

Supplementary Materials: Computational Approaches for the Discovery of Human Proteasome Inhibitors: An Overview

Romina A. Guedes ¹, Patrícia Serra ¹, Jorge A. R. Salvador ^{2,3} and Rita C. Guedes ^{1,*}

Table S1. Computational studies on the field of proteasome inhibitors.

Reference	Software	PDB ID	Active site	Database/compound(s) studied
Kazi <i>et al.</i> [1]	Autodock	1JD2	β_5	Genistein
Smith <i>et al.</i> [2]	Autodock	1JD2	β_5	(-)EGCG
Rydzewski <i>et al.</i> [3]	MOE	1IRU	β_5	Vinyl sulfones
Yang <i>et al.</i> [4]	Autodock	1JD2	β_5	Pristimerin
Milacic <i>et al.</i> [5]	Autodock	1JD2	β_5	Curcumin
Leban <i>et al.</i> [6]	ProPose	1IRU	β_5	Peptide-semicarbazones
Zhang <i>et al.</i> [7]	GOLD	Crystal structures of MG101-proteasome complex		MG132
Basse <i>et al.</i> [8]	MD: Amber (Divcon and Antechamber modules – determination of partial atomic charges)		β_5	Chembridge compound collection (~300000 molecules)
Zhu <i>et al.</i> [9]	GOLD	2F16	β_5	Dipeptidyl boronic acids
Kanwar <i>et al.</i> [10] (Smith <i>et al.</i> [2])	AutoDock	1JD2	β_5	Catechol-O-methyltransferase-resistant EGCG analogs
Shi <i>et al.</i> [11]	AutoDock	Eukaryotic yeast proteasome		Organotin compounds (butyltins and phenyltins)
Bonfili <i>et al.</i> [12]	InsightII	1IRU		EGCG oxidation derivative
Ma <i>et al.</i> [13]	GOLD	Yeast proteasome:MG101 complex		Peptide aldehyde derivatives

Table S1. *Cont.*

Reference	Software	PDB ID	Active site	Database/compound(s) studied
Xu <i>et al.</i> [14]			β_5	Naphthoquinone derivatives
Pham <i>et al.</i> [15]		1IRU	β_1, β_2 and β_5	Cerpegin derivatives
Santoro <i>et al.</i> [16]	AutoDock Vina	2F16	β_5	Cationic and anionic porphyrins
Hovhannisyany <i>et al.</i> [17]	AutoDock	1IRU	β_5	Cerpegin derivatives
Maréchal <i>et al.</i> [18]	MS-Dock, LigandFit and Surflex.	Constitutive 20S proteasome	β_5	ChemBridge compound collection
(same procedure as Basse <i>et al.</i> [8])				
Jiang <i>et al.</i> [19]	AutoDock Vina	2F16	β_1, β_2 and β_5	Marchantin M
Orabi <i>et al.</i> [20]	Surflex-Dock interfaced with SYBYL-X	1R0P and 1JD2	β_1, β_2 and β_5	TMC-95A, bortezomib and syringic acid derivatives
Zuo <i>et al.</i> [21]	GLIDE	2F16 and 1JD2		Amino acid Schiff base copper complexes; bortezomib as control
Bordessa <i>et al.</i> [22]	GOLD	1IRU	β_5	Library of pseudopeptides
Kawamura <i>et al.</i> [23]	Glide	3GPT	β_5	Salinosporamide A derivatives
Li <i>et al.</i> [24]	Ph4 SB LigandScout Noncovalent docking: LibDock Covalent docking: GOLD MD: Desmond software ADME: QikProp	3UNB	β_5	Epoxyketones
Hasegawa <i>et al.</i> [25]	MD: Chem3D MOE	3UNB 3UNB 3UNB —	β_1, β_2 and β_5	Tamoxifen derivatives (RID-A – RID-H) Ridaifen-F derivatives
Scarbaci <i>et al.</i> [26]	ASEDock GOLD	3D29 2F16	β_5	Peptidomimetic boronates

Table S1. *Cont.*

Reference	Software	PDB ID	Active site	Database/compound(s) studied
Troiano et. al. [27]	GOLD	2F16	β_5	Pseudopeptide boronates
Voss et al. [28]	MOE	4R02	β_5	α -Keto phenylamides
Miller et al. [29]	FRED		β_5	345 447 compounds included in the University of Cincinnati library
			β_5	Non-peptide, reversible proteasome inhibitor with a pyrazole scaffold
Scotti et al. [30]	MM-PBSA and MM-GBSA MD: semi-empirical PM3 calculations MOE	1G65 (for β_1) 4LQI (for β_5)	β_1 β_5	Naphthoquinone dipeptide derivatives Naphthoquinone dipeptide derivatives
Xu et al. [31]	Discovery Studio, Ligandfit protocol,	3SDK	β_5	Linear peptide
Pundir et al. [32]	MOE	2F16 and 1IRU	β_1 , β_2 and β_5	4-piperazinylquinoline scaffold and a sulfonyl pharmacophore
Sun et al. [33]	AutoDock MD: Sander module (AMBER 11) Ab initio: Gaussian	4NO8	β_5	Furan-based peptides (dipeptidic and tripeptidic inhibitors)
		4NO8	β_5	Tripeptide derivative (furan-based)

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