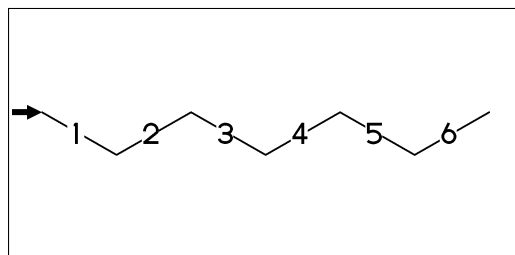


## No.1 Chain (1)

plus(+):anticlockwise,minus(-)clockwise  
bold arrow is default angle and position

```
<30,-60,60,-60,60,-60,60
```

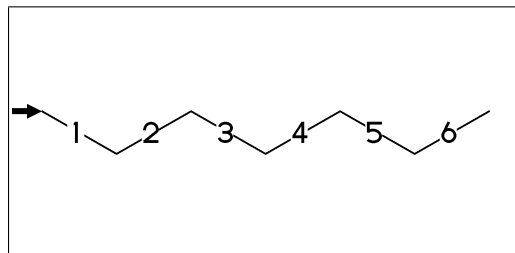


## No.2 Chain (2)

!,: take 60 or -60 depend on  
current angle and enviroment

```
!6
```

```
** !6: !,!,!,!,!,!
```

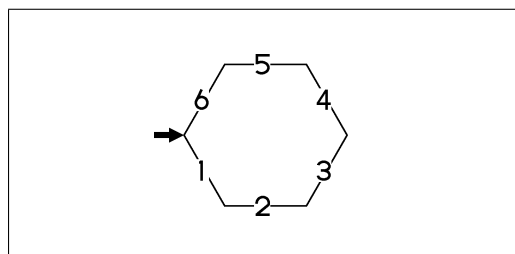


## No.3 Ring

six membered ring

```
?6
```

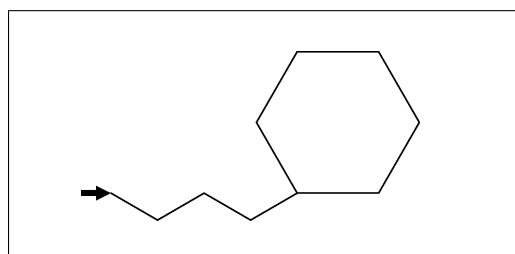
```
** ?6 : <-120,60,60,60,60,60,&1  
&1 : make bond connect to A1
```



## No.4 Rotate current angle

<angle:rotate current angle

```
<30,!4,<30,?6
```

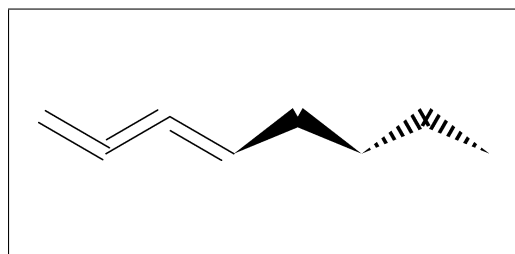


## No.5 Change bond type (1)

~bond change bond

```
dm:double,dl:double(left),dr:double(right),  
wf:wedge forward,wb:wedge backward,  
zf:wedge dotted,zb:wedge dotted backward
```

```
<30,!~dm,!~dl,!~dr,!~wf,!~wb,!~zf,!~zb
```

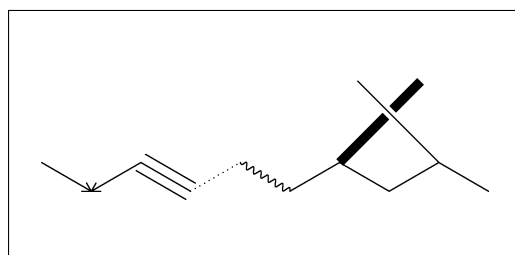


## No.6 Change bond type (2)

Bn=bond type : \$(Bn)bond type (change bond type at Bn)

```
vf:vector forward, vb:vector backward,  
tm:triple, wv:waved, bd:broad single,  
ov:over line
```

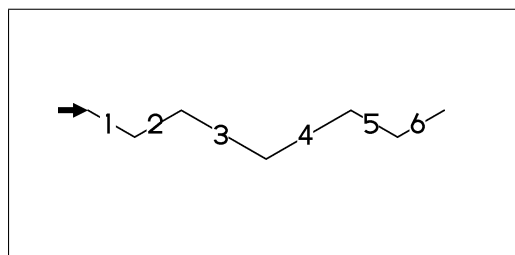
```
<30,!9,1=vf,2=vb,3=tm,4=dt,5=wv,  
@(7~bd~-45'2,9~ov~45'2)/Me
```



**No.7 Change bond length (1)**

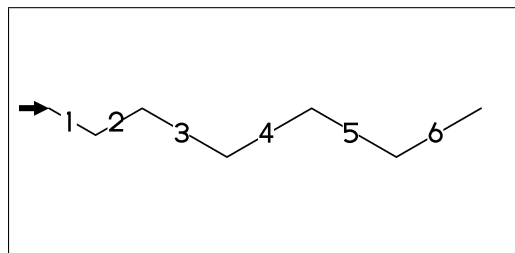
Bn'length : change bond length at Bn

<30,!2,!2'1.2,!2

**No.8 Change bond length (2)**

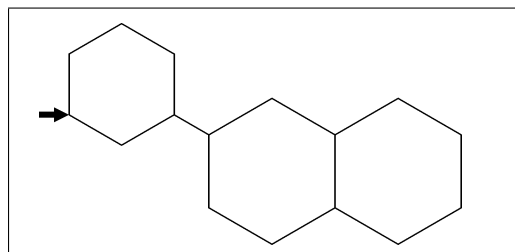
''length : change all bond length after

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

**No.9 Change chain length (3)**

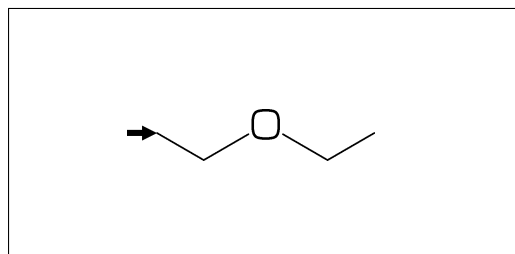
?n'length : change ring length

<30,?6,3\,|,?6'1.2,4=?6

**No.10 Change atom (1)**

Insert hetero atom

<30,!2,0,!2

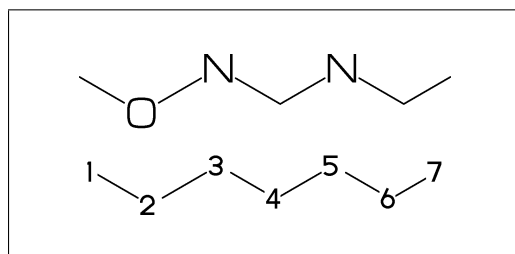
**No.11 Change atom (2)**

2:0 : change A2 C to O

@(3,5)N : change A3,A5 C to N

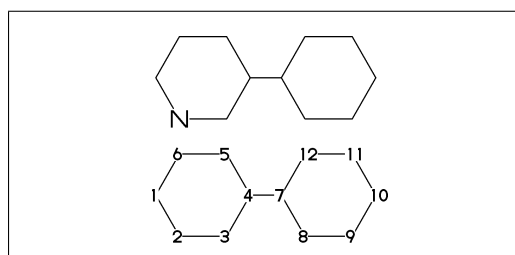
<30,!6,2:0,@(3,5)N

An(n:numeric): atom number

**No.12 Change atom (3)**

2:N : change A2 C to N

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

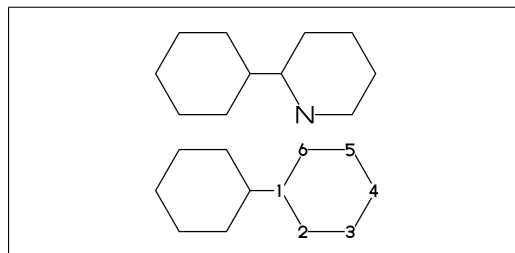


**No.13 Change atom (brock address)**

2:N : change A2(brock address) C to N

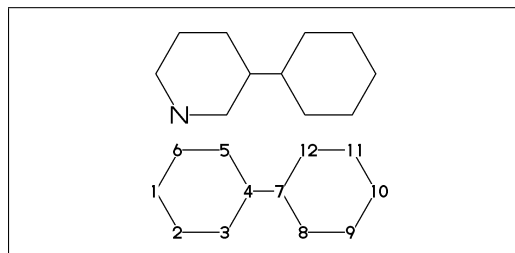
?6,4\,|,?6,2:N

| : divide brock

**No.14 Change atoma (absolute address)**

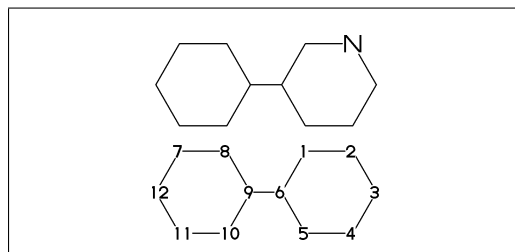
#2:N : change A#2 C to N

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

**No.15 Change atom (relative address)**

-2:N : change A(-2) C to N

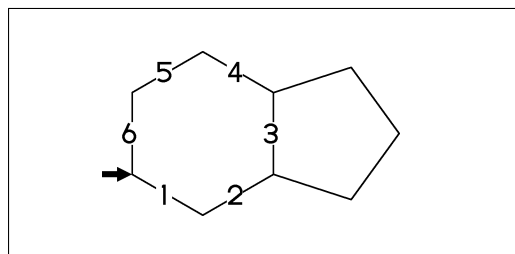
?6,4\,?6,-2:N

**No.16 Fuse ring (attached 1 bond)**

?6,3=?5 : fuse ?5 at B3

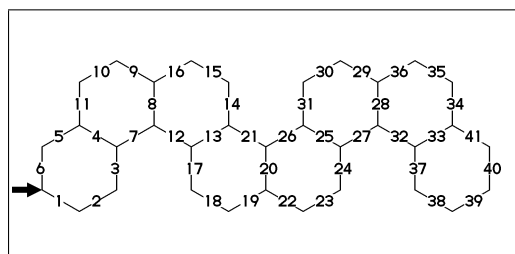
?6,3=?5

Bn(n:numeric): bond number

**No.17 Fuse multi ring (attached 1 bond)**

?6,\$(-3,-4,-4,-2,-2,-4,-4)?6

?6,\$(4,8,13,20,25,28,33)?6

**No.18 Fuse ring (attached 2 bond)**

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

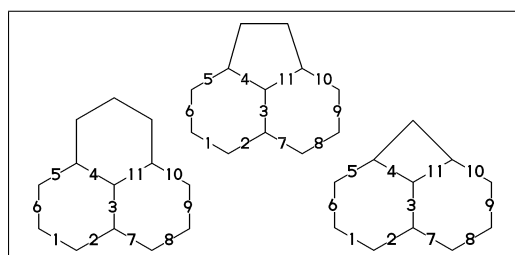
(4,11)=?5[3] : fuse 3/5 ring to B11..B4

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

MCd(1,.7)( 0,0)(<30,?6,3=?6,(11,4)=?6[4])

MCd(1,.6)(.5,1)(<30,?6,3=?6,(11,4)=?5[3])

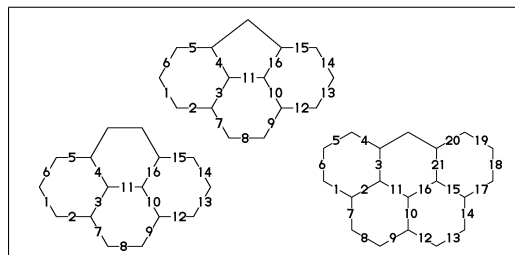
MCd(1,.6)( 1,0)(<30,?6,3=?6,(11,4)=?4[2])



### No.19 Fuse ring (attached 3,4 bond)

```
(16,4)=?6[3] : fuse 3/6 ring to B16..B4
(16,4)=?5[2] : fuse 2/5 ring to B16..B4
(21,3)=?6[2] : fuse 2/6 ring to B21..B3

MCd(1,.55)( 0, 0)(?6,$(3,10)?6,(16,4)=?6[3])
MCd(1,.55)(.43,1)(?6,$(3,10)?6,(16,4)=?5[2])
MCd(1,.53)(1,0)(<30,?6,$(2,10,15)?6,(21,3)=?6[2])
```

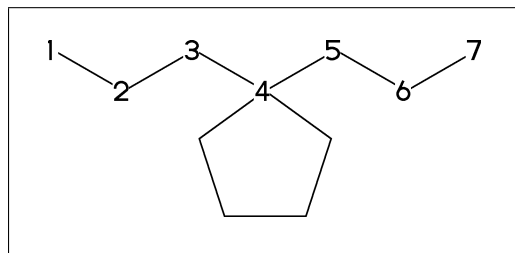


### No.20 Spiro ring

```
4*,?5 : add ?5(5 membered ring) at A4

<30,!6,4*,?5

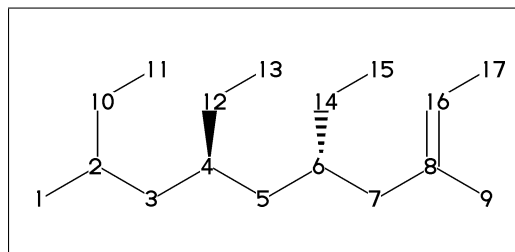
An* : jump to An
```



### No.21 Branch bond (1)

```
2\ : 2*,0      4*\ : 4*,0~wf
6\* : 6*,0~zf  8\\ : 8*,0~dm

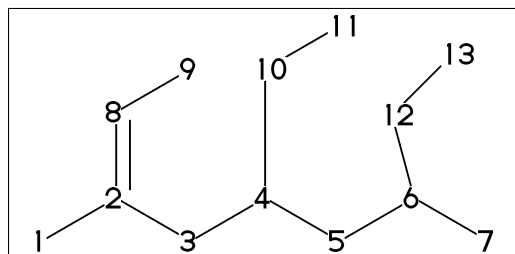
MCf(<30,!8,2\,! ,4*\,! ,6\*,! ,8\\,! )
```



### No.22 Branch bond (2)

```
2\~dr : 2*,0~dr
4\'1.5 : 4*,0\'1.5
6\^15 : 6*,0^15

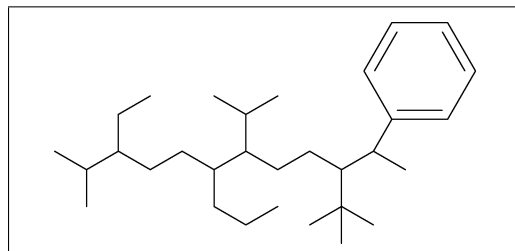
MCf(<-30,!6,2\~dr,! ,4\'1.5,! ,6\^15,-60)
```



### No.23 Insert substituent(1)

```
MCf(<30,
!,/Me,!,/Et,!3,/Pr,!,/iPr,!3,/tBu,!,/Ph^-30,! )

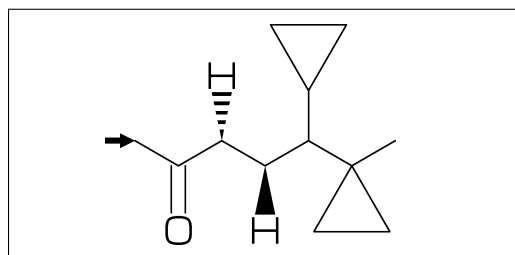
** Me:methyl Et:ethyl Pr:propyl iPr:isopropyl
   tBu:tertial buthyl Ph:phenyl
```



### No.24 Insert substituent(2)

```
/ : single      // : double
*/ : wedge forward /* : wedge backward
** : direct

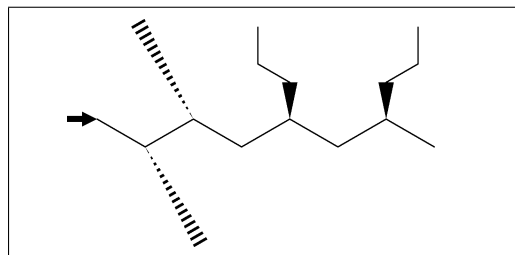
MCf(<30,! ,//0,! ,/*H,! ,*/H,! ,/?3,! ,**?3,! )
```



### No.25 Insert substituent(3)

~,^,',> : change type,angle,length,enviroment of substituent

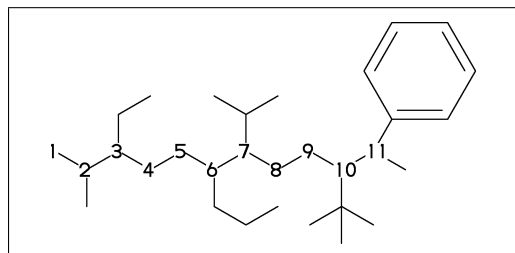
```
MCf(<30,! '1,/Me~zf '2^30,! '1,/Me~zf '2^30,
    !2 '1,*/Pr>lr,!2 '1,*/Pr>r1,! '1)
```



### No.26 Add substituent(1)

```
sw_numberA:=1; numberA_end:=_skeletonA_end;
MCf(<30,!11,
    2:/Me,3:/Et,6:/Pr,7:/iPr,10:/tBu,11:/Ph^30)
```

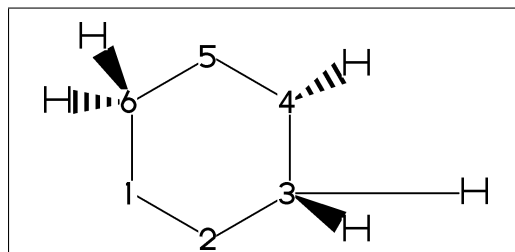
```
** _skeletonA_end :
    end number of molecular skeleton atom
```



### No.27 Add substituent(2)

~,^,',> : change type,angle,length,enviroment of substituent

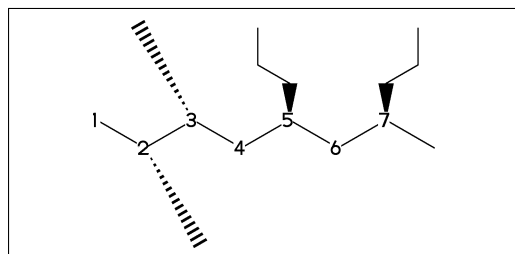
```
sw_numberA:=1; numberA_end:=_skeletonA_end;
MCf(<30,?6,
    @(3 '2^30,3~wf,4~zf,6~wf^30,6~zf^30)/H)
```



### No.28 Add substituent(3)

~,^,',> : change type,angle,length,enviroment of substituent

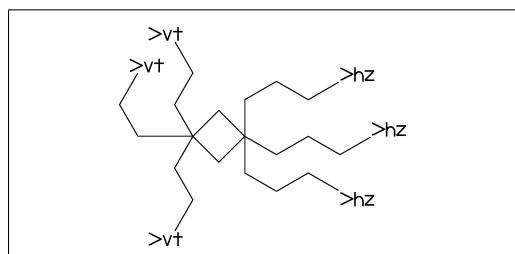
```
sw_numberA:=1; numberA_end:=_skeletonA_end;
MCF(<30,!7 '1,
    @(2,3)/Me '2^30,5:*/Pr>lr,7:*/Pr>r1)
```



### No.29 Chain stretch direction environment (1)

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

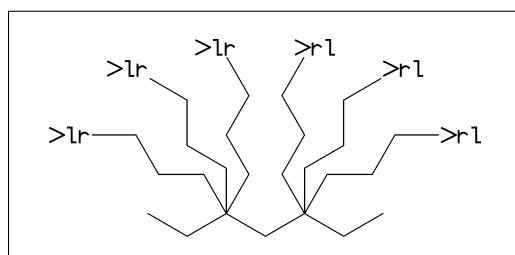
```
?4,
    @(3^-90,3^-30,3^90)/'(!3,"{>hz}")>hz,
    @(1^-60,1 '1.5,1^60)/'(!2,"{>vt}")>vt
```



### No.30 Chain stretch direction environment (2)

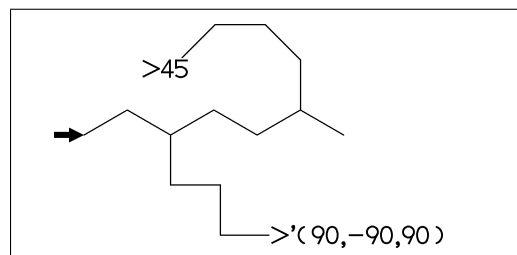
>lr : left-right enviroment  
>r1 : right-left enviroment

```
<30,!6,
    @(3^-30,3,3^30)/'(!3,"{>lr}")>lr,
    @(5^-30,5,5^30)/'(!3,"{>r1}")>r1
```



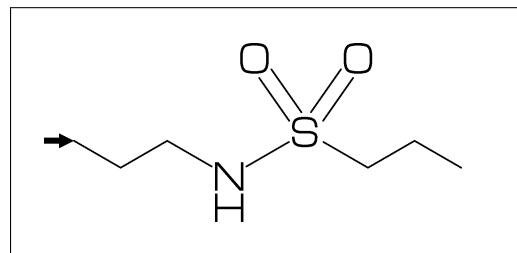
**No.31 Chain stretch direction environment (3)**

>45 : fixed angle environment  
 >'(-90,90,-90) : multi angle environment  
  
 <-30,!6,@(2>45)/'(!3,"{>45}"),  
 @(6>'(-90,90,-90))/'(!2,"{>(-90,90,-90)}")

**No.32 Change atom and Substituent**

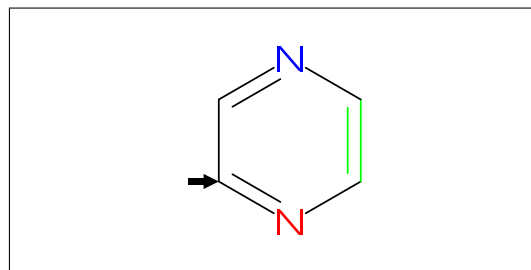
NH,S00 : inset hetero atom and substituent simultaneously

<30,!3,NH,! ,S00,!3

**No.33 Change color**

@(5)green : change color of A5 green  
 \$(3)red : change color of B3 red

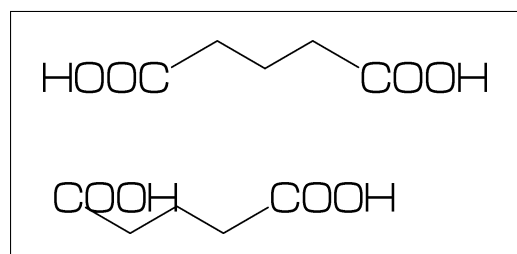
<30,Ph,@(2,5)N,  
 2:red,5:blue,3=green

**No.34 Chain start multiple characters**

if chain start multi character string,  
 use !0 instead of !

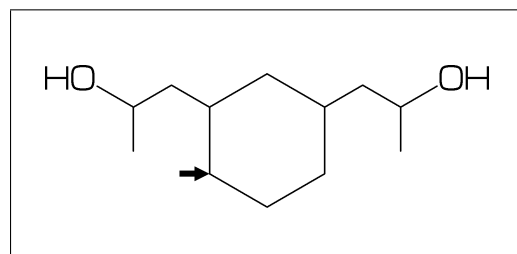
MCd( 1,1)(0 ,0.9)(<30,COOH,!0,!3,COOH)

MCd(.8,1)(0.3,0.1)(<30,COOH,!4,COOH)

**No.35 User definition**

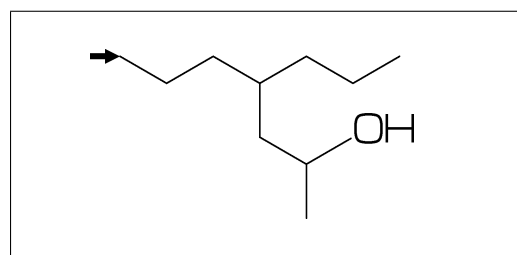
iBuOH : user defined substructure

iBuOH:= '(!,/Me,! ,OH)  
 MCf(<30,?6,@(4,6)/iBuOH)

**No.36 Inline definition**

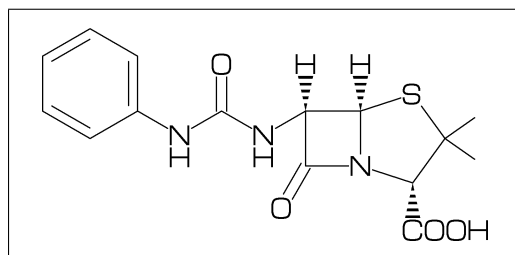
Insert user defined substructure

<30,!3,/ '(!,/Me,! ,OH),!3



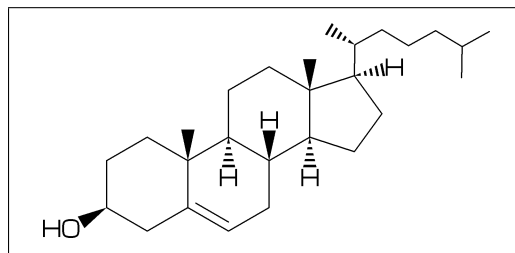
No.37 Example(1) Ampicillin

<45,?4,2:N,2=?5,-1:S,  
 @(3^45,4^-45)/\*H,1://0^15,  
 5:/\*COOH^-18,@(6^35,6^-35)/Me,  
 4\^75,NH,!,//0,! ,NH,! ,Ph



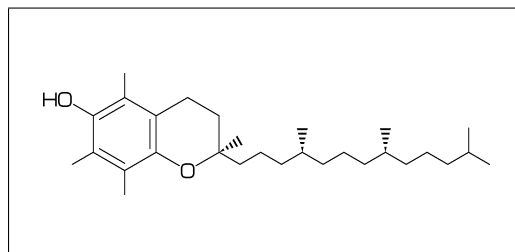
No.38 Example(2) Cholesterol

<30,?6,\$(-4,-2)?6,-4=?5,7=d1,  
 1:\*/OH,@(4,12)\*/Me^60,9:\*/H^60,  
 10:\*/H^180,@(11,-1)\*/H^-60,  
 -1\^17,/\*Me,!4,/Me,! ,



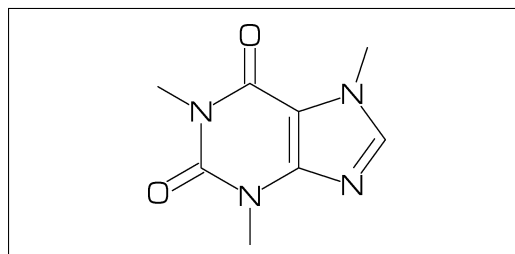
No.39 Example(3) alfa-Tocopherol

<30,Ph,3=?6,  
 7:0,@(1,2,5)/Me,8:/\*Me^60,6:/OH,  
 8\,|,!12,@(4,8)\*/Me,12:/Me



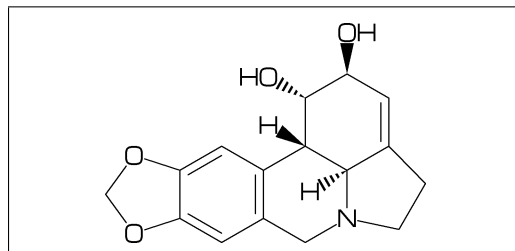
No.40 Example(4) Caffeine

<30,?6,-4=?5,\$(3,8)d1,  
 @(2,6,7,9)N,@(2,6,9)/Me,  
 @(1,5)//0



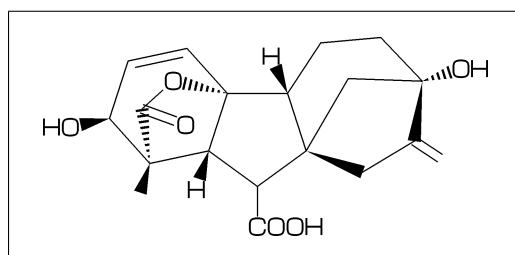
No.41 Example(5) Lycorine

<30,Ph,-4=?6,-2=?6,6=?5,(9,12)=?5[3],  
 13=d1,8:N,@(15,17)0,  
 9:\*/H^180,10:\*/H^60,13:\*/OH,14:\*/OH



No.42 Example(6) Gibberellin

<12,?6^1.3,3=?5,9=?7,12\^160^1.6,&8,  
 4\^155~zf^1.2,0,55,//0^180^1,&2~zb,  
 5=d1,11=wf,13=wb,7:/COOH,11://Me,1:\*/OH,  
 12:\*/OH,2:\*/Me,@(3^-60,9^60)\*/H

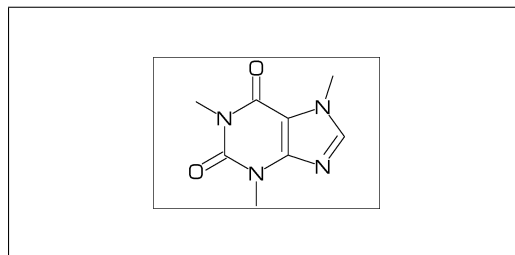


**No.43 Font size**

```

beginfont("EN:Caffeine")
font_wd#:=30mm#; %<==font width
font_ht#:=20mm#; %<==font height
sw_font_frame:=1;
MCf(<30,?6,-4=?5,$(3,8)d1,@(2,6,7,9)N,
    @(2,6,9)/Me,@(1,5)//O)
endfont

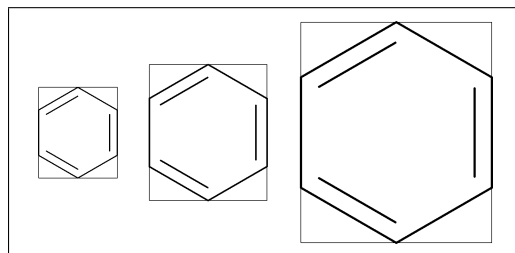
```

**No.44 Max ratio bond/width length**

```

max_bond_width:=0.10;
MCd(1,1)( 0, .5)(<30,Ph)
max_bond_width:=0.15; %<== default
MCd(1,1)(.33,.5)(<30,Ph)
max_bond_width:=0.30;
MCd(1,1)( 1, .5)(<30,Ph)

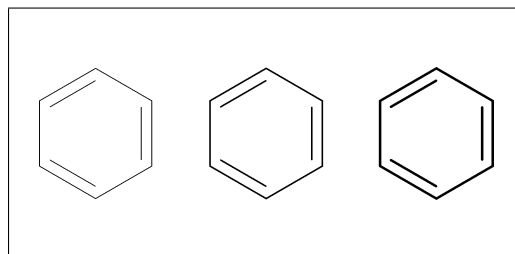
```

**No.45 Ratio thickness/bond length**

```

ratio_thickness_bond:= 0.005;
MCd(1,.6)(0, .5)(<30,Ph)
ratio_thickness_bond:= 0.015; %<== default
MCd(1,.6)(.5,.5)(<30,Ph)
ratio_thickness_bond:= 0.030;
MCd(1,.6)(1, .5)(<30,Ph)

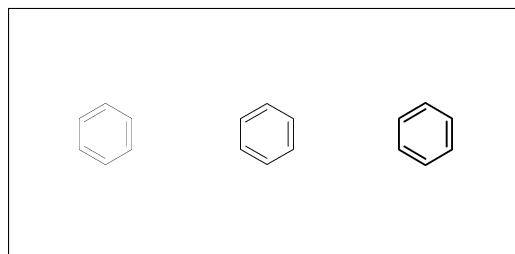
```

**No.46 Offset thickness of bond**

```

beginfont() offset_thickness#:=0pt#;
MCd(1,.3)(0, .5)(<30,Ph) endfont
beginfont() offset_thickness#:=0.2pt#; %<== default
MCd(1,.3)(.5,.5)(<30,Ph) endfont
beginfont() offset_thickness#:=0.5pt#;
MCd(1,.3)(1, .5)(<30,Ph) endfont

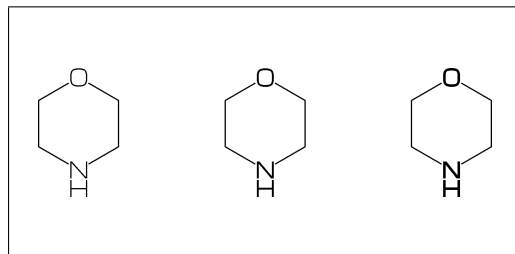
```

**No.47 Ratio char/bond thickness**

```

ratio_char_bond:=1.0;
MCd(1,.6)(0, .5)(<30,?6,5:O,2:NH)
ratio_char_bond:=1.5; %<== default
MCd(1,.6)(.5,.5)(<30,?6,5:O,2:NH)
ratio_char_bond:=2.0;
MCd(1,.6)(1, .5)(<30,?6,5:O,2:NH)

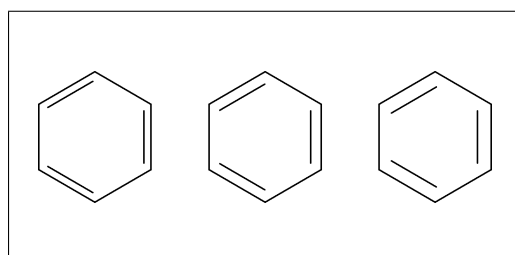
```

**No.48 Ratio bondgap/bond length**

```

ratio_bondgap_bond:= 0.10;
MCd(1,.6)(0, .5)(<30,Ph)
ratio_bondgap_bond:= 0.15; %<== default
MCd(1,.6)(.5,.5)(<30,Ph)
ratio_bondgap_bond:= 0.20;
MCd(1,.6)(1, .5)(<30,Ph)

```



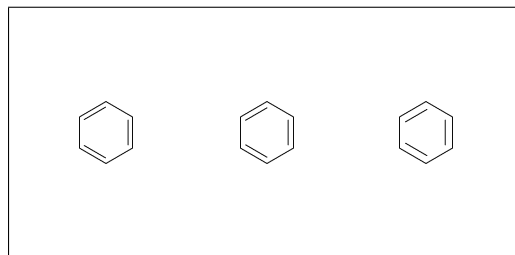


**No.49 Offset of doublebond gap**

```

beginfont() offset_bond_gap#:=0.0pt#;
MCd(1,.3)(0, .5)(<30,Ph) endfont
beginfont() offset_bond_gap#:=0.3pt#; %<== default
MCd(1,.3)(.5,.5)(<30,Ph) endfont
beginfont() offset_bond_gap#:=1.0pt#;
MCd(1,.3)(1, .5)(<30,Ph) endfont

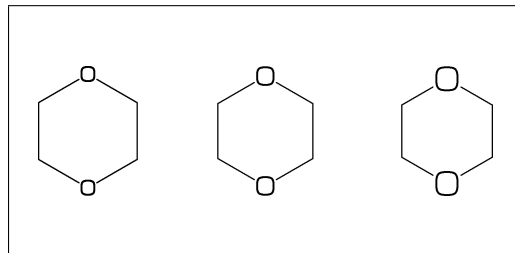
```

**No.50 Ratio atom/bond length**

```

ratio_atom_bond:= 0.25;
MCd(1,.6)(0, .5)(<30,?6,@(2,5)O)
ratio_atom_bond:= 0.36; %<== default
MCd(1,.6)(.5,.5)(<30,?6,@(2,5)O)
ratio_atom_bond:= 0.45;
MCd(1,.6)(1, .5)(<30,?6,@(2,5)O)

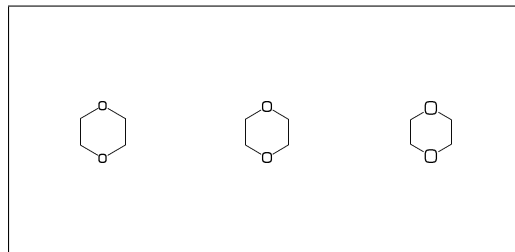
```

**No.51 Offset of atom width**

```

beginfont() offset_atom#:=0.0pt#;
MCd(1,.3)(0, .5)(<30,Ph,@(2,4,6)N) endfont
beginfont() offset_atom#:=0.8pt#; %<== default
MCd(1,.3)(.5,.5)(<30,Ph,@(2,4,6)N) endfont
beginfont() offset_atom#:=2.0pt#;
MCd(1,.3)(1, .5)(<30,Ph,@(2,4,6)N) endfont

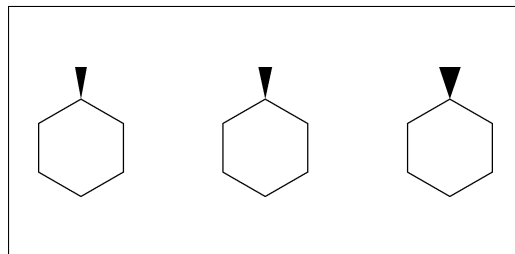
```

**No.52 Ratio wedge/bond length**

```

ratio_wedge_bond:=0.10;
MCd(1,.6)(0, .5)(<30,?6,5:*/Me)
ratio_wedge_bond:=0.12; %<== default
MCd(1,.6)(.5,.5)(<30,?6,5:*/Me)
ratio_wedge_bond:=0.20;
MCd(1,.6)(1, .5)(<30,?6,5:*/Me)

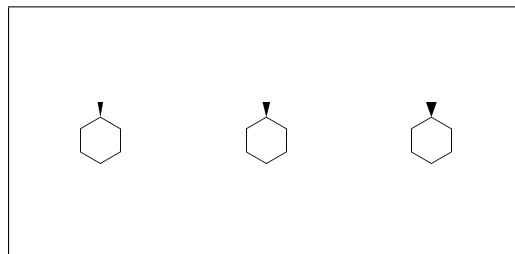
```

**No.53 Offset of wedge width**

```

beginfont("EN:Offset_wedge")
offset_wedge#:=0.0pt#;
MCd(1,.3)(0, .5)(<30,?6,5:*/Me) endfont
beginfont() offset_wedge#:=0.4pt#; %<== default
MCd(1,.3)(.5,.5)(<30,?6,5:*/Me) endfont
beginfont() offset_wedge#:=1.0pt#;
MCd(1,.3)(1, .5)(<30,?6,5:*/Me) endfont

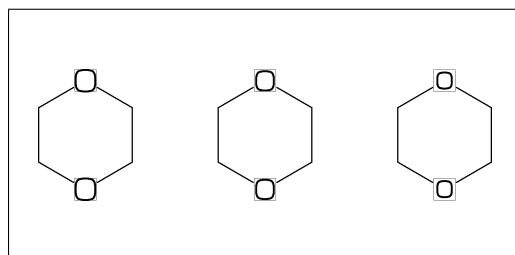
```

**No.54 Ratio font atom gap/atom length**

```

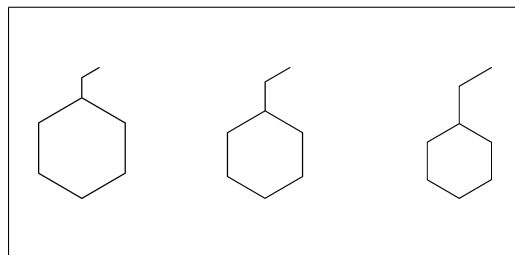
ratio_atomgap_atom:=0.0;
MCd(1,.6)(0, .5)(<30,?6,@(2,5)O)
ratio_atomgap_atom:=0.050; %<== default
MCd(1,.6)(.5,.5)(<30,?6,@(2,5)O)
ratio_atomgap_atom:=0.12;
MCd(1,.6)(1, .5)(<30,?6,@(2,5)O)

```

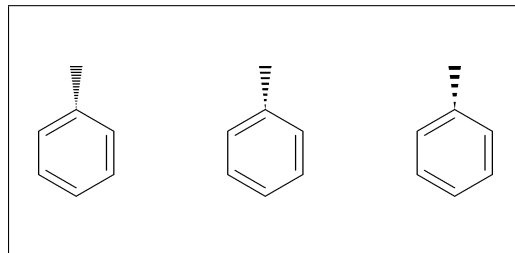


**No.55 Ratio chain/ring length**

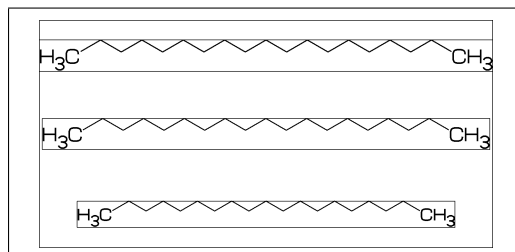
```
ratio_chain_ring:= 0.4;
MCd(1,.6)(0, .5)(<30,?6,5:/Et)
ratio_chain_ring:= 0.66;          %<== default
MCd(1,.6)(.5,.5)(<30,?6,5:/Et)
ratio_chain_ring:= 1.0;
MCd(1,.6)(1, .5)(<30,?6,5:/Et)
```

**No.56 Ratio zebra gap/bond length**

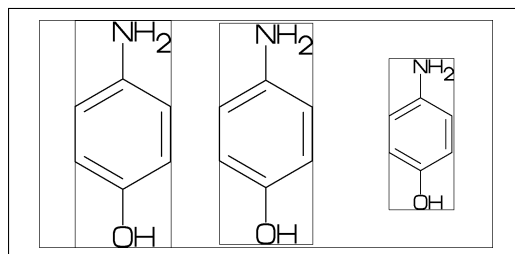
```
ratio_zebragap_bond:=0.06;
MCd(1,.6)(0, .5)(<30,Ph,5:/*Me'1)
ratio_zebragap_bond:=0.12;      %<== default
MCd(1,.6)(.5,.5)(<30,Ph,5:/*Me'1)
ratio_zebragap_bond:=0.20;
MCd(1,.6)(1, .5)(<30,Ph,5:/*Me'1)
```

**No.57 Margin left and right**

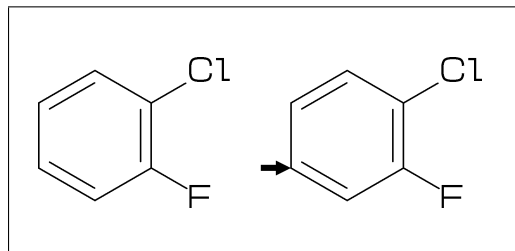
```
margin_left_right:=0mm;
MCd(1,1)(0.5,0.9)(<30,CH3,!0,!17,CH3)
margin_left_right:=0.4mm;      %<== default
MCd(1,1)(0.5,0.5)(<30,CH3,!0,!17,CH3)
margin_left_right:=5mm;
MCd(1,1)(0.5,0.1)(<30,CH3,!0,!17,CH3)
```

**No.58 Margin top and bottom**

```
margin_top_bottom:=0mm;
MCd(1,1)(0.1,0.5)(<30,Ph,2:/OH,5:/NH2)
margin_top_bottom:=0.4mm;      %<== default
MCd(1,1)(0.5,0.5)(<30,Ph,2:/OH,5:/NH2)
margin_top_bottom:=5mm;
MCd(1,1)(0.9,0.5)(<30,Ph,2:/OH,5:/NH2)
```

**No.59 Switch Start Vector**

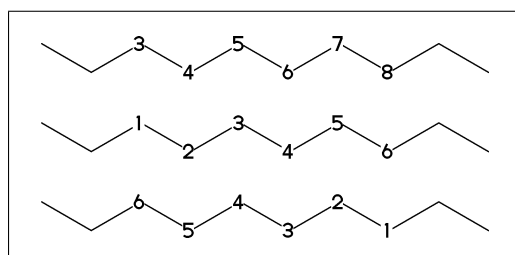
```
MCd(1,.8)( 0,0.5)(<30,Ph,4:/Cl,3:/F)
sw_start_vector:=1;
MCd(1,.8)( 1,0.5)(<30,Ph,4:/Cl,3:/F)
```

**No.60 Switch Numbering atom**

```
numberA_start:=3; numberA_end:=8;

sw_numberA:=1; MCd(1,1)(.5,.9)(<30,!9)
sw_numberA:=2; MCd(1,1)(.5,.5)(<30,!9)
sw_numberA:=3; MCd(1,1)(.5,.1)(<30,!9)

** default: numberA_start=1 numberA_end=4095
```



**No.61 Switch Numbering bond**

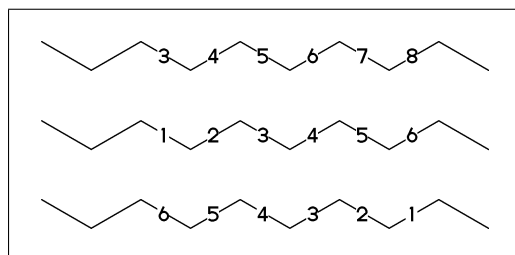
```

numberB_start:=3; numberB_end:=8;

sw_numberB:=1; MCd(1,1)(.5,.9)(<30,!9)
sw_numberB:=2; MCd(1,1)(.5,.5)(<30,!9)
sw_numberB:=3; MCd(1,1)(.5,.1)(<30,!9)

** default: numberB_start=1 numberB_end=4095

```

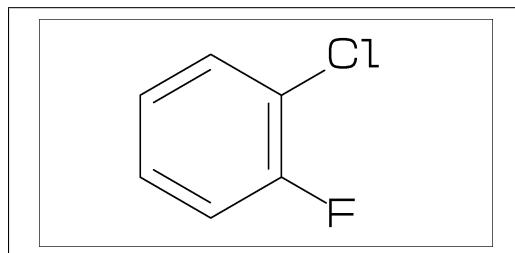
**No.62 Switch font frame**

```

sw_font_frame:=1;

MCf(<30,Ph,4:/Cl,3:/F)

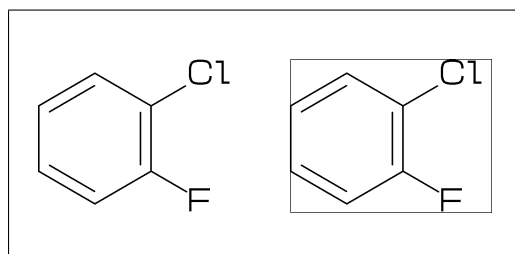
```

**No.63 Switch molecular frame**

```

MCd(1,.8)(0,0.5)(<30,Ph,4:/Cl,3:/F)
sw_mol_frame:=1;
MCd(1,.8)(1,0.5)(<30,Ph,4:/Cl,3:/F)

```

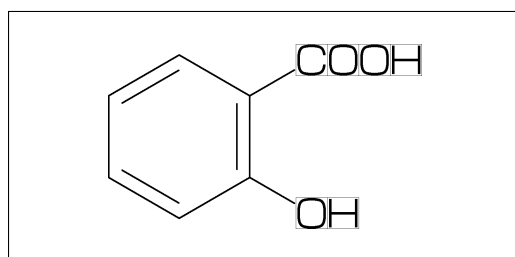
**No.64 Switch atom frame**

```

sw_atom_frame:=1;

MCf(<30,Ph,4:/COOH,3:/OH)

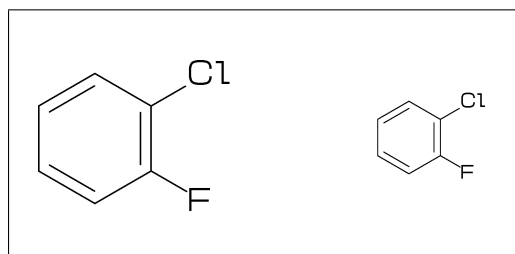
```

**No.65 Switch solid mode**

```

MCd(1,.8)( 0,0.5)(<30,Ph,4:/Cl,3:/F)
sw_solid:=1; ratio_bond_width:=0.08;
MCd(1,.8)( 1,0.5)(<30,Ph,4:/Cl,3:/F)

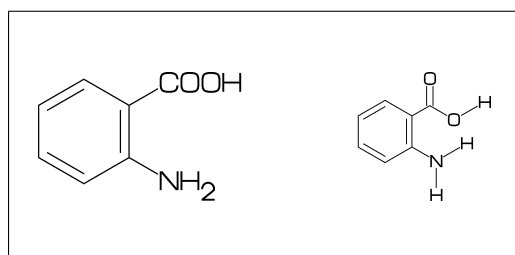
```

**No.66 Switch Expand**

```

MCd(1,.6)(0,0.5)(<30,Ph,4:/COOH,3:/NH2)
sw_expand:=1;
MCd(1,.6)(1,0.5)(<30,Ph,4:/COOH,3:/NH2)

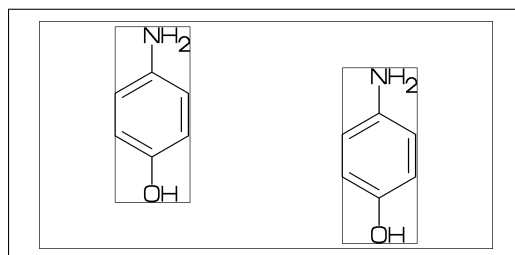
```



**No.67 Function MCd (draw)**

```
MCd(a,b)(c,d)(...)
  a: ratio molecular width/font width
  b: ratio molecular hight/font hight
  c: x axis position  d:y axis position
```

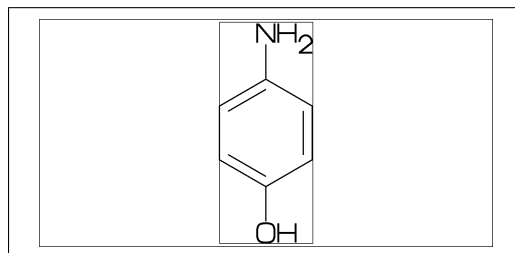
```
MCd(1,0.8)(0.2,0.9)(<30,Ph,2:/OH,5:/NH2)
MCd(1,0.8)(0.8,0.1)(<30,Ph,2:/OH,5:/NH2)
```

**No.68 Function MCf (fit draw)**

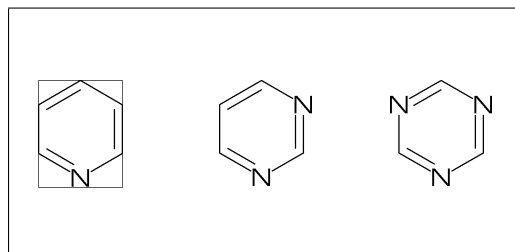
```
MCf(...) : MCd(1,1)(0.5,0.5)(...)

sw_font_frame:=1;  sw_mol_frame:=1;

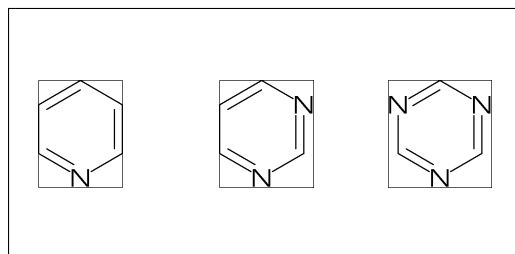
MCf(<30,Ph,2:/OH,5:/NH2)
```

**No.69 Local setting**

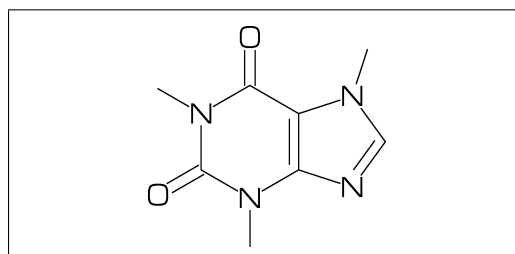
```
beginfont("N0:1")
  sw_mol_frame:=1; % <== Local setting
  MCd(1,.5)(0.0,0.5)(<30,Ph,@(2)N) endfont
beginfont("N0:2")
  MCd(1,.5)(0.5,0.5)(<30,Ph,@(2,4)N) endfont
beginfont("N0:3")
  MCd(1,.5)(1.0,0.5)(<30,Ph,@(2,4,6)N) endfont
```

**No.70 Global setting**

```
sw_mol_frame:=1; % <== Global setting
beginfont("N0:1")
  MCd(1,.5)(0.0,0.5)(<30,Ph,@(2)N) endfont
beginfont("N0:2")
  MCd(1,.5)(0.5,0.5)(<30,Ph,@(2,4)N) endfont
beginfont("N0:3")
  MCd(1,.5)(1.0,0.5)(<30,Ph,@(2,4,6)N) endfont
```

**No.71 Output molecular infomation**

```
beginfont() sw_info_weight:=sw_info_formula:=1;
MCf(...) endfont
%% Output to mcf_man_soc-info.aux %%
\INFO{{F:mcf_man_soc}{C:82}{MWc:194.19174}
  {FMc:C8H10N4O2}}%
MWc:calculated molecular weight
FMc:calculated molecular formula
```

**No.72 Output additional infomation**

```
beginfont("EN:Caffeine","CAS:58-08-2")
MCf(...) endfont
%% Output to mcf_man_soc-info.aux %%
\INFO{{F:mcf_man_soc}{C:83}{EN:Caffeine}
  {CAS:58-08-2}}%
*F:filename *C:char number EN:molecular name
CAS:CAS number *:default output
```

