Supplementary Materials

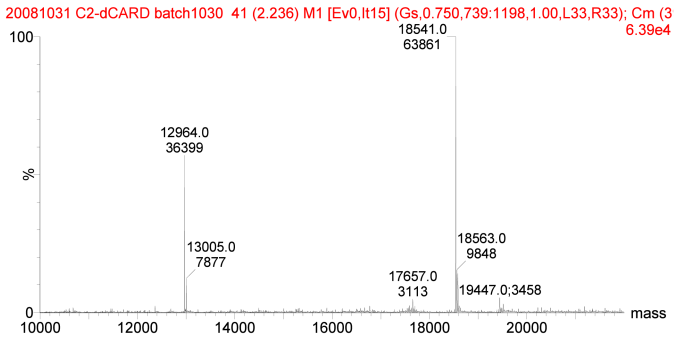
Table S1. X-ray data collection and refinement statistics

	Apo-casp2	Casp2/ VDVAD	Casp2/ ADVAD	Casp2/ DVAD[d]	Casp2/ DVAD[e]	T380A/ VDVAD
Data collection statistics						
Wavelength (Å)	1.11	1.11	1.11	1.11	1.11	1.11
Resolution (Å)	2.24	2.07	1.77	2.33	1.80	1.90
Reflection (observed/unique)	240485/ 33253	267526/ 37412	429434/ 59418	189720/ 26321	404978/ 55954	345933/ 47911
Completeness (%)	100(100)	100(100)	99.8(100)	100(100)	99.9(100)	100(100)
Redundancy	7.2(7.3)	7.2(7.2)	7.2(7.2)	7.2(7.2)	7.2(7.3)	7.2(7.3)
I/σ(I)	41.2(5.51)	25.4(5.23)	55.9(6.32)	37.8(10.0)	49.2(8.35)	39.1(7.93)
R_{merge}[a]	0.50(0.10)	0.55(0.17)	0.50(0.089)	0.32(0.120)	0.48(0.10)	0.43(0.11)
Refinement Statistics						
Space group	$P2_12_1\ 2_1$	$P2_12_1\ 2_1$	$P2_12_1\ 2_1$	$P2_12_1\ 2_1$	$P2_12_1\ 2_1$	$P2_12_1\ 2_1$
Unit cell parameters	a=74.16 b=82.80 c=112.00	a=63.32 b=97.69 c=96.85	a=62.92 b=96.62 c=97.97	a=62.87 b=95.86 c=98.14	a=63.00 b=96.86 c=97.93	a=62.91 b=97.06 c=98.25
Monomers per A.U.	2	2	2	2	2	2
Protein atoms	4045	4143	4114	4103	4076	4132
Water molecules	132	315	244	208	307	291
R_{free}[b] (%)	0.23	0.21	0.21	0.23	0.21	0.20
R_{crys}[c] (%)	0.19	0.16	0.18	0.17	0.17	0.18
Bonds (Å)	0.024	0.023	0.017	0.022	0.017	0.014
Angles (°)	2.0	1.8	1.6	1.8	1.7	1.4
Favored	99.3	98.9	99.6	97.0	99.8	99.8
Generously allowed	0.7	1.1	0.4	3.0	0.2	0.2
Disallowed	0	0.2	0	0	0	0

[a] $R_{merge} = \Sigma|I_o - \langle I \rangle|/\Sigma\langle I \rangle$ summed over all observations and reflections.
[b] $R_{free} = R_{cryst}$ calculated for 5% of reflections omitted from the refinement.
[c] $R_{cryst} = \Sigma|F_o - F_c|/\Sigma|F_o|$.
[d] high Ac-DVAD-CHO concentration structure.
[e] low Ac-DVAD-CHO concentration structure.

Figure S1. A) The mass spectrum, and B) the SDS-PAGE of purified wild type caspase-2.

A.



B.

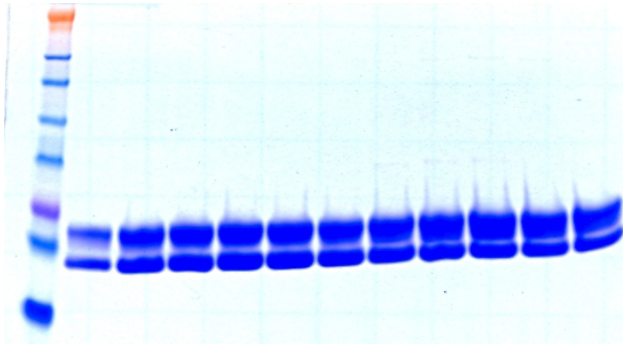


Figure S2. The electron density map of peptide inhibitors. The $2F_o$-F_c map is contoured at σ=1. Color scheme same as in Figure 1. Only the low concentration structure of Casp2/DVAD is shown here.

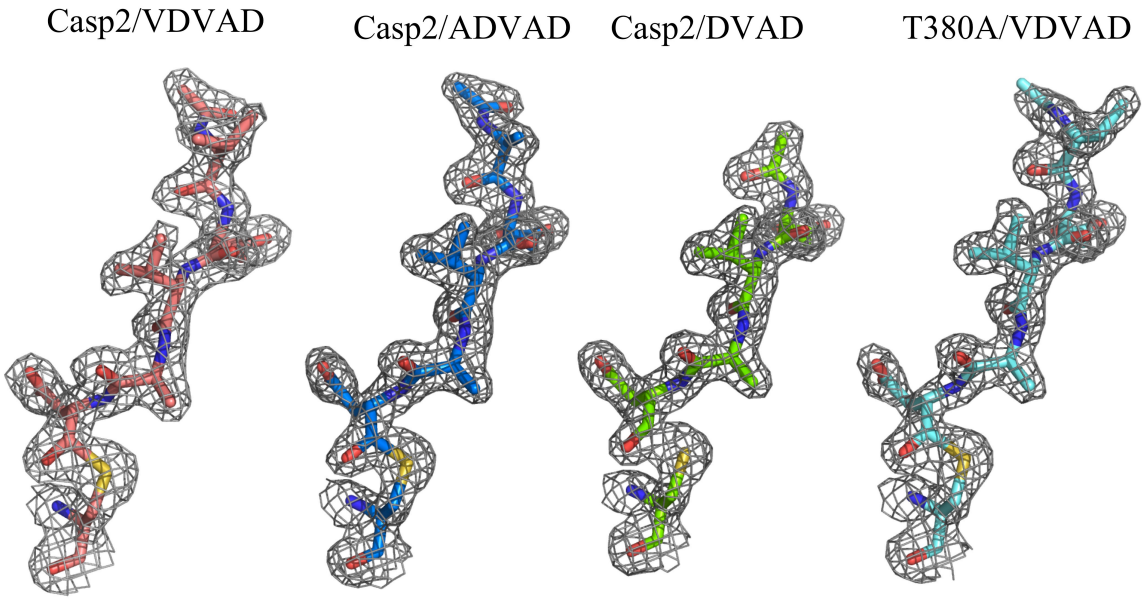
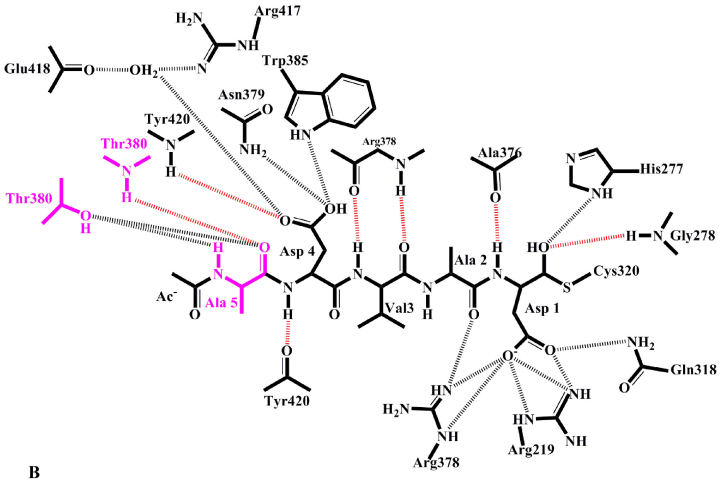
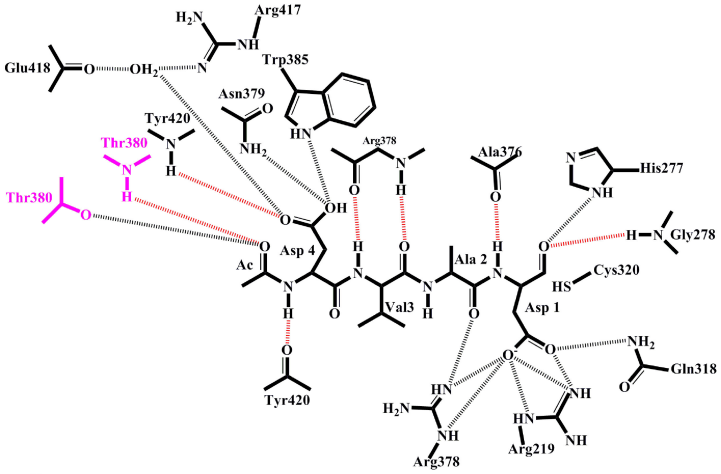


Figure S3. Schematic diagrams of caspase-2 interactions with peptide inhibitors. Only the low concentration structure of Casp2/DVAD is shown here. Backbone hydrogen bonds are shown in black dotted lines, main chain hydrogen bonds are shown in red dotted lines. Hydrophobic interactions are shown in wavy lines. The P5 residue and its interacting residues are shown in magenta. A) Casp2/ADVAD; B) Casp2/DVAD; C) T380A/VDVAD

A



B



C

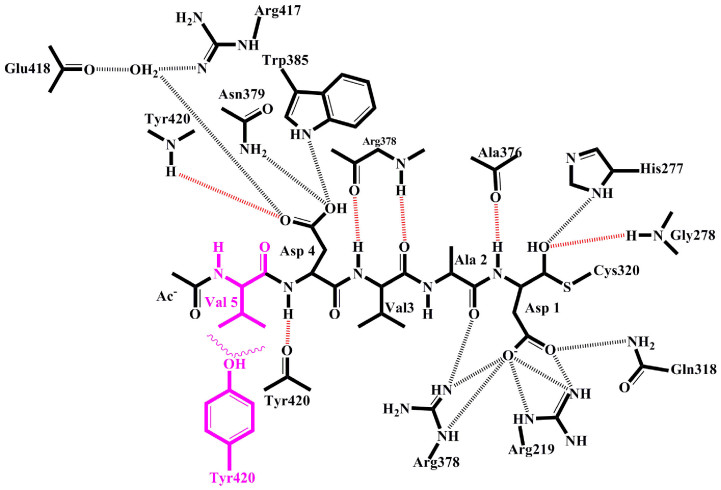


Figure S4. The Hill Coefficient of caspase-2 is 1.0.