The Stanford Mechanism thermo datafile (thermo.dat) placed in R:\m-y-crfel\COMMON\FlameMaster\Mechanisms\Stanford and /g/m-y-crfel2/COMMON/Xu\_Flames has an error in A1CH3CH3 species. All atoms (N,C,O,H) are represented as 0 and I get the error "molecular weight is not appropriate for species A1CH3CH3."

A1CH3CH3 G3B3 H 0C 0O 0N 0G 300.000 3000.000 1000.000 1

-1.95577967E+00 7.09552723E-02-4.19975432E-05 1.18372259E-08-1.28339716E-12 2

-6.91883225E+01 3.59161008E+01-3.46066830E+00 7.17789316E-02-2.55611032E-05 3

-1.74870775E-08 1.22856956E-11 1.62314629E+02 4.36521185E+01 2.21996114E+04 4

The elemental composition for A1CH3CH3 is C8H10. You can correct it as H  10C   8O   0N   0G in the thermo file.

However, TheSoot.chthermo file looks correct:

A1CH3CH3 000000N 0H 10O 0C 8AR 0G 300 5000 1000 1

-1.95577967E+00 7.09552723E-02-4.19975432E-05 1.18372259E-08-1.28339716E-12 2

-6.91883225E+01 3.59161008E+01-3.46066830E+00 7.17789316E-02-2.55611032E-05 3

-1.74870775E-08 1.22856956E-11 1.62314629E+02 4.36521185E+01 4

So 2 questions:

1. Which one does the .pre file actually use during its generation? This determines whether our .pre file is also wrong for this part.
2. TheSoot.chthermo file looks older, so does it generate the thermo.dat file? If yes, why this mistake can happen?