| Clone# | Peptide Sequence |  |  |
|--------|------------------|--|--|
| 1      | CPGKGLPSC        |  |  |
| 2      | CPGKGLPSC        |  |  |
| 3      | CPFPAKILC        |  |  |
| 4      | CTKPAKALC        |  |  |
| 5      | CIHAPYAKC        |  |  |
| 6      | CPGKGLPSC        |  |  |
| 7      | 7 CPFPALELC      |  |  |
| 8      | CPAKIGQEC        |  |  |
| 9      | ND               |  |  |
| 10     | CKHAPYALC        |  |  |

**Supplemental Table 1: Peptide Sequences of Isolated Phage Clones.** Sequences of displayed peptides from enriched individual phage clones evaluated in **Fig. 1A**. *ND* = not determined.

|   | CPFPALELC:Fab             | CPGKGLPSC:Fab            |  |
|---|---------------------------|--------------------------|--|
| Data collection                           |                           |                          |  |
| Space group                               | C121                      | P 21 21 21               |  |
| Cell dimensions                           |                           |                          |  |
| a, b, c (Å)                               | 130.18, 55.23, 73.86      | 72.43, 203.51, 225.92    |  |
| α, β, γ (°)                               | 90, 118.696, 90           | 90, 90, 90               |  |
| Resolution (Å)                            | 24.46 - 1.8 (1.864 - 1.8) | 20.0 - 3.0 (3.107 - 3.0) |  |
| R <sub>merge</sub>                        | 0.06451 (0.4702)          | 0.2699 (0.8219)          |  |
| Ι / σΙ                                    | 21.67 (2.05)              | 4.08 (1.63)              |  |
| <i>CC</i> <sub>1/2</sub>                  | 0.999 (0.848)             | 0.963 (0.534)            |  |
| Completeness (%)                          | 96.99 (79.61)             | 97.83 (99.21)            |  |
| Multiplicity                              | 8.3 (2.8)                 | 3.3 (3.3)                |  |
|   |                           |                          |  |
| Refinement                                |                           |                          |  |
| Resolution (Å)                            |                           |                          |  |
| Number of reflections                     | 41567                     | 66291                    |  |
| R <sub>work</sub> / R <sub>free</sub> (%) | 18.6 / 22.5               | 23.89 / 28.82            |  |
| Number of atoms                           |                           |                          |  |
| macromolecules                            | 3348                      | 19964                    |  |
| ligands                                   | 13                        | 0                        |  |
| solvent                                   | 541                       | 0                        |  |
| R.M.S. deviations                         |                           |                          |  |
| Bond lengths (Å)                          | 0.010                     | 0.003                    |  |
| Bond angles (°)                           | 1.282                     | 0.542                    |  |
| Ramachandran                              |                           |                          |  |
| Favored / allowed / disallowed            | 98.6 / 1.2 / 0.23         | 96.29 / 3.60 / 0.12      |  |
| PDB Code                                  | 8G2M                      | 8G8N                     |  |

Supplemental Table 2: Crystallographic analysis and refinement statistics for peptide:aCTLA4 crystal structures.

| Protease | $k_{cat}/K_{m} (M^{-1}.s^{-1})$ | SD (M <sup>-1</sup> .s <sup>-1</sup> ) |  |
|----------|---------------------------------|--|--|
| MMP-1    | 1.4E+04                         | 5.0E+02                                |  |
| MMP-2    | 3.1E+04                         | 3.5E+03                                |  |
| MMP-7    | 2.2E+04                         | 2.0E+03                                |  |
| MMP-9    | 4.6E+04                         | 4.5E+03                                |  |
| MMP-10   | 1.2E+03                         | 0                                      |  |
| MMP-14   | 2.4E+03                         | 1.0E+02                                |  |

Supplemental Table 3: Catalytic efficiency for activation of XTX101 with recombinant human MMPs. SD was calculated from 2 independent experiments.

| Group | Treatment            | Dose<br>(mg/kg) | Tumor<br>Volume<br>(mm <sup>3</sup> ) <sup>a</sup> on<br>Day 16 | TGI (%) <sup>b</sup> | Complete<br>Responses | <i>p</i> value <sup>°</sup> |
|-------|----------------------|-----------------|---|----------------------|-----------------------|-----------------------------|
| 1     | Isotype Control      | 10              | 2220 ± 161  | -                    | 0/8                   | -                           |
| 2     | lpilimumab<br>analog | 1               | 773 ± 158   | 65.2                 | 0/8                   | 0.0002                      |
| 3     | lpilimumab<br>analog | 3               | 227 ± 57  | 89.8                 | 2/8                   | <0.0001                     |
| 4     | XTX100               | 1               | 213 ± 50  | 90.4                 | 3/8                   | <0.0001                     |
| 5     | XTX100               | 3               | 135 ± 23  | 93.9                 | 6/8                   | <0.0001                     |
| 6     | XTX100               | 10              | 134 ± 32  | 94                   | 4/8                   | <0.0001                     |
| 7     | XTX101               | 1               | 434 ± 140   | 80.5                 | 2/8                   | <0.0001                     |
| 8     | XTX101               | 3               | 194 ± 32  | 91.2                 | 3/8                   | <0.0001                     |
| 9     | XTX101               | 10              | 133 ± 31  | 94                   | 5/8                   | <0.0001                     |

Supplemental Table 4: Results from XTX101 in MB49 Model Study. Tumor volume measurements, TGI calculations, and complete responses from MB49 tumor model study. <sup>a</sup>Mean  $\pm$  SEM. <sup>b</sup>Tumor Growth Inhibition (TGI) = (1-T/C) x 100%; T and C are mean tumor volumes of treatment and vehicle control groups respectively on Day 16. <sup>c</sup>A 2-way repeated measures analysis of variance (ANOVA) with Bonferroni's post-hoc test was performed to determine the statistical significance of treatment versus isotype control. Day 16 results were tabulated.

| Group | Treatment                              | Tumor Volume (mm <sup>3</sup> ) <sup>a</sup><br>on Day 14 | TGI (%) <sup>b</sup> | <i>p</i> value <sup>°</sup> |
|-------|--|---|----------------------|-----------------------------|
| 1     | Isotype control 10 mg/kg               | 1446 ± 132  | -                    | -                           |
| 2     | XTX101 0.3 mg/kg                       | 1000 ± 109  | 34.22                | 0.8354                      |
| 3     | RMP1-14 10 mg/kg                       | 931 ± 171   | 39.56                | 0.3722                      |
| 4     | XTX101 0.3 mg/kg +<br>RMP1-14 10 mg/kg | 374 ± 125   | 82.34                | 0.0002                      |

Supplemental Table 5: Results from XTX101 + anti-PD-1 Combination Therapy in MC38 Tumor Model Study. Tumor volume measurements and TGI calculations from MC38 tumor model study. <sup>a</sup>Mean  $\pm$  SEM. <sup>b</sup>Tumor Growth Inhibition (TGI) = (1-T/C) x 100%; T and C are mean tumor volumes of treatment and vehicle control groups respectively on Day 14.

<sup>c</sup>Compared to isotype control (Group 1) by Kruskal-Wallis test with Dunn's multiple comparison test on day 14 post-treatment.