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Research Article

Molecular docking analysis of Bcl-2 with phytocompounds

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Abstract:

The Bcl-2 protein is liked in several cancers and drug resistance to therapy is also known in this context. There are many Bcl-2 inhibitors under clinical trials. It is of further interest to design new Bcl2 inhibitors from phyto compounds such as artesunate, bruceantin, maytansin, Salvicine, indicine N-oxide, kamebanin and oxyacanthine. We report the optimal binding features of these compounds with Bcl-2 for further consideration towards *in vitro* and *in vivo* validation.

Keywords: Breast cancer, bioactive compounds, Bcl-2, molecular docking

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Background:

Cancer related issues **[1-6]** are linked to the BCL-2 family of proteins **[7-12]**. BCL-2 is a known cancer target with several potential inhibitors under validation. Therefore, it is of interest to design and develop new compounds from plant source with improved binding features with the BCL-2 protein. Hence, we report the molecular docking analysis of Bcl-2 with phytocompounds.

Methodology:

BCL-2 structure:

The structure data of Bcl-2 protein (PDB ID: 2W3L) was downloaded from the protein databank (PDB) **[13]** and processed for further analysis.

Ligand data:

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6

7

The structures of phytocompounds such as artesunate, bruceantin, maytansin, Salvicine, indicine N-oxide, kamebanin, and oxyacanthine were downloaded from the pubchem database in SDF format and converted to PDB format using the Online Smiles Translator.

Active site prediction:

Bruceantin

Maytansin

Kamebanin

Oxvacanthine

Indicine N-oxide

Salvicine

Binding site prediction of Bcl-2 was completed using MetaPocket 2.0 server [14].

Molecular docking:

PatchDock **[15, 16]** was used for the molecular docking analysis of BCL-2 with phytocompounds such as artesunate, bruceantin, maytansin, Salvicine, indicine N-oxide, kamebanin and oxyacanthine.

Results and Discussion:

BCL2 is a known cancer target. Therefore, it is of interest to design new Bcl2 inhibitors from phyto compounds such as artesunate, bruceantin, maytansin, Salvicine, indicine N-oxide, kamebanin and oxyacanthine. The predicted active site residues in BCL-2 are LYS 22, GLN 25, ARG 26, THR 55, ASP 62, SER 64, ARG 66, TYR 67, ARG 68, PHE 71, LEU 80, ARG 86, ASN 102, GLY 104, VAL 107 and GLU 111. The molecular docking analysis data of Bcl-2 with the phyto-compounds are given in **Table 1**. Detailed interaction between BCL-2 and the compounds are shown in **Figure 1**. The residues ARG 26, ARG 68, ARG 66, SER 64, ARG 86, ARG 68, GLY 104, LYS 22, SER 20, ASN 34, LYS 22, LYS 270, SER 351, ARG 469, and LYS 345 are found to be interacting with the phyto compounds (**Figure 1**). Thus, we report the optimal binding features of these compounds with Bcl-2 for further consideration towards *in vitro* and *in vivo* validation.

Conclusion:

No of

67

102

131

37

40

31

3.24

3.3

3.34

2.04

2.17

2.47

1.75

1.95

3.08

2 7 9

non-bonded interaction 148

We report compounds with improved binding features with Bcl-2 for further consideration towards *in vitro* and *in vivo* analysis.

S. No	Compound Name	Score (kcal/mol)	ACE	Hydrogen bonds	Bond length
1	Artesunate	4814	-211.33	ARG 26- NH-O	2.46

-104.71

-110.4

-126.9

-130.62

-140.03

-102

ARG 68-NE-O

SER 64 OG-O

ARG 86 NE-O

ARG 68 NE-O

GLY 104 N-O

LYS 22 NZ-O

SER 64 OG-O

ARG 66 NE-O

ARG 26 NH2-O

ARG 66- NH2-O

Table 1: Molecular docking analysis of Bcl-2 with phyto-compounds

5714

773.1

4946

4226

4002

6368

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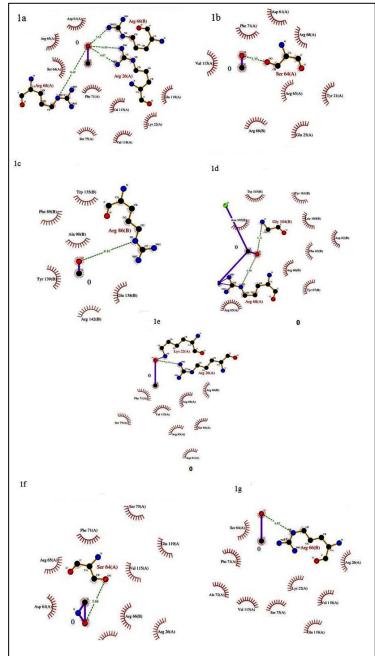


Figure 1: Interaction of BcI-2 and (a) artesunate; (b) bruceantin; (c) maytansin; (d) salvicine; (e) indicine N-oxide; (f) kamebanin and (g) oxyacanthine is shown using ligplot.

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