

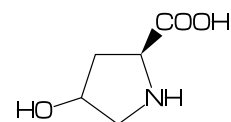
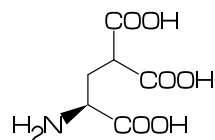
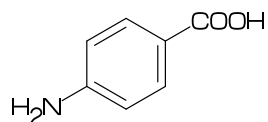
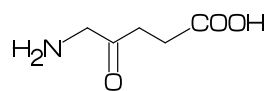
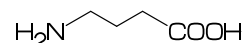
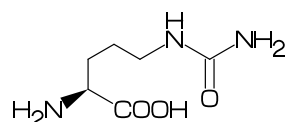
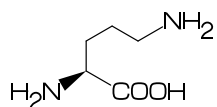
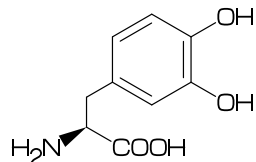
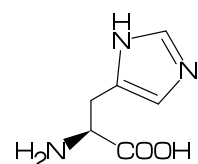
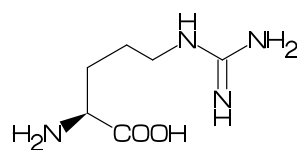
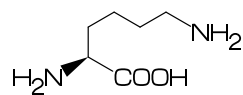
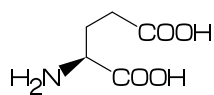
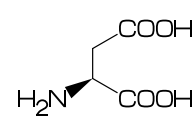
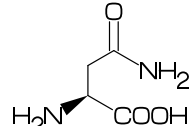
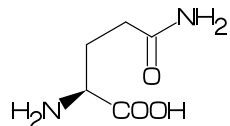
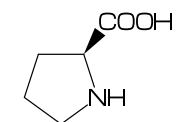
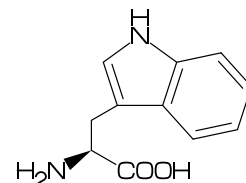
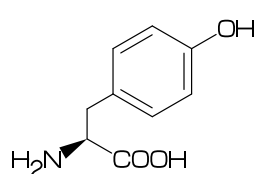
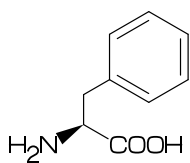
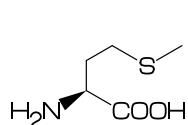
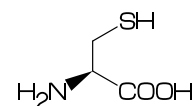
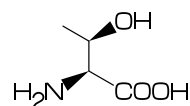
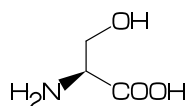
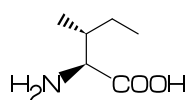
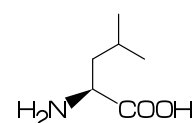
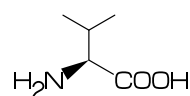
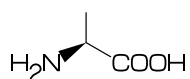
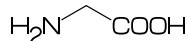
Molecular Coding Format manual

Akira Yamaji

May 8, 2022

Located at <http://www.ctan.org/pkg/mcf2graph>

Suggestion or request mail to: mcf2graph@gmail.com



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1 Introduction

Molecular Coding Format(MCF) is new linear notation represent chemical structure diagrams. This Coding is named from programming technique such as operator, array, scope, macro, addressing, etc. mcf2graph convert from MCF to PNG, SVG, EPS, MOL file. It is also able to calculate molecular weight, exact mass, molecular formula.

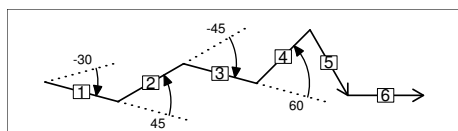
2 MCF syntax

2.1 Make bond

2.1.1 Chain

real number plus (+): counterclockwise
 real number minus(-): clockwise
 \$n (0<=n<360): absolute angle

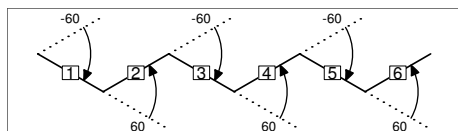
<10,-30,45,-45,60,\$300,\$0



2.1.2 Chain use !,!n

! : take value 60 or -60 depend on current angle and environment
 !6 : !,!,!,!,!

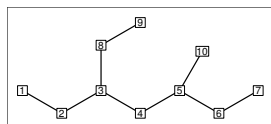
<-30,!6



2.1.3 Jump to atom

@n : Jump to An
 ** An: atom number(-999<=n<=4095)

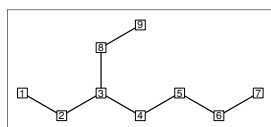
<-30,!6,@3,0,!,@5,-30



2.1.4 Branch bond

\ : 0

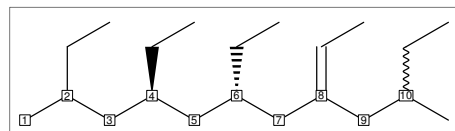
<-30,!6,@3,\,!



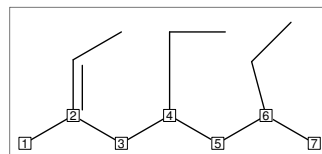
2.1.5 Branch modified bond

\ : 0
 *\ : 0~wf
 * : 0~zf
 \\ : 0~dm
 ** : 0~wv

<30,!8,
 @2,\,!,@4,*\,!,@6,*,!,@8,\\,!,@10,**,!



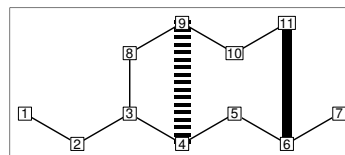
<30,!6,
 \~dr,! : 0~dr,!
 \^1.5,-90 : 0^1.5,-90
 \^15,-60 : 0^15,-60



2.1.6 Connect atom

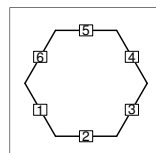
&n : Connect to An

<-30,!6,@3,\,!3,&6~bd,@9,&4~bz



2.1.7 Ring

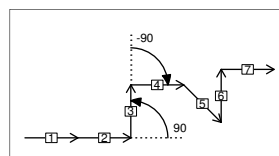
?n : n membered ring(3<=n<=20)
 ?6 : <-120,60,60,60,60,60,&1
 ?6



2.1.8 Rotate current angle

<angle : rotate current angle

0,0,<90,0,<-90,0,<\$315,0,<\$90,0,<\$0,0



2.2 Change bond type

2.2.1 Double, triple, wedge, vector

(Double, triple)

a~type : ~type, a

dm : double middle

dl : double left side

dr : double right side

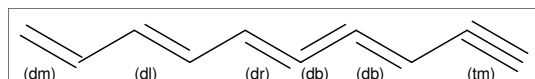
db : double left or right side

tm : triple

!! : !~db / !!! : !~tm

<-30,!~dm,!~dl,!~dr,!~db,!~db,!~tm

<-30,!~dm,!~dl,!~dr,!! ,!! ,!,!!!



(Wedge, Vector)

wf: wedge forward

wb: wedge backward

zf: hashed(zebra stripe) wedge forward

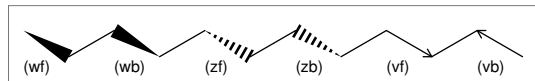
zb: hashed(zebra stripe) wedge backward

vf: vector forward

vb: vector backward

<-30,

!~wf,!~wb,!~zf,!~zb,!~vf,!~vb



(Dotted, wave)

Bn=bond type : change bond type at Bn

dt : dotted / wv : wave

bd : broad / bz : broad dotted

<-30,!7,1=dt,3=wv,5=bd,7=bz



2.2.2 Over line

si_ : single over line

wf_ : wedge forward over line

wb_ : wedge backward over line

zf_ : hashed wedge forward over line

zb_ : hashed wedge backward over line

bd_ : broad over line

dl_ : double left over line

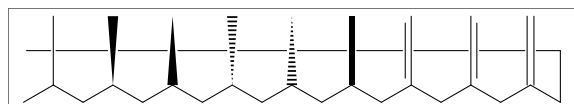
dr_ : double right over line

dm_ : double over line

<30,!8,!60,90'18,

{2~si_,4~wf_,6~wb_,8~zf_,10~zb_,

12~bd_,14~dl_,16~dr_,18~dm_}:/_2



2.2.3 Steric ring

wf_r : wedge forward (half width)

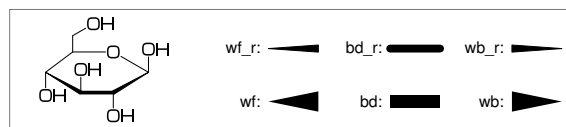
bd_r : broad (half width, rounded)

wb_r : wedge backward (half width)

#1.25,-30~wf_r,30~bd_r'1,30~wb_r,

120,0,30,&1,##,#.5,6~\$90:!/OH,

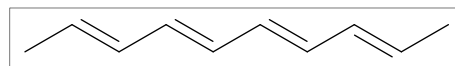
{1~\$-90,2~\$90,3~\$-90,4~\$90}:/OH,



2.2.4 Change multiple bond type

{2,4,6,8'}=dl : 2=dl,4=dl,6=dl,8=dr

<30,!7,{2,4,6,8'}=dl

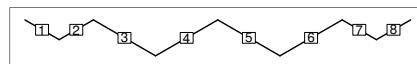


2.3 Change bond length

2.3.1 Chain length

(!,!n)'length : change length of !,!n

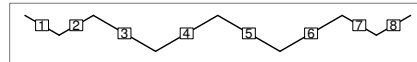
<-30,!2,!4'1.2,!2



#n : bond length=n

: reset bond length

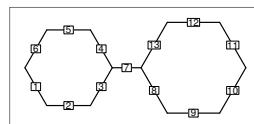
<-30,!2,#1.2,!4,##,!2



2.3.2 Ring length

?n'length : change ring length

?6,@4,\,?6'1.2

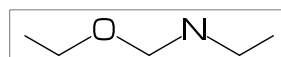


2.4 Change atom

2.4.1 Insert atom

Insert hetero atom

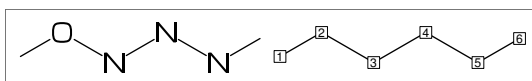
<-30,!2,0,!2,N,!2



2.4.2 Addressed atom

2:0 : change A2 C to O
 {3,4}:N : change A3,A4 C to N

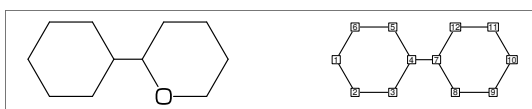
<30,!4,2:0,{3,4}:N



2.4.3 Brock address

| : divide brock

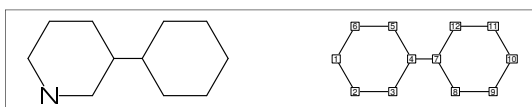
?6,@4,\,|,?6,2:0



2.4.4 Reset brock address

|| : reset brock address

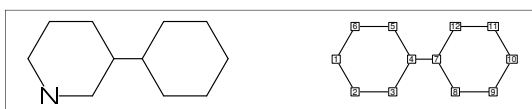
?6,@4,\,|,?6,||,2:N



2.4.5 Absolute address

\$2:N : change A\$2 C to N **1<=n<=3095

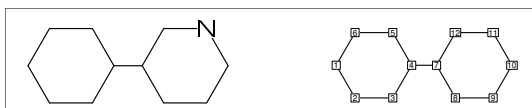
?6,@4,\,|,?6,\$2:N



2.4.6 Relative address

-2:N : change A(-2) C to N ** -999<=n<=-1

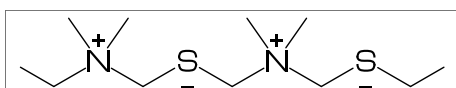
?6,@4,\,?6,-2:N



2.4.7 Charged atom

p_ : positive / n_ : negative

<-30,!2,N,??,p_,!2,S,n_^180,
 !6,7:N,7:??,9:S,7:n_,9:n_^180



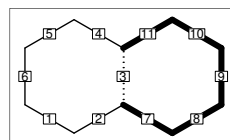
2.5 Fuse ring

(Attached 1 bond)

?6,3=?6 : fuse ?6 at B3

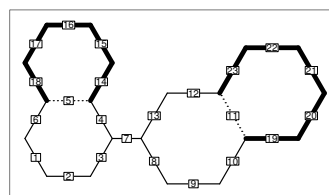
** Bn(n:-999<=n<=4095): bond number

?6,3=?6



** fused ring size depend on
 attached bond length

?6,@4,\,?6'1.2,5=?6,11=?6

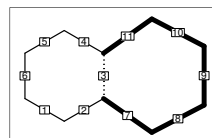


?6,3=?6[13] : fuse ?6[13] at B3

?6[13]: 6 membered ring scaled 13/10

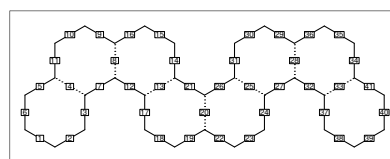
** ?m[n] (5<=m<=8,11<=n<=15)

?6,3=?6[13]



?6,{-3,-4,-4,-2,-2,-4,-4}=?6

?6,{4,8,13,20,25,28,33}=?6



(Attached 2 bond)

(4,11)=?6 : fuse 4/6 ring to B11..B4

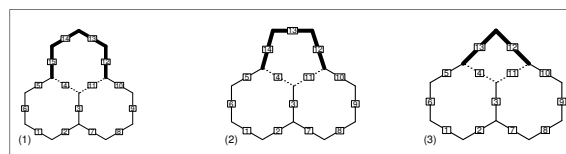
(4,11)=?5 : fuse 3/5 ring to B11..B4

(4,11)=?4 : fuse 2/4 ring to B11..B4

1:<30,?6,3=?6,(11,4)=?6

2:<30,?6,3=?6,(11,4)=?5

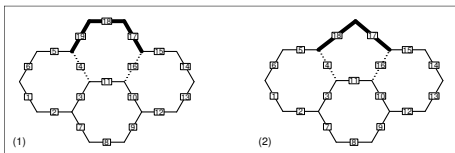
3:<30,?6,3=?6,(11,4)=?4



(Attached 3 bond)

(16,4)=?6[3] or {(16',4)}=?6
: fuse 3/6 ring to B16..B4
(16,4)=?5[2] or {(16',4)}=?5
: fuse 2/5 ring to B16..B4
** ?m[n] (5<=m<=6,n=m-3)

1:?6,{3,10,(16',4)}=?6
2:?6,{3,10}=?6,(16,4)=?5[2]

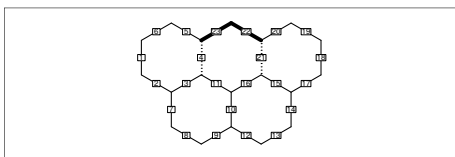


(Attached 4 bond)

(21,4)=?6[2] or {(21',4')}=?6
: fuse 2/6 ring to B21..B4

<-30,?6,{3,10,15,(21',4')}=?6

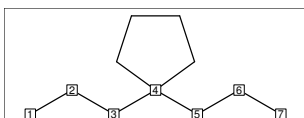
** ?m[n] (m=6,n=2)



2.6 Spiro ring

@4,?5 : add ?5 at A4

<30,!6,@4,?5



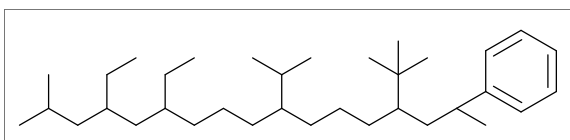
2.7 Group

2.7.1 Insert group

/ : group start single bond

/_ : methyl /! : ethyl
/!2 : propyl /?! : isopropyl
/??! : tert-butyl /Ph : phenyl

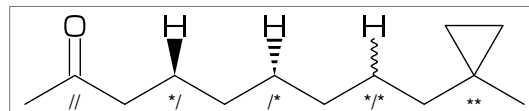
<30,!/_,!2,/!,!2,/!2,!4,/?!,
!4,/??!,!2,/Ph^-60,!



2.7.2 Insert modified group

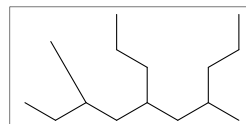
// : double (double middle)
*/ : wedge forward
/* : hashed wedge forward
** : wave
** : direct

<30,!//0,!2,*H,!2,*H,!2,*H,!2,**?3,!



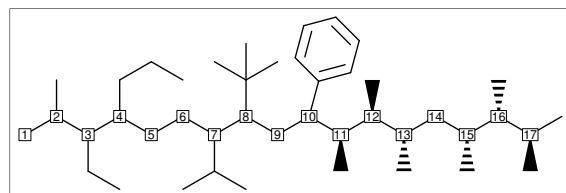
~ : change type
^ : change angle
' : change length
> : change environment

<-30,'^1,!,
/_'^2^30,!2,/!2>lr,!2,/!2>r1,!)



2.7.3 Add group

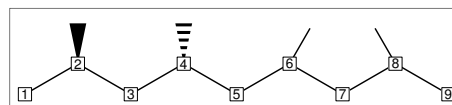
<30,!17,2:/_,3:/!,4:/!2,7:/iPr,
8:/tBu,10:/'(Ph^0.6)^-15,
{11,12,13'}:*/_,{15,16,17'}:/*_



2.7.4 Add modified group

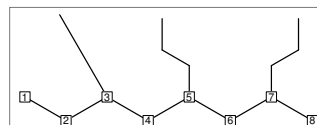
~,^,' : change type,angle,length

<30,!6,{2~wf,4~zf,6^-30,8^\$120}:/_



^,',> : change angle,length,environment

<-30,!7^1,3:/_'^2^30,5:/!2>lr,7:/!2>r1

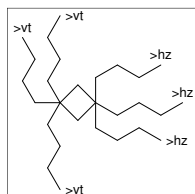


2.8 Chain environment

2.8.1 Horizontal,vertical

>hz : horizontal environment (default)
>vt : vertical environment

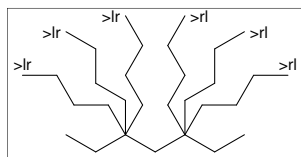
```
?4,  
{3^-90,3^-30,3^90}:/!3>hz,  
{1^-60,1,1^60}:/!3>vt
```



2.8.2 Left-right,right-left

>lr : left-right environment
>rl : right-left environment

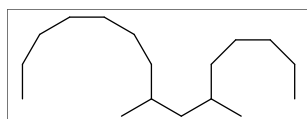
```
<-30,!6,  
{3^-30,3,3^30}:/!3>lr,  
{5^-30,5,5^30}:/!3>rl
```



2.8.3 Fixed rotate angle

>n : rotate n

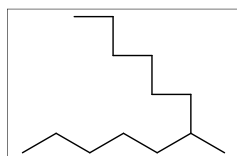
```
<30,!4,  
2:/!6>30, % 2:\,30,30,30,30,30,30  
4:/!4>-45 % 4:\,-45,-45,-45,-45
```



2.8.4 Multiple rotate angle

>'(90,-90,...) : rotate 90,-90,...

```
<30,!6,6>'(90,-90,90,-90,90):/!5
```

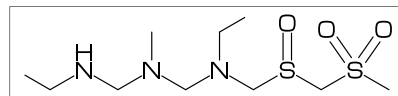


2.9 Miscellaneous

2.9.1 Abbreviated parts

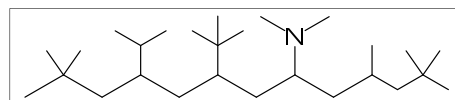
```
NH : N,/H~n1 N! : N,/_ N!2 : N,/!  
SO : S,//0 SOO : S,//0^35,/^-35
```

```
<-30,!2,NH,!2,N!,!2,N!2,SO,!2,SOO,!
```



```
?! : /_,!  
/?? : /_^35,/_-35  
/?! : isopropyl /??? : tert-butyl  
/N?! : dimethylamino
```

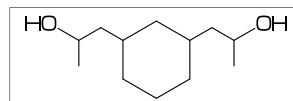
```
<30,!9'1,?!,! ,??,! ,2:??,4:/??,6:/??!,8:/N?!
```



2.9.2 Parts definition

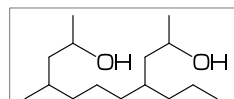
'(..) : user defined parts

```
iBuOH:= '(!,/_,! ,OH);  
MC(<30,!6,{4,6}:/iBuOH)
```



2.9.3 Parts inline definition

```
<30,!8,{2,6}:/'(!,/_,! ,OH)
```



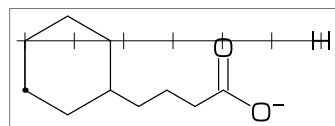
2.9.4 Move position

@(x,y) : Move l*(x,y) from current position

@\$(x,y) : Move l*(x,y) from origin(@)

** l=bond length of ring

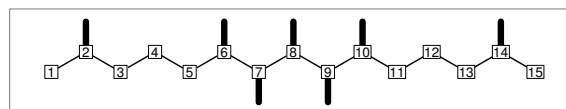
```
<30,!6,@3,!4,//0,! ,0,n_^60,@$(6,1),H,p_^15
```



2.9.5 Serial number

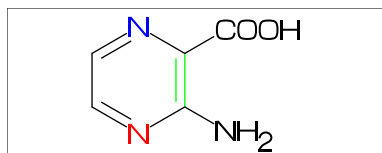
```
6:10 : 6,7,8,9,10
```

```
<30,!14,{2,6:10,14}:/_~bd_r^0.5
```



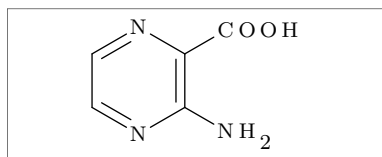
2.9.6 Change color

```
beginfig()
MC(
  <30,Ph,{2,5}:N,3:/NH2,4:/COOH,
  %-----
  2:red,      % red   A2
  5:blue,    % blue  A5
  3:green,   % green B3
  %-----
)
endfig
```



2.9.7 Change font

```
beginfig()
%-----
atomfont:="cmr8";
%-----
MC(<30,Ph,{2,5}:N,3:/NH2,4:/COOH)
endfig
```

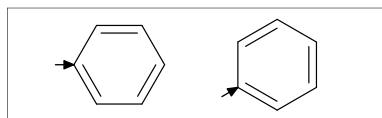


3 Option parameter

3.1 Angle parameter

mangle=0 ** default

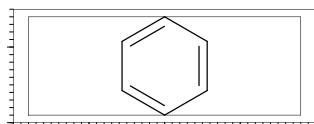
```
MCat(0.2,0.5)(Ph)
mangle:=30;
MCat(0.8,0.5)(Ph)
```



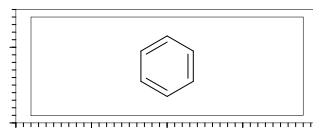
3.2 Size/Ratio parameter

3.2.1 Bond length

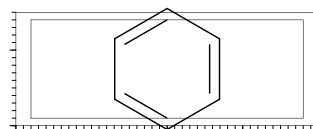
(fit to figure size)
blength=0 ** default



(ratio bond/figure width)
blength=0.1 ** (0<blength<=1)
blength=60mm(width)*0.1=6mm

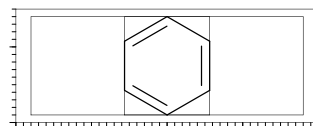


(bond length)
blength=9mm
** (blength>1) ignore msize(w,h)

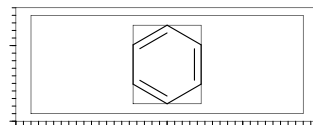


3.2.2 Molecular size

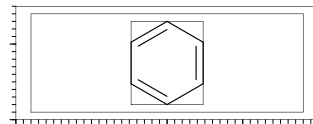
msize=(1,1) ** default



msize=(0.25,1)
msize=40mm-4mm*0.25=9mm

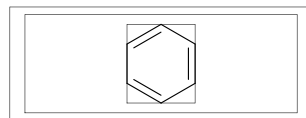


msize=(11mm,11mm)

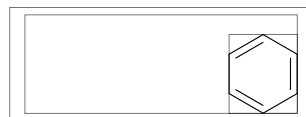


3.2.3 Molecular position

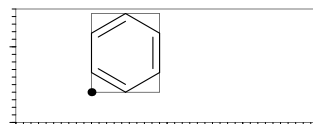
mposition=(0.5,0.5) ** default



mposition=(1,0)



mposition=(10mm,4mm)



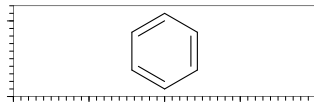
3.3 Size parameter

3.3.1 Figure size

`fsize=(figure width,figure height)`

**** default:** (30mm,20mm)

`fsize=(40mm,15mm)`

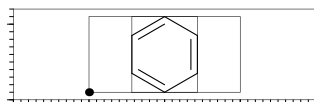


3.3.2 Figure margin

`fmargin=(margin left right,top bottom)`

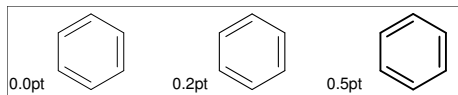
**** default:** (0.4mm,0.4mm)

`fmargin=(10mm,2mm)`



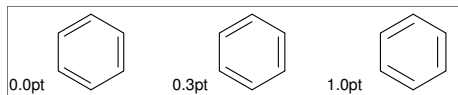
3.3.3 Offset thickness of bond

default: `offset_thickness=0.2pt`



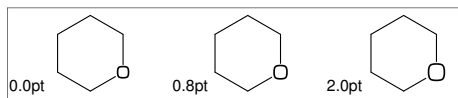
3.3.4 Offset of double bond gap

default: `offset_bond_gap=0.3pt`



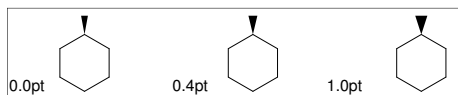
3.3.5 Offset of atom width

default: `offset_atom=0.8pt`



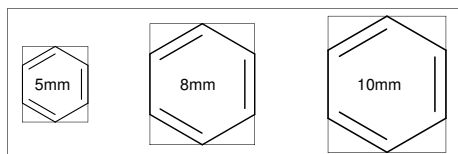
3.3.6 Offset of wedge width

default: `offset_wedge=0.4pt`



3.3.7 Max bond length

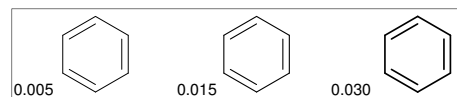
default: `max_blength=10mm`



3.4 Ratio parameter

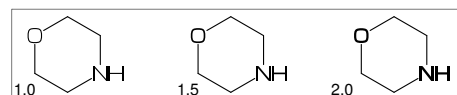
3.4.1 Thickness/bond length

default: `ratio_thickness_bond=0.015`



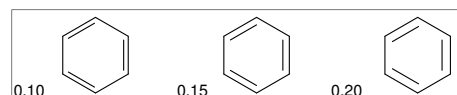
3.4.2 Char/bond thickness

default: `ratio_char_bond=1.5`



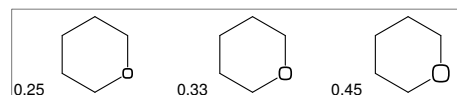
3.4.3 Bond gap/bond length

default: `ratio_bondgap_bond= 0.15`



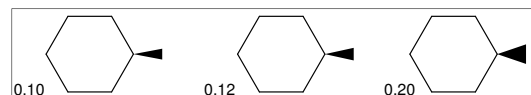
3.4.4 Atom/bond length

default: `ratio_atom_bond= 0.36`



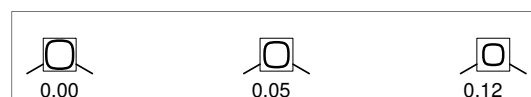
3.4.5 Wedge/bond length

default: `ratio_wedge_bond=0.12`



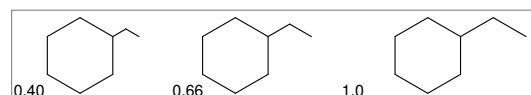
3.4.6 Figure atom gap/atom length

default: `ratio_atomgap_atom= 0.050`



3.4.7 Chain/ring length

default: `ratio_chain_ring= 0.66`



3.4.8 Hash gap/bond length

default: `ratio_hashgap_bond=0.12`

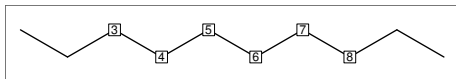


3.5 Drawing mode

3.5.1 Numbering atom

```
sw_numbering=Atom
numbering_start:=3;
numbering_end:=8;
default: sw_numbering=0
```

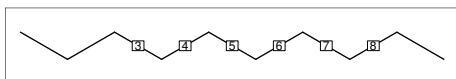
```
sw_numbering:=Atom;
MC(<-30,!9)
```



3.5.2 Numbering bond

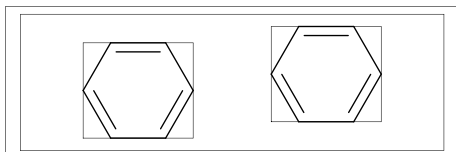
```
sw_numbering=Bond
numbering_start:=3;
numbering_end:=8;
default: sw_numbering=0
```

```
sw_numbering:=Bond;
MC(<-30,!9)
```

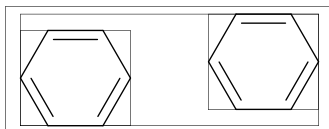


3.5.3 Trimming mode

```
sw_trimming:=0; ** default
msize:=(1,0.7);
MCat(0.2,0.3)(Ph)
MCat(0.8,0.7)(Ph)
```

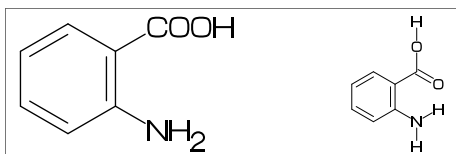


```
sw_trimming:=1;
MCat(0.2,0.3)(Ph)
MCat(0.8,0.7)(Ph)
```



3.5.4 Expand mode

```
MCat(0, .5)(<30,Ph,4:/COOH,3:/NH2)
sw_expand:=1;
MCat(1, .5)(<30,Ph,4:/COOH,3:/NH2)
** default: sw_expand=0
```



3.5.5 Abbreviate group

```
** default: sw_abbreviate=Group
```



3.5.6 Abbreviate bond type

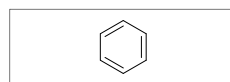
```
** default: sw_abbreviate=Bond
```



3.6 Frame

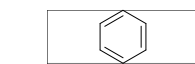
3.6.1 Figure frame

```
** default:sw_frame=0
(Draw figure frame)
fmargin:=(5mm,2mm);
sw_frame=Outside
```



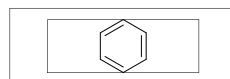
(Frame inside margin)

```
sw_frame=Inside
```



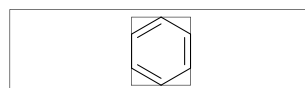
(Draw both frame)

```
sw_frame=Bothside=Inside+Outside
```



3.6.2 Molecular frame

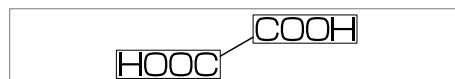
```
sw_frame=Mol
** default:sw_frame=0
```



3.6.3 Atom frame

```
sw_frame=Atom
** default: sw_frame=0
```

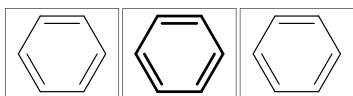
```
MC(<30,COOH,! ,COOH)
```



3.7 Parameter setting

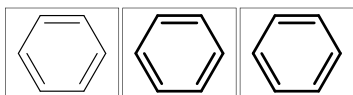
3.7.1 Local parameter setting

```
beginfigm()  
  MC(Ph)  
endfigm  
beginfigm()  
  %-----  
  ratio_thickness_bond:=0.05;  
  %-----  
  MC(Ph)  
endfigm  
beginfigm()  
  MC(Ph)  
endfigm
```



3.7.2 Global parameter setting

```
beginfigm()  
  MC(Ph)  
endfigm  
%-----  
ratio_thickness_bond:=0.05;  
%-----  
beginfigm()  
  MC(Ph)  
endfigm  
beginfigm()  
  MC(Ph)  
endfigm
```



4 Function

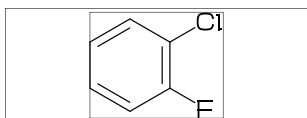
4.1 Function MC()

(Draw molecule)

```
msize=(a,b)      **default (1,1)  
mposition=(c,d)  **default (0.5,0.5)
```

a: ratio molecular width/figure width
b: ratio molecular height/figure height
c: x axis position
d: y axis position

```
beginfigm()  
  MC(<30,Ph,3:/F,4:/Cl)  
endfigm
```



4.2 Function MCat()

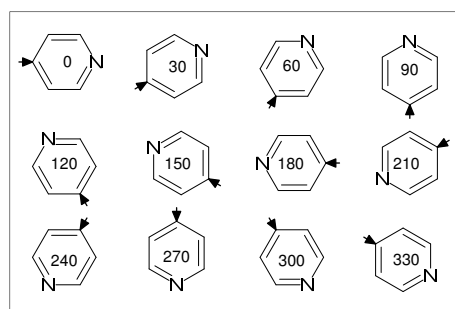
(Draw molecule at mposition)

MCat(c,d)(....) :

mposition:=(c,d); MC(....)

c: x axis position
d: y axis position

```
defaultsize:=5bp;  
fsize:=(60mm,40mm); fmargin:=(3mm,3mm);  
blength:=0.07; sw_frame:=Outside;  
mangle:=0;  
for i=1 step -0.5 until 0:  
  for j=0 step 0.33 until 1:  
    MCat(j,i)(Ph,4:N)  
    add(drawarrow((A1+A1up**aw)..A1);  
        label(decimal(mangle),  
            p0+(0.5w,0.5h));  
    )  
    mangle:=mangle+30;  
  endfor  
endfor
```



4.3 Function mc_check()

(immediately compile)

```
beginfigm("EN:Pyridine")  
  MC(<30,Ph,2:N)  
endfigm
```

(check mcf and compile)

** mc_check(mc) : error count

```
beginfigm("EN:Pyridine",  
  ":<30,Ph,}2:N") % ** extra '}'  
  if mc_check(mc)=0: MC(scantokens(mc)) fi  
endfigm
```



mc_check(mc)=0 mc_check(mc)>=1

4.4 Function add()

(Add label to molecule)

w: molecular width
h: molecular height
aw: atom font size
em: label font size
p0: origin of molecular structure
l: bond length

An: atom number
A[m]: atom position
A[m]ang: branch angle of A[m]
A[m]up: dir A[m]ang
A[m]left: dir A[m]ang+90
A[m]right: dir A[m]ang-90
A[m]down: dir A[m]ang+180

Bn: bond number
B[m]: bond(path)
B[m]s: bond start position
B[m]m: bond middle position
B[m]e: bond end position
B[m]ang: bond angle
B[m]up: dir B[m]ang
B[m]left: dir B[m]ang+90
B[m]right: dir B[m]ang-90
B[m]down: dir B[m]ang+180

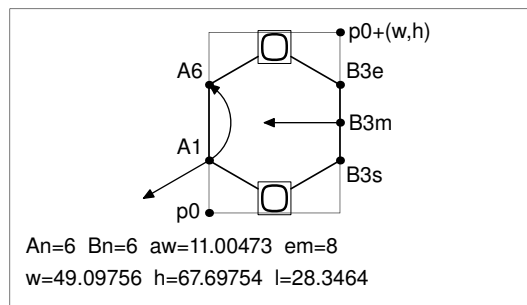
plus : '+' circled
minus : '-' circled
circlediam = 0.6aw (default)
circlepen = 0.2bp (default)

lonenpair r: ':' rotated r
lonenpairdiam = 0.3aw (default)
lonenpairspace = 0.7aw (default)

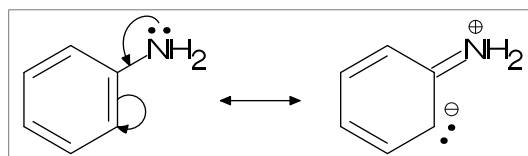
** : scaled
<< : rotated
a /* b : point b of a

```
beginfigm("EN:add() 1")
  fsize:=(70mm,40mm);
  sw_frame:=Bothside;
  max_blength:=10mm;
  msize:=(.91,.9);
  MCat(.5,.85)(<30,?6,{2,5}:0)
  add(
    defaultscale:=.8;
    labeloffset:=.3aw;
    dotlabel.lft("p0",p0);
    dotlabel.rft("p0+(w,h)",p0+(w,h));
    dotlabel.ulft("A1",A1);
    drawarrow A1..A1+__*1<<A1ang;
    dotlabel.lrt("B3s",B3s);
    dotlabel.rft("B3m",B3m);
    drawarrow B3m..B3m+__*1<<(B3ang+90);
    dotlabel.ulft("A6",A6);
```

```
drawarrow A1{A1down}..A6;
dotlabel.urft("B3e",B3e);
label.rft("An="&decimal(An)&
  " Bn="&decimal(Bn)&
  " aw="&decimal(aw)&
  " em="&decimal(em),
  p0+(-9em,-1.5em));
label.rft("w="&decimal(w)&
  " h="&decimal(h)&
  " l="&decimal(l),
  p0+(-9em,-3em));
)
endfigm
```



```
beginfigm("EN:add() 2")
  fsize:=(60mm,20mm);
  msize:=(1,0.85);
  %-----
  MCat(0,0)(<30,Ph,3=d1,4:/NH2)
  %-----
  add(
    labeloffset:=.7aw;
    label.top(lone_pair 90,A7);
    drawarrow
      (A7+up**1.2aw){A7left}
      ..{B7right}B7/*0.3;
    drawarrow
      B3m..A3+B2up**1.5aw..{A3down}A3;
  )
  %-----
  MCat(1,0)(<30,?6,{1,5}=d1,4:/NH2)
  %-----
  add(
    labeloffset:=.7aw;
    label.top(plus,A7);
    label.urft(minus,A3);
    label(lonenpair A3ang,A3+A3up**0.7aw);
  )
  %-----
  ext(drawdblarrow (.4w,.4h)..(.55w,.4h));
  %-----
endfigm
```



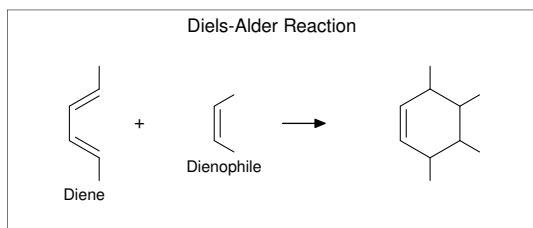
4.5 Function ext()

(Extra label to figure)

```
w:      figure width
h:      figure height
w0:     figure width-2xpart(fmargint)
h0:     figure height-2ypart(fmargint)
aw:     atom font size
em:     label font size
p0:     fmargint

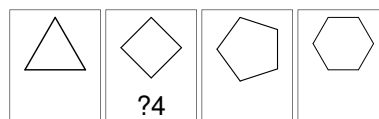
n:      molecular number
p[m]:   molecular origin position
w[m]:   molecular width
h[m]:   molecular height

ratio_thickness_char:
pen thickness / char width
%-----
beginfig()
  fsize:=(70mm,30mm);
  blength:=0.065;
  %-----
  MCat(0.1,0.5)(
    <-210,60'1,60'1,60'1,{1,3}=d1,
    1:/R1,4:/R2^-60
  )
  add(
    defaultscale:=0.6;
    label.bot("Diene",p0+(0.5w,0));
  )
  MCat(0.4,0.5)(
    <-30,-60'1,1=d1,1:/R3,2:/R4^60
    add(defaultscale:=0.6;
      label.bot("Dienophile",p0+(.5w,0));
    )
  )
  MCat(0.9,0.5)(
    <30,?6,6=d1,2:/R2,3:/R4,4:/R3,5:/R1
  )
  %-----
  ext(
    drawarrow (.52w,.5h)..(.6w,.5h);
    defaultscale:=0.7;
    label("+", (0.25w,0.5h));
    ratio_thickness_char:=0.125;
    label.bot("Diels-Alder Reaction",
      (.5w,h));
  )
  %-----
endfigm
```



4.5.1 Local ext() setting

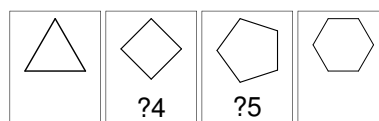
```
beginfig("EN:?3")
  fsize:=(12mm,15mm);
  MCat(0.5,1)(<30,?3)
endfigm
beginfig("EN:?4")
  fsize:=(12mm,15mm);
  MCat(0.5,1)(?4)
  %-----
  ext(label.top(inf_EN,(0.5w,0));)
  %-----
endfigm
beginfig("EN:?5")
  fsize:=(12mm,15mm);
  MCat(0.5,1)(?5)
endfigm
beginfig("EN:?5")
  fsize:=(12mm,15mm);
  MCat(0.5,1)(?6)
endfigm
```



4.5.2 Global ext() setting

```
ext_clear: reset global ext()

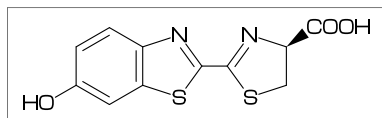
beginfig("EN:?3")
  fsize:=(12mm,15mm);
  MCat(0.5,1)(<30,?3)
endfigm
%-----
ext(label.top(inf_EN,(0.5w,0));)
%-----
beginfig("EN:?4")
  fsize:=(12mm,15mm);
  MCat(0.5,1)(?4)
endfigm
beginfig("EN:?5")
  fsize:=(12mm,15mm);
  MCat(0.5,1)(?5)
endfigm
%-----
ext_clear;
%-----
beginfig("EN:?6")
  fsize:=(12mm,15mm);
  MCat(0.5,1)(?6)
endfigm
```



5 MCF example

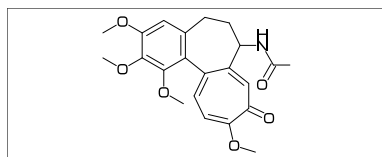
5.1 Luciferin

```
(use library file 'mcf_library')
beginfigm("f:mcf_library",
  "t:EN", "v:Luciferin")
  fsize:=(50mm,15mm);
  if mc_check(mc)=0: MC(scantokens(mc)) fi
endfigm
```



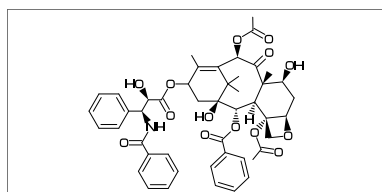
5.2 Colchicine

```
beginfigm("EN:Colchicine", "MW:385.41",
  %-----
  ": <30,Ph,{1,2,6}:/O!,-4,-5}=?7, ",
  ": {-1,-4,-6}=d1,-2://0,-3:/O!, ",
  ": @9,\,NH,! ,//0,! ")
  %-----
  fsize:=(50mm,20mm);
  if mc_check(mc)=0: MC(scantokens(mc)) fi
endfigm
```



5.3 Paclitaxel

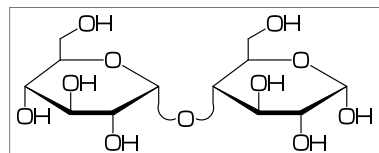
```
beginfigm("EN:Paclitaxel", "MW:853.91",
  %-----
  ": ?6,5=d1,@3,#1,36,45,45,45,45,##, ",
  ": &5",
  ": -4=?6,-4=?4,-1=wb,-3=wf,-1:0,||, ",
  ": 4:??,6:/_{3^-60,15}:*/OH, ",
  ": 8:/*H^-60,",
  ": 9:*/_^-60,10://0, ",
  ": @1,\,0,! ,//0,! ,*/OH,! ,/Ph,60~wf, ",
  ": NH,-60,//0,60,Ph, ",
  ": @7,\*,0,-45,//0,60,Ph, ",
  ": @11,\*,0,-60,//0,60, ",
  ": @12,\*^-15,0,60,//0,-60 ")
  %-----
  fsize:=(50mm,25mm);
  if mc_check(mc)=0: MC(scantokens(mc)) fi
endfigm
```



5.4 Maltose

```
(bond type for glycan)
arc_lb : arc left > bottom
arc_br : arc bottom right
```

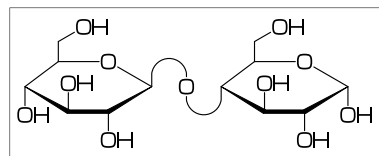
```
beginfigm("EN:Maltose", "MW:342.3",
  %-----
  ": #1.25,-30~wf_r,30~bd_r'1,30~wb_r, ",
  ": 120,0,30,&1,##, ",
  ": #.5,{1^$-90,2^$90,3^$-90}:/OH, ",
  ": 6^$90:/!OH, ",
  ": @4,$-50~arc_lb'1,0,$50~arc_br'1,<$0, ",
  ": |,#1.25,-30~wf_r,30~bd_r'1,30~wb_r, ",
  ": 120,0,30,&1,##, ",
  ": #.5,{2^$90,3^$-90,4^$-90}:/OH, ",
  ": 6^$90:/!OH ")
  %-----
  fsize:=(50mm,20mm);
  if mc_check(mc)=0: MC(scantokens(mc)) fi
endfigm
```



5.5 Cellobiose

```
(bond type for glycan)
arc_lbr : arc left > bottom > right
arc_ltr : arc left > top > right
```

```
beginfigm("EN:Cellobiose", "MW:342.3",
  %-----
  ": #1.25,-30~wf_r,30~bd_r'1,30~wb_r, ",
  ": 120,0,30,&1,##, ",
  ": #.5,{1^$-90,2^$90,3^$-90}:/OH, ",
  ": 6^$90:/!OH, ",
  ": @4,$0~arc_ltr,0,$0~arc_lbr, ",
  ": |,#1.25,-30~wf_r,30~bd_r'1,30~wb_r, ",
  ": 120,0,30,&1,##, ",
  ": #.5,{2^$90,3^$-90,4^$-90}:/OH, ",
  ": 6^$90:/!OH ")
  %-----
  fsize:=(50mm,20mm);
  if mc_check(mc)=0: MC(scantokens(mc)) fi
endfigm
```



6 Example to use mcf2graph

6.1 MetaPost source file

```
%-----
input mcf2graph;                                > input main macro
%-----
sw_output:=Info;      % aux(information) file output on > global setting
%% sw_output:=Report; > report output
%% sw_output:=MOL2k;  > MOL file output
fsize:=(60mm,40mm);  % (figure width,figure height) >
tag1:="J";           > jobname
tag2:="C";           > char No
tag3:="mw";          % calculated molecular weight >
tag4:="fm";          % calculated molecular formula >
outputformat:="png"; hppp:=vppp:=0.1;           > PNG output
outputtemplate:="%j-%3c.png";                  >
%-----
beginfigm("EN:Ampicillin", "MW:349.405")        > information
  MC(<45,?4,-3=?5,2:N,7:S,                      > immediately compile
    3^45:/*H,1://O^15,5:/*COOH^-18,6:??,        >
    @4,*\^15,NH,!,//O,!/*NH2,! ,Ph)           >
endfigm                                          >
%-----
beginfigm("EN:Cholesterol", "MW:386.65",        >information
  %----- >
  ": <30,?6,{-4,-2}?6,-4=?5,7=d1, " ,          > mc1
  ": 10:/*H^180,11:/*H^-60,17:/*H^-54, " ,     > mc2
  ": {4,12}:*/_^60, " ,                        > mc3
  ": @-1,18,/*_,-60,!3,?! " )                 > mc4
  %----- >
  if mc_check(mc)=0: MC(scantokens(mc)) fi      > mc=mc1 - mc4
endfigm                                          >
%-----
beginfigm("f:mcf_library.mcf", "t:EN", "v:Adenine") > from mcf_library.mcf
  if mc_check(mc)=0: MC(scantokens(mc)) fi      > select EN="Adenine"
endfigm                                          >
%-----
beginfigm("t:EN", "v:Guanine")                  > select EN="Guanine"
  if mc_check(mc)=0: MC(scantokens(mc)) fi
endfigm
%-----
beginfigm("t:EN", "v:Cytosine")                 > select EN="Cytosine"
  if mc_check(mc)=0: MC(scantokens(mc)) fi
endfigm                                          >
%-----
beginfigm("t:n", "v+:4")                        > v+:4 = select No.4
  if mc_check(mc)=0: MC(scantokens(mc)) fi      > keep file open
endfigm                                          >
%-----
forever:
%% %% %% %% %% beginfigm("f:mcf_library", "v+:*") > select all
  beginfigm("f:mcf_library", "t:EXA", "v+:1")    > 'v+:1'= select EXA=1
    if f_EOF=0: if mc_check(mc)=0: MC(scantokens(mc)) fi fi > keep file open
  endfigm                                          >
  exitif f_EOF=1;                                  > exit if file end
endfor
%-----
bye
```

6.2 Molecular library file

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% molecular library file   mcf_library.mcf   by Akira Yamaji   2022.03.13
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% tag1:var1;tag2:var2;tag3:var3   ....
% first character of line "%" comment out
% first character of line "+" begin MCF
% first string   of line "+-" end MCF
% first string   of line "%-" end header
% Cat = Category
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%-----
Cat:biological;EN:Adenine;MW:135.13
+
<30,?6,3=?5,{1,3,5,9}=d1,{2,6,9}:N,5:/NH2,7:NH
%-----
Cat:biological;EN:Guanine;MW:151.13
+
<30,?6,3=?5,{1,3,9}=d1,{2,9}:N,{6,7}:NH,5://0,1:/NH2
%-----
Cat:biological;EN:Cytosine;MW:111.10
+
<30,?6,{4,6}=d1,4:N,3://0,2:NH,5:/NH2
%-----
Cat:biological;EN:Thymine;MW:126.11
+
<30,?6,3=d1,{2,6}:NH,{1,5}://0,4:/_
%-----
Cat:biological;EN:Uracil;MW:112.09
+
<30,?6,6=d1,{3,5}://0,{2,4}:NH
%-----
Cat:biological;EN:Geraniol;MW:154.25
+
<30,!8,OH,{2,6}=dr,{2,6}:/_
%-----
Cat:biological;EN:Limonene;MW:136.24
+
<30,?6,2=d1,2:/_,@5,*\,/_,!!
%-----
Cat:biological;EN:l-Menthol;MW:156.27
+
<30,?6,2:/*?!,5:*/_ ,3:*/OH
%-----
Cat:biological;EN:Vanillin;MW:152.15
+
<30,Ph,2:/OH,3:/O!,5:/CHO
%-----
Cat:biological;EN:Allicin;MW:162.28
+
<-30,!!,!2,S0,!,S,!2,!!
%-----
Cat:biological;EN:Stearic acid;MW:284.48
+
<30,!17,COOH
%-----
```


6.3 Function mc_query()

(Example)

```
%-----  
% mc_query()  
%  
% "f:filename" : input file name (default "mcf_library.mcf")  
% "o:filename" : output file name (default "temp.mcf")  
% "s:sort-key" : sort by sort-key  
%  
% operator : = , <> , <= , >= , < , >  
%  
% filter 1 : Cat=biological  
% filter 2 : MW>=285  
% filter 3 : MW<=295  
%-----  
mc_query("s:EN","Cat=biological","MW>=285","MW<=295");  
%-----  
forever:  
  beginfigm("f:temp","v+:*") % use file temp.mcf / select all  
    if f_EOF=0: if mc_check(mc)=0: MC(scantokens(mc)) fi fi  
  endfigm  
  exitif f_EOF=1;  
endfor  
%-----
```

(output)

```
Cat:biological;EN:Atoropin;MW:289.375;EXA:1  
+  
<30,0,!,//0,!,!,Ph,@$1,\~zb^-60,|,?7'1.1,@6,*\^190'1.25,N!,&3~wb,$3:/!OH~wv  
+-----  
Cat:biological;EN:Cianidanol;MW:290.27;EXA:1  
+  
<30,Ph,3=?6,@8,*\,Ph,7:0,{1,5,13,14}:/OH,9:/*OH  
+-----  
Cat:biological;EN:Lycorine;MW:287.315;EXA:1  
+  
<30,Ph,{-4,-2}=?6,{6,(9,12)}=?5,13=dl,8:N,{15,17}:0,  
9:/*H^180,10:*/H^60,13:*/OH,14:/*OH  
+-----  
Cat:biological;EN:Morphine;MW:285.343;EXA:1  
+  
<30,Ph,{2,-4}=?6,(1,12)=?5[2],-1:0,-1=zb,  
@7,60~wf'0.75,70~si_ '1.3,45,N!,&9~wb,15=dl,6:/OH,8^180:*/H,12:/*OH  
+-----  
Cat:biological;EN:Piperine;MW:285.343;EXA:1  
+  
<30,Ph,|,-1=?5,{1,3}:0,@$4,\,!!,,!!,,!!,,//0,!,|,?6,1:N  
+-----
```

6.4 Information aux file output

(Option parameter setting)

```
sw_output:=Info;          %% tag1:var1;tag2:var2
sw_output:=Info+Table;   %% tag1;tag2 var1;var2
```

(Command line)

```
>mpost -s ahlengh=1 FILENAME (sw_output=Info)
>mpost -s ahlengh=2 FILENAME (sw_output=Info+Table)
```

(Source)

```
beginfigm("EN:Ampicillin")    .... endfigm
beginfigm("EN:Cholesterol")   .... endfigm
beginfigm("EN:Limonin")       .... endfigm
beginfigm("EN:beta-Carotene") .... endfigm
```

(Setting)

```
tag1:="J"; tag2:="C"; tag3:="mw"; tag4:="fm"; tag5:="EN";
```

(Output)

(sw_output=Info)

```
F:mcf_man_soc;C:1;mw:349.40462;fm:C16H19N3O4S;EN:Ampicillin
F:mcf_man_soc;C:2;mw:386.6532;fm:C27H46O;EN:Cholesterol
F:mcf_exa_soc;C:3;mw:470.5113;fm:C26H30O8;EN:Limonin
F:mcf_exa_soc;C:4;mw:536.8722;fm:C40H56;EN:beta-Carotene
```

(sw_output=Info+Table)

```
F;C;mw;fm
mcf_man_soc;1;349.40462;C16H19N3O4S;Ampicillin
mcf_man_soc;2;386.6532;C27H46O;Cholesterol
mcf_exa_soc;3;470.5113;C26H30O8;Limonin
mcf_exa_soc;4;536.8722;C40H56;beta-Carotene
```

(aux_delimiter="/")

```
F:mcf_man_soc/C:1/mw:349.40462/fm:C16H19N3O4S/EN:Ampicillin
F:mcf_man_soc/C:2/mw:386.6532/fm:C27H46O/EN:Cholesterol
F:mcf_exa_soc/C:3/mw:470.5113/fm:C26H30O8/EN:Limonin
F:mcf_exa_soc/C:4/mw:536.8722/fm:C40H56/EN:beta-Carotene
```

(Tag)

```
J  : jobname
C  : char number
NO : serial number
EN : english name
JN : japanese name
FM : formula from literature data
MW : molecular weight from literature data
MI : monoisotopic mass from literature data
USE : the use
mw  : molecular weight calculated
mi  : monoisotopic mass calculated
fm  : molecular formula calculated
w   : figure width
h   : figure height
```

6.5 MCF aux file output

(Option parameter setting)

```
sw_output:=Mcode;          %% output 'temp-mc.aux'
```

(Command line)

```
>mpost -s ahlength=3 FILENAME (sw_output=Info+Mcode)
```

(Output mcf file)

```
sw_output=Mcode           %% file name = 'temp-mc.aux'
```

(result)

```
<30,?6,3=?5,{1,3,5,9}=d1,{2,6,9}:N,5:/NH2,7:NH
```

(Output library file)

```
sw_output=Info+Mcode      %% file name = 'jobname-lib.aux'
```

(result)

```
Cat:biological;EN:Adenine;MW:135.13;EXA:1
```

```
+
```

```
<30,?6,3=?5,{1,3,5,9}=d1,{2,6,9}:N,5:/NH2,7:NH
```

```
+-----
```

(LuaLaTeX example)

```
%-----  
\begin{mplibcode}  
  beginfigm("t:EN","v:Vancomycin")  
    sw_output:=Mcode;      %%% output temp-mc.aux %%%  
  endfigm;  
\end{mplibcode}  
%-----  
\verbatiminput{temp-mc.aux}  
%-----
```

(result)

```
file name = 'temp-mc.aux'
```

```
<30,?6,@4,?6,@-4,\,!3,<-12,?5,@-3,<-12,?6,-3=?6,@-3,*\,!3,  
?6,@-4,?6,@6,\,!/*Me^-40,*OH^20,!//0,!1,OH,  
3=wb,11=d1,15=dr,17=wf,19=wf,38=wb,{5,7,16,24,25,33,42}:0,  
32:*/H^60,10:/Me,{12,31}:*/_ ,27://_ ,37:/*_ ,28:/OH,{3,29}:/*OH
```

6.6 Report output

(Option parameter setting)

```
sw_output:=Report;          %% file name = 'jobname-report.aux'
```

(Command line)

```
>mpost -s ahlenth=7 FILENAME
```

(Output)

```
=====
No[3],Name<Cytosine>,Category<biological>,File<mcf_library.mcf>
-----
<30,?6,{4,6}=dl,4:N,3://0,2:NH,5:/NH2
-----
Row[1],Length[37],Commands[7],&Code[59],Warning[0]
-----
=[1]({}=[1]), :[4]({}: [0]), '() [0]
@[0],&[0],<[1],~[0],^[0],'[0],>[0],|[0],|[0],#[0],##[0]
-----
Width[30.92432],Height[42.36536], Shift x[0],Shift y[-12.99213]
Bond length[11.33856],Atom size[4.8819]
-----
Atom[9],Bond[9],Ring[1],Hide H[2]
< NO. ><atom(s) >( x axis , y axis )<bond><hideH><chg>
A1 C ( 0 , 0 ) 3 1
A2 N ( 1 , 0 ) 3
A3 C ( 2 , 0 ) 4
A4 N ( 2 , 1 ) 3
A5 C ( 1 , 2 ) 4
A6 C ( 0 , 1 ) 3 1
A7 O ( 3 , 0 ) 2
A8 H ( 1 , -1 ) 1
A9 NH2 ( 1 , 2 ) 1
-----
< NO. >< bond (sdt)><angle +( +- )><length ( pt )>
B1 1 -> 2 ( 1 ) 330 ( -30) 1 ( 11)
B2 2 -> 3 ( 1 ) 30 ( 30) 1 ( 11)
B3 3 -> 4 ( 1 ) 90 ( 90) 1 ( 11)
B4 4 -> 5 ( 2 ) 150 ( 150) 1 ( 11)
B5 5 -> 6 ( 1 ) 210 ( -150) 1 ( 11)
B6 6 -> 1 ( 2 ) 270 ( -90) 1 ( 11)
B7 3 -> 7 ( 2 ) 330 ( -30) 0.66 ( 7)
B8 2 -> 8 ( 1 ) 270 ( -90) 0.36 ( 4)
B9 5 -> 9 ( 1 ) 90 ( 90) 0.66 ( 7)
-----
<atom>( atom wt ) [ mi wt ] < cnt > < sum wt > [ sum mi wt ]
C ( 12.0107) [ 12 ] * 4 48.04279 [ 48 ]
H ( 1.00793) [ 1.00783 ] * 5 5.03967 [ 5.03914 ]
N ( 14.0067) [ 14.00307 ] * 3 42.0201 [ 42.0092 ]
O ( 15.9994) [ 15.99492 ] * 1 15.9994 [ 15.99492 ]
Molecular Weight [Mono Isotopic] = 111.1019 [ 111.04326 ]
-----
Weight Calc: 111.1019 / Input: 111.10 / weight gap= 0.00195
Fomula Calc: C4H5N3O / Input:
=====
```

6.7 MOL file output

(Option parameter setting)

```
sw_output:=MOL2k;    % MOL(V2000)
sw_output:=MOL3k;    % MOL(V3000)
```

(Command line)

```
>mpost -s ahlength=5 FILENAME    % MOL(V2000)
>mpost -s ahlength=6 FILENAME    % MOL(V3000)
```

(Output)

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
```

```
-MCFtoMOL- EN:Caffeine
```

```
14 15 0 0 0 0 0 0 0 0999 V2000
      0      0      0 C  0 0 0 0
  0.86603    -0.5      0 N  0 0 0 0
  1.73206      0      0 C  0 0 0 0
  1.73206      1      0 C  0 0 0 0
  0.86603     1.5      0 C  0 0 0 0
      0      1      0 N  0 0 0 0
  2.6831   -0.30902    0 N  0 0 0 0
  3.27089      0.5      0 C  0 0 0 0
  2.6831    1.30902    0 N  0 0 0 0
  0.86603   -1.36383    0 C  0 0 0 0
 -0.76894    1.44394    0 C  0 0 0 0
 -0.76894   -0.44394    0 D  0 0 0 0
  0.86603    2.36383    0 D  0 0 0 0
  2.95299    2.1396    0 C  0 0 0 0
  1  2  1  0      0  0
  2  3  1  0      0  0
  3  4  2  0      0  0
  4  5  1  0      0  0
  5  6  1  0      0  0
  6  1  1  0      0  0
  3  7  1  0      0  0
  7  8  2  0      0  0
  8  9  1  0      0  0
  9  4  1  0      0  0
  2 10  1  0      0  0
  6 11  1  0      0  0
  1 12  2  0      0  0
  5 13  2  0      0  0
  9 14  1  0      0  0
```

```
M  END
```

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
```

6.8 LuaTeX file example

```

\documentclass{article}
\usepackage{luamplib}%
\usepackage[T1]{fontenc}%
\usepackage{textcomp}%
\mplibcodeinherit{enable}%
\mplibverbatim{enable}%
\mplibnumbersystem{double}%
\everymplib{%
  if unknown Ph1: input mcf2graph; fi
  sw_output:=Fig; max_blength:=4.5mm;
  defaultfont:="uhvr8r"; defaultsize:=8bp; defaultscale:=1;
}%
\begin{document}
\noindent%
%-----
\begin{mplibcode}
  fsize:=(50mm,50mm);
  beginfigm("NO:1","EN:Limonin","MW:470.51",
    %-----
    ": <30,?6,{-3,-4}=?6,          ",
    ": -5=?3,-2=wf,-1=wb,6=?5,-4=?6,-5=wf, ",
    ": {13,15,17,20}:0,{3,12,21}://0,      ",
    ": {4~wf^60,8~zf^60,18^35,18^-35}:/_,   ",
    ": {1^60,5^180,16^60}:/*H,            ",
    ": @14,\*,|,?5,{1,4}=d1,3:0          ")
    %-----
  if mc_check(mc)=0: MC(scantokens(mc)) fi
  endfigm
\end{mplibcode}\\
%-----
\begin{mplibcode}
  fsize:=(80mm,50mm);
  beginfigm("NO:2","EN:beta-carotene","MW:536.87",
    %-----
    ": <30,?6,3=d1,{3,5^35,5^-35}:/_,      ",
    ": @4,\,|,!18,{1,3,5,7,9,11,13,15,17}=dr, ",
    ": {3,7,12,16}:/_,                      ",
    ": |,?6,6=d1,{6,2^35,2^-35}:/_        ")
    %-----
  if mc_check(mc)=0: MC(scantokens(mc)) fi
  endfigm
\end{mplibcode}\\
%-----
\begin{mplibcode}
  fsize:=(50mm,50mm);
  beginfigm("NO:3","EN:Gibberellin A3","MW:346.37",
    %-----
    ": <18,?5,3=?7,5=?6[12],              ",
    ": @8,160'1.3,&3,13=d1,6=wf,8=wb,      ",
    ": @5,40~zf'1,0,60,//0^180,&14~zb,    ",
    ": 2:/COOH,7://_,13:*/OH,8:*/OH,      ",
    ": 14:*/_,{1^60,4^60}:/*H            ")
    %-----
  if mc_check(mc)=0: MC(scantokens(mc)) fi
  endfigm;
%-----
\end{mplibcode}\\
\end{document}

```

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