Electronic Supplementary Material (ESI) for Molecular Systems Design & Engineering.

Supplementary materials

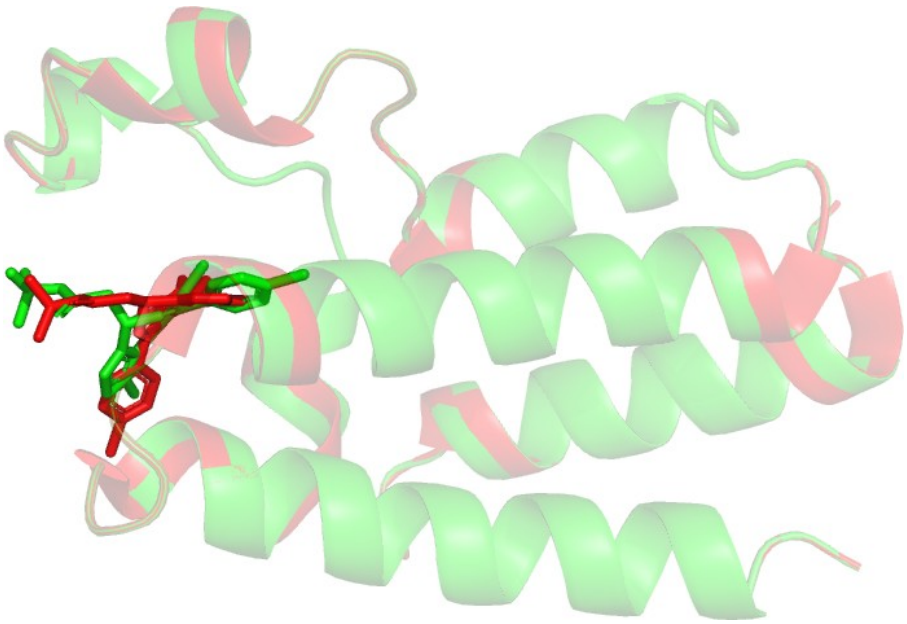

Fig. S1. Conformations of experimental complex (JQ-1 in green) and re-docked complex (JQ-1 in red).

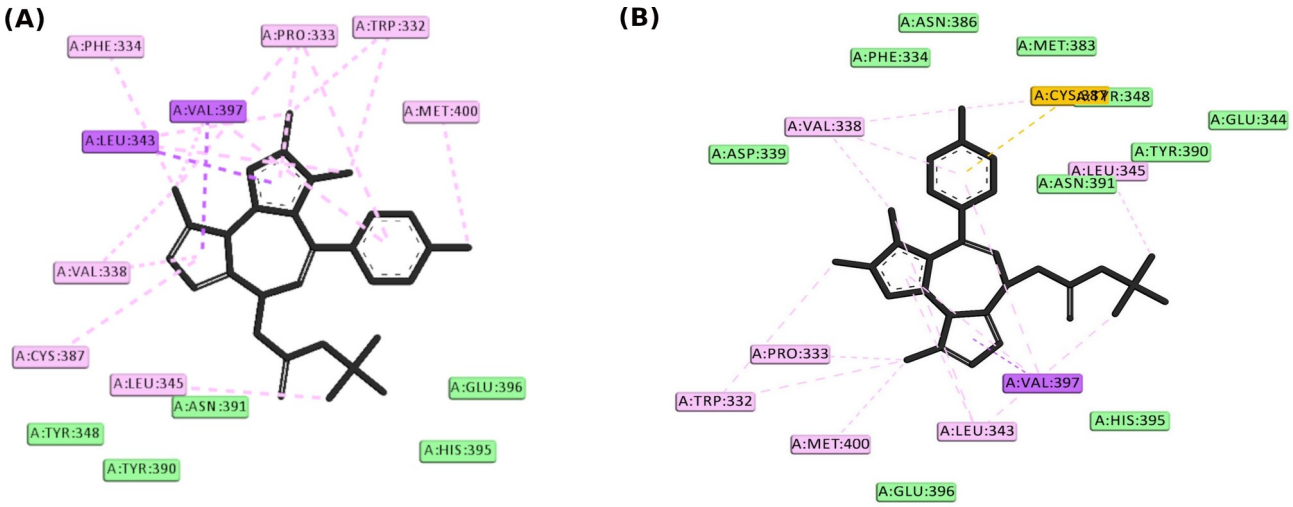

Fig. S2. 2D interaction of experimentally co-crystallized molecule (JQ-1) **(A)** and re-docked JQ-1 **(B)**.

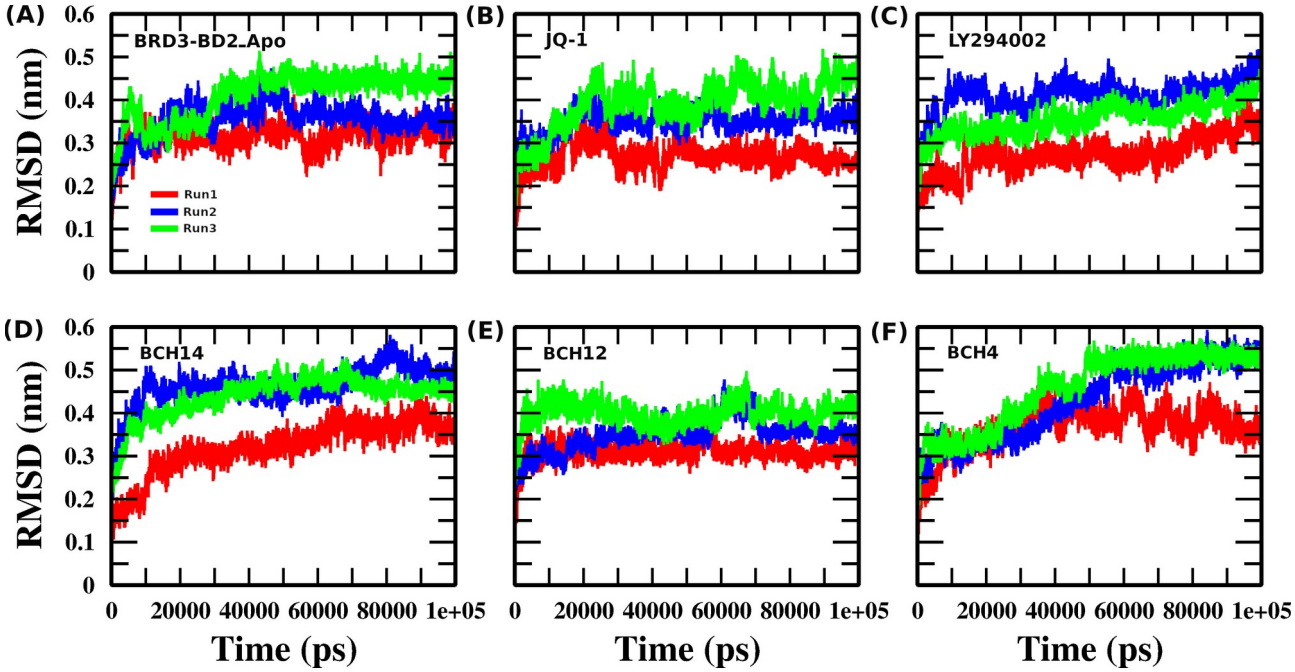

Fig. S3. RMSD trajectories of BRD3-BD2_Apo and selected complexes in triplicates; run1 (red), run2 (blue) and run3 (green) **(A)** BRD3-BD2-Apo, **(B)** JQ-1, **(C)** LY294002, **(D)** BCH14, **(E)** BCH12, and **(F)** BCH4.

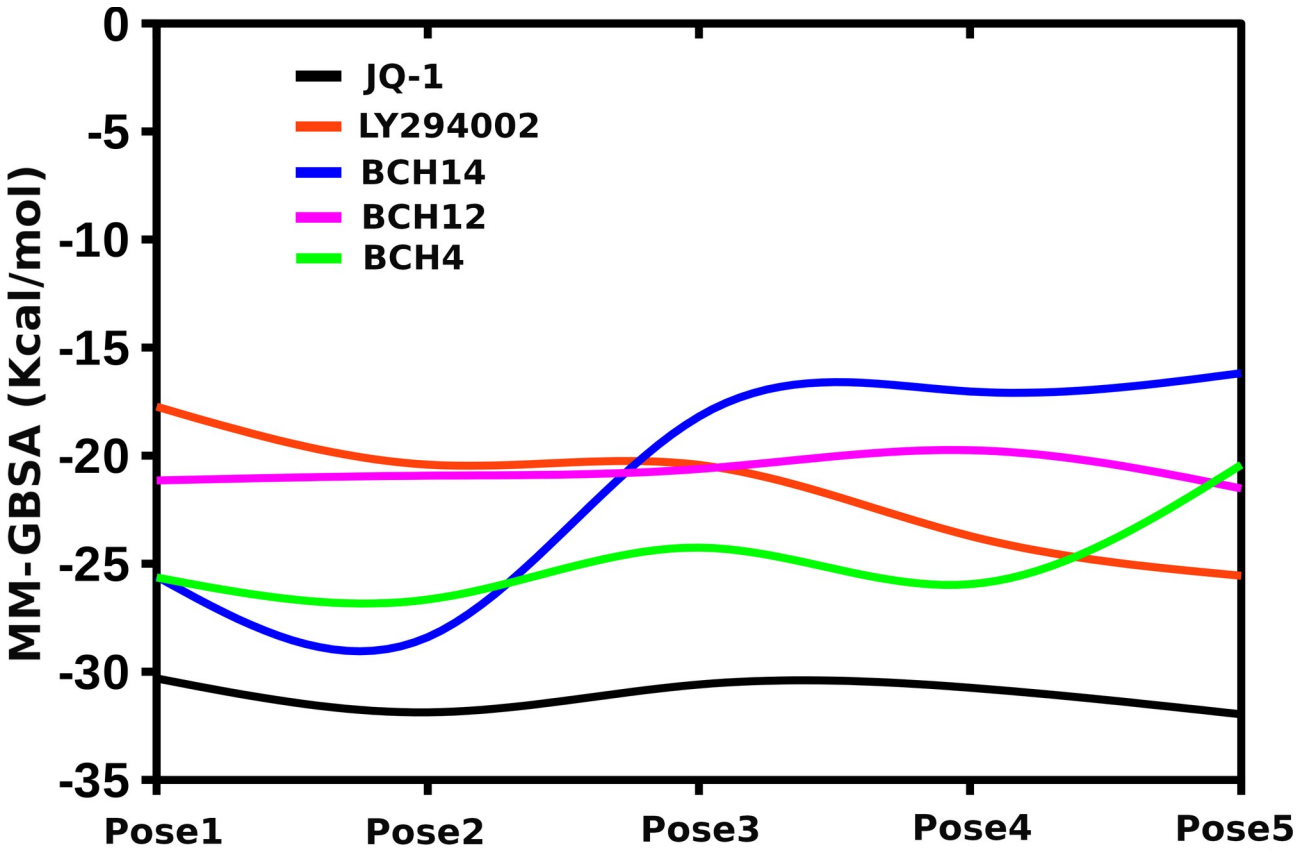

Fig. S4. Radius of gyration analysis; JQ-1 (black), LY294002 (red), BCH14 (blue), BCH12 (magenta) and BCH4 (green).

Table S1. CDOCKER interaction energy of selected seventeen BCH molecules and two reference inhibitors (JQ-1 and LY294002).

S. No.	Molecules	CDOCKER interaction energy
1.	BCH1	-33.32
2.	BCH2	-31.61
3.	BCH3	-31.98
4.	**BCH4**	**-48.72**
5.	BCH5	-40.62
6.	BCH6	-37.55
7.	BCH7	-34.39
8.	BCH8	-40.60
9.	BCH9	-37.34
10.	BCH10	-36.96
11.	BCH11	-35.89
12.	**BCH12**	**-48.78**
13.	BCH13	-31.30
14.	**BCH14**	**-48.14**
15.	BCH15	-40.04
16.	BCH16	-37.03
17.	BCH17	-32.00
18.	**JQ-1**	**-41.27**
19.	**LY294002**	**-32.27**

Table S2. Interaction analysis of JQ-1, LY294002, BCH4, BCH12 and BCH14 complexes.

Complexes	Hydrogen bond	π-sigma interaction	π-anion interaction	π-π T-shaped interaction	π-alkyl interaction	Hydrophobic interactions
JQ-1	-	Val397	Cys387	-	Trp332, Pro333, Val338, Leu343, Leu345, Met400	Phe334, Asp339, Glu344, Tyr348, Met383, Asn386, Tyr390, Asn391, His395, Glu396
LY294002	-	-	-	-	Pro333, Val338, Leu343, Cys387, Val397	Trp332, Phe334, Leu345, Tyr348, Try390, Asn391, His395, Glu396
BCH4	Pro333, Lys336	-	Cys387	Trp332	Phe334, Val338, Leu343, His395, Val397, Met400	Tyr335, Pro337, Leu345, Tyr348, Met383, Asn386, Tyr390, Asn391, Glu396
BCH12	Leu343, Cys387	-	-	Trp332	Phe333, Lys336, Val338, Leu345, Tyr348, Tyr390, His395, Val397	Phe334, Tyr335, Pro337, Asp339, Asn386, Asn391, Leu396
BCH14	-	-	Cys387	Trp332	Pro333, Val338, Leu343, His395, Val397, Met400	Phe334, Tyr335, Lys336, Pro337, Leu345, Tyr348, Met383, Asn386, Tyr390, Asn391, Glu396,

Table. S3. Average RMSD values of BRD3-BD2_Apo, JQ-1, LY294002, BCH4, BCH12 and BCH14 systems.

Complexes	**Average RMSD (**nm)
BRD3-BD2_Apo	0.315 nm
JQ-1	0.278 nm
LY294002	0.274 nm
BCH4	0.319 nm
BCH12	0.299 nm
BCH14	0.364 nm

Table S4. Highest RMSF peak value of ZA-loop, αA and αB regions.

Complexes	Highest RMSF peak value of ZA-loop region (336-352 residue)	Highest RMSF peak value of αA, and αB regions (363-367, and 372-380 residue)
BRD3-BD2_Apo	0.36 nm	0.40 nm
JQ-1	0.58 nm	0.45 nm
LY294002	0.41 nm	0.42 nm
BCH4	0.41 nm	0.45 nm
BCH12	0.40 nm	0.28 nm
BCH14	0.41 nm	0.45 nm

Table. S5. Cluster RMSD of backbone Cα atoms of selected systems.

Complexes	**Average RMSD (**nm)	**clusters**
BRD3-BD2_Apo	0.200419	51
JQ-1	0.185601	51
LY294002	0.198332	51
BCH4	0.19081	51
BCH12	0.175217	48
BCH14	0.203788	51