Protein Folding Problem

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par(mfrow=c(2,2))  
# First :   
  
#Residual plot : vs fitted values  
plot(m2$fitted.values, m2$residuals, xlab="Fitted Values", ylab="Residuals ")  
  
#Histogram of Residuals  
hist(m2$residuals, xlab="Residuals", main="Histogram of residuals")  
  
#Residual vs index  
plot (1: nrow(pro) , m2$residuals , xlab = "Index", ylab = "Residuals")  
  
#QQ plot of Residuals  
qqnorm(m2$residuals)  
qqline(m2$residuals, col="red", lwd=2)

