Check list for submitting Mass Chain Evaluations

• Run FMTCHK and correct all errors
• Run ConsistencyCheck and correct any issues
• Ensure that all relevant references from NSR have been included
• Ensure that Jπi values in the Adopted Levels are given with justification
• Ensure that T_{1/2} values in the Adopted Levels are traceable
• Ensure that Eg, Ig, Mult and MR in the Adopted Gammas are traceable
• Check that G.S. and isomer properties in Adopted Levels match exactly those corresponding properties in the parent records
• Ensure that all isomers are flagged with M (or M1,M2...) in column 78-79
• Check band drawings for incorrectly flagged levels or missing flags
• Ensure the J^π, Mult, and MR values in Decay Datasets are identical to those in the Adopted Levels
• Confirm that the latest version of BrIcc has been run on all datasets requiring ICC values
• Ensure the procedure for the normalization for decay datasets is clearly indicated

• Confirm that all decay datasets have been updated with latest Q values and log ft or HF codes run with updated Q values.

• Check that XUNDL datasets have not been exactly copied into evaluation (XUNDL datasets should be merged with existing datasets, not adopted as is)
• Check the reference titles for keynumbers that don’t belong to the evaluation