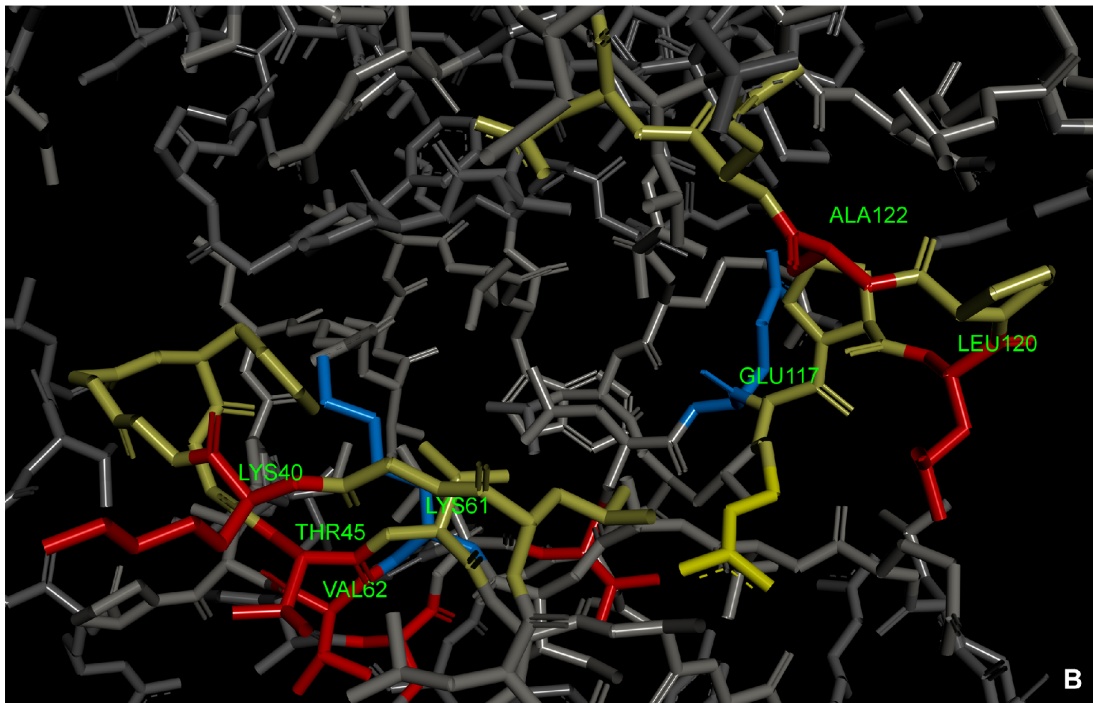


## SUPPLEMENTARY FIGURE AND TABLE

PIM1	129	YQVGP	LLGSGGFG	<u>SVYSG</u>	IRVSDNLPVAIKHVEKDRI	SDWGE	LPNGTRV	PMEVLLK	KVS						
PIM2	32	YRLGP	LLGKGGFG	TVFAG	HRLTDRLQVAIKVIPRNRV	LGWSP	LSDSVTC	PLEVALL	KVG						
PIM3	40	YQVGA	VLLGSGGFG	TVYAG	SRIADGLPVAVKHVV	KERVTE	WGS	LGGATV	PLEVLLR	KVG					
PIM1	189	S	-GFS	GVIRLLD	WFERPDS	<u>SVLIL</u>	ERPEPV	QDLDF	FITERGALQEELARS	FFWQV	LEAV				
PIM2	92	AGGG	HPGVIRLLD	WFETQ	EGFMLVLERPL	PAQDL	LDYITE	KGPLG	EGSP	RCCFFG	QVVA	IR			
PIM3	99	AAGG	ARGVIRLLD	WFERPD	GFLLV	LERPE	PAQDL	LDYITE	KGPLG	EGSP	RCCFFG	QVVA	IR		
PIM1	247	RHCH	NCGV	LHRDI	KDENILIDL	NRGEL	KLIDFG	SGALL	KDVTY	DFD	GRVY	SPPEW	IRY		
PIM2	152	QHCH	SRGV	VHRDI	KDENILIDL	RRGCA	KLIDFG	SGALL	HDE	PYTFD	GRVY	SPPEW	ISR		
PIM3	159	RHCH	SCGV	VHRDI	KDENLL	VDLR	SGEL	KLIDFG	SGALL	KDVTY	DFD	GRVY	SPPEW	IRY	
PIM1	307	HRYH	GRSA	AVWS	LGYLL	DMVCG	DIPFE	HDEE	IRGQ	VFFR	QRVS	SECQ	HLIR	WCLAL	LRP
PIM2	212	HQYH	ALPAT	VWSL	GILGYLL	DMVCG	DIPFER	DQEIL	EAEL	HFP	AHVSP	DCCAL	IR	RCLAP	KP
PIM3	219	HRYH	GRSAT	VWSL	GVLLY	DMVCG	DIPFE	QDEE	ILRG	LLFR	RRVS	SPECQ	QLIR	WCL	SLRP
PIM1	367	SDR	PTFEE	IQN	HPWM										
PIM2	272	SSR	PSLEE	ILL	DPWM										
PIM3	279	SER	PSLDQ	IAA	HPWM										

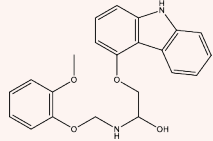
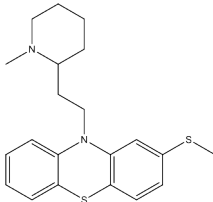
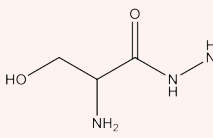
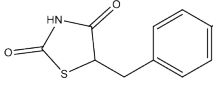
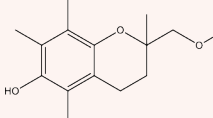
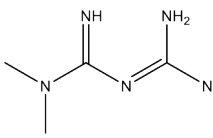
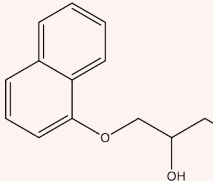
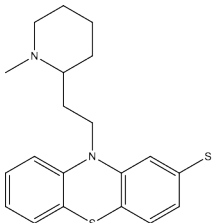
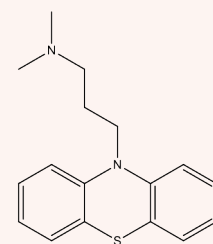
A



B

**Supplementary Figure S1: Sequence alignment of kinase domains and structure-based differences between PIM1 and PIM2.** (A) Sequence alignment of kinase domains of PIM1, PIM2 and PIM3, the differences are underlined with red background or words. The amino acids that form part of the ATP binding are marked with blue boxes; (B) The active site (yellow) of PIM2, LYS40, THR45, VAL62, LEU120 and ALA122 (red) are differences in the protein sequence. LYS61 and GLU117 (blue) are amino acids with conformational differences between PIM1 and PIM2, which influence the effect on PIM2 of PIM1 inhibitors with crystallographic structure.

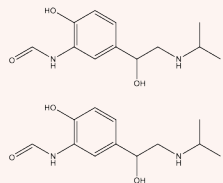
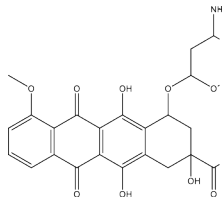
**Supplementary Table S1: The MTT assay of candidate small-molecule PIM inhibitors from Drugbank**

Number	Name	CAS NO.	Structure	Inhibitory ratio (%)
P1	Carvedilol	72956-09-3		51.77537144
P2	Lansoprazole	103577-45-3		22.66431629
P3	Benserazide hydrochloride	14919-77-8		10.12339461
P4	Rosiglitazone hydrochloride	302543-62-0		46.81440443
P5	Troglitazone	97322-87-7		6.925207756
P6	Metformin HCL	1115-70-4		11.20624528
P7	Propranolol Hydrochloride	318-98-9		3.878116343
P8	thioridazine hydrochloride	130-61-0		59.12868295
P9	Chlorpromazine	50-53-3		93.95618232

(Continued)

Number	Name	CAS NO.	Structure	Inhibitory ratio (%)
P10	Hydroxychloroquine sulfate	747-36-4		
P11	Primaquine diphosphate	63-45-6		39.56182322
P12	Ethambutol Hydrochloride	1070-11-7		10.75295895
P13	Lincomycin Hydrochloride	859-18-7		29.84134979
P14	cisapride	81098-60-4		38.10123395
P15	xantinol nicotinate	437-74-1		11.45807101
P16	Valaciclovir	124832-26-4		
P17	Fluoxetine hydrochloride	56296-78-7		12.36464367
P18	Flavoxate Hydrochloride	3717-88-2		-1.284311257

(Continued)

Number	Name	CAS NO.	Structure	Inhibitory ratio (%)
P19	Formoterol Fumarate	43229-80-7		0.138504155
P20	Daunorubicin hydrochloride	23541-50-6		91.26164694