_2\text{O} + \text{CO}_2 \rightleftharpoons \text{H}_2\text{CO}_3 \quad [\text{R } 4]$$

With version 3.3 referencing and the use of  $\mathcal{A}\mathcal{M}\mathcal{S}$ math's `\intertext` also function properly:

```
1 \begin{reactions}  
2 A + 2 B &-> 3 C + D \label{rxn:test}  
3 \intertext{Some text in between aligned reactions}  
4 3 E + F &<=> G + 1/2 H  
5 \end{reactions}  
6 See reaction \ref{rxn:test}.
```

$$A + 2 B \longrightarrow 3 C + D \quad \{5\}$$

Some text in between aligned reactions

$$3 E + F \rightleftharpoons G + \frac{1}{2} H \quad \{6\}$$

See reaction 5.

In the standard setting, i.e. using `method = chemformula` you should not use `\mch` and its relatives inside the reaction environments. They will very likely mess with spacing. In the standard setting charges inside the environments automatically recognize the setting of the option `circled` so there's also no need for the charge commands.

## 18.2. 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

---

<sup>30</sup> Provided by the mathtools package

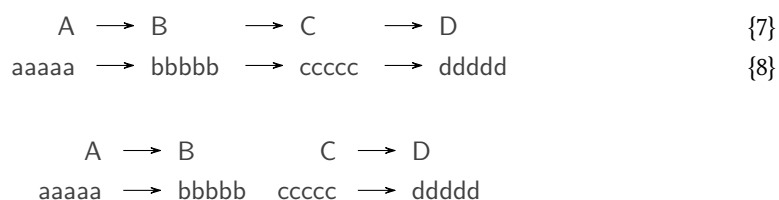
- `\DeclareChemReaction[star]{reaction}{equation}` and
- `\DeclareChemReaction[star]{reactions}{align}`.

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

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

With this the reactionsat environment is defined.

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



### 18.3. List of Reactions

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

- `\listoreactions`

```
1 \listoreactions
```

## List of reactions

Reaction {1} . . . . .	33
Reaction {2} . . . . .	33
Reaction {3} . . . . .	33
Reaction [R 4] . . . . .	34
Reaction {5} . . . . .	34
Reaction {6} . . . . .	34
Reaction {7} . . . . .	35
Reaction {8} . . . . .	35
Reaction {9}: Autoprotolyse . . . . .	36
Reaction {10}: first step of chain . . . . .	36
Reaction {11}: second step of chain . . . . .	36
Reaction {12}: Synthese von Alkanen . . . . .	59

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

**reaction** ► **list-name** = <name of the list> → Let's you set the name of the list manually. Default = List of reactions

**reaction** ► **list-entry** = <prefix to each entry> → Let's you set a prefix to each list entry. Default = Reaction

**option** Both default option values recognize the package option **german**.

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.

```

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

```

$$2 \text{H}_2\text{O} \rightleftharpoons \text{H}_3\text{O}^+ + \text{OH}^- \quad \{9\}$$

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

► `\AddRxnDesc{<description>}`

```

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

```

$$\text{Cl}\cdot + \text{CH}_4 \longrightarrow \text{HCl} + \cdot\text{CH}_3 \quad \{10\}$$

$$\cdot\text{CH}_3 + \text{Cl}_2 \longrightarrow \text{CH}_3\text{Cl} + \text{Cl}\cdot \quad \{11\}$$

Note: you don't have to use the phantom commands if you haven't changed the format of the atoms, see section 30 on page 56.

## 19. Phases

### 19.1. Basics

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

- `\sld` → (s)
- `\lqd` → (l)
- `\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.

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

$$\text{C(s)} + 2 \text{H}_2\text{O(l)} \longrightarrow \text{CO}_2\text{(g)} + 2 \text{H}_2\text{(g)}$$
  
To make it complete: NaCl(aq).

With the package option `language = german` (see section 4) you get the german versions.

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 → Switch the position of the phase indicator. Default = side

`phases` ► `space` = <dim> → Change the default spacing between compound a phase indicator if `pos` = side.  
A TeX dimension. Default = .1333em

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

$$\text{C}_{\text{(s)}} + 2 \text{H}_2\text{O}_{\text{(l)}} \longrightarrow \text{CO}_{2\text{(g)}} + 2 \text{H}_{2\text{(g)}}$$
  
To make it complete: NaCl<sub>(aq)</sub>.

## 19.2. 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.

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

NaOH(aq,∞) H<sub>2</sub>O (cd) U(cr) A(lc)

NaOH<sub>(aq,∞)</sub> H<sub>2</sub>O<sub>(cd)</sub> U<sub>(cr)</sub> A<sub>(lc)</sub>

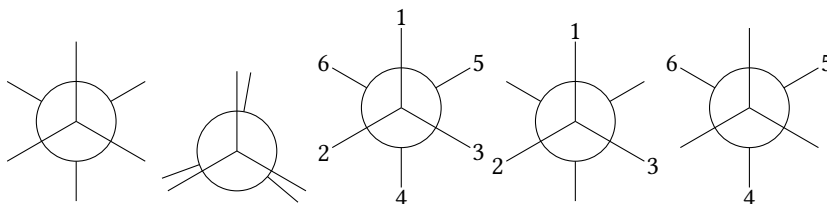
## 20. Newman Projections

`CHEMMACROS` provides the command

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

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

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



Several options allow customization:

`newman` ► `angle` = `<angle>` → default angle

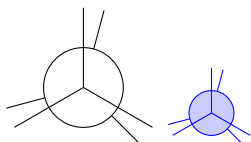
`newman` ► `scale` = `<factor>` → scale the whole projection

**newman** ► **ring** = <tikz> → customize the ring with **TikZ** keys

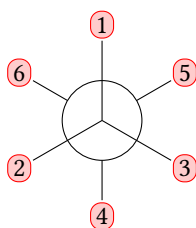
**newman** ► **atoms** = <tikz> → customize the nodes within which the atoms are set

**newman** ► **back-atoms** = <tikz> → explicitly customize the back atoms

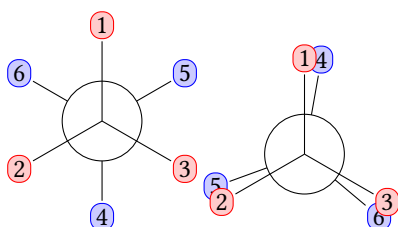
```
1 \chemsetup[newman]{angle=45} \newman{}
2 \newman[scale=.75,ring={draw=blue,fill=blue!20}]{}
```



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



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



## 21. 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

sp<sup>2</sup>

sp<sup>3</sup>

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



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

**orbital** ► **phase** =  $\pm/-$  → changes the phase of the orbital (all types)

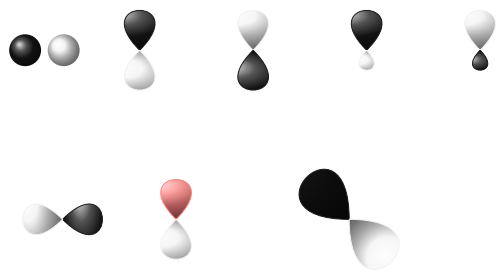
**orbital** ► **scale** = <factor> → changes the size of the orbital (all types)

**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)

```
1 \orbital{s} \orbital[phase=-]{s}
2 \orbital{p} \orbital[phase=-]{p}
3 \orbital{sp3} \orbital[phase=-]{sp3}
4
5 \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 **TikZ** behaviour can be changed.

**orbital** ► **overlay** = true/false → the orbital “doesn’t need space”; it is displayed with the **TikZ** option overlay.

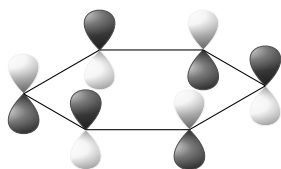
**orbital** ► **opacity** = <num> → the orbital becomes transparent; <value> can have values between 1 (fully opaque) to 0 (invisible).



```

1 \hspace{1cm}
2 \chemsetup[orbital]{
3   overlay,
4   p/color = black!70
5 }
6 \setbondoffset{0pt}
7 \chemfig{?\orbital{p}-[1.3]{\orbital[phase=-]{p}}-[:30,1.1]\orbital{p}
8   }-[:150,.9]{\orbital[phase=-]{p}}-[4,1.3]\orbital{p}-[:150,1.1]{\orbital[phase
9   =-]{p}}??}
10 \vspace{7mm}

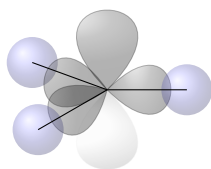
```



```

1 \hspace{2cm}
2 \setbondoffset{0pt}
3 \chemsetup[orbital]{
4   overlay ,
5   opacity = .75 ,
6   p/scale = 1.6 ,
7   s/color = blue!50 ,
8   s/scale = 1.6
9 }
10 \chemfig{\orbital{s}-[:20]{\orbital[scale=2]{p}}{\orbital[half,angle=0]{p}}{\
11   orbital[angle=170,half]{p}}{\orbital[angle=-150,half]{p}}(-[:150]\orbital{s})
12   -\orbital{s}}
13 \vspace{1cm}

```



## Part III.

# chemformula

## 22. Setup

All of **CHEMFORMULA**'s options belong to the module **chemformula**. This means they can be setup with

```

1 \chemsetup[chemformula]{<options>} or
2 \chemsetup[chemformula/<option1>,chemformula/<option2>}

```

## 23. The Basic Principle

**CHEMFORMULA** offers one main command.

► **\ch**[<options>]{<input>}

The usage will seem very familiar to you if you're familiar with mhchem:

1	<b>\ch</b> {H2O} \\\	$\text{H}_2\text{O}$
2	<b>\ch</b> {Sb2O3} \\\	$\text{Sb}_2\text{O}_3$
3	<b>\ch</b> {H+} \\\	$\text{H}^+$
4	<b>\ch</b> {CrO4^2-} \\\	$\text{CrO}_4^{2-}$
5	<b>\ch</b> {AgCl2-} \\\	$\text{AgCl}_2^-$
6	<b>\ch</b> {[AgCl2]-} \\\	$[\text{AgCl}_2]^-$
7	<b>\ch</b> {Y^{99+}} \\\	$\text{Y}^{99+}$
8	<b>\ch</b> {Y^{99+}} \\\	$\text{Y}^{99+}$
9	<b>\ch</b> {H2_{(aq)}} \\\	$\text{H}_{2(\text{aq})}$
10	<b>\ch</b> {NO3-} \\\	$\text{NO}_3^-$
11	<b>\ch</b> {(NH4)2S} \\\	$(\text{NH}_4)_2\text{S}$
12	<b>\ch</b> {^{227}_{90}Th+} \\\	$^{227}_{90}\text{Th}^+$
13	<b>\$V_{\ch{H2O}}\$</b> \\\	$V_{\text{H}_2\text{O}}$
14	<b>\ch</b> {Ce^{IV}} \\\	$\text{Ce}^{\text{IV}}$
15	<b>\ch</b> {KCr(SO4)2 * 12 H2O}	$\text{KCr}(\text{SO}_4)_2 \cdot 12 \text{H}_2\text{O}$

However, there are differences. The most notable one: **CHEMFORMULA** distinguishes between different types of input. These different parts *have* to be separated with blanks:

► **\ch**{part1 part2 part3 part4}

A blank in the input *never* is a blank in the output. This role of the blank strictly holds and disregarding it can have unexpected results and even lead to errors.

Another notable difference: **CHEMFORMULA** tries to avoid math mode whenever possible:

1	<b>\ch</b> {A + B ->[a] C} \\\	$A + B \xrightarrow{a} C$
2	<b>\ce</b> {A + B ->[a] C}	$A + B \xrightarrow{a} C$

This means that **\ch**{2H2O} is recognized as a *single* part, which in this case is recognized as a compound.

1	<b>\ch</b> {2H2O} \\\	$2\text{H}_2\text{O}$
2	<b>\ch</b> {2 H2O}	$2\text{H}_2\text{O}$

This also means, that a part cannot contain a blank since this will automatically divide it into two parts. If you need an extra blank in the output you need to use ~. However, since commands in

most cases gobble a space after them a input like `\ch{\command ABC}` will be treated as a single part. If you want or need to divide them you need to add an empty group: `\ch{\command{ } ABC}`. The different input types are described in the following sections.

There are some options to customize the output of the `\ch` command. They can either be applied locally using the optional argument or can be set globally using the `setup` command. All options of `CHEMFORMULA` belong to the module `chemformula`.

► `\chemsetup[chemformula]{<options>}`

## 24. Stoichiometric Factors

A stoichiometric factor may only contain of numbers and the signs `.`, `_`/`()`

1	<code>\ch{2} \\\</code>	
2	<code>\ch{12}</code>	
3		2
4	% decimals:	12
5	<code>\ch{3.5} \\\</code>	3.5
6	<code>\ch{5,75}</code>	5.75
7		$\frac{3}{2}$
8	% fractions:	$1\frac{1}{2}$
9	<code>\ch{3/2} \\\</code>	
10	<code>\ch{1_1/2}</code>	

You have to be a little bit careful with the right syntax but I believe it is rather intuitive.

```
1 this won't work but will result in an error: \ch{1/1_1}
```

If stoichiometric factors are enclosed with parentheses the fractions are not recognized. What's inside the parenthesis is typeset as is.

1	<code>\ch{(1/2) H2O} \ch{1/2 H2O} \ch{0.5 H2O}</code>	$(1/2)\text{H}_2\text{O}$ $\frac{1}{2}\text{H}_2\text{O}$ $0.5\text{H}_2\text{O}$
---	---	---

You can find many examples like the following for stoichiometric factors in parentheses in the IUPAC Green Book [[Coh+08](#)]:



There are a few possibilities to customize the output.

- `decimal-marker` = `<marker>` → the symbol to indicate the decimal. Default = `.`
- `frac-style` = `math/xfrac/nicefrac` → determines how fractions are displayed. Default = `math`
- `stoich-space` = `<dim>` → The space that is placed after the stoichiometric factor. Default = `.1667em`

```
1 \ch[decimal-marker={,}]{3.5} \ch[decimal-marker={\cdot}]{3,5}
```

3,5 3·5

The option `frac-style = xfrac` uses the `\sfrac` command of the `xfrac` package. The output strongly depends on the font you use.

```
1 \ch[frac-style=xfrac]{3/2} \ch[frac-style=xfrac]{1_1/2}
```

$\frac{3}{2}$   $1\frac{1}{2}$

**CHEMFORMULA** defines the instance `formula-text-frac` which you can redefine to your needs. See the `xfrac` documentation for further information. The default definition is this:

```
1 \DeclareInstance{xfrac}{chemformula-text-frac}{text}
2 {
3   slash-left-kern = -.15em ,
4   slash-right-kern = -.15em
5 }
```

This document uses the font Linux Libertine and the following definition:

```
1 \DeclareInstance{xfrac}{chemformula-text-frac}{text}
2 {
3   scale-factor = 1 ,
4   denominator-bot-sep = -.2ex ,
5   denominator-format = \scriptsize #1 ,
6   numerator-top-sep = -.2ex ,
7   numerator-format = \scriptsize #1
8 }
```

The option `frac-style = nicefrac` uses the `\nicefrac` command of the `nicefrac` package.

```
1 \ch[frac-style=nicefrac]{3/2} \ch[frac-style=nicefrac]{1_1/2}
```

$\frac{3}{2}$   $1\frac{1}{2}$

The option `stoich-space` allows you to customize the space between stoichiometric factor and the group following after it.

```
1 \ch{2 H2O} \ \ 2 H2O
2 \ch[stoich-space=.3em]{2 H2O} 2 H2O
```

## 25. Compounds

**CHEMFORMULA** determines compounds as the type that “doesn’t fit in anywhere else”. This point will become more clear when you know what the other types are.

1	<code>\ch{H2SO4} \</code>	$\text{H}_2\text{SO}_4$
2	<code>\ch{[Cu(NH3)4]^2+}</code>	$[\text{Cu}(\text{NH}_3)_4]^{2+}$

### 25.1. Adducts

**CHEMFORMULA** has two identifiers which will create adducts.

► `\ch{A.B}` →

► `\ch{A*B}` →

1	<code>\ch{CaSO4.H2O} \</code>	$\text{CaSO}_4 \cdot \text{H}_2\text{O}$
2	<code>\ch{CaSO4*H2O}</code>	$\text{CaSO}_4 \cdot \text{H}_2\text{O}$

Since numbers in a compound always are treated as subscripts (see section 25.2) you sometimes need to introduce stoichiometric factors for the right output:

1	<code>\ch{Na3PO4*12H2O} \</code>	$\text{Na}_3\text{PO}_4 \cdot 12\text{H}_2\text{O}$
2	<code>\ch{Na3PO4* 12 H2O} \</code>	$\text{Na}_3\text{PO}_4 \cdot 12 \text{H}_2\text{O}$
3	<code>\ch{Na3PO4 * 12 H2O}</code>	$\text{Na}_3\text{PO}_4 \cdot 12 \text{H}_2\text{O}$

### 25.2. Subscripts

*All* numbers in a compound are treated as subscripts.

1	<code>\ch{H2SO4}</code>	$\text{H}_2\text{SO}_4$
---	-------------------------	-------------------------

If you want a letter to be a subscript you can use the math syntax:

1	<code>\ch{A_nB_m}</code>	$A_nB_m$
---	--------------------------	----------

The subscript recognizes groups. You can also use math inside it.

1	<code>\ch{A_{n\$}B_{m\$}} \</code>	$A_nB_m$
2	<code>\ch{NaCl_{(aq)}}</code>	$\text{NaCl}_{(\text{aq})}$

### 25.3. Commands

Commands are allowed in a compound:

1	<code>\ch{\textbf{A2}B3} \ch{A2\color{red}B3}</code>	$A_2B_3$ $A_2B_3$
---	--	-------------------

However, if the commands demand numbers as argument, e.g. space commands or CHEMMACROS' `\ox` command the direct use will fail. This is because the numbers are treated as subscripts *before* the command expands.

1	<code>\ch{A\hspace{2mm}B}</code> will raise an error because <code>\hspace</code> sees something like this: <code>\hspace{\$_2\$mm}</code> .
---	--

See section 27.1 for a way around this.

## 25.4. Charges and Other Superscripts

**Basics** If a compound *ends* with a plus or minus sign it will be treated as charge sign and typeset as superscript. In other places a plus is treated as a triple bond and a dash will be used as a single bond, see section 25.5.

1	<code>\ch{A+B} \ch{AB+} \</code>	$A=B$ $AB^+$
2	<code>\ch{A-B} \ch{AB-}</code>	$A-B$ $AB^-$

For longer charge groups or other superscripts you can use the math syntax. It recognizes groups and you can use math inside them. Inside these groups neither + nor - are treated as bonds. If a dot . is inside a superscript it is treated as indicator for a radical. A \* gives the excited state.

1	<code>\ch{A^{x-}} \</code>	$A^{x-}$
2	<code>\ch{A^x-} \</code>	$A^{x-}$
3	<code>\ch{A^{x}-} \</code>	$A^{x-}$
4	<code>\ch{A^{x-\$}} \</code>	$A^{x-}$
5	<code>\ch{RNO2^{-.}} \</code>	$RNO_2^{--}$
6	<code>\ch{^31H} \</code>	$^3H$
7	<code>\ch{^{14}6C} \</code>	$^{14}C$
8	<code>\ch{^{58}_{26}Fe} \</code>	$^{58}_{26}Fe$
9	<code>\ch{NO^*}</code>	$NO^*$

Ions and ion composites with more than one charge can be typeset quite as easy:

1	<code>\ch{SO4^2-} \ch{Ca^2+ SO4^2-}</code>	$SO_4^{2-}$ $Ca^{2+}SO_4^{2-}$
---	--	--------------------------------

**Charge Commands** You don't need to use `\mch` and related commands inside `\ch`. Indeed, you *shouldn't* use them as they might mess with the subscript and superscript alignment. The CHEMMACROS option circled is obeyed by `\ch`.

1	<code>\chemsetup[option]{circled=all}</code>	$H^{\oplus} + OH^{\ominus} \rightleftharpoons H_2O$
2	<code>\ch{H+ + OH- &lt;=&gt; H2O}</code>	

**Behaviour** The superscripts behave differently depending on their position in a compound, if there are super- and subscripts following each other directly.

```

1 \ch{^33B} \ch{{}^33B} \ch{3^3B} \ch{B^3} \ch{B3^3} \\
2 \ch{^{23}_{123}B} \ch{{}^{23}_{123}B} \ch{{}_{123}^{23}B} \ch{B^{23}} \ch{B
  _{123}^{23}} \\
3 \ch{^{123}_{23}B} \ch{{}^{123}_{23}B} \ch{{}_{23}^{123}B} \ch{B^{123}} \ch{B
  23^{123}}

3B 3B 3B B3 B33
23B 23B 23B B23 B2323
123B 123B 123B B123 B123123
123B 123B 123B B123 B23123

```

- If a compound *starts* with a sub- or superscript both sub- and superscript are aligned to the *right* else to the *left*.
- If a *does not start* with a sub- or superscript and there is both a sub- and a superscript, the superscript is shifted additionally by a length determined from the option `charge-hshift = <dim>`, also see page 47f.

The second point follows IUPAC's recommendations:

In writing the formula for a complex ion, spacing for charge number can be added (staggered arrangement), as well as parentheses:  $\text{SO}_4^{2-}$ ,  $(\text{SO}_4)^{2-}$  The staggered arrangement is now recommended.

*IUPAC Green Book [Coh+08, p. 51]*

## 25.5. Bonds

There are three kinds of bonds:

1	single: <code>\ch{CH3-CH3}</code> \\	single: $\text{CH}_3\text{--CH}_3$
2	double: <code>\ch{CH2=CH2}</code> \\	double: $\text{CH}_2=\text{CH}_2$
3	triple: <code>\ch{CH\equiv CH}</code>	triple: $\text{CH}\equiv\text{CH}$

## 25.6. Customization

These options allow you to customize the output of the compounds:

- `subscript-vshift = <dim>` → Extra vertical shift of the subscripts. Default = 0pt
- `subscript-style = text/math` → Style that is used to typeset the subscripts. Default = text
- `charge-hshift = <dim>` → Shift of superscripts when following a subscript. Default = .5ex
- `charge-vshift = <dim>` → Extra vertical shift of the superscripts. Default = 0pt
- `charge-style = text/math` → Style that is used to typeset the superscripts. Default = text
- `adduct-space = <dim>` → Space to the left and the right of the adduct point. Default = .1333em

- **bond-length** = <dim> → The length of the bonds. Default is the length of an endash as measured by `\settowidth{<len>}{\textendash}`.
- **bond-offset** = <dim> → Space between bond and atoms. Default = 0pt

Maybe you have noticed that charges of certain ions are shifted to the right. They are shifted if they *follow* a subscript which follows IUPAC recommendations [Coh+08, p. 51]. The amount of the shift can be set with the option **charge-hshift**.

<pre> 1 \ch{SO4^2-} \ch{NH4+} \ch{Na+} \\ 2 \chemsetup[chemformula]{charge-hshift=.5ex} 3 \ch{SO4^2-} \ch{NH4+} \ch{Na+} \\ 4 \chemsetup[chemformula]{charge-hshift=.5pt} 5 \ch{SO4^2-} \ch{NH4+} \ch{Na+} </pre>	$\text{SO}_4^{2-} \text{NH}_4^+ \text{Na}^+$ $\text{SO}_4^{2-} \text{NH}_4^+ \text{Na}^+$ $\text{SO}_4^{2-} \text{NH}_4^+ \text{Na}^+$
---	--

Despite IUPAC's recommendation **CHEMFORMULA** does not make a fully staggered arrangements in the default setting as I find it hard to read in some cases and ugly in others. Since this is a subjective decision **CHEMFORMULA** not only let's you define the absolute amount of the shift but also provides a possibility for full staggered arrangements. For this you have to use **charge-hshift = full**.

<pre> 1 \ch[charge-hshift=0pt]{C5H11+} \ch[charge-hshift=0pt]{SO4^2-} \\ 2 \ch{C5H11+} \ch{SO4^2-} \\ 3 \ch[charge-hshift=1ex]{C5H11+} \ch[charge-hshift=1ex]{SO4^2-} \\ 4 \ch[charge-hshift=full]{C5H11+} \ch[charge-hshift=full]{SO4^2-} </pre>	$\text{C}_5\text{H}_{11}^+ \text{SO}_4^{2-}$ $\text{C}_5\text{H}_{11}^+ \text{SO}_4^{2-}$ $\text{C}_5\text{H}_{11}^+ \text{SO}_4^{2-}$ $\text{C}_5\text{H}_{11}^+ \text{SO}_4^{2-}$
---	--

If you don't want the charges to be typeset in text mode you can switch to math mode:

<pre> 1 \ch{M^x+} \ch{SO4^2-} \\ 2 \chemsetup[chemformula]{charge-style = math} 3 \ch{M^x+} \ch{SO4^2-} </pre>	$M^{x+} \text{SO}_4^{2-}$ $M^{x+} \text{SO}_4^{2-}$
--	--

The option **subscript-vshift** can be used to adjust the vertical shift of the subscripts:

<pre> 1 \ch{H2SO4} \ch{Na3PO4} \\ 2 \chemsetup[chemformula]{subscript-vshift=.5ex} 3 \ch{H2SO4} \ch{Na3PO4} \\ 4 \chemsetup[chemformula]{subscript-vshift=-.2ex} 5 \ch{H2SO4} \ch{Na3PO4} </pre>	$\text{H}_2\text{SO}_4 \text{Na}_3\text{PO}_4$ $\text{H}_2\text{SO}_4 \text{Na}_3\text{PO}_4$ $\text{H}_2\text{SO}_4 \text{Na}_3\text{PO}_4$
--	--



$$\text{H}_2\text{SO}_4 \text{ Na}_3\text{PO}_4$$

$$\text{H}_2\text{SO}_4 \text{ Na}_3\text{PO}_4$$

$$\text{H}_2\text{SO}_4 \text{ Na}_3\text{PO}_4$$

You can choose the mode subscripts are typeset in the same way as it is possible for the charges:

```
1 \ch{A_nB_m} \ch{H2SO4} \\\
2 \chemsetup[chemformula]{subscript-style = math}
3 \ch{A_nB_m} \ch{H2SO4}
```

$$A_nB_m \text{ H}_2\text{SO}_4$$

$$A_nB_m \text{ H}_2\text{SO}_4$$

The option `adduct-space` sets the space left and right to the adduct symbol `.`.

```
1 \ch{Na3PO3*H2O} \\\
2 \chemsetup[chemformula]{adduct-space=.2em}
3 \ch{Na3PO3*H2O}
```

$$\text{Na}_3\text{PO}_3 \cdot \text{H}_2\text{O}$$

$$\text{Na}_3\text{PO}_3 \cdot \text{H}_2\text{O}$$

Changing the length of the bonds:

```
1 \chemsetup[chemformula]{bond-length=4mm}%
2 single: \ch{CH3-CH3} \\\
3 double: \ch{CH2=CH2} \\\
4 triple: \ch{CH#CH}
```

$$\text{single: CH}_3\text{—CH}_3$$

$$\text{double: CH}_2\text{=CH}_2$$

$$\text{triple: CH}\equiv\text{CH}$$

You can change the distance between bond and atom, too:

```
1 \ch{H-H + N+N + O=O} \\\
2 \ch[bond-offset=1pt]{H-H + N+N + O=O}
```

$$\text{H-H + N}\equiv\text{N + O=O}$$

$$\text{H-H + N}\equiv\text{N + O=O}$$

## 26. Special Input Types

There are some “special type” input groups.

### 26.1. Single Token Groups

The first kind are groups which consist of only one token, namely of the following ones:

- `\ch{ + }` → `+` creates the plus sign between compounds with space around it:  
`\ch{2 Na + Cl2}`  $2 \text{ Na} + \text{Cl}_2$
- `\ch{ v }` →  $\downarrow$  sign for precipitate: `\ch{BaSO4 v}`  $\text{BaSO}_4\downarrow$
- `\ch{ ^ }` →  $\uparrow$  sign for escaping gas<sup>31</sup>: `\ch{H2 ^}`  $\text{H}_2\uparrow$

The space left and right of the plus sign can be set with this option:

- `plus-space = <dim>` → Default = `.3em`

<sup>31</sup> Is this the correct English term? Please correct me if it isn't.

1	<code>\ch{A + B}\</code>	$A + B$
2	<code>\ch[plus-space=4pt]{A + B}</code>	$A + B$

## 26.2. Option Input

This is an experimental feature and may well be dropped in future versions.

Sometimes you might want to apply an option only to a part of a, say, reaction. Of course you have the possibility to use `\ch` several times.

1	<code>\ch{H2O +}\textcolor{red}{\ch{H2SO4}}\ch{-&gt; H3O+ + HSO4-} \</code>
2	<code>\ch{H2O +}\ch[subscript-vshift=2pt]{H2SO4}\ch{-&gt; H3O+ + HSO4-}</code>

$H_2O + H_2SO_4$	$\longrightarrow$	$H_3O^+ + HSO_4^-$
$H_2O + H_2SO_4$	$\longrightarrow$	$H_3O^+ + HSO_4^-$

This, however, interrupts the input in your source and *may* mess with the spacing. That's why there is an alternative:

- `\ch{ @<options> }`  → The options specified this way will be valid *only* until the next compound is set.

1	<code>\ch{H2O +}\textcolor{red}{\ch{H2SO4}}\ch{-&gt; H3O+ + HSO4-} \</code>
2	<code>\ch{H2O + @\format=\color{red}} H2SO4 -&gt; H3O+ + HSO4-} \</code>
3	<code>or of course:\</code>
4	<code>\ch{H2O + \textcolor{red}{H2SO4} -&gt; H3O+ + HSO4-}\[1em]</code>
5	<code>\ch{H2O +}\ch[subscript-vshift=2pt]{H2SO4}\ch{-&gt; H3O+ + HSO4-} \</code>
6	<code>\ch{H2O + @\subscript-vshift=2pt} H2SO4 -&gt; H3O+ + HSO4-}</code>

$H_2O + H_2SO_4$	$\longrightarrow$	$H_3O^+ + HSO_4^-$
$H_2O + H_2SO_4$	$\longrightarrow$	$H_3O^+ + HSO_4^-$
or of course:		
$H_2O + H_2SO_4$	$\longrightarrow$	$H_3O^+ + HSO_4^-$
$H_2O + H_2SO_4$	$\longrightarrow$	$H_3O^+ + HSO_4^-$
$H_2O + H_2SO_4$	$\longrightarrow$	$H_3O^+ + HSO_4^-$
$H_2O + H_2SO_4$	$\longrightarrow$	$H_3O^+ + HSO_4^-$

## 27. Escaped Input

In some cases it may be desirable to prevent `CHEMFORMULA` from parsing the input. This can be done in two ways.

### 27.1. Text

If you put something between " " or ' ' then the input will be treated as normal text, except that spaces are not allowed and have to be input with `~`.

- `\ch{ "<escaped text>" }`

► `\ch{ '<escaped text>' }`

```
1 \ch{"\ox{2,Ca}" 0} \\
2 \ch{"\ldots\," Na + "\ldots\," Cl2 -> "\ldots\," NaCl} \\
3 \ch{'A~->~B'}
```

$$\overset{\text{II}}{\text{CaO}}$$

$$\dots \text{Na} + \dots \text{Cl}_2 \longrightarrow \dots \text{NaCl}$$

$$\text{A} \rightarrow \text{B}$$

In many cases you won't need to escape the input. But when you get into trouble when using a command inside `\ch` try hiding it.

## 27.2. Math

If you especially want to input math you just enclose it with `$ $`. This output is different from the escaped text as it is followed by a space.

► `\ch{ $<escaped math>$ }`

<pre>1 escaped text: \ch{"\$x\$" H2O} \\ 2 escaped math: \ch{"\$x\$ H2O"} \\ 3 \ch{"\$2n\$ Na + \$n\$ Cl2 -&gt; \$2n\$ NaCl"}</pre>	<p>escaped text: <math>x\text{H}_2\text{O}</math></p> <p>escaped math: <math>x\text{H}_2\text{O}</math></p> $2n\text{Na} + n\text{Cl}_2 \longrightarrow 2n\text{NaCl}$
---	--

The space that is inserted after a math group can be edited:

► `math-space = <dim> → Default = .1667em`

<pre>1 \ch{"\$2n\$ Na + \$n\$ Cl2 -&gt; \$2n\$ NaCl"} \\ 2 \chemsetup{chemformula}{math-space=.25em} 3 \ch{"\$2n\$ Na + \$n\$ Cl2 -&gt; \$2n\$ NaCl"} \\ 4 \ch{"\$A-&gt;B\$"} \\</pre>	$2n\text{Na} + n\text{Cl}_2 \longrightarrow 2n\text{NaCl}$ $2n\text{Na} + n\text{Cl}_2 \longrightarrow 2n\text{NaCl}$ $A- > B$
--	--

## 28. Arrows

### 28.1. Arrow types

Arrows are input in the same intuitive way they are with `mhchem`. There are various different types:

- `\ch{ -> } → →` standard right arrow
- `\ch{ <- } → ←` standard left arrow
- `\ch{ -/> } → ⇏` does not react (right)
- `\ch{ </- } → ⇏` does not react (left)

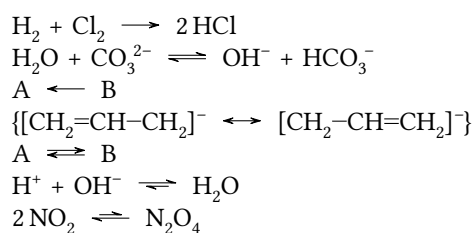
- `\ch{ <-> }` →  $\longleftrightarrow$  resonance arrow
- `\ch{ <> }` →  $\rightleftharpoons$  reaction in both directions
- `\ch{ == }` →  $=$  stoichiometric equation
- `\ch{ <=> }` →  $\rightleftharpoons$  equilibrium arrow
- `\ch{ <=>> }` →  $\rightleftharpoons$  unbalanced equilibrium arrow to the right
- `\ch{ <=>< }` →  $\rightleftharpoons$  unbalanced equilibrium arrow to the left
- `\ch{ <o> }` →  $\longleftrightarrow$  isolobal arrow

All these arrows are drawn with **TikZ**.

```

1 \ch{H2 + Cl2 -> 2 HCl} \\
2 \ch{H2O + CO3^{2-} <=> OH- + HCO3-} \\
3 \ch{A <- B} \\
4 \ch{\{[CH2=CH-CH2]- <-> [CH2-CH=CH2]- \}} \\
5 \ch{A <> B} \\
6 \ch{H+ + OH- <=>> H2O} \\
7 \ch{2 NO2 <=>< N2O4}

```



## 28.2. Labels

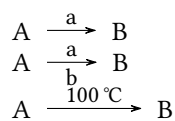
The arrows take two optional arguments to label them.

- `\ch{ ->[<above>][<below>] }`

```

1 \ch{A ->[a] B} \\
2 \ch{A ->[a][b] B} \\
3 \ch{A ->[\SI{100}{\celsius}] B}

```

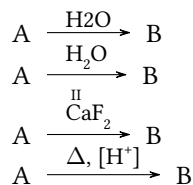


The label text can be parsed separately from the arrow. The recipe is easy: leave blanks.

```

1 \ch{A ->[H2O] B} \\
2 \ch{A ->[ H2O ] B} \\
3 \ch{A ->[ "\text{ox}\{2,Ca\}" F2 ] B} \\
4 \ch{A ->[\Delta, [H^+]] B}

```

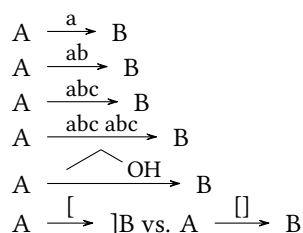


If you leave the blanks `CHEMFORMULA` treats the groups inside the square brackets as separated input types. The arrow reads its arguments *afterwards*. As you can see the arrows “grow” with the length of the labels. What stays constant is the part that protrudes the labels. As you also can see in the last example square brackets inside the arrow arguments should be produced using `\[` and `\]`. They keep their usual meaning outside `\ch`. These commands are necessary since the usual grouping (i.e. hiding the brackets inside curly brackets) doesn’t work due to the way `\ch` reads its argument.

```

1 \ch{A ->[a] B} \\
2 \ch{A ->[ab] B} \\
3 \ch{A ->[abc] B} \\
4 \ch{A ->[abc~abc] B} \\
5 % needs the 'chemfig' package:
6 \setatomsep{15pt}
7 \ch{A ->[ "\chemfig{[:-30]-[:-30]OH}" ] B} \\
8 \ch{A ->[[ ] B} vs. \ch{A ->[\[ \] B}

```



### 28.3. Customization

These are the options which enable you to customize the arrows:

- `arrow-offset` = <dim> → This is the length that an arrow protrudes a label on both sides. This means an empty arrow’s length is two times `arrow-offset`. Default = 1.5ex
- `arrow-yshift` = <dim> → Shifts an arrow up (positive value) or down (negative value). Default = 0pt
- `arrow-ratio` = <factor> → The ratio of the arrow lengths of the unbalanced equilibrium. .4 would mean that the length of the shorter arrow is 0.4× the length of the longer arrow. Default = .6
- `compound-sep` = <dim> → The space between compounds and the arrows. Default = 1ex
- `label-offset` = <dim> → The space between the labels and the arrows. Default = 2pt
- `label-style` = <font command> → The relative font size of the labels. Default = `\footnotesize`

The following code shows the effect of the different options on the `<=>` arrow:

```

1 standard: \ch{A <=>[x][y] B} \\
2 longer: \ch[arrow-offset=12pt]{A <=>[x][y] B} \\
3 higher: \ch[arrow-yshift=2pt]{A <=>[x][y] B} \\
4 more balanced: \ch[arrow-ratio=.8]{A <=>[x][y] B} \\
5 labels further away: \ch[label-offset=4pt]{A <=>[x][y] B} \\
6 larger distance to compounds: \ch[compound-sep=2ex]{A <=>[x][y] B} \\
7 smaller labels: \ch[label-style=\tiny]{A <=>[x][y] B}

```

standard: A  $\xrightarrow[y]{x}$  B  
 longer: A  $\xrightarrow[y]{x}$  B  
 higher: A  $\xrightarrow[y]{x}$  B  
 more balanced: A  $\xrightarrow[y]{x}$  B  
 labels further away: A  $\xrightarrow[y]{x}$  B  
 larger distance to compounds: A  $\xrightarrow[y]{x}$  B  
 smaller labels: A  $\xrightarrow[y]{x}$  B

## 28.4. Modify Arrow Types

The arrows are defined with the command

► `\DeclareChemArrow{<tokens>}{<tikz>}`

{<tokens>} is the sequence of tokens that is replaced with the actual arrow code. For example the basic arrow is defined via

```

1 \DeclareChemArrow{>}{\draw[-cf] (cf_arrow_start) -- (cf_arrow_end) ;}

```

In order to define arrows yourself you need to know the basics of **TikZ**<sup>32</sup>. There are some predefined coordinates you can and should use:

(cf\_arrow\_start) The beginning of the arrow.

(cf\_arrow\_end) The end of the arrow.

(cf\_arrow\_mid) The mid of the arrow.

(cf\_arrow\_mid\_start) The beginning of the shorter arrow in types like <=>.

(cf\_arrow\_mid\_end) The end of the shorter arrow in types like <=>.

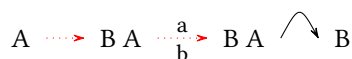
cf, left cf, right cf **CHEMFORMULA**'s own arrow heads.

```

1 \DeclareChemArrow{.>}{\draw[-cf,dotted,red] (cf_arrow_start) -- (cf_arrow_end);}
2 \DeclareChemArrow{n>}{\draw[-cf] (cf_arrow_start) .. controls ([yshift=3ex]cf_
   arrow_mid) .. (cf_arrow_end);}
3 \ch{A .> B} \ch{A n>[a][b] B} \ch{A n> B}

```

<sup>32</sup> Please see the pgfmanual for details.



If you want to redefine an existing arrow there are two commands you can use:

► `\RenewChemArrow{<tokens>}{<tikz>}`

► `\ShowChemArrow{<tokens>}`

The second one gives the current definition, the first one redefines an existing arrow.

```
1 \texttt{\ShowChemArrow{->}} \\  
2 \RenewChemArrow{->}{\draw[->,red] (cf_arrow_start) -- (cf_arrow_end) ;}  
3 \texttt{\ShowChemArrow{->}} \\  
4 \ch{A -> B}  
  
\draw [-cf](cf_arrow_start) (cf_arrow_end);  
\draw [->,red] (cf_arrow_start) (cf_arrow_end) ;  
A  $\longrightarrow$  B
```

## 29. Names

### 29.1. Syntax

**CHEMFORMULA** has a built-in syntax to write text under a compound. In a way it works very similar to the arrows.

► `\ch{ !(<name>)( <formula> ) }`

If an exclamation mark is followed by a pair of parentheses **CHEMFORMULA** will parse it this way:

1	<code>\ch{!(ethanol)( CH<sub>2</sub>CH<sub>2</sub>OH )}</code>	$\text{CH}_2\text{CH}_2\text{OH}$ ethanol
---	--	--

The same what's true for the arrows arguments holds for these arguments: if you leave blanks the different parts will be treated according to their input type before the text is set below the formula.

1	<code>\ch{!(water)(H<sub>2</sub>O)} \quad</code>	
2	<code>\ch{!( "\textcolor{blue}{water}" )( H<sub>2</sub>O )} \quad</code>	
3	<code>\ch{!( \$2n-1\$ )( H<sub>2</sub>O )} \quad</code>	
4	<code>\ch{!( H<sub>2</sub>O )( H<sub>2</sub>O )} \quad</code>	
5	<code>\ch{!(oxonium)( H<sub>3</sub>O<sup>+</sup> )}</code>	

$\text{H}_2\text{O}$ water	$\text{H}_2\text{O}$ <span style="color: blue;">water</span>	$\text{H}_2\text{O}$ $2n - 1$	$\text{H}_2\text{O}$ $\text{H}_2\text{O}$	$\text{H}_3\text{O}^+$ oxonium
-------------------------------	---	----------------------------------	--	-----------------------------------

If for some reason you want to insert an exclamation mark *without* it creating a name you only have to make sure it isn't followed by parentheses.

```

1 \ch{H2O~(!)} \ \ H2O (!)
2 \ch{A!{}} \ \ A!()

```

## 29.2. Customization

**CHEMFORMULA** provides two options to customize the output of the names:

- **name-format** = <commands> → The format of the name. This can be arbitrary input. Default = `\scriptsize\centering`
- **name-width** = <dim>/auto → The width of the box where the label is put into. auto will detect the width of the name and set the box to this width. Default = auto

```

1 \ch{!(acid)( H2SO4 ) -> B} \ \
2 \ch[name-format=\sffamily\small]{!(acid)( H2SO4 ) -> B} \ \
3 \ch[name-format=\scriptsize N:~]{!(acid)( H2SO4 ) -> B} \ \
4 \ch[name-width=3em,name-format=\scriptsize\raggedright]{!(acid)( H2SO4 ) -> B}

```

$$\text{H}_2\text{SO}_4 \rightarrow \text{B}$$

$$\text{acid} \text{H}_2\text{SO}_4 \rightarrow \text{B}$$

$$\text{acid} \text{H}_2\text{SO}_4 \rightarrow \text{B}$$

$$\text{N: acid} \text{H}_2\text{SO}_4 \rightarrow \text{B}$$

$$\text{acid} \text{H}_2\text{SO}_4 \rightarrow \text{B}$$

## 30. Format and Font

In the standard setting **CHEMFORMULA** doesn't make any default changes to the font of the formula output. Let's take a look at a nonsense input which shows all features:

```

1 \newcommand*\sample{\ch{H2C-C+C-CH=CH+ + CrO4^2- <=>[x][y] 2.5 Cl^{-.} + 3_1/2 Na
   *OH_{(aq)} + !(name)( A^n ) "\LaTeXe"}}
2 \sample

```

$$\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightleftharpoons[\text{y}]{\text{x}} 2.5 \text{Cl}^{-.} + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^n \text{\LaTeXe}$$

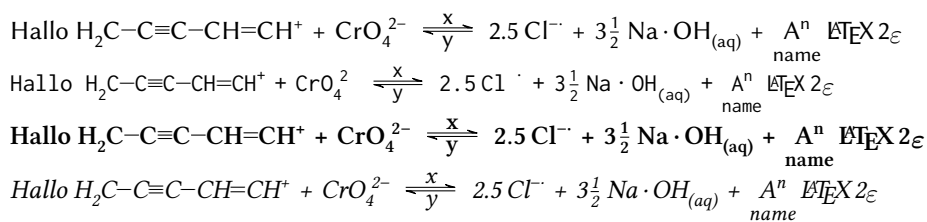
Now we're going to change different aspects of the font a look what happens:

```

1 \sffamily Hallo \sample \ \
2 \ttfamily Hallo \sample \normalfont \ \
3 \bfseries Hallo \sample \normalfont \ \
4 \itshape Hallo \sample

```





As you can see most features adapt to the surrounding font.

If you want to change the default format you need to use this option:

- **format** = <anything> → Adds arbitrary code before the output of `\ch`.

```

1 \definecolor{newblue}{rgb}{.1,.1,.5}\chemsetup[chemformula]{format=\color{newblue}
  }\sffamily}
2 \sffamily Hallo \sample \\
3 \ttfamily Hallo \sample \normalfont \\
4 \bfseries Hallo \sample \normalfont \\
5 \itshape Hallo \sample

Halo H2C-C≡C-CH=CH+ + CrO42-  $\xrightleftharpoons[\text{y}]{\text{x}}$  2.5 Cl- + 3½ Na · OH(aq) +  $\overset{\text{A}^n}{\underset{\text{name}}{\text{L}^{\text{A}}\text{T}_{\text{E}}\text{X} 2_{\varepsilon}}}$ 
Halo H2C-C≡C-CH=CH+ + CrO42-  $\xrightleftharpoons[\text{y}]{\text{x}}$  2.5 Cl- + 3½ Na · OH(aq) +  $\overset{\text{A}^n}{\underset{\text{name}}{\text{L}^{\text{A}}\text{E}^{\text{X}} 2_{\varepsilon}}}$ 
Halo H2C-C≡C-CH=CH+ + CrO42-  $\xrightleftharpoons[\text{y}]{\text{x}}$  2.5 Cl- + 3½ Na · OH(aq) +  $\overset{\text{A}^n}{\underset{\text{name}}{\text{B}^{\text{L}}\text{E}^{\text{X}} 2_{\varepsilon}}}$ 
Halo H2C-C≡C-CH=CH+ + CrO42-  $\xrightleftharpoons[\text{y}]{\text{x}}$  2.5 Cl- + 3½ Na · OH(aq) +  $\overset{\text{A}^n}{\underset{\text{name}}{\text{L}^{\text{A}}\text{T}_{\text{E}}\text{X} 2_{\varepsilon}}}$ 

```

You can also specifically change the fontfamily, fontseries and fontshape of the output.

- **font-family** = <family> → Changes the fontfamily of the output with `\fontfamily{<family>}\selectfont`.
- **font-series** = <series> → Changes the fontseries of the output with `\fontseries{<series>}\selectfont`.
- **font-shape** = <shape> → Changes the fontshape of the output with `\fontshape{<shape>}\selectfont`.

```

1 \chemsetup[chemformula]{font-series=bx}
2 Hallo \sample \\
3 \sffamily Hallo \sample \normalfont \\
4 \chemsetup[chemformula]{font-family=lmr,font-series=m} Hallo \sample \normalfont
  \\
5 \itshape Hallo \sample

```

Hallo $\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$
Hallo $\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$
Hallo $\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$
Hallo $\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$

If you're using  $\text{\LaTeX}$  or  $\text{\LuaTeX}$  and have loaded `fontspec`<sup>33</sup> you have the possibility to set the font with it:

- `font-spec` = {<font>} or with options
- `font-spec` = {[<options>]<font>}

1	<code>\chemsetup[chemformula]{font-spec={Linux Biolinum O}} \sample \</code>
2	<code>\chemsetup[chemformula]{font-spec={[[Color=darkgray]Augie}} \sample \</code>
3	<code>\chemsetup[chemformula]{font-spec={Tipbrush Script}} \sample \</code>
4	<code>\chemsetup[chemformula]{font-spec={Latin Modern Sans}} \sample \</code>
5	<code>\bfseries \sample \normalfont \</code>
6	<code>\chemsetup[chemformula]{font-spec={Feathergraphy Decoration}} \sample</code>

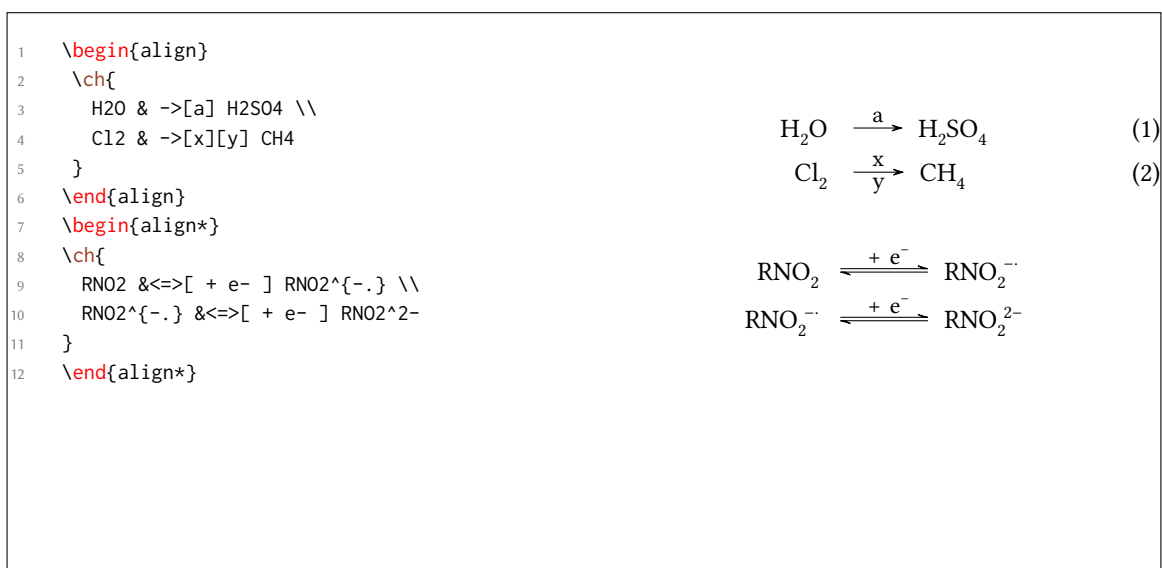
  

$\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$
$\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$
$\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$
$\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$
$\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$
$\text{H}_2\text{C}-\text{C}\equiv\text{C}-\text{CH}=\text{CH}^+ + \text{CrO}_4^{2-} \xrightarrow{\frac{x}{y}} 2.5 \text{Cl}^- + 3\frac{1}{2} \text{Na} \cdot \text{OH}_{(\text{aq})} + \text{A}^{\text{n}}$	$\text{\LaTeX 2\epsilon}$

## 31. Usage In Math Equations

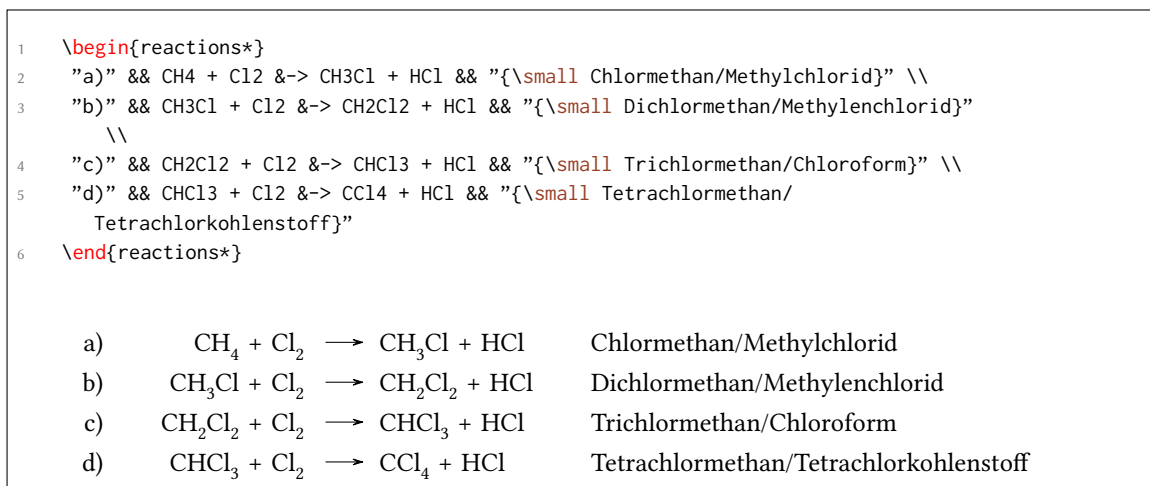
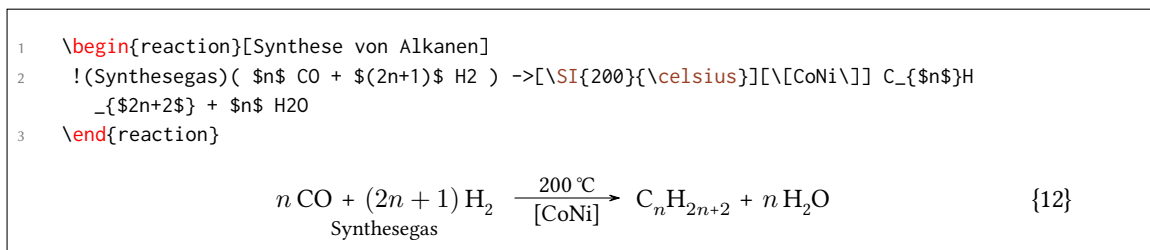
The `\ch` command can be used inside math equations. It recognizes `\` and `&` and passes them on. However, you can't use the optional arguments of `\` inside `\ch`.

<sup>33</sup> CTAN: `fontspec`



## 32. Further Examples

This section presents some examples of a possible usage.



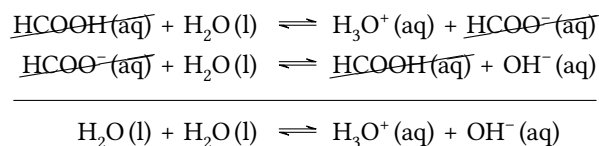
$$\begin{array}{l} \text{C}^{\delta-}\text{-M}^{\delta+} \quad (\longleftrightarrow) \quad \text{C}^{\delta+}\text{-Br}^{\delta-} \\ \text{X}\cdot + \cdot\text{Y} \rightleftharpoons \text{X-Y} + \text{Bindungsenergie} \\ \text{CH}_4(\text{g}) + 2 \text{O}_2(\text{g}) \longrightarrow \text{CO}_2(\text{g}) + \text{H}_2\text{O}(\text{l}) + \Delta H^\ominus \\ \Delta_f H^\ominus \quad \quad \quad \text{??} \quad \quad \quad 0 \quad \quad \quad -94.3 \quad -57.9 \quad -192.1 \end{array}$$
$$\begin{array}{l} \text{CH}_3\text{MgBr} + \text{Cu}^{\text{I}}\text{X} \longrightarrow \text{„CH}_3\text{Cu}^{\text{I}}\text{“} + \text{MgBrX} \quad \text{X} = \text{Br, I, CN} \\ 2 \text{ MeLi} + \text{CuI} \longrightarrow \text{Me}_2\text{CuLi} + \text{Li} \\ \text{Dimethylcuprat (Gilman-Cuprat)} \end{array}$$
$$\begin{array}{lll} \text{H}_3\text{C}-\text{CH}_3 + \text{Cl}_2 & \xrightarrow[h\nu]{\Delta} & \text{H}_3\text{CCH}_2\text{Cl} + \text{HCl} & \Delta H = -27.1 \text{ kJ} \\ \text{H}_3\text{C}-\text{CH}_3 + \text{Cl}\cdot & \longrightarrow & \text{H}_3\text{CCH}_2\cdot + \text{HCl} & \Delta H = -5.0 \text{ kJ} \\ \text{H}_3\text{C}-\text{CH}_2\cdot + \text{Cl}_2 & \longrightarrow & \text{H}_3\text{CCH}_2\text{Cl} + \text{Cl}\cdot & \Delta H = -23.0 \text{ kJ} \end{array}$$

```

1 % needs 'cancel'
2 \begin{align*}
3 \quad \text{\texttt{\textbackslash ch\{cancel\HCOOH\aq\} + H2O\lqd\}} \&=> \text{\texttt{\textbackslash H3O^+\aq\}} + \text{\texttt{\textbackslash cancel\{HCOO^-\aq\}}} \text{\texttt{\textbackslash \}}
4 \quad \text{\texttt{\textbackslash ch\{cancel\{HCOO^-\aq\} + H2O\lqd\}}} \&=> \text{\texttt{\textbackslash cancel\{HCOOH\aq\} + OH^-\aq\}} \text{\texttt{\textbackslash \[-1ex\}}
5 \quad \text{\texttt{\textbackslash cline\{1-2\}}}
6 \quad \text{\texttt{\textbackslash ch\{H2O\lqd\} + H2O\lqd\}} \&=> \text{\texttt{\textbackslash H3O^+\aq\}} + \text{\texttt{\textbackslash OH^-\aq\}}
7 \end{align*}

```

60



## Part IV.

# ghsystem

### 33. Setup

All of `GHSYSTEM`'s options belong to the module `ghsystem`. This means they can be setup with

```

1 \chemsetup[ghsystem]{<options>} or
2 \chemsetup{ghsystem/<option1>,ghsystem/<option2>}

```

### 34. Get Hazard and Precautionary Statements

#### 34.1. Simple Statements

The general usage is simple: you use the command

- `\ghs[<options>]{<type>}{<number>}`
- `\ghs*[<options>]{<type>}{<number>}`

There are three types available: h, euh and p. The `{<type>}` argument is case insensitive, so just type them in as you like.

```

1 \ghs{h}{200} \\\
2 \ghs{H}{224} \\\
3 \ghs{euh}{001} \\\
4 \ghs{Euh}{202} \\\
5 \ghs{p}{201}

```

H200: Unstable explosives.  
H224: Extremely flammable liquid and vapour.  
EUH001: Explosive when dry.  
EUH202: Cyanoacrylate. Danger. Bonds skin and eyes in seconds. Keep out of the reach of children.  
P201: Obtain special instructions before use.

The starred version hides the identifier and only gives the statement. If you want to hide the statement itself instead you can use the option:

- `hide = true/false`

There is an option to customize the output, too.

- `space = <space command> → Space between <type> and <number>.`

1	<code>\ghs{h}{200} \\</code>	H200: Unstable explosives.
2	<code>\ghs[space=\,]{h}{200} \\</code>	H 200: Unstable explosives.
3	<code>\ghs*{h}{200} \\</code>	Unstable explosives.
4	<code>\ghs[hide]{h}{200}</code>	H200

## 34.2. Statements with Placeholders

Some of the statements contain placeholders. They can be one of the following:

- *<state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard>*
- *<state specific effect if known>*
- *<or state all organs affected, if known>*
- *<name of sensitising substance>*

Except the last one which needs to be filled in, they are hidden per default. They can be made visible with the option

► `fill-in = true/false` → Show placeholders. Default = false

1	<code>\ghs{h}{340} \\</code>	H340: May cause genetic defects.
2	<code>\ghs[fill-in]{h}{340} \\</code>	H340: May cause genetic defects. <i>&lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
3	<code>\ghs{h}{360} \\</code>	H360: May damage fertility or the unborn child.
4	<code>\ghs[fill-in]{h}{360} \\</code>	H360: May damage fertility or the unborn child. <i>&lt;state specific effect if known&gt; &lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
5	<code>\ghs{h}{370} \\</code>	H370: Causes damage to organs.
6	<code>\ghs[fill-in]{h}{370} \\</code>	H370: Causes damage to organs <i>&lt;or state all organs affected, if known&gt;. &lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
7	<code>\ghs{euh}{208} \\</code>	EUH208: Contains <i>&lt;name of sensitising substance&gt;</i> . May produce an allergic reaction.
8	<code>\ghs[fill-in]{euh}{208}</code>	EUH208: Contains <i>&lt;name of sensitising substance&gt;</i> . May produce an allergic reaction.

These placeholders can be replaced with one of these options:

- `exposure = <text>` → exposure placeholder
- `effect = <text>` → effect placeholder
- `organs = <text>` → organ placeholder

- **substance** = <text> → substance placeholder

```

1 \ghs[exposure=This is how you get exposed.]{h}{340} \\
2 \ghs[effect=These are the effects.]{h}{360} \\
3 \ghs[organs=to this organ]{h}{370} \\
4 \ghs[substance=substance]{euh}{208}

```

H340: May cause genetic defects. This is how you get exposed.  
H360: May damage fertility or the unborn child. These are the effects.  
H370: Causes damage to this organ.  
EUH208: Contains substance. May produce an allergic reaction.

### 34.3. Statements with Gaps

Some of the statements have gaps that can be filled.

```

1 \ghs{p}{301} \\
2 \ghs{p}{401} \\
3 \ghs{p}{411} \\
4 \ghs{p}{413}

```

P301: IF SWALLOWED:  
P401: Store ...  
P411: Store at temperatures not exceeding °C/°F.  
P413: Store bulk masses greater than kg/lbs at temperatures not exceeding °C/°F.

These gaps can be filled using these options:

- **text** = <text>
- **dots** = <text>
- **C-temperature** = <num>
- **F-temperature** = <num>
- **kg-mass** = <num>
- **lbs-mass** = <num>

```

1 \ghs[dots=contact physician!]{p}{301} \\
2 \ghs[text=here]{p}{401} \\
3 \ghs[C-temperature=50, F-temperature=122]{p}{411} \\
4 \ghs[kg-mass=5.0, lbs-mass=11, C-temperature=50, F-temperature=122]{p}{413}

```

P301: IF SWALLOWED:  
P401: Store ...  
P411: Store at temperatures not exceeding 50 °C/122 °F.  
P413: Store bulk masses greater than 5.0 kg/11 lbs at temperatures not exceeding 50 °C/122 °F.

## 34.4. Combined Statements

There are some combinations of statements. They are input with a + between the numbers:

```
1 \ghs{p}{235+410} \\  
2 \ghs{p}{301+330+331}
```

P235 + P410: Keep cool. Protect from sunlight.

P301 + P330 + P331: IF SWALLOWED: rinse mouth. Do NOT induce vomiting.

Note that you can only get combinations that officially exist. *You can't combine freely.*

## 35. Pictograms

### 35.1. The Pictures

The GHS defines a number of pictograms:



The command

► `\ghspic[<options>]{<name>}`

loads them. Table 3 shows all available pictograms and their names. To be more precise: it shows the names to use with the `\ghspic` command. The file names are `ghsystem_<name>.<filetype>` where `<filetype>` is `eps`, `jpg` or `png`, see also section 35.2.

```
1 \ghspic{skull}
```



If you don't like the default size you can change it using this option:

► `scale = <factor>` → Scales the pictogram. Default = 1

The pictures are actually quite large. The default setting scales them by a factor of  $\frac{1}{20}$ .

```
1 \ghspic[scale=2]{skull}
```



If you want to use some specific `\includegraphics` options, e.g. if you want to rotate the pictogram for some reason, use this option:

► `includegraphics = {<includegraphics keyvals>}`












1 \ghspic[includegraphics={angle=90}]{skull}



Table 3: All available GHS pictograms.

name	pictogram	name	pictogram
explos		explos-1	
explos-2		explos-3	
explos-4		explos-5	
explos-6			
flame		flame-2-white	
flame-2-black		flame-3-white	
flame-3-black		flame-4-1	
flame-4-2		flame-4-3-white	
flame-4-3-black		flame-5-2-white	
flame-5-2-black			
flame-0		flame-0-5-1	
bottle		bottle-2-black	

name	pictogram	name	pictogram
bottle-2-white			
acid		acid-8	
skull		skull-2	
skull-6			
exclam			
health			
aqpol			

### 35.2. Picture Type Depending on Engine

As you probably know you can't use every picture type with every compiler engine. pdf<sub>T</sub><sub>E</sub>X in DVI mode *needs* eps pictures while pdf<sub>T</sub><sub>E</sub>X in PDF mode, X<sub>Y</sub><sub>T</sub><sub>E</sub>X and Lua<sub>T</sub><sub>E</sub>X convert eps pictures into pdf files, given they have the rights to write in the directory the pictures are saved in.

However, the latter can include jpg and png without any problems, while pdf<sub>T</sub><sub>E</sub>X in DVI mode can't.

To resolve this [GHSYSTEM](#) tests which engine is used and if pdf<sub>T</sub><sub>E</sub>X which mode is used and then chooses either eps or png for the pictograms. You are free to choose the picture type yourself with the option

► `pic-type = eps/jpg/png`

## 36. Available Languages

Right now the H and P statements are only available in English, German or Italian. The package adapts the package option `german` but does not (yet) recognize language settings by [babel](#)<sup>35</sup> or [polyglossia](#)<sup>36</sup>.

You can also choose the language explicitly.

► `language = english/german/italian`

<sup>35</sup> CTAN: [babel](#) <sup>36</sup> CTAN: [polyglossia](#)

1	<code>\ghs{h}{201}</code>	H201: Explosive; mass explosion hazard.
2		
3	<code>\chemsetup[ghsystem]{language=german}</code>	H201: Explosiv, Gefahr der Massenexplosion.
4	<code>\ghs{h}{201}</code>	

I will add other languages some time in future. This may take a while, though. If you would be willing to contribute and write the statements of another language please feel free to contact me<sup>37</sup>. I would provide you with a template file, a pdf containing the official translations, and help to all your questions.

## 37. List of All Statements

If for some reason you want to list all sentences you can use

► `\ghslistall[<options>]`

This command has a number of options to customize the table, which is created with the `longtable` environment of the `longtable` package.

- `table-head-number` = <text> → Default = Identifier
- `table-head-text` = <text> → Default = Statement
- `table-next-page` = <text> → Default = continues on next page
- `table-caption` = <text> → As <text> in `\caption{<text>}`. Default = All H, EUH, and P Statements.
- `table-caption-short` = <text> → As <short> in `\caption[<short>]{<text>}`.
- `table-label` = <text> → The label to refer to the table with `\ref` and similar commands. Default = `tab:ghs-hp-statements`
- `table-row-sep` = <dim> → The separation of the table rows. A  $\text{\TeX}$  dimension. Default = 3pt
- `table-rules` = `default`/`booktabs`/`none` → The style of the horizontal rules in the table. `default` uses `\hline`, `booktabs` uses `\toprule`, `\midrule` or `\bottomrule`, resp. This option needs the `booktabs`<sup>38</sup> package which you have to load yourself then. Default = `default`
- `table-top-head-rule` = `default`/`booktabs`/`none` → Change top rule explicitly. Default = `default`
- `table-head-rule` = `default`/`booktabs`/`none` → Change rule below head explicitly. Default = `default`
- `table-foot-rule` = `default`/`booktabs`/`none` → Change foot rule explicitly. Default = `default`
- `table-last-foot-rule` = `default`/`booktabs`/`none` → Change last foot rule explicitly. Default = `default`

The code below shows how [Table 4](#) was created:

<sup>37</sup> [contact@mychemistry.eu](mailto:contact@mychemistry.eu)    <sup>38</sup> CTAN: `booktabs`

Table 4: All H, EUH, and P Statements.

Identifier	Statement
H200	Unstable explosives.
H201	Explosive; mass explosion hazard.
H202	Explosive, severe projection hazard.
H203	Explosive; fire, blast or projection hazard.
H204	Fire or projection hazard.
H205	May mass explode in fire.
H220	Extremely flammable gas.
H221	Flammable gas.
H222	Extremely flammable aerosol.
H223	Flammable aerosol.
H224	Extremely flammable liquid and vapour.
H225	Highly flammable liquid and vapour.
H226	Flammable liquid and vapour.
H228	Flammable solid.
H240	Heating may cause an explosion.
H241	Heating may cause a fire or explosion.
H242	Heating may cause a fire.
H250	Catches fire spontaneously if exposed to air.
H251	Self-heating; may catch fire.
H252	Self-heating in large quantities; may catch fire.
H260	In contact with water releases flammable gases which may ignite spontaneously.
H261	In contact with water releases flammable gases.
H270	May cause or intensify fire; oxidiser.
H271	May cause fire or explosion; strong oxidiser.
H272	May intensify fire; oxidiser.
H280	Contains gas under pressure; may explode if heated.
H281	Contains refrigerated gas; may cause cryogenic burns or injury.
H290	May be corrosive to metals.
H300	Fatal if swallowed.
H301	Toxic if swallowed.

*continues on next page*

Identifier	Statement
H302	Harmful if swallowed.
H304	May be fatal if swallowed and enters airways.
H310	Fatal in contact with skin.
H311	Toxic in contact with skin.
H312	Harmful in contact with skin.
H314	Causes severe skin burns and eye damage.
H315	Causes skin irritation.
H317	May cause an allergic skin reaction.
H318	Causes serious eye damage.
H319	Causes serious eye irritation.
H330	Fatal if inhaled.
H331	Toxic if inhaled.
H332	Harmful if inhaled.
H334	May cause allergy or asthma symptoms or breathing difficulties if inhaled.
H335	May cause respiratory irritation.
H336	May cause drowsiness or dizziness.
H340	May cause genetic defects. <i>&lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
H341	Suspected of causing genetic defects. <i>&lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
H350	May cause cancer. <i>&lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
H351	Suspected of causing cancer. <i>&lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
H360	May damage fertility or the unborn child. <i>&lt;state specific effect if known&gt; &lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
H361	Suspected of damaging fertility or the unborn child. <i>&lt;state specific effect if known&gt; &lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
H362	May cause harm to breast-fed children.
H370	Causes damage to organs <i>&lt;or state all organs affected, if known&gt;. &lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>

*continues on next page*

Identifier	Statement
H371	May cause damage to organs <i>&lt;or state all organs affected, if known&gt;</i> . <i>&lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
H372	Causes damage to organs <i>&lt;or state all organs affected, if known&gt;</i> through prolonged or repeated exposure. <i>&lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
H373	May cause damage to organs <i>&lt;or state all organs affected, if known&gt;</i> through prolonged or repeated exposure. <i>&lt;state route of exposure if it is conclusively proven that no other routes of exposure cause the hazard&gt;</i>
H400	Very toxic to aquatic life.
H410	Very toxic to aquatic life with long lasting effects.
H411	Toxic to aquatic life with long lasting effects.
H412	Harmful to aquatic life with long lasting effects.
H413	May cause long lasting harmful effects to aquatic life.
H350i	May cause cancer by inhalation.
H360F	May damage fertility.
H360D	May damage the unborn child.
H361f	Suspected of damaging fertility.
H361d	Suspected of damaging the unborn child.
H360FD	May damage fertility. May damage the unborn child.
H361fd	Suspected of damaging fertility. Suspected of damaging the unborn child.
H360Fd	May damage fertility. Suspected of damaging the unborn child.
H360Df	May damage the unborn child. Suspected of damaging fertility.
EUH001	Explosive when dry.
EUH006	Explosive with or without contact with air.
EUH014	Reacts violently with water.
EUH018	In use may form flammable/explosive vapour-air mixture.
EUH019	May form explosive peroxides.
EUH044	Risk of explosion if heated under confinement.
EUH029	Contact with water liberates toxic gas.
EUH031	Contact with acids liberates toxic gas.
EUH032	Contact with acids liberates very toxic gas.
EUH066	Repeated exposure may cause skin dryness or cracking.
EUH070	Toxic by eye contact.
EUH071	Corrosive to the respiratory tract.

*continues on next page*

Identifier	Statement
EUH059	Hazardous to the ozone layer.
EUH201	Contains lead. Should not be used on surfaces liable to be chewed or sucked by children.
EUH201A	Warning! contains lead.
EUH202	Cyanoacrylate. Danger. Bonds skin and eyes in seconds. Keep out of the reach of children.
EUH203	Contains chromium(VI). May produce an allergic reaction.
EUH204	Contains isocyanates. May produce an allergic reaction.
EUH205	Contains epoxy constituents. May produce an allergic reaction.
EUH206	Warning! Do not use together with other products. May release dangerous gases (chlorine).
EUH207	Warning! Contains cadmium. Dangerous fumes are formed during use. See information supplied by the manufacturer. Comply with the safety instructions.
EUH208	Contains <name of sensitising substance>. May produce an allergic reaction.
EUH209	Can become highly flammable in use.
EUH209A	Can become flammable in use.
EUH210	Safety data sheet available on request.
EUH401	To avoid risks to human health and the environment, comply with the instructions for use.
P101	If medical advice is needed, have product container or label at hand.
P102	Keep out of reach of children.
P103	Read label before use.
P201	Obtain special instructions before use.
P202	Do not handle until all safety precautions have been read and understood.
P210	Keep away from heat/sparks/open flames/hot surfaces. — No smoking.
P211	Do not spray on an open flame or other ignition source.
P220	Keep/Store away from clothing/.../combustible materials.
P221	Take any precaution to avoid mixing with combustibles ...
P222	Do not allow contact with air.
P223	Keep away from any possible contact with water, because of violent reaction and possible flash fire.
P230	Keep wetted with ...
P231	Handle under inert gas.
P232	Protect from moisture.

*continues on next page*

Identifier	Statement
P233	Keep container tightly closed.
P234	Keep only in original container.
P235	Keep cool.
P240	Ground/bond container and receiving equipment.
P241	Use explosion-proof electrical/ventilating/lighting/... equipment.
P242	Use only non-sparking tools.
P243	Take precautionary measures against static discharge.
P244	Keep reduction valves free from grease and oil.
P250	Do not subject to grinding/shock/.../friction.
P251	Pressurized container: Do not pierce or burn, even after use.
P260	Do not breathe dust/fume/gas/mist/vapours/spray.
P261	Avoid breathing dust/fume/gas/mist/vapours/spray.
P262	Do not get in eyes, on skin, or on clothing.
P263	Avoid contact during pregnancy/while nursing.
P264	Wash ... thoroughly after handling.
P270	Do not eat, drink or smoke when using this product.
P271	Use only outdoors or in a well-ventilated area.
P272	Contaminated work clothing should not be allowed out of the workplace.
P273	Avoid release to the environment.
P280	Wear protective gloves/protective clothing/eye protection/face protection.
P281	Use personal protective equipment as required.
P282	Wear cold insulating gloves/face shield/eye protection.
P283	Wear fire/flame resistant/retardant clothing.
P284	Wear respiratory protection.
P285	In case of inadequate ventilation wear respiratory protection.
P231 + P231	Handle under inert gas. Protect from moisture.
P235 + P410	Keep cool. Protect from sunlight.
P301	IF SWALLOWED:
P302	IF ON SKIN:
P303	IF ON SKIN (or hair):
P304	IF INHALED:
P305	IF IN EYES:
P306	IF ON CLOTHING:
P307	IF exposed:

*continues on next page*



Identifier	Statement
P308	IF exposed or concerned:
P309	IF exposed or if you feel unwell:
P310	Immediately call a POISON CENTER or doctor/physician.
P311	Call a POISON CENTER or doctor/physician.
P312	Call a POISON CENTER or doctor/physician if you feel unwell.
P313	Get medical advice/attention.
P314	Get medical advice/attention if you feel unwell.
P315	Get immediate medical advice/attention.
P320	Specific treatment is urgent (see ... on this label).
P321	Specific treatment (see ... on this label).
P322	Specific measures (see ... on this label).
P330	Rinse mouth.
P331	Do NOT induce vomiting.
P332	If skin irritation occurs:
P333	If skin irritation or rash occurs:
P334	Immerse in cool water/wrap in wet bandages.
P335	Brush off loose particles from skin.
P336	Thaw frosted parts with lukewarm water. Do not rub affected area.
P337	If eye irritation persists:
P338	Remove contact lenses, if present and easy to do. Continue rinsing.
P340	Remove victim to fresh air and keep at rest in a position comfortable for breathing.
P341	If breathing is difficult, remove victim to fresh air and keep at rest in a position comfortable for breathing.
P342	If experiencing respiratory symptoms:
P350	Gently wash with plenty of soap and water.
P351	Rinse cautiously with water for several minutes.
P352	Wash with plenty of soap and water.
P353	Rinse skin with water/shower.
P360	Rinse immediately contaminated clothing and skin with plenty of water before removing clothes.
P361	Remove/Take off immediately all contaminated clothing.
P362	Take off contaminated clothing and wash before reuse.
P363	Wash contaminated clothing before reuse.
P370	In case of fire:
P371	In case of major fire and large quantities:

*continues on next page*

Identifier	Statement
P372	Explosion risk in case of fire.
P373	DO NOT fight fire when fire reaches explosives.
P374	Fight fire with normal precautions from a reasonable distance.
P375	Fight fire remotely due to the risk of explosion.
P376	Stop leak if safe to do so.
P377	Leaking gas fire: Do not extinguish, unless leak can be stopped safely.
P378	Use ... for extinction.
P380	Evacuate area.
P381	Eliminate all ignition sources if safe to do so.
P390	Absorb spillage to prevent material damage.
P391	Collect spillage.
P301 + P310	IF SWALLOWED: Immediately call a POISON CENTER or doctor/physician.
P301 + P312	IF SWALLOWED: Call a POISON CENTER or doctor/physician if you feel unwell.
P301 + P330 + P331	IF SWALLOWED: rinse mouth. Do NOT induce vomiting.
P302 + P334	IF ON SKIN: Immerse in cool water/wrap in wet bandages.
P302 + P350	IF ON SKIN: Gently wash with plenty of soap and water.
P302 + P352	IF ON SKIN: Wash with plenty of soap and water.
P303 + P361 + P353	IF ON SKIN (or hair): Remove/Take off immediately all contaminated clothing. Rinse skin with water/shower.
P304 + P340	IF INHALED: Remove victim to fresh air and keep at rest in a position comfortable for breathing.
P304 + P341	IF INHALED: If breathing is difficult, remove victim to fresh air and keep at rest in a position comfortable for breathing.
P305 + P351 + P338	IF IN EYES: Rinse cautiously with water for several minutes. Remove contact lenses, if present and easy to do. Continue rinsing.
P306 + P360	IF ON CLOTHING: Rinse immediately contaminated clothing and skin with plenty of water before removing clothes.
P307 + P311	IF exposed: Call a POISON CENTER or doctor/physician.
P308 + P313	IF exposed or concerned: Get medical advice/attention.
P309 + P311	IF exposed or if you feel unwell: Call a POISON CENTER or doctor/physician.
P332 + P313	If skin irritation occurs: Get medical advice/attention.
P333 + P313	If skin irritation or rash occurs: Get medical advice/attention.

*continues on next page*

Identifier	Statement
P335 + P334	Brush off loose particles from skin. Immerse in cool water/wrap in wet bandages.
P337 + P313	If eye irritation persists: Get medical advice/attention.
P342 + P311	If experiencing respiratory symptoms: Call a POISON CENTER or doctor/physician.
P370 + P376	In case of fire: Stop leak if safe to do so.
P370 + P378	In case of fire: Use ... for extinction.
P370 + P380	In case of fire: Evacuate area.
P370 + P380 + P375	In case of fire: Evacuate area. Fight fire remotely due to the risk of explosion.
P371 + P380 + P375	In case of major fire and large quantities: Evacuate area. Fight fire remotely due to the risk of explosion.
P401	Store ...
P402	Store in a dry place.
P403	Store in a well-ventilated place.
P404	Store in a closed container.
P405	Store locked up.
P406	Store in corrosive resistant/... container with a resistant inner liner.
P407	Maintain air gap between stacks/pallets.
P410	Protect from sunlight.
P411	Store at temperatures not exceeding °C/°F.
P412	Store at temperatures not exceeding 50 °C/122 °F.
P413	Store bulk masses greater than kg/lbs at temperatures not exceeding °C/°F.
P420	Store away from other materials.
P422	Store contents under ...
P402 + P404	Store in a dry place. Store in a closed container.
P403 + P233	Store in a well-ventilated place. Keep container tightly closed.
P403 + P235	Store in a well-ventilated place. Keep cool.
P410 + P403	Protect from sunlight. Store in a well-ventilated place.
P410 + P412	Protect from sunlight. Do not expose to temperatures exceeding 50 °C/122 °F.
P411 + P235	Store at temperatures not exceeding °C/°F . Keep cool.
P501	Dispose of contents/container to ...

# Part V.

## Appendix

### Overview: Options and Customization

#### Options

In the table below all options provided by CHEMMACROS for customization are listed. All options that belong to a module can be set with

► `\chemsetup[<module>]{<keyval>}` or

► `\chemsetup{<module>/<keyval>}`.

Some options can be set without value. Then the underlined value is used. The options belonging to the modules `chemformula` and `ghsystem` are not listed here.

option	module	values	default	
package options:				
<code>bpchem</code>	option	<u>true</u> /false	false	page 5
<code>circled</code>	option	formal/ <u>all</u> /none	formal	page 5
<code>circletype</code>	option	chem/math	chem	page 6
<code>cmversion</code>	option	1/2/bundle	bundle	page 6
<code>ghsystem</code>	option	<u>true</u> /false	true	page 6
<code>iupac</code>	option	auto/restricted/strict	auto	page 6
<code>language</code>	option	<language>	english	page 6
<code>method</code>	option	chemformula/formula	formula	page 6
<code>Nu</code>	option	chemmacros/mathspec	chemmacros	page 6
<code>strict</code>	option	<u>true</u> /false	false	page 6
<code>synchronize</code>	option	<u>true</u> /false	false	page 6
<code>greek</code>	option	math/textgreek/ <u>upgreek</u>	upgreek	page 6
<code>version</code>	option			page 7
<code>xspace</code>	option	<u>true</u> /false	true	page 6
<code>\ba, \Nu:</code>				
<code>elpair</code>	particle	<u>dots</u> /dash/false	false	page 10
IUPAC commands:				
<code>break-space</code>	iupac	<dim>	.01em	page 12
<code>bridge-number</code>	iupac	sub/super	sub	page 15
<code>coord-use-hyphen</code>	iupac	<u>true</u> /false	true	page 15
<code>hyphen-pre-space</code>	iupac	<dim>	.01em	page 12
<code>hyphen-post-space</code>	iupac	<dim>	-.03em	page 12
<code>\DeclareChemLatin:</code>				
<code>format</code>	latin	<anything>	<code>\itshape</code>	page 17
<code>\pch, \mch, \fpch, \fmch:</code>				
<code>append</code>	charges	<u>true</u> /false	false	page 19
acid/base:				
<code>p-style</code>	acid-base	slanted/italics/upright	upright	page 18
<code>\ox:</code>				
<code>parse</code>	ox	<u>true</u> /false	true	page 19

option	module	values	default	
roman	ox	<u>true/false</u>	true	page 19
pos	ox	top/super/side	top	page 20
explicit-sign	ox	<u>true/false</u>	false	page 20
decimal-marker	ox	comma/point	point	page 20
\OX, \redox:				
dist	redox	<dim>	.6em	page 23
sep	redox	<dim>	.2em	page 23
\Enthalpy, \Entropy, \Gibbs:				
exponent		<anything>	\standardstate	page 25
delta		<anything>/false		page 25
subscript		left/right		page 25
unit		<unit>		page 25
\DeclareChemState, \RenewChemState:				
exponent		<anything>	\standardstate	page 25
delta		<anything>/false		page 25
subscript		<anything>		page 25
subscript-left		<u>true/false</u>		page 26
\State:				
exponent	state	<anything>	\standardstate	page 26
delta	state	<anything>/false		page 26
subscript-left	state	<u>true/false</u>		page 26
\NMR:				
unit	nmr	<unit>	\mega\hertz	page 28
nucleus	nmr	{<num>,<atom symbol>}	{1,H}	page 28
format	nmr	<anything>		page 28
pos-number	nmr	side/sub	side	page 28
coupling-unit	nmr	<unit>	\hertz	page 28
parse	nmr	<u>true/false</u>	true	page 29
delta	nmr	<anything>		page 29
list	nmr	<u>true/false</u>	false	page 29
list-setup	nmr		see text	page 29
use-equal	nmr	<u>true/false</u>	true	page 29
\DeclareChemReaction:				
star		<u>true/false</u>	false	page 34
arg		<u>true/false</u>	false	page 34
list-name	reaction	<anything>	List of reactions	page 36
list-entry	reaction	<anything>	Reaction	page 36
\mhName:				
align	mhName	<alignment>	\centering	page 32
format	mhName	<commands>		page 32
fontsize	mhName	<fontsize>	\tiny	page 32
width	mhName	<dim>		page 32
phases:				
pos	phases	side/sub	side	page 37
space	phases	<dim>	.1333em	page 37
\newman:				
angle	newman	<angle>	0	page 38
scale	newman	<factor>	1	page 38
ring	newman	<tikz>		page 39
atoms	newman	<tikz>		page 39

option	module	values	default	
<code>back-atoms</code>	<code>newman</code>	<code>&lt;tikz&gt;</code>		page 39
<code>\orbital &lt;type&gt; = s/p/sp/sp2/sp3:</code>				
<code>phase</code>	<code>orbital/&lt;type&gt;</code>	<code>+/-</code>	<code>+</code>	page 40
<code>scale</code>	<code>orbital/&lt;type&gt;</code>	<code>&lt;factor&gt;</code>	<code>1</code>	page 40
<code>color</code>	<code>orbital/&lt;type&gt;</code>	<code>&lt;color&gt;</code>	<code>black</code>	page 40
<code>angle</code>	<code>orbital/&lt;type&gt;</code>	<code>&lt;angle&gt;</code>	<code>90</code>	page 40
<code>half</code>	<code>orbital/p</code>	<code>true/false</code>	<code>false</code>	page 40
<code>overlay</code>	<code>orbital</code>	<code>true/false</code>	<code>false</code>	page 40
<code>opacity</code>	<code>ornital</code>	<code>&lt;num&gt;</code>	<code>1</code>	page 40

## Commands

Quite a number of commands has been presented with which the possibilities of CHEMMACROS can be expanded. They are listed below for a quick overview.

- ▶ `\DeclareChemArrow` → Define new arrow, see page 54.
- ▶ `\RenewChemArrow` → Redefine existing arrow.
- ▶ `\DeclareChemIUPAC` → Define new IUPAC command, see page 16.
- ▶ `\RenewChemIUPAC` → Redefine IUPAC command.
- ▶ `\DeclareChemLatin` → Define new latin phrases, see page 16.
- ▶ `\RenewChemLatin` → Redefine latin phrases.
- ▶ `\DeclareChemNMR` → Define new NMR command, see page 27.
- ▶ `\RenewChemNMR` → Redefine NMR command.
- ▶ `\DeclareChemParticle` → Define new particle, see page 11.
- ▶ `\RenewChemParticle` → Redefine particle.
- ▶ `\DeclareChemPhase` → Define new phases command, see page 38.
- ▶ `\RenewChemPhase` → Redefine phases command.
- ▶ `\DeclareChemReaction` → Define new reaction environment, see page 34.
- ▶ `\DeclareChemState` → Define new state command, see page 25.
- ▶ `\RenewChemState` → Redefine state command.

## Suggestions and Bug Reports

Feedback on [CHEMMACROS](#), [CHEMFORMULA](#) and [GHSYSTEM](#) is highly appreciated and welcome! Especially [CHEMFORMULA](#) and [GHSYSTEM](#) are still in beta testing phase so even if I repeat myself: feedback is highly 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<sup>39</sup>.

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 Lüdigg
- Dr. Paul King
- Jonas Rivetti (Special thanks for his translation of the hazard and precautionary statements into Italian!)
- Christoph Schäfer

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<sup>39</sup> [contact@mychemistry.eu](mailto:contact@mychemistry.eu)

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

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