Table S1. A summary of transcriptomic pre-processing

Sample		Raw		Trimming			Mapping	
		reads	GC (%)	Clean reads	GC (%)	Rate (%)	Uniquely mapped read rate (%)	Overall alignment rate (%)
Control	1	32,037,606	48, 47	31,832,325	47	99	86.90	98.14
	2	30,138,785	48, 47	29,956,656	47	99	86.90	98.19
	3	38,342,983	48	38,094,731	48	99	86.17	98.24
	4	36,457,769	48	36,228,390	48	99	86.92	98.09
BA (3 μg/mL)	1	37,369,090	48	37,133,398	48	99	86.60	98.19
	2	35,330,686	48	35,100,432	48	99	87.17	98.16
	3	37,290,950	48, 47	37,055,387	47	99	87.30	98.15
	4	35,386,985	48	35,189,457	48	99	86.08	98.33
Mean		35,294,357	48	35,073,847	48	99	86.76	98.19

GC, guanine-cytosine content; BA, betulinic acid.

Table S2. Docking scores of ligands [betulinic acid, positive controls, and DMSO (negative control)] binding binding to IR and IGF1R kinase domains

Target proteins	**IR**				**IGF1R**	
PDB ID	**1IR3**		**3ETA**		**5E1S**	
Ligands	**Score (kcal/mol)**	**RMSD (Å)**	**Score (kcal/mol)**	**RMSD (Å)**	**Score (kcal/mol)**	**RMSD (Å)**
Betulinic acid	-7.26±0.27	7.06±10.14	-7.43±0.28	11.19±11.84	-6.98±0.43	9.46±7.90
Positive controls	-7.63±2.52 (351)	2.64±1.13 (351)	-7.78±0.29 (351)	5.06±8.95 (351)	-7.73±0.40 (BI885578)	3.35±1.74 (BI885578)
	-8.22±0.25 (ANP)	1.61±0.78 (ANP)	-6.40±0.26 (ANP)	19.14±12.69 (ANP)		
DMSO	-2.27±0.16	20.73±10.78	-2.32±0.15	12.71±10.93	-2.18±0.14	14.658±10.67

Root-mean-square deviation (RMSD) values for re-docked co-crystal ligand conformers were calculated to validate the docking process. IR, insulin receptor; IGF1R, insulin-like growth factor 1 receptor.