Supporting Information

Kaiserman et al. 10.1073/pnas.0811968106

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hGzmA   1   IIGGNEVTPHSRPYMVLLSLDRKT----ICAGALIAKDWVLTAAHCNLNKRSQVILGAHSITREEPTKQI
hGzmB   1   IIGGHEAKPHSRPYMAYLMIWDQK-SLKRCGGFLIQDDFVLTAAHC-WGSSINVTLGAHNIKEQEPTQQF
mGzmC   1   IIGGNEISPHSRPYMAYYEFLKVGGKKMFCGGFLVRDKFVLTAAHC-KGRSMTVTLGAHNIKAKEETQQI

hGzmA   67  MLVKKEFPYPCYDPATREGDLKLLQLTEKAKINKYVTILHLPKKGDDVKPGTMCQVAGWGRTHNSASWSD
hGzmB   69  IPVKRPIPHPAYNPKNFSNDIMLLQLERKAKRTRAVQPLRLPSNKAQVKPGQTCSVAGWGQTAPLGKHSH
mGzmC   70  IPVAKAIPHPDYNPDDRSNDIMLLKLVRNAKRTRAVRPLNLPRRNAHVKPGDECYVAGWGKVTPDGEFPK

hGzmA   137 TLREVNITIIDRKVCNDRNHYNFNPVIGMNMVCAGSLRGGRDSC~NGDSGSPLLCEGVFRGVTSFGLENK
hGzmB   139 TLQEVKMTVQEDRKCESDLRHYYD---STIELCVGDPEIKKTSF~KGDSGGPLVCNKVAQGIVSYGRN--
mGzmC   140 TLHEVKLTVQKDQVCESQFQSSYN---RANEICVGDSK~IKGASFEEDSGGPLVCKRAAAGIVSYGQT--

hGzmA   206 CGDPRGPGVYILLSKKHLNWIIMTIKGAV
hGzmB   202 --NGMPPRACTKVSS-FVHWIKKTMKRY-
mGzmC   203 --DGSAPQVFTRVLS-FVSWIKKTMKHS-
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Fig. S1. Register shift in granzyme C. Structural alignment of granzyme C with human granzyme A and granzyme B. Amino acids are colored by hydrophobicity: orange, hydrophobic; green, polar; blue, basic; red, acidic; magenta, cysteine. Residues involved in the gzmC register shift are background colored and are aligned based on the structure. Arrow indicates the direction of register shift.

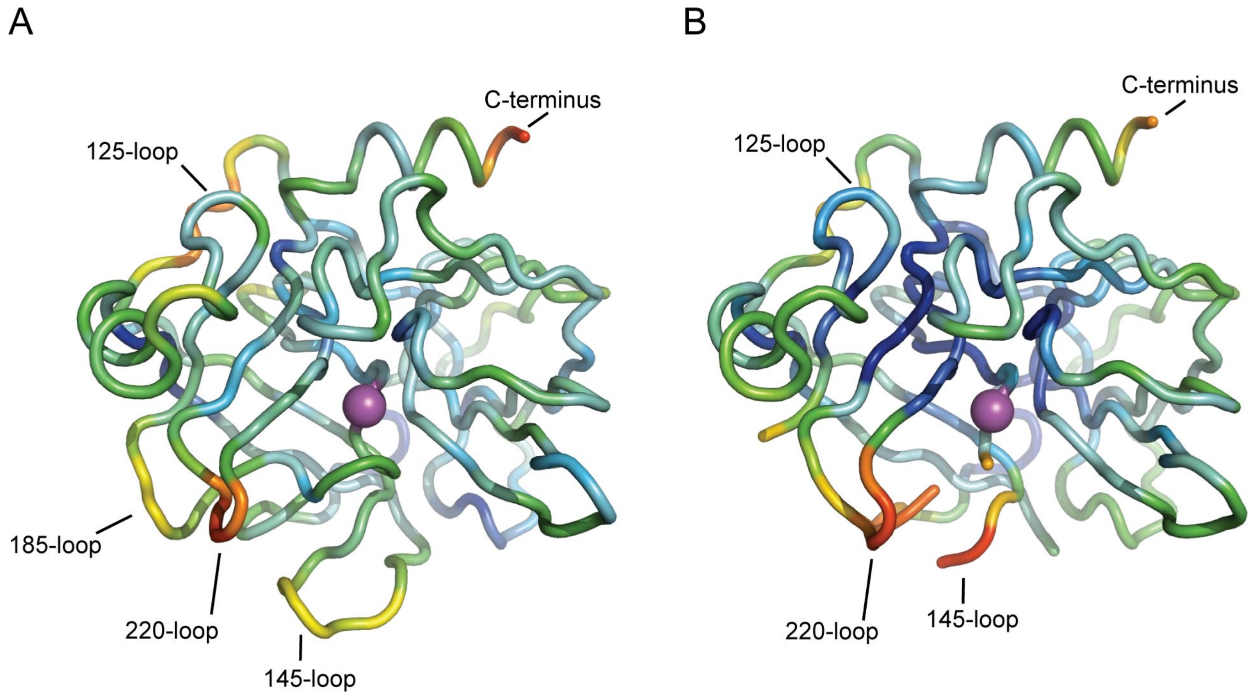

Fig. S2. Granzyme C *B* factors. (*A*) Representation of WT granzyme C colored according to *B* factor from 40 Å^2 (blue) to 70 Å^2 (red). The active-site Ser-195 is shown as a magenta ball, and regions of high B factor are labeled. (*B*) Representation of granzyme C E192R/E193G mutant colored according to *B* factor from 20 Å^2 (blue) to 65 Å^2 (red). The active-site Ser-195 is shown as a magenta ball. Note that the 145- and 185-loops could not be fully modeled.

Other Supporting Information Files

Table S1 (PDF)