

## XP commands

**ARAD** a b s key | a=rad b=rad s=space r  
**ATYP** t c key | t=-4 to 10 c= 1 to 15  
**BACK** c i | c= 1 to 15 i=0 to 3  
**BANG** key | bond & angle  
**CELL**  $\lambda$  a b c  $\alpha$   $\beta$   $\gamma$   
**CENT** key | centroid  
**CENT/X** key | add to coords  
**DEMO**  
**DIAG** key | diagonal drawing  
**DIAG/B** | BOX diagonal  
**DRAW** plotfile | send plotfile to  
print/file  
**ECHO** text  
**EDEN** key | electron density  
**EGSD** path | path for example files  
**END**  
**ENVI** d key | enviroment r1+r1+d  
[d=0.5]  
<Esc> | stop  
**EXAM** template | template=DOS or UNIX  
command  
**EXIT** file | filename (opt) print  
output  
**EYES** n | n=1 mono n=2 stereo  
**FILE** file | write \*.ins file=\*  
**FMOL** key, d | make mole r1+r2+d  
[d=0.5]  
**FMOL** REST | make molecule less  
current  
**FMOL/N** | not listing to screen  
**FUSE** | complement of GROW  
**GAPS** o s | o=gap bond/atom s=shade  
**GROW** d key | r1+r2+d [d=0.5]  
**HADD** t d U key | t=1 to 9  
d=0.96(0.08)U=-1.2  
**HIMP** d key | d=distance [d=0.96]  
**HLPD** path | path to help files  
**INFO** key | atom info  
**INVT** x y z key | invert atoms thru x,y,z  
**ISOT** key | make isotropic  
**JOIN** t key | t= 1 to 7  
**KILL** key | delete  
**LABL** c s | c=0 to 4 : s [s=600]  
**LIBR** key | libration  
**LINE** two atoms | l.s. line thru atoms  
**LINK** t key | t=0 to 7  
**LITE** I d s p | I=2 to 20 d=0 to 1  
p=4 to 20  
**LOSE** filename | delete filename  
**MATR** p11 p12 p13 p21 p22 p23 p31 p32 p33  
**MATR** n | n=1(a); n=2(b); n=3(c)  
**MATR** h,k,l | perp. to h,k,l  
**MGEN** k dX dY dZ X Y Z  
**MODL** key s d | s=[def=3.0A]  
d=[def=0.25]  
**MOVE** dx dy dz sign  
**MPLN** key | least-square plane  
**MPLN/N** | no output  
**NAME** old new c | c=sfaccode  
**NEWM** two atoms | newman projection  
**NEXT** filename | read save file  
**NOPL** | clear plane info  
**OFIT** key | orthogonal fit  
**ORTH** filename | orthogonal file  
**ORTH/F** filename | include unit-cell  
**PACK** d2 d1 d | packing diagram  
**PAGE** | form feed  
**PART** n | n=part number  
**PART/S** n atom | change part number  
**PAWS** | pause  
**PBOX** w d x y z | w=[def=20] d=[def=8]  
**PERS** br key | br=[def=0.05]  
**PGEN** key dX dY dZ X Y Z  
**PICK** key | atom pick  
**POLP** key | polyhedral fill (plot)  
**POLY** key | polyhedral fill  
**POST** plotfile | poster/plotfile maker  
**PREV** | previous matrix  
**PRIN** | print buffer  
**PROJ** d k | d=rotation degree  
**PROJ/P** | alpha-carbon traces  
**PRUN** nb key | nb=max. # of bonds  
**PRUN** d1 d2 key | prun below d1 above d2  
**PUSH** dx dy dz sign  
**QUIT**  
**RASD** code | rast device  
code=L,F,C,D  
**RAST** filename | raster file  
**READ** filetype | read file to END  
**REAP** filetype | read file to EOF  
**RESI** n c | n=number c=class  
**RESI/S** n c atom | chage class number  
**RIDE** key | riding model  
**RING** c key | find rings c = bondtype  
**ROTA** n,p; ... | n=1(x),2(y),3(z)  
p=degrees  
**ROTA** two atoms | about atoms  
**SAVE** filename | save snapshot (see  
NEXT)  
**SFIL** s d key | space s=-3,0,3;  
d=[def=50]  
**SGEN** sym key | symmetry expansion  
**SORT** a1 a2...an | atom sort  
**SORT/H** | hydrogens sorted  
**SORT/N** | sorts in numeric order  
**SORT/R** | sorts in numeric  
residue order  
**SORT/P** | sorts in residue order  
**SPIX** key | space fill screen  
**SPOT** I m p | I=4 to 20; m=deg p=deg  
**SRCH** keys d | search r1+r2+d  
**SYMM** symmetry operator  
**TELP** s p b d | s=-3,0,3 p=% b=br  
d=view d  
**TELP/P** | alpha-carbon traces  
**TITL** text  
**TORS** key | torsion angle  
**UNDO** key | undo BOND  
**UNIQ** key d | r1+r2+d  
**USER** path | change path  
**VIEW** plotfile | screen view  
**WAIT** wt key | atom weights  
**WIPE** | screen clear  
**ZOOM** scale  
keywords :  
**atom names**, **TYPEn**, **ALL**, **TO**, **LESS**, **CELL**,  
**REST** and **LPT**.