Electronic Supplementary Material (ESI) for Molecular BioSystems.

Structural identification of HER2 receptor model binding pocket to optimize lead compounds: a combined experimental and computational approach

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Supporting Information

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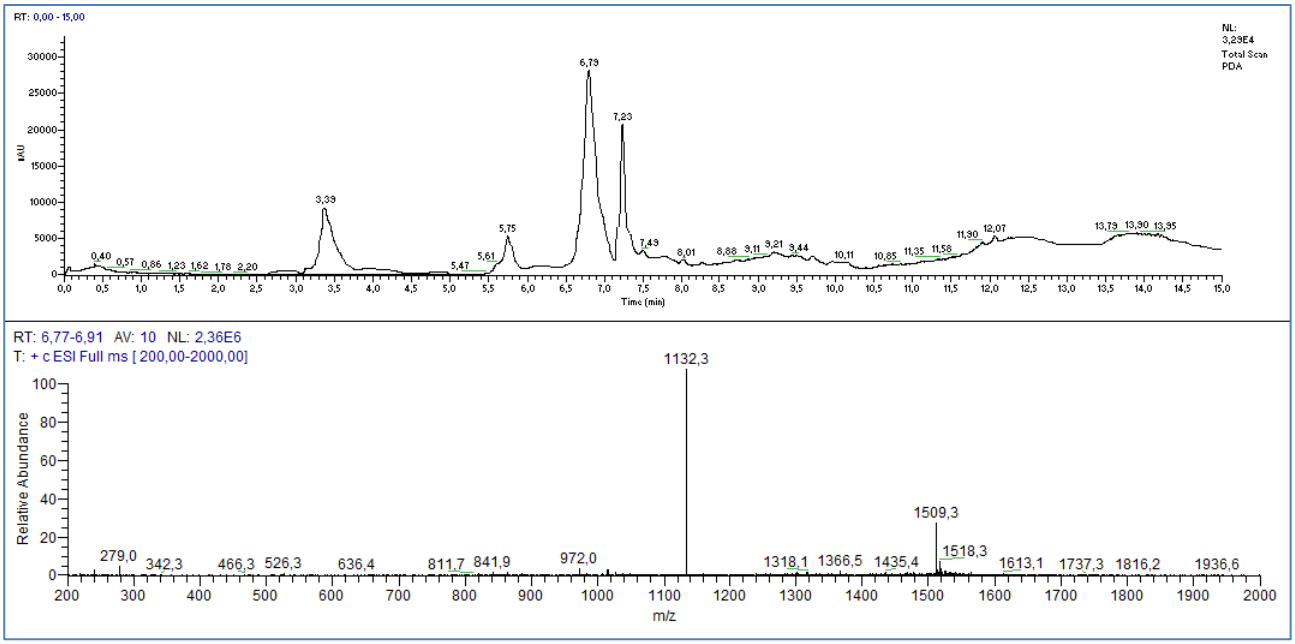
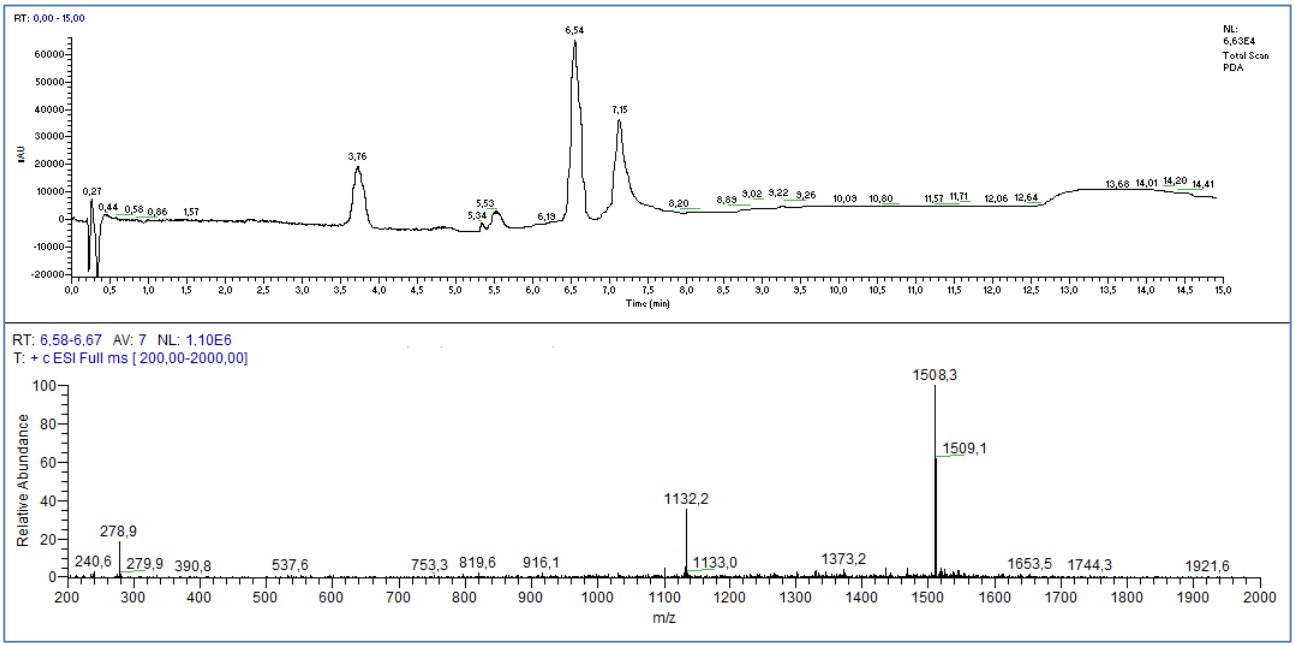
1. LC-MS spectra of mutated HER2-DIVMP

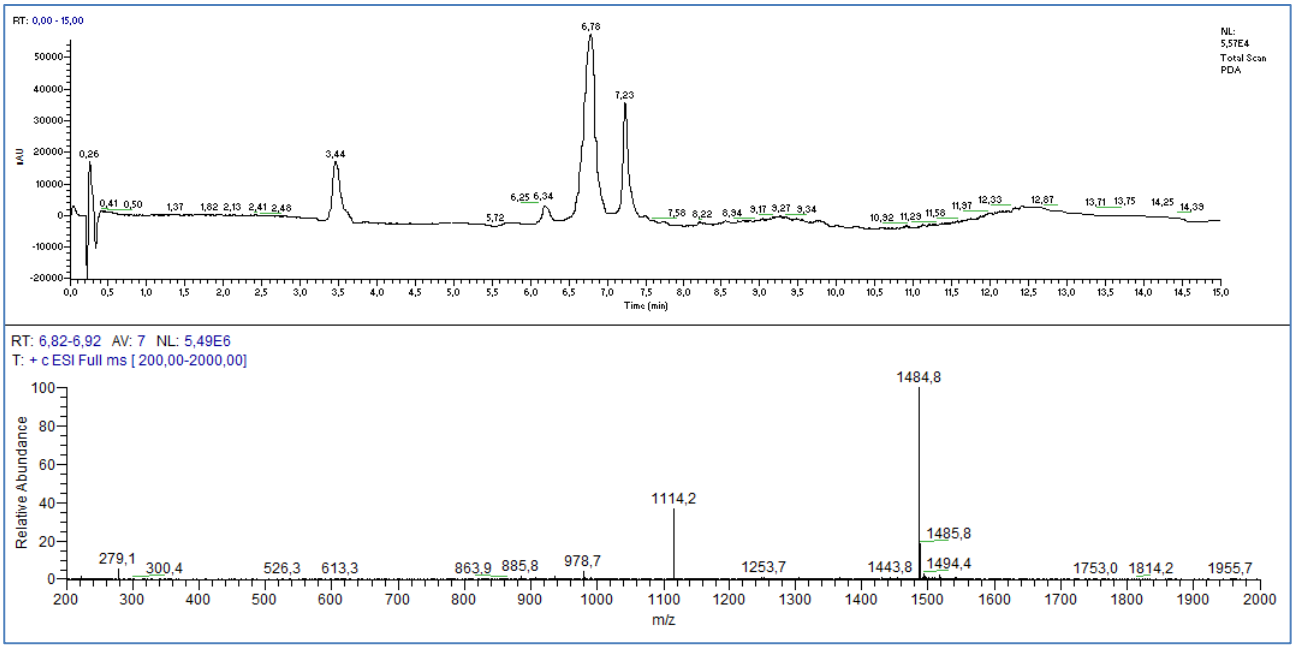
HER2-DIVMP(K569G)



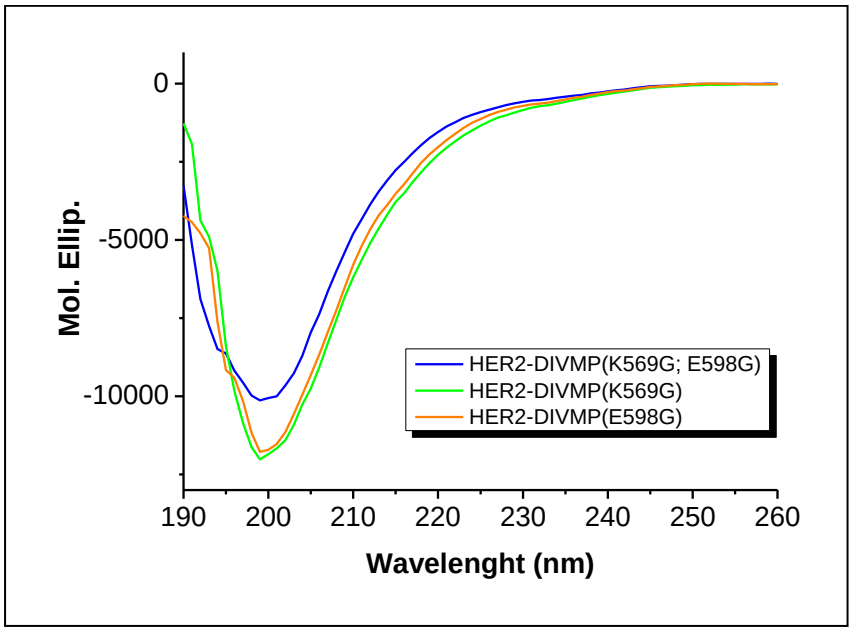
HER2-DIVMP(E598G)

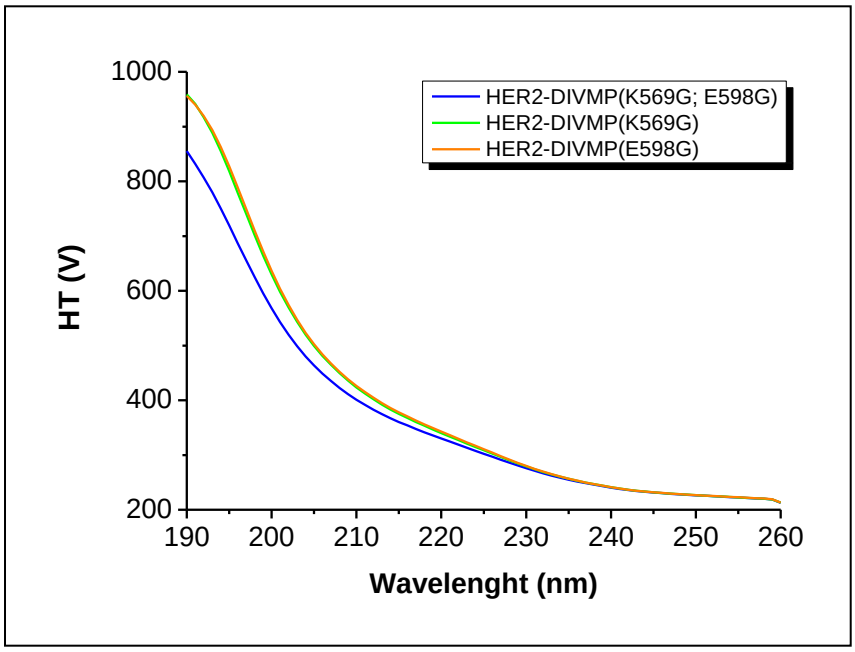


HER2-DIVMP(K569G;E598G)



2. CD spectra of mutated HER2-DIVMP





3. MD analysis

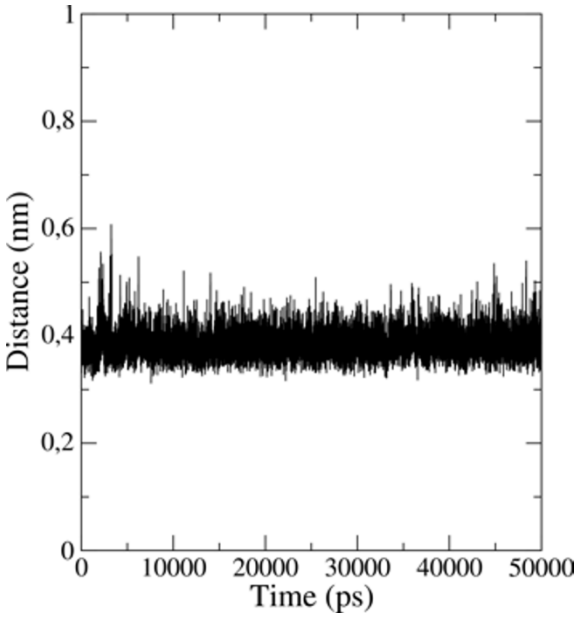


Figure S1. Distance between the side chains of K569 (CG, CD atoms) and V29 (CG1, CG2 atoms) computed along the simulation for model_docking system.

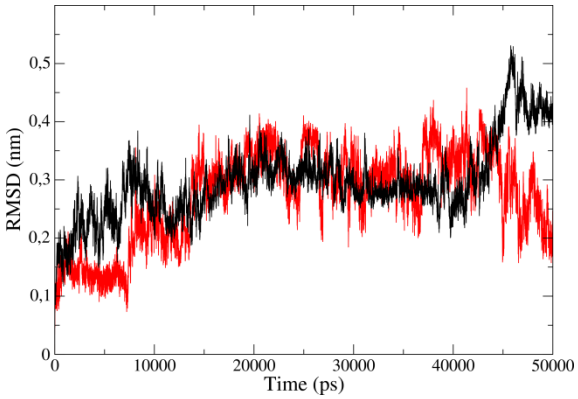


Figure S2. Root mean square deviation (RMSD) of the Cα carbon atoms positions as a function of time for model_ docking_seed simulation. HER2-DIVMP (black line) and A9 (red line).

Table S1: Percentage of occurrence (%) of hydrogen bonds between A9 and HER2-DIVMP in model_RX are estimated using 30000 MD trajectory frames (only values above 10% are reported)

A9	**HER2-DIVMP**	%
GLN 27 (OE1)	LYS 569 (HZ3)	14.9
VAL 29 (H)	GLU 598 (O)	39.4
ASN 30 (H)	GLU 598 (O)	13.8
ASN 30 (D22)	GLU 597 (O)	22.1
ALA 34 (H)	ALA 566 (O)	12.8
ALA 34 (H)	CYS 565 (O)	35.8

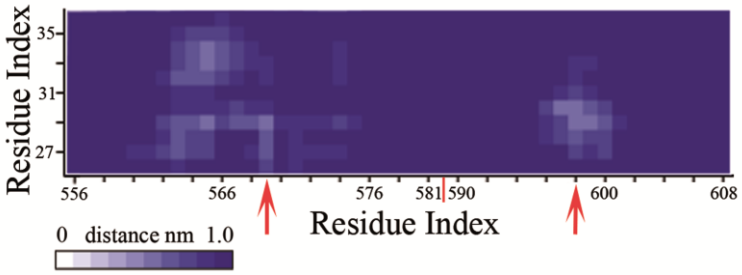


Figure S3. Graphical map of the contacts between A9 and HER2-DIVMP in model_docking_seed system. The regions of the receptor involved in ligand binding during the simulation time are colored by the average of the distance. Red arrows indicate the positions of K569 and E598.

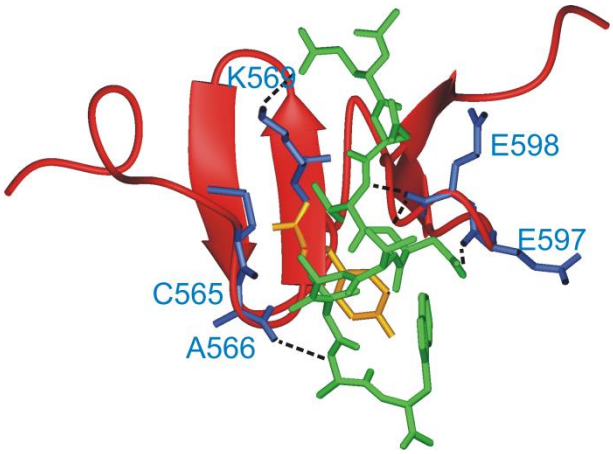


Figure S4. MD representative structure for the model_docking_seed system. HER2-DIVMP is displayed as red cartoon; A9 peptide residues are displayed in green sticks. HER2 residues involved into interaction with A9 are labeled and represented as blue sticks.