ACCSCIENCE PUBLISHING

Gene & Protein in Disease

ORIGINAL RESEARCH ARTICLE

Analysis of multi-disease targeting effect of phytochemicals by ampk stimulation– diabetes: A computational approach

Supplementary File

Supplementary Table S1. Molecular docking analysis of binding energy, distance between ligand and target, and the type of molecular interaction between control drugs and active compound of *C. roseus* against AMPK1

Compounds	Vina score (kcal/mol)	Ligand	Distance (Å)	Target protein	Category	Type of interaction
AMPK1-Metformin	−4.0	UNL1:H	2.45	A: LEU200:O	Hydrogen bond	Conventional H-bond
		UNL1:HN2	2.20	A: LEU200:O	Hydrogen bond	Conventional H-bond
		UNL1:N	5.57	A: GLU205:OE2	Electrostatic attraction	Attractive charge interaction
		UNL1:N	4.27	A: GLU205:OE2	Electrostatic attraction	Attractive charge interaction
		UNL1:N	3.95	A: GLU205:OE2	Electrostatic attraction	Attractive charge interaction
		UNL1:N	3.06	A: GLU194:OE2	Electrostatic attraction	Attractive charge interaction
		UNL1:N	4.79	A: GLU194:OE2	Electrostatic attraction	Attractive charge interaction
		UNL1:N	2.96	A: GLU194:OE2	Electrostatic attraction	Attractive charge interaction
		UNL1:H	1.84	A: GLU205:OE2	Electrostatic attraction	Salt Bridge; Attractive charge
		UNL1:N	4.16	A: PHE180	Non-covalent molecular interaction	Pi-cation interaction
		UNL1:N	4.91	A: PHE180	Non-covalent molecular interaction	Pi-cation interaction
		UNL1:H	2.55	A: ALA202:HN	*Intrinsic interactions*	Unfavorable donor-donor
AMPK1-Vindolinine	−7.4	UNL1:O	2.66	A: ARG182:HH21	Hydrogen bond	Conventional H-bond
		UNL1:O	3.08	A: ARG182:HE	Hydrogen bond	Conventional H-bond
		UNL1:H	2.20	A: LEU462:O	Hydrogen bond	Conventional H-bond
		UNL1	5.39	A: LEU462	Hydrophobic	Pi-alkyl interaction
		UNL1:C	5.14	A: TYR 463	Hydrophobic	Pi-alkyl interaction
		UNL1	4.13	A: TYR 441	Hydrophobic	Pi-pi stacked interaction
		UNL1:N	3.97	A: ARG182:NH2	*Intrinsic interactions*	Unfavorable positive-positive
AMPK1-Vindoline	−6.3	UNL1:O	2.31	A: ARG182:HH22	Hydrogen bond	Conventional H-bond
		UNL1:NH	2.30	A: LEU462:O	Hydrogen bond	Conventional H-bond
		UNL1:C	3.62	A: GLY198:O	Hydrogen bond	Carbon H-bond interaction
		UNL1:C	3.59	A: GLY198:O	Hydrogen bond	Carbon H-bond interaction
		UNL1:C	3.56	A: GLN461:OE1	Hydrogen bond	Carbon H-bond interaction
		UNL1	5.20	A: LEU200	Hydrophobic	Alkyl interaction
		UNL1	5.47	A: TYR463	Hydrophobic	Pi-alkyl interaction
AMPK1-(+) Vindorosine (CID: 261578)	−6.3	UNL1:H	2.08	UNL1:O	Hydrogen bond	Conventional H-bond
		UNL1:C	3.5	A: PHE180	Hydrophobic	Pi-sigma interaction
		UNL1:C	4.48	A: PHE180	Hydrophobic	Pi-alkyl interaction
		UNL1:C	4.61	A: LEU200	Hydrophobic	Alkyl interaction

(Cont'd...)

Supplementary Table S1. ***(Continued)***

Compounds	Vina score (kcal/mol)	Ligand	Distance (Å)	Target protein	Category	Type of interaction
AMPK1-Cr-1 (CID: 5315746)	−6.4	UNL1:H	1.95	A: GLY198:O	Hydrogen bond	Conventional H-bond
		UNL1:O	2.57	A: ARG 182:HH12	Hydrogen bond	Conventional H-bond
		UNL1:C	3.54	A: SER 197:O	Hydrogen bond	Carbon H-bond interaction
		UNL1:C	3.67	A: GLY198:O	Hydrogen bond	Carbon H-bond interaction
		UNL1:C	3.37	A: GLN464:O	Hydrogen bond	Carbon H-bond interaction
		UNL1:C	3.69	UNL1	Hydrophobic	Pi-sigma interaction
		UNL1:C	4.42	A: ARG199	Hydrophobic	Alkyl interaction
		UNL1:C	4.44	A: LEU200	Hydrophobic	Alkyl interaction
		UNL1:N	4.11	A: ARG199:NH1	*Intrinsic interactions*	Unfavorable positive-positive
AMPK1- Cr-2 (CID: 59908094)	−6.1	UNL1:C	3.51	A: TYR463	Hydrophobic	Pi-sigma interaction
		UNL1:C	3.55	A: PHE180	Hydrophobic	Pi-sigma interaction
		UNL1:C	4.25	A: TYR463	Hydrophobic	Pi-alkyl interaction
		UNL1:C	5.28	A: LEU200	Hydrophobic	Alkyl interaction

Abbreviations: UNL: *C. roseus* active compounds; LEU: Leucine; GLU: Glutamic acid; PHE: Phenylalanine; ALA: Alanine; ARG: Arginine; GLY: Glycine; GLN: Glutamine; TYR: Tyrosine; VAL: Valine; SER: Serine; *C. roseus*: *Catharanthus roseus*

Supplementary Table S2. Molecular docking analysis of binding energy, distance between ligand and target, and the type of molecular interaction between control drugs and active compound of *C. roseus* against AMPK2

Docking compounds	Vina score (kcal/mol)	Ligand	Distance (Å)	Target protein	Category	Type of interaction
AMPK2-Metformin	−4.2	UNL1:HN	2.33	A: ASP261:O	Hydrogen bond	Conventional H-bond
		UNL1:H	2.11	A: ASP261:O	Hydrogen bond	Conventional H-bond
		UNL1:HN2	2.40	A: HIS247:ND1	Hydrogen bond	Conventional H-bond
		UNL1:H	2.40	A: THR243:O	Hydrogen bond	Conventional H-bond
		UNL1:C	3.54	A: ASP261:OD1	Hydrogen bond	Carbon H-bond
		UNL1:N	4.45	A: ASP261:OD1	Electrostatic attraction	Attractive charge
		UNL1:N	5.18	A: ASP261:OD1	Electrostatic attraction	Attractive charge
AMPK2-Vindoline	−6.2	UNL1:O	2.21	A: ARG263:HH21	Hydrogen bond	Conventional H-bond
		UNL1:O	2.29	A: ARG263:HH21	Hydrogen bond	Conventional H-bond
		UNL1:O	2.62	A: LYS260:HA	Hydrogen bond	Carbon H-bond
		UNL1:O	2.80	A: ARG263:HD2	Hydrogen bond	Carbon H-bond
		UNL1:C	5.22	A: LEU272	Hydrophobic	Alkyl interaction
		UNL1:C	3.87	A: ARG263	Hydrophobic	Alkyl interaction
		UNL1:N	5.36	A: GLU279:OE2	Electrostatic attraction	Attractive charge
		UNL1:O	2.97	A: ASP280:OD1	*Intrinsic interactions*	Unfavorable acceptor-acceptor
AMPK2-Vindolinine	−5.6	UNL1:C	3.45	A: GLU264:OE2	Hydrogen bond	Carbon H-bond
		UNL1:N	4.77	A: GLU264:OE2	Electrostatic attraction	Attractive charge
		UNL1:N	5.16	A: ASP280:OD1	Electrostatic attraction	Attractive charge
		UNL1	3.95	A: ASP280:OD1	Non-covalent molecular interaction	Pi-anion interaction
		UNL1	3.97	A: LYS269:NZ	Non-covalent molecular interaction	Pi-cation interaction
		UNL1	5.36	A: ARG263	Hydrophobic	Pi-alkyl interaction

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Supplementary Table S2. ***(Continued)***

Docking compounds	Vina score (kcal/mol)	Ligand	Distance (Å)	Target protein	Category	Type of interaction
AMPK2-(+) Vindorosin (CID: 261578)	−5.6	UNL1:O	2.10	A: ARG263:HE	Hydrogen bond	Conventional H-bond
		UNL1:O	2.41	A: ARG263:HH21	Hydrogen bond	Conventional H-bond
		UNL1:O	3.0	A: ARG263:HH22	Hydrogen bond	Conventional H-bond
		UNL1:C	3.65	A: GLU264:OE2	Hydrogen bond	Carbon H-bond
		UNL1:C	4.17	A: LYS260	Hydrophobic	Alkyl interaction
		UNL1:C	3.77	A: LYS260	Hydrophobic	Alkyl interaction
		UNL1:N	4.62	A: GLU264:OE2	Electrostatic attraction	Attractive charge
		UNL1	3.86	A: GLU279:OE2	Non-covalent molecular interaction	Pi-anion interaction
AMPK2-CR-1 (CID: 5315746)	−5.3	UNL1:O	2.63	A: ARG263:HH21	Hydrogen bond	Conventional H-bond
		UNL1:O	2.32	A: ARG263:HE	Hydrogen bond	Conventional H-bond
		UNL1:N	4.92	A: GLU264:OE2	Electrostatic attraction	Attractive Charge
		UNL1:N	4.78	A: GLU279:OE2	Electrostatic attraction	Attractive Charge
		UNL1:C	4.13	A: ARG263	Hydrophobic	Alkyl interaction
		UNL1:C	4.21	A: LYS260	Hydrophobic	Alkyl interaction
		UNL1:C	3.73	UNL1	Hydrophobic	Pi-sigma interaction
AMPK2-CR-2 (CID: 59908094)	−5.3	UNL1:H	3.01	UNL1:O	Hydrogen bond	Conventional H-bond
		UNL1:O	2.30	A: LYS260:HZ3	Hydrogen bond	Conventional H-bond
		UNL1:C	3.73	A: GLU264:OE2	Hydrogen bond	Carbon H-bond
		UNL1:C	3.71	A: LYS260:O	Hydrogen bond	Carbon H-bond
		UNL1:N	3.45	A: GLU279:OE1	Electrostatic attraction	Attractive charge
		UNL1:N	3.81	A: LYS260:NZ	*Intrinsic interactions*	Unfavorable positive-positive

Abbreviations: UNL: *C. roseus* active compounds; ASP: Aspartic acid; HIS: Histidine; THR: Threonine; ARG: Arginine; LYS: Lysine; LEU: Leucine; GLU: Glutamic acid; *C. roseus*: *Catharanthus roseus*