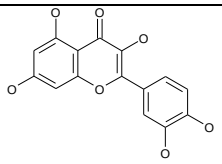
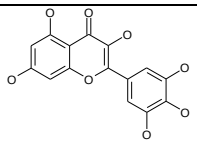
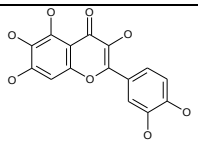
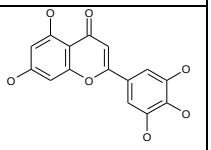
Supplementary Table 1. Data Processing and Refinement Statistics

	PIM1 + **Quercetin**	PIM1 + **Myricetin**	PIM1 + **Quercetagetin**	PIM1 + **5,7,3',4',5'-penta-hydroxyflavone**
Chemical Structure				
Data Processing				
Space group	$P6_5$	$P6_5$	$P6_5$	$P6_5$
Cell dimension	a=b=97.76Å, c=81.19Å, α=β =90°, γ=120°	a=b=98.71Å, c=80.59Å, α=β =90°, γ=120°	a=b=97.76Å, c=80.97Å, α=β =90°, γ=120°	a=b=98.65Å, c=80.47Å, α=β =90°, γ=120°
Resolution (Å)	2.24	2.00	2.44	2.85
Unique reflections	20716	30667	16041	10523
R_{sym} [a,b]	0.079 (0.53)	0.129 (0.681)	0.084 (0.635)	0.138 (0.983)
Redundancy [b]	5.3 (4.5)	5.0 (4.9)	6.0 (5.1)	4.9 (4.9)
Completeness (%) [b]	98.5 (99.5)	99.9 (99.9)	100 (100)	100 (100)
$\langle I/\sigma_I \rangle$ [b]	8.5 (1.4)	7.9 (1.5)	13.4 (2.3)	9.5 (1.6)
Refinement				
Reflections used	20049	28657	15599	9976
R-factor [c]	0.187	0.193	0.189	0.208
R_{free} [d]	0.220	0.218	0.229	0.262
RMS bond length (Å)	0.011	0.010	0.013	0.013
RMS bond angle (°)	1.365	1.361	1.497	1.545
RMS torsion angle (°)	2.927	3.049	3.190	2.949

[a] $R_{sym} = \sum|I-\langle I\rangle| / \sum I$, where I is the intensity of a reflection and $\langle I\rangle$ is the mean intensity of multiple observations of that reflection as well as its symmetry mates. [b] Values in parenthesis refer to the highest resolution shell. [c] R-factor = $\sum||F_o|-|F_c|| / \sum|F_o|$, where F_o and F_c are the observed and calculated structure factors of a given reflection respectively, [d] R_{free} was calculated by setting aside 5% of the reflections randomly.

Supplementary Figure 1. Identification of PIM1 effects on clonogenic growth by siRNA knockdown. Potential human *pim-1* siRNA sequences were designed using an on-line program (http://www.ambion.com/techlib/misc/siRNA_finder.html), based on GenBank sequence NM_002648. Three sequences were evaluated: #21 (nucleotides 743-764), #27 (nucleotides 1199-1220), and #30 (nucleotides 1221-1239). Mammalian expression plasmids encoding these potential siRNA sequences were constructed in pSILENCER (Ambion). Candidate sequences were validated by their ability to prevent expression of human *pim-1* protein in a transient transfection model in human U2OS osteosarcoma cells. The ability of the siRNA constructs to block expression of the transiently co-expressed *pim-1* cDNA was evaluated by immunoblotting.

To characterize the effect of *pim-1* inhibition on the clonogenic growth of prostate epithelial cells, we transfected pSILENCER plasmids encoding either control sequences or *pim-1* #21 siRNA sequences into RWPE1 and RWPE2 cells. The target cells were first plated at low density into 10cm plates. After 24hrs plasmid (10μg/plate), precomplexed with Fugene 6 transfection reagent, was added and allowed to remain in contact with the cells for 24hr. The medium was then replaced with medium containing 5μg/mL puromycin. After an additional 48hrs, this medium was then changed to either complete medium without puromycin (RWPE1) or medium containing 2.5μg/mL puromycin (RWPE2). Culture was continued for an additional 10-14 days to allow formation of colonies. The plates were then rinsed twice with PBS, fixed with 4% paraformaldehyde in PBS, then stained with crystal violet.

A. Characterization of pSILENCER plasmids encoding active human *pim-1* siRNA sequences. U2OS cells were transiently transfected with an expression plasmid encoding the human *pim-1* cDNA, along with plasmids for control or candidate *pim-1* siRNA sequences. 48hrs later, the cells were lysed and examined by immunoblotting to measure expression of PIM1. siRNA #21 was the most efficient at blocking transcription of a *pim-1* cDNA. C = inactive, control siRNA sequence in pSILENCER **B.** Transfection of RWPE1 and RWPE2 cells with *pim-1* siRNA-encoding plasmids markedly decreases clonogenic growth.