Note added in proof
(for CCP4–bound users only)

If you intend to use *GraphEnt* to calculate **FOM–weighted protein density maps,** then it is strongly suggested to use σA coefficients for the calculation, as follows :

– Use SIGMAA to obtain the required coefficients. If you use REFMAC you already have them in the .mtz file written by it.

– Start the program with 'graphent <my_file.mtz>'

– For a (2Fo–Fc) map, chose (in this order) the columns :
2FOFCWT, SIGFP, PH2FOFCWT where SIGFP is the standard deviation of your native structure factor amplitudes.

– For a (Fo–Fc) map, chose (in this order) the columns :
FOFCWT, SIGFP, PHFOFCWT

– If your .mtz file comes directly from a SIGMAA run, the coefficients will be : FWT, SIGFP, PHFWT and DELFWT, SIGFP, PHDELFWT.

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Please note that depending on how high (or low) the figure of merit is, this procedure may underestimate the standard deviations of the coefficients. The result is that the maps may be somewhat sharper than they ought to.