

# typsium

Typeset chemical formulas and reactions.

v0.3.2

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<https://github.com/Typsium/typsium>

**Typsium Community**

[https://github.com/  
Typsium](https://github.com/Typsium)

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## What is Tysium?

Tysium is a tool for writing beautiful chemical equations easily.

First, we import **tysium**:

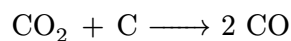
```
1 #import "@preview/tysium:0.3.2":*
```

typ

## Chemical Equations

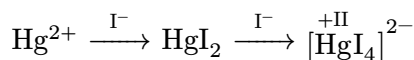
```
1 #ce("CO2 + C -> 2CO")
```

typ



```
1 #ce("Hg^2+ ->[I-] HgI2 ->[I-] [Hg^+II I4]^2-")
```

typ



## Formulas

```
1 $ce("H2O")$
```

typ



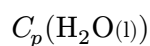
```
1 $ce("Sb2O3")$
```

typ



```
1 $C_p (ce("H2O(l)"))$
```

typ



## Charges

```
1 #ce("H+")
```

typ



We try to understand the intent behind many different ways of writing the same Compound:

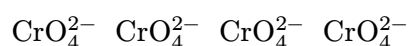
```
1 #ce("CrO4-2")
```

typ

```
2 #ce("CrO4^2-")
```

```
3 #ce("CrO-2_4")
```

```
4 #ce("CrO_4^2-")
```



```
1 #ce("[AgCl2]-")
```

typ



```
1 #ce("Y^99+")
```

typ



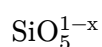
```
1 #ce("Fe^II Fe^III_2O4")
```

typ



```
1 #ce("SiO5^(1-x)")
```

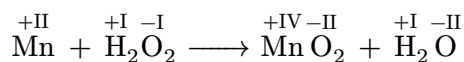
typ



## Oxidation Numbers

Use double ^ to add oxidation numbers to individual elements in your compound. This can also be combined with charges, but only if the oxidation numbers appear after the charges are declared.

```
1 #ce("Mn^^2 + H2^^1O2^^-1 -> Mn^^4O2^^-2 + H2^^1O^^-2") typ
```



## Unpaired Electrons

You can add a radical dot to your molecules like this:

```
1 #ce("CO^.") typ
```



The appearance of the radical can be further customized by the set-element show rule.

## Stoichiometric Numbers

Spaces get moved to before the molecule, since there shouldn't be a space between stoichiometric numbers and the molecule.

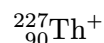
```
1 #ce("2H2O")\ typ
2 #ce("2 H2O")\
3 #ce("$1/2$H2O")\
```



## Isotopes

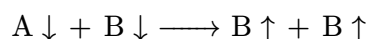
When writing Isotopes it is important that this specific order is used. Otherwise the notation is similar to counts and charges, just before the Symbol.

```
1 #ce("^227_90Th+") typ
```



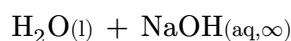
## Precipitation arrows

```
1 #ce("A v +B v &-> B ^ +B ^") typ
```



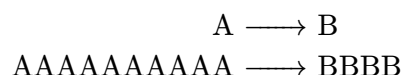
## Aggregation states

```
1 #ce("NaCl(aq) + He(g) + C(s)")\ typ
2 #ce("H2O(l) + NaOH(aq,oo)")\
```



## Alignment

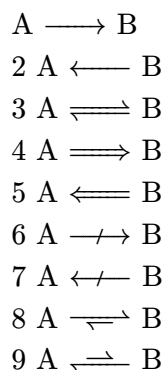
```
1 $ typ
2 #ce("A &-> B")\
3 #ce("AAAAAAAAA &-> BBBB")\
4 $
```



## Arrows

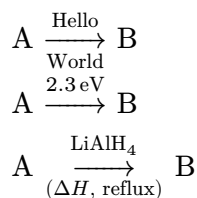
There exist many different kinds of arrows:

```
1 #ce("1A -> B")\
2 #ce("2A <- B")\
3 #ce("3A <=> B")\
4 #ce("4A => B")\
5 #ce("5A <= B")\
6 #ce("6A -/> B")\
7 #ce("7A </- B")\
8 #ce("8A <=>> B")\
9 #ce("9A <=> B")\
```



You can add any content you like on top of arrows, including full reactions or content from other packages.

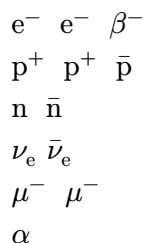
```
1 #ce("A ->[Hello][World] B")
2
3 #ce[A ->[#qty("2.3", "electronvolt")]
  B]
4
5 #ce[A ->[LiAlH4][($Delta H$, reflux)]
  B]
```



## Particles

You can use shorthand versions of particle names to display nicely rendered particles

```
1 #ce("electron") #ce("e-")
  #ce("beta-") \
2 #ce("proton") #ce("p+")
  #ce("antiproton")\
3 #ce("neutron") #ce("antineutron")\
4 #ce(" neutrino antineutrino")\
5 #ce("mu-") #ce("muon-")\
6 #ce("alpha")\
```

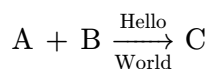


## Show Rules

### set-arrow

Use this to permanently modify what gets drawn on top of all arrows. Don't use this if you are looking to add content on top of just one arrow. Use the squared brackets after the arrow instead. These will overwrite the show rule for the specific instance.

```
1 #show: set-arrow(
2   top:[Hello],
3   bottom:[World],
4 )
5 #ce("A + B -> C")
```



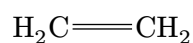
## Parameters

```
set-arrow(  
  top,  
  bottom  
) -> show rule
```

## set-bond

Use this to modify the way bonds get drawn

```
1 #show: set-bond(  
2   length: 2em  
3 )  
4 #ce("H2C==CH2")
```



## Parameters

```
set-bond(  
  length,  
  spacing,  
  stroke,  
  non-covalent-stroke  
) -> show rule
```

### length

Width of the bond

Default: 0.5em

### spacing

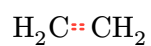
Vertical spacing between each bond line

Default: 0.15em

### stroke

stroke settings used to draw the normal bonds

```
1 #show: set-bond(  
2   stroke: stroke(Paint: red,  
3   thickness: 1pt, cap: "round",  
4   dash: "dotted")  
3 )  
4 #ce("H2C==CH2")
```



Default: (thickness: 0.5pt,)

## non-covalent-stroke

stroke settings used to draw the non covalent bonds

Default: (thickness: 0.5pt, dash: ("dot",),)

## set-element

Use this to modify how elements are displayed.

### Parameters

```
set-element(  
  spaced-charge: bool,  
  roman-oxidation: bool,  
  roman-charge: bool,  
  radical-symbol: content,  
  negative-symbol: content,  
  positive-symbol: content,  
  affect-layout: bool  
)
```

### spaced-charge bool

This will offset the charge symbol to the right so that it's not directly above the count. This may be more useful for ACS notation.

```
1 #ce("NH4-") typ  
2 #show: set-element(spaced-charge:  
  true)  
3 #ce("NH4-")
```

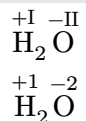


Default: false

### roman-oxidation bool

This will determine whether oxidation numbers will be shown using roman numerals or arabic numerals.

```
1 #ce("H2^10^-2") typ  
2 #show: set-element(roman-oxidation:  
  false)  
3 #ce("H2^10^-2")
```



Default: true

### roman-charge bool

This will determine whether charges will be shown using roman numerals or arabic numerals.

```
1 #ce("Fe+3") typ  
2 #show: set-element(roman-charge:  
  true)  
3 #ce("Fe^3")
```

Fe<sup>3+</sup>  
Fe<sup>III</sup>

Default: `false`

### radical-symbol content

Customise the appearance of the radical dot.

```
1 #ce("Br^.") typ  
2 #show: set-element(radical-symbol:  
  sym.dot)  
3 #ce("Br^.")
```

Br<sup>•</sup>  
Br<sup>'</sup>

Default: `sym.bullet`

### negative-symbol content

Customise the appearance of the minus symbol.

```
1 #ce("Cl-") typ  
2 #show: set-element(negative-symbol:  
  sym.minus.o)  
3 #ce("Cl-")
```

Cl<sup>-</sup>  
Cl<sup>⊖</sup>

Default: `math.minus`

### positive-symbol content

Customise the appearance of the plus symbol.

```
1 #ce("Na+") typ  
2 #show: set-element(positive-symbol:  
  sym.plus.o)  
3 #ce("Na+")
```

Na<sup>+</sup>  
Na<sup>⊕</sup>

Default: `math.plus`

## **affect-layout** bool

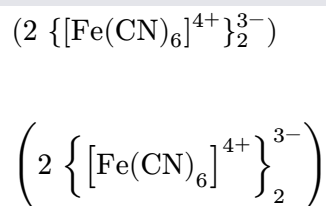
There are some edge cases where elements may be affecting layout. Turn this option off if you are having issues

Default: true

## **set-group**

Use this to modify how groups are displayed in your document

```
1 #ce("(2{[Fe(CN)6]^4+}2-3)") typ
2
3 #show: set-group(
4   grow-brackets:true,
5   affect-layout:true,
6 )
7
8 #ce("(2{[Fe(CN)6]^4+}2-3)")
```



### **Parameters**

```
set-group(
  grow-brackets,
  affect-layout
) -> show rule
```

### **grow-brackets**

Brackets will stay the same size by default. Enabling this option will pair Brackets and scale them to wrap around the inner content, dependent on bracket depth.

Default: false

### **affect-layout**

Counts and Charges will always stay at the same position by default, Enabling this option will move counts to the bottoms of brackets and move charges to the top of brackets, dependent on bracket depth. this will not look good inside a block paragraph because it affects the layout.

Default: false

## **set-molecule**

Use this to modify how molecules are displayed in your document

## Parameters

```
set-molecule(  
  count-spacing: content,  
  bond-spacing  
)
```

### count-spacing `content`

the content used for the spacing between the stoichiometric number and the rest of the molecule

Default: `sym.space.nobreak`

### bond-spacing

spacing applied in front of and behind of bonds

Default: `h(0.1em)`

## set-reaction

Use this to modify the way reactions get drawn

```
1 #show: set-reaction(  
2   plus-spacing: box(fill:red,  
3   arrow-spacing: h(2em),  
4 )  
5 #ce("A + B -> C")
```



## Parameters

```
set-reaction(  
  plus-spacing,  
  arrow-spacing,  
  molecule-spacing,  
  group-spacing-correction  
) -> show rule
```

### plus-spacing

spacing applied in front of and behind + symbols

Default: `h(0.4em, weak: true)`

### arrow-spacing

spacing applied in front of and behind of reaction arrows

Default: `h(0.4em, weak: true)`

**molecule-spacing**

spacing applied between molecules

Default: `sym.space.nobreak`

**group-spacing-correction**

spacing applied so that groups don't have big empty space after them

Default: `h(-0.4em)`