rmsd before Boxplot using best by energy Methods 14 classic-abinitio sade mc ffi9 02 12 sade mc final sade remc sade remc ffi9 02 sade remc final 112y 2mr9 1acw 1ail 1crn 1enh 1rop 1utg 1zdd 1wqc Protein

RMSD (Lower is better)

10

8

6