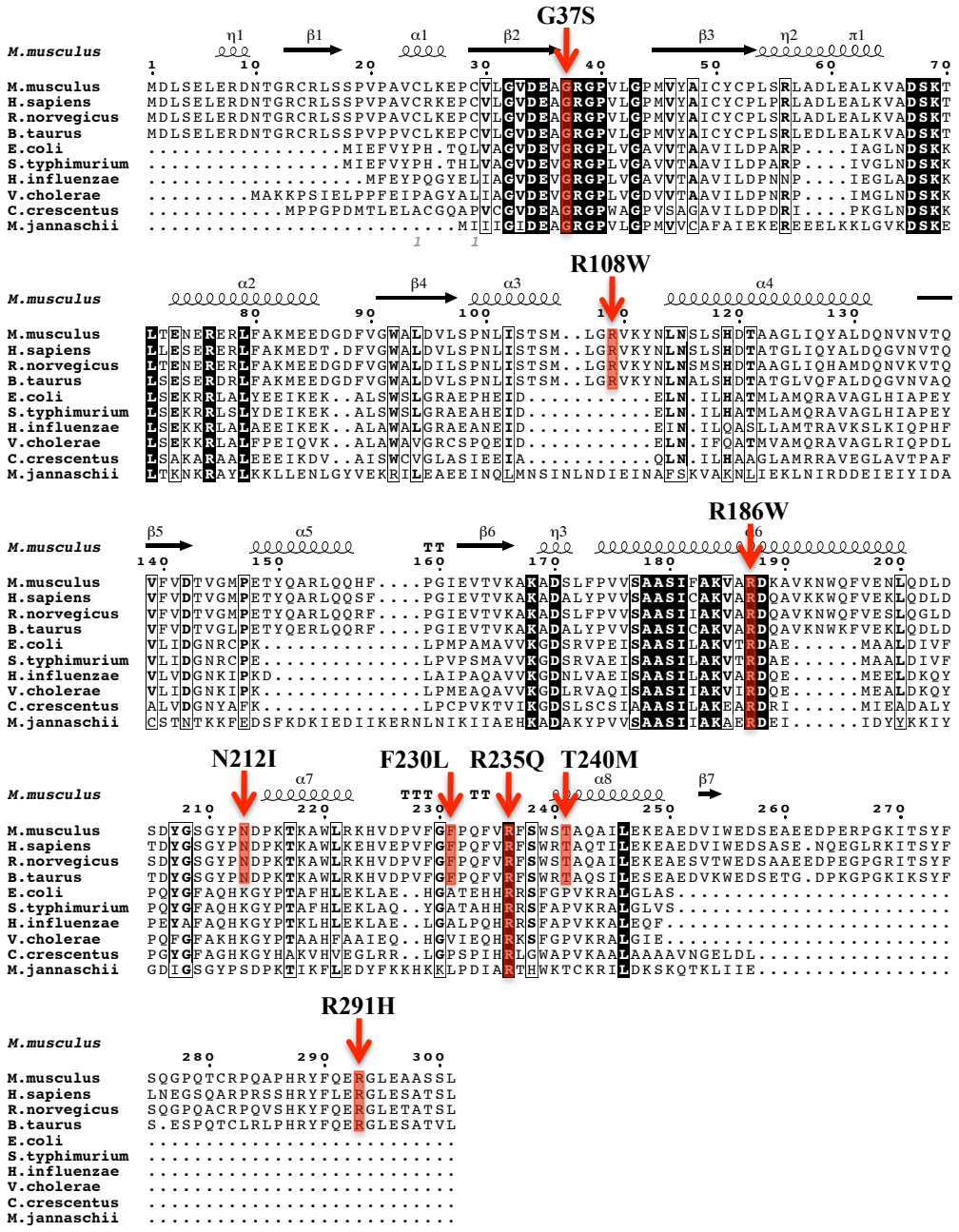
Supplemental Figures

Supplemental Figure 1

Structure-based sequence alignment We used Clustal W to align the primary amino acid sequences of RNase H2s from the following organisms (UniProt accession number): Mus musculus (Q9CWY8), Homo sapiens (O75792), Rattus norvegicus (Q5U209), Bos taurus (Q2TBT5), Escherichia coli (P10442), Salmonella typhimurium (P0A2C1), Haemophilus influenzae (Q4QLM7), Vibrio cholerae (P52021), Caulobacter crescentus (B8GZ34), Methanocaldococcus jannaschii (Q57599). The crystal structure of the mouse RNase H2 (Protein Data Bank code 3KIO) was then aligned to the results using ESPript 2.2 (26) under default conditions. Residues highlighted in black are strictly conserved, those in bold have similarity within their group, and those framed have similarity across groups.



Supplemental Figure 2

Site-directed mutations were introduced into the *RNASEH2A* expression construct and the RNase H2 mutant complexes were purified as described under "EXPERIMENTAL PROCEDURES." Approximately 6 μg of the indicated RNase H2 complex was subjected to 15% SDS-PAGE, and the gel was stained with Coomassie Brilliant Blue (lanes 2–10). The positions of migration of the molecular weight standards (lane 1) and RNase H2 subunits are indicated.