

Table S1. Cell cycle distribution of A549 cells treated with QAs and controls.

Compound	G0/G1	S	G2/M
DMSO	81	7	12
250 nM QA ₁	11	4	85
250 nM QA ₂	12	7	81
250 nM QA ₃	10	6	84
100 nM colchicine	18	5	77
50 nM pironetin	17	7	76

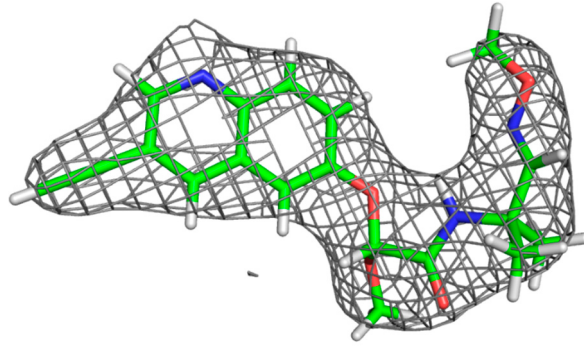
Values represent percentages (%).

Table S2. X-ray data collection and refinement statistics.

Data Collection ^a	
Wavelength, Å	1
Space group	P 21 21 21
Resolution range, Å	47.98 – 2.495 (2.584 – 2.495)
Unit cell a, b, c (Å) α , β , γ (°)	104.907 157.474 180.678 90 90 90
No. of observed reflections	1396075 (122343)
No. of unique reflections	104223 (9893)
Mean I/sigma (I)	13.94 (0.76)
R-merge	0.2069 (3.31)
R-meas	0.2151 (3.451)
CC1/2 ^b	0.998 (0.231)
CC *	0.999 (0.613)
Refinement	
R-work	0.2041 (0.3525)
R-free	0.2559 (0.3691)
Macromolecules	16643
Ligands	207
Protein residues	2089
RMS (bonds) (Å)	0.011
RMS (angles) (°)	1.11
Ramachandran favored (%) ^c	96
Ramachandran outliers (%) ^c	0.048
B-factors	
Average B-factor	72.02
Macromolecules	72.23
Ligands	66.22
Solvent	55.29

^a Highest resolution shell statistics are in parentheses. ^b As defined by Karplus and Diederichs (PMID: 22628654). ^c As defined by MolProbity (PMID: 15215462)

(a)



(b)

	1	10	20	30	40	50	60	70	80	90
Bos torus	MREIVHIQAG	QCG-NQIGAK	FWQVTSDEHG	IDPTGSYHGD	SDLQLERINV	YYNEATGNKY	VPRAILVDLE	PGTMDSVRS	PFGQIFRPDN	
Erysiphe necator	MREIVHLQTG	QCG-NQIGAA	FWQVTSDEHG	LDGSGVYNGT	SDLQLERTNV	YFNEASGNKY	VPRAVLVDLE	PGTMDAVRAG	PFGQLFRPDN	
Pythium ultimum	MRELVHIQGG	QCG-NQIGAK	FWQVTSDEHG	VDPTGSYHGD	SDLQLERINV	YYNEATGGRY	VPRAILMDLE	PGTMDSVRAG	PFGQLFRPDN	
Zymoseptoria tritici	MREIVHLQTG	QCVSNQIGAA	FWQVTSDEHG	LDGSGVYNGT	SDLQLERMNV	YFNEASGNKY	VPRAVLVDLE	PGTMDAVRAG	PFGQLFRPDN	
Phytophthora infestans	MRELVHIQGG	QCG-NQIGAK	FWQVTSDEHG	VDPTGSYHGD	SDLQLERINV	YYNEATGGRY	VPRAILMDLE	PGTMDSVRAG	PFGQLFRPDN	
	★					★				
	100	110	120	130	140	150	160	170	180	
Bos torus	FVFGQSGAGN	NWAKGHYTEG	AELVDSVLVDV	VRKEESGDCD	LQGFQITHSL	GGGTGSGMGT	LLISKIREFY	PDRIMNTFSV	MPSPKVS DTV	
Erysiphe necator	FVFGQSGAGN	NWAKGHYTEG	AELVDQVLVDV	VRKEAEGDCD	LQGFQITHSL	GGGTGAGMGT	LLISKIREEF	PDRMMATFSV	VPSPKVS DTV	
Pythium ultimum	FVFGQSGAGN	NWAKGHYTEG	AELIDSVLVDV	ARKEAEGDCD	LQGFQITHSL	GGGTGSGMGT	LLISKIREFY	PDRIMCTYSV	CPSPKVS DTV	
Zymoseptoria tritici	FVFGQSGAGN	NWAKGHYTEG	AELVDQVLVDV	VRKEAEGDCD	LQGFQITHSL	GGGTGAGMGT	LLISKIREEF	PDRMMATFSV	MPSPKVS DTV	
Phytophthora infestans	FVFGQSGAGN	NWAKGHYTEG	AELIDSVLVDV	VRKEAEGDCD	LQGFQITHSL	GGGTGSGMGT	LLISKIREFY	PDRIMCTYSV	CPSPKVS DTV	
					★			★		
	190	200	210	220	230	240	250	260	270	
Bos torus	VEPYNATLSV	HQLVENTDET	YCIDNEALYD	ICFRTLKLTT	PTYGDLNHLV	SATMSGVITTC	LRFPQGLNAD	LRKLAVNMVP	FPRLHFFMPG	
Erysiphe necator	VEPYNATLSV	HQLVENSDET	FCIDNEALYE	ICMRTLKLSN	PSYGDLNHLV	SAVMSGVITTC	LRFPQGLNSD	LRKLAVNMVP	FPRLHFFMVG	
Pythium ultimum	VEPYNATLSV	HQLVENADEV	MCLDNEALYD	ICFRTLKLTT	PTYGDLNHLV	CAAMSGITTC	LRFPQGLNSD	LRKLAVNLIP	FPRLHFFMIG	
Zymoseptoria tritici	VEPYNATLSV	HQLVENSDET	FCIDNEALYD	ICMRTLKLSN	PSYGDLNHLV	SAVMSGVITTC	LRFPQGLNSD	LRKLAVNMVP	FPRLHFFMVG	
Phytophthora infestans	VEPYNATLSV	HQLVENADEV	MCLDNEALYD	ICFRTLKLTT	PTYGDLNHLV	CAAMSGITTC	LRFPQGLNSD	LRKLAVNLIP	FPRLHFFMIG	
		★	★			★	★	★	★	★
	280	290	300	310	320	330	340	350	360	
Bos torus	FAPLTSRGSQ	QYRALTVPEL	TQQMFDSKNM	MAACDPRHGR	YLTVAAILFRG	RMSMKEVDEQ	MLNVQNKNS	YFVEWIPNNV	KTAVCDIPPR	
Erysiphe necator	FAPLTSRGAH	SFRAVTPEL	TQQMYDPKNM	MAASDFRNGR	YLTCSAIFRG	KVSMKEVDEQ	MRNVQNKNS	YFVEWIPNNV	QTALCSIPPR	
Pythium ultimum	FAPLTSRGSQ	QYRALTVPEL	TQQQFDAKNM	MCAADPRHGR	YLTAAACMFRG	RMSTKEVDEQ	MLNVQNKNS	YFVEWIPNNI	KASVCDIPPK	
Zymoseptoria tritici	FAPLTSRGAH	SFRAVTPEL	TQQIFDPKNM	MAASDFRNGR	YLTCSAIFRG	KVSMKEVDEQ	IRNVQNKNTA	YFVEWIPNNV	QTALCSIPPR	
Phytophthora infestans	FAPLTSRGSQ	QYRALTVPEL	TQQQFDAKNM	MCAADPRHGR	YLTAAACMFRG	RMSTKEVDEQ	MLNVQNKNS	YFVEWIPNNI	KASVCDIPPK	
					★				★	★
	370	380	390	400	410	420	430	440	448	
Bos torus	GLKMSATFIG	NSTAIQELFK	RISQFTAMF	RRKAFLHWYT	GEGMDEMEFT	EAESNMNDLV	SEYQQYQDAT	ADEQGE-FEE	EEGEDEA	
Erysiphe necator	GLKMSSTFVG	NSTSIQELFK	RVGDQFTAMF	RRKAFLHWYT	GEGMDEMEFT	EAESNMNDLV	HEYQQYQDAS	ISEGEEDYEE	EPQVENEE	
Pythium ultimum	GLKMSSTFVG	NSTAIQEMFK	RVSEQFTAMF	RRKAFLHWYT	GEGMDEMEFT	EAESNMNDLV	SEYQQYQDAT	AEEEGE-FDE	DEEMDEM	
Zymoseptoria tritici	GLKMSSTFVG	NSTSIQELFK	RVGDQFSAMF	RRKAFLHWYT	GEGMDEMEFT	EAESNMNDLV	SEYQQYQDAS	VSDAEEYDE	EAPLEGEE	
Phytophthora infestans	GLKMSSTFIG	NSTAIQEMFK	RVSEQFTAMF	RRKAFLHWYT	GEGMDEMEFT	EAESNMNDLV	SEYQQYQDAT	AEEEGE-FDE	DEEMDEM	
		★								

Figure S1. Electron density map and multiple sequence alignment. (a) Electron density map showing fitting of QA1 in the electron density; (b) Multiple sequence alignment of mammalian beta-tubulin with beta-tubulin from important fungal phytopathogens. Amino acid residues involved in QA1 are highlighted by black stars.