

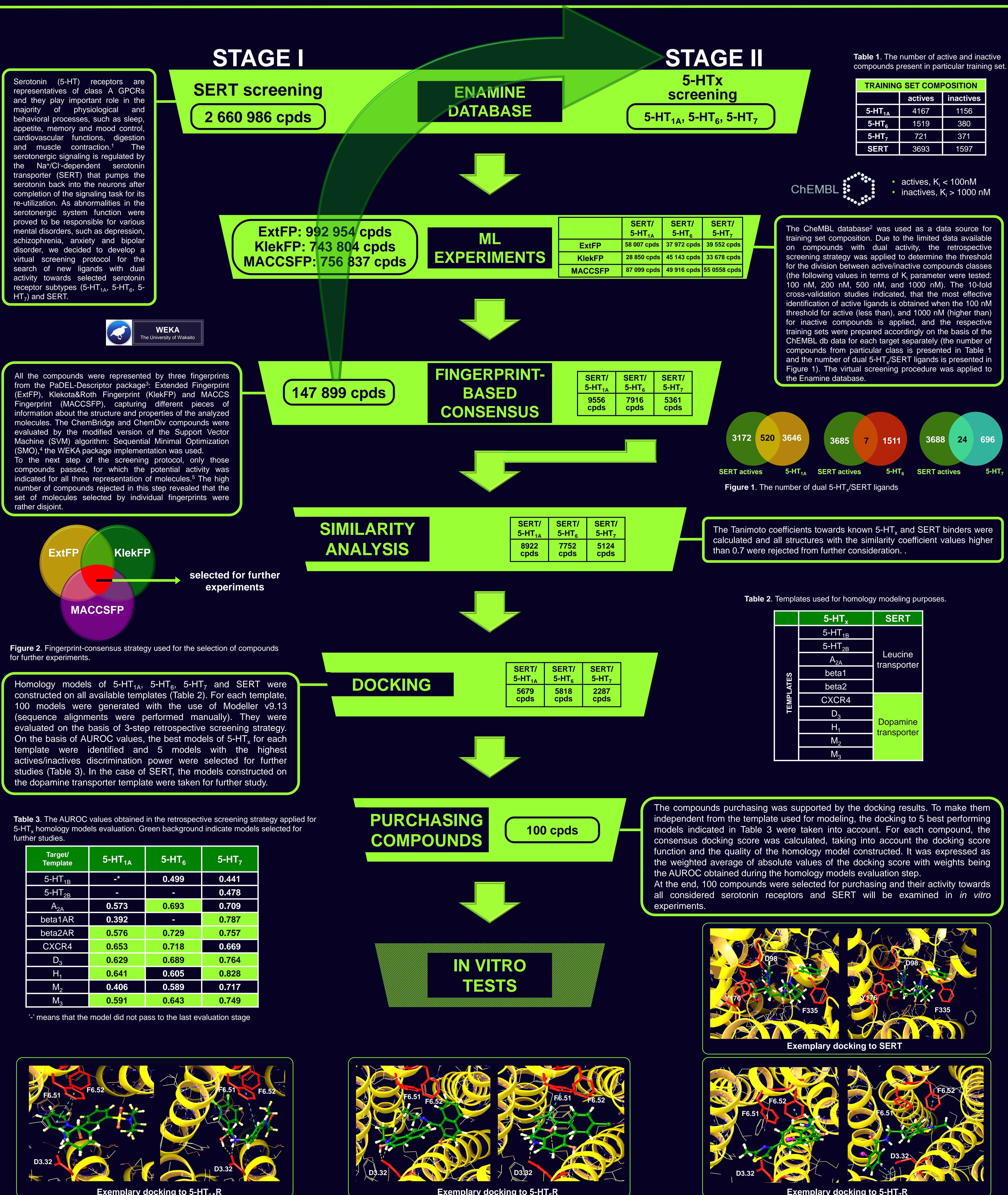
Because two is always better than one – towards the search of dual 5-HT_x-SERT ligands

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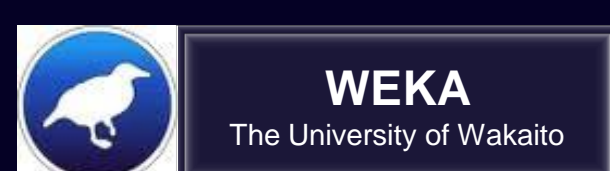
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Serotonin (5-HT) receptors are representatives of class A GPCRs and they play important role in the majority of physiological and behavioral processes, such as sleep, appetite, memory and mood control, cardiovascular functions, digestion and muscle contraction.¹ The serotonergic signaling is regulated by the Na⁺/Cl⁻-dependent serotonin transporter (SERT) that pumps the serotonin back into the neurons after completion of the signaling task for its re-utilization. As abnormalities in the serotonergic system function were proved to be responsible for various mental disorders, such as depression, schizophrenia, anxiety and bipolar disorder, we decided to develop a virtual screening protocol for the search of new ligands with dual activity towards selected serotonin receptor subtypes (5-HT_{1A}, 5-HT₆, 5-HT₇) and SERT.



All the compounds were represented by three fingerprints from the PaDEL-Descriptor package³: Extended Fingerprint (ExtFP), Klekota&Roth Fingerprint (KlekFP) and MACCS Fingerprint (MACCSFP), capturing different pieces of information about the structure and properties of the analyzed molecules. The ChemBridge and ChemDiv compounds were evaluated by the modified version of the Support Vector Machine (SVM) algorithm: Sequential Minimal Optimization (SMO),⁴ the WEKA package implementation was used. To the next step of the screening protocol, only those compounds passed, for which the potential activity was indicated for all three representation of molecules.⁵ The high number of compounds rejected in this step revealed that the set of molecules selected by individual fingerprints were rather disjoint.

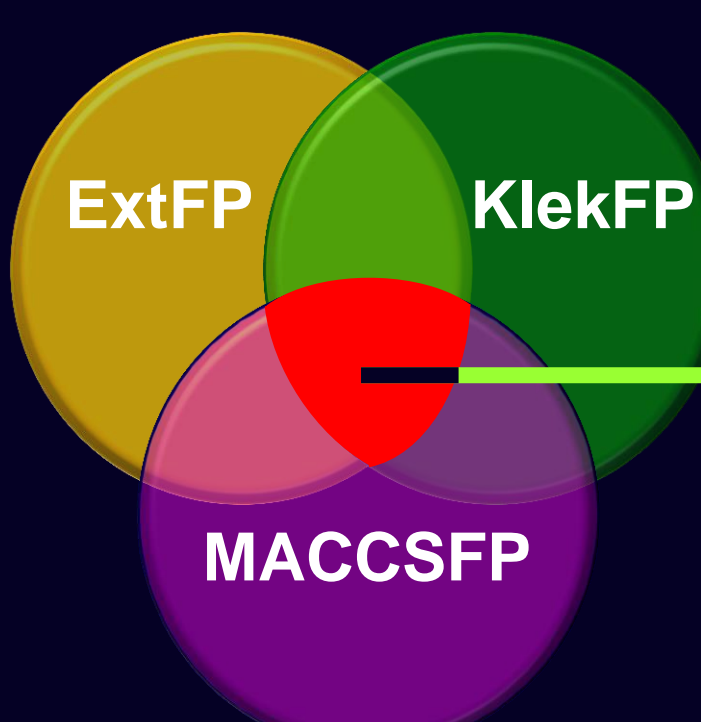


Figure 2. Fingerprint-consensus strategy used for the selection of compounds for further experiments.

Homology models of 5-HT_{1A}, 5-HT₆, 5-HT₇ and SERT were constructed on all available templates (Table 2). For each template, 100 models were generated with the use of Modeller v9.13 (sequence alignments were performed manually). They were evaluated on the basis of 3-step retrospective screening strategy. On the basis of AUROC values, the best models of 5-HT_x for each template were identified and 5 models with the highest actives/inactives discrimination power were selected for further studies (Table 3). In the case of SERT, the models constructed on the dopamine transporter template were taken for further study.

Table 3. The AUROC values obtained in the retrospective screening strategy applied for 5-HT_x homology models evaluation. Green background indicate models selected for further studies.

Target/ Template	5-HT _{1A}	5-HT ₆	5-HT ₇
5-HT _{1B}	-*	0.499	0.441
5-HT _{2B}	-	-	0.478
A _{2A}	0.573	0.693	0.709
beta1AR	0.392	-	0.787
beta2AR	0.576	0.729	0.757
CXCR4	0.653	0.718	0.669
D ₃	0.629	0.689	0.764
H ₁	0.641	0.605	0.828
M ₂	0.406	0.589	0.717
M ₃	0.591	0.643	0.749

* means that the model did not pass to the last evaluation stage

Table 1. The number of active and inactive compounds present in particular training set.

TRAINING SET COMPOSITION		
	actives	inactives
5-HT _{1A}	4167	1156
5-HT ₆	1519	380
5-HT ₇	721	371
SERT	3693	1597



- actives, K_i < 100nM
- inactives, K_i > 1000 nM

The ChEMBL database² was used as a data source for training set composition. Due to the limited data available on compounds with dual activity, the retrospective screening strategy was applied to determine the threshold for the division between active/inactive compounds classes (the following values in terms of K_i parameter were tested: 100 nM, 200 nM, 500 nM, and 1000 nM). The 10-fold cross-validation studies indicated, that the most effective identification of active ligands is obtained when the 100 nM threshold for active (less than), and 1000 nM (higher than) for inactive compounds is applied, and the respective training sets were prepared accordingly on the basis of the ChEMBL db data for each target separately (the number of compounds from particular class is presented in Table 1 and the number of dual 5-HT_x/SERT ligands is presented in Figure 1). The virtual screening procedure was applied to the Enamine database.

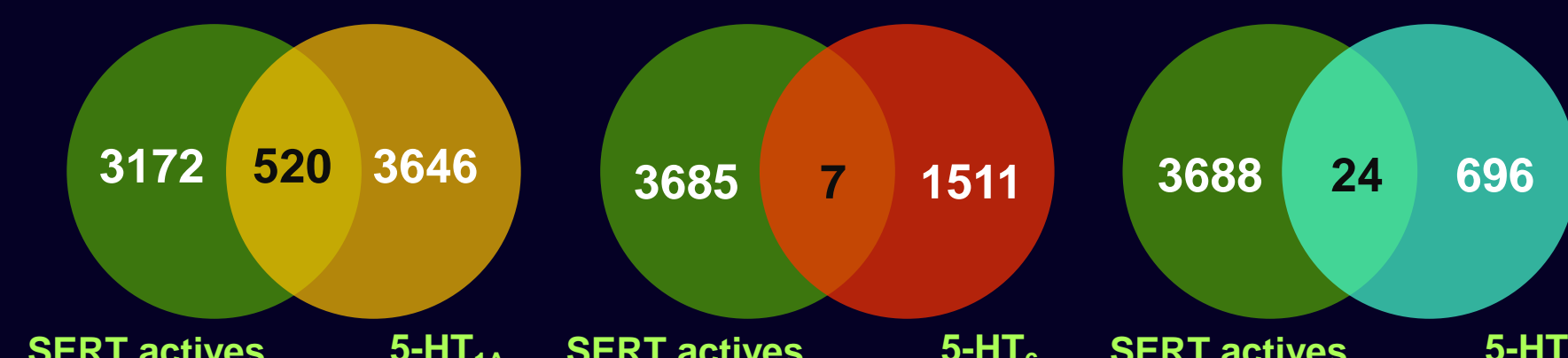


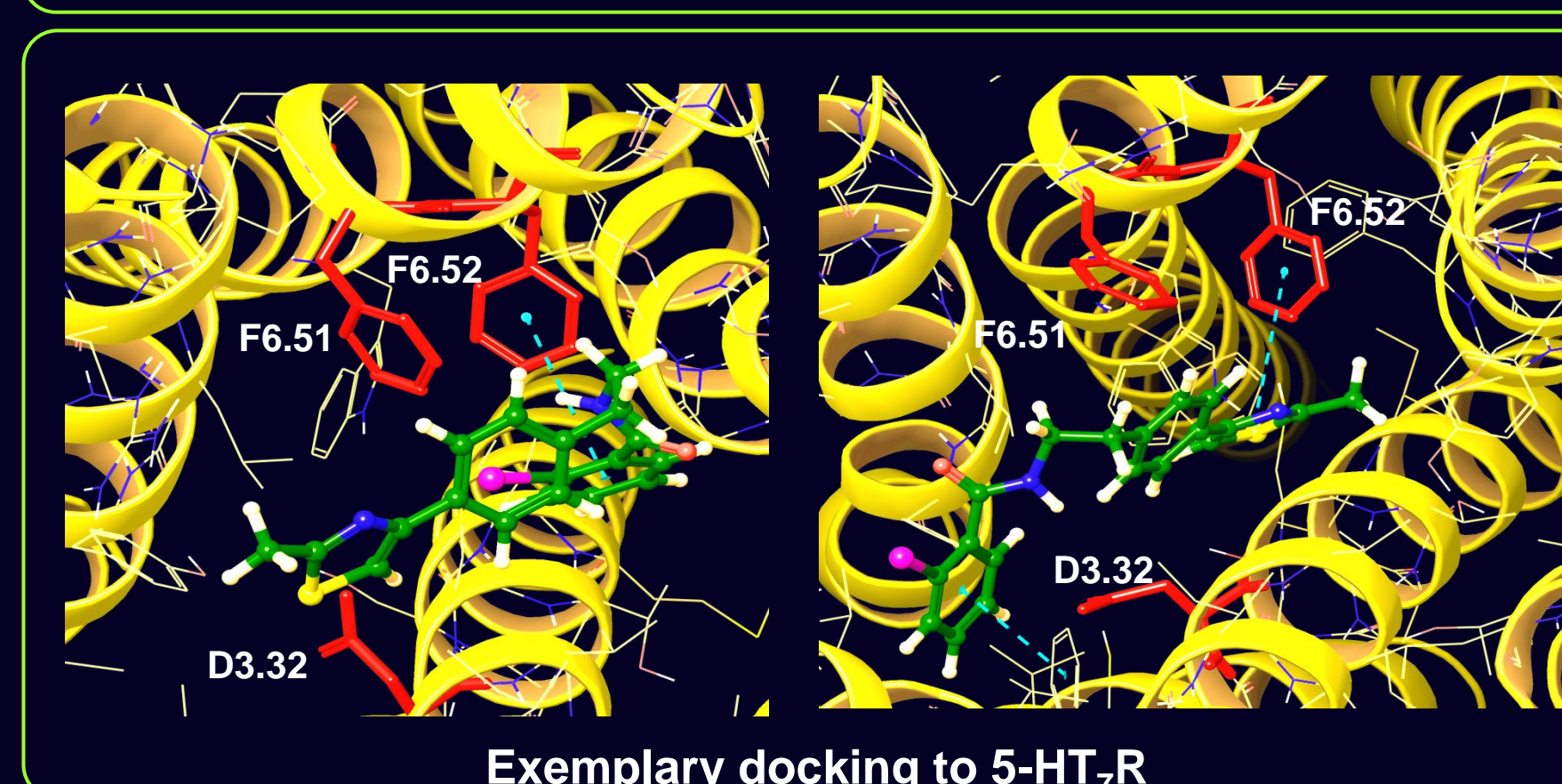
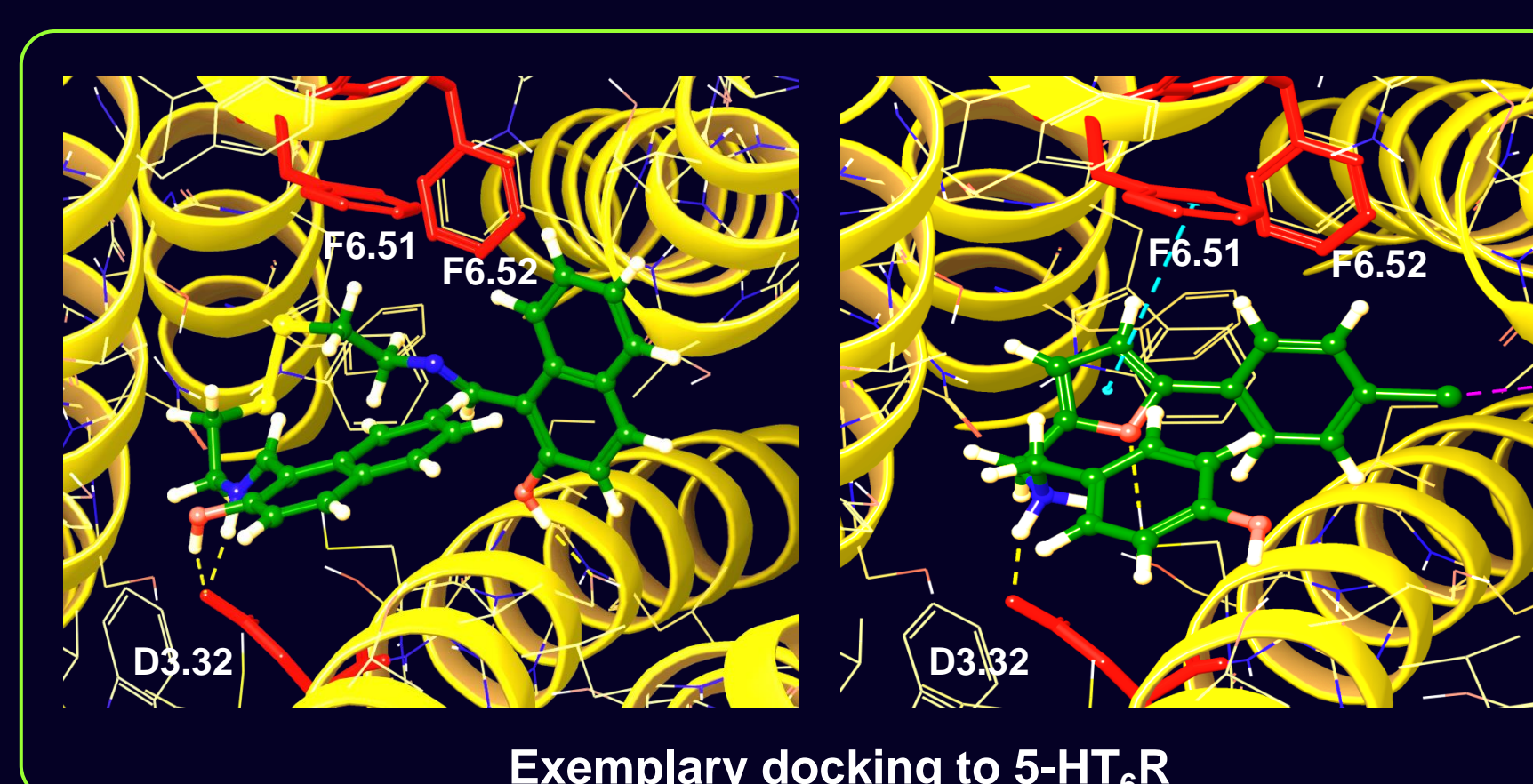
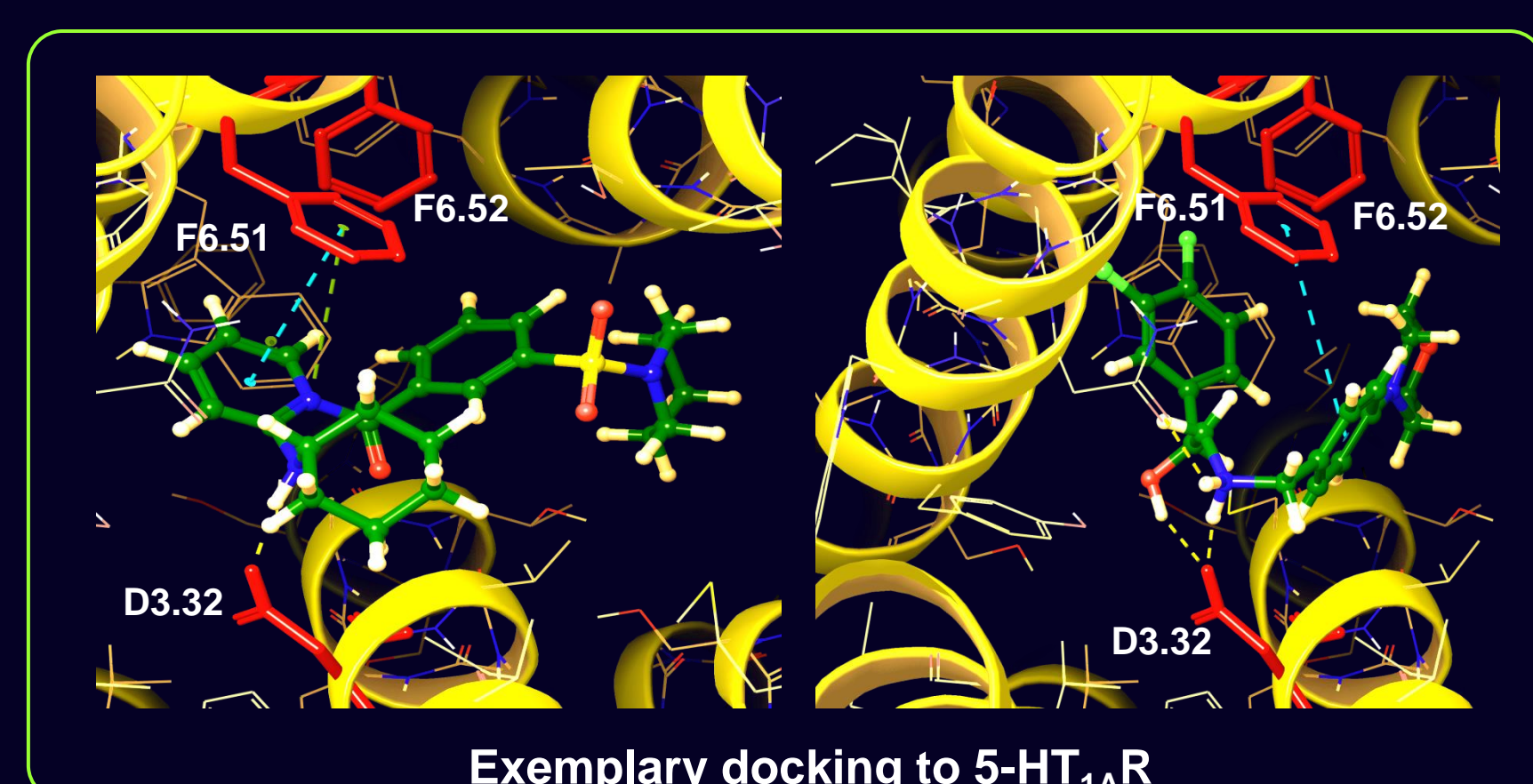
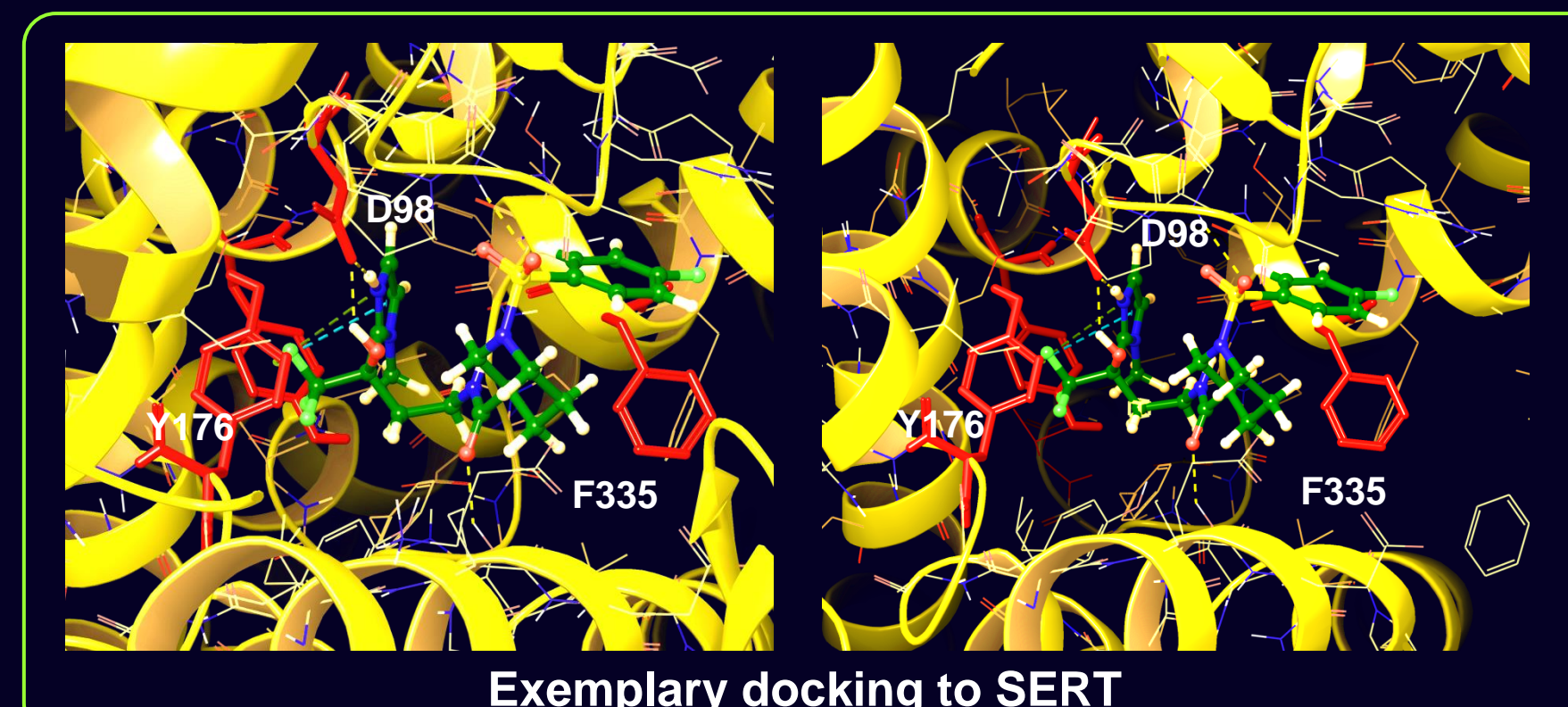
Figure 1. The number of dual 5-HT_x/SERT ligands

The Tanimoto coefficients towards known 5-HT_x and SERT binders were calculated and all structures with the similarity coefficient values higher than 0.7 were rejected from further consideration.

Table 2. Templates used for homology modeling purposes.

	5-HT _x	SERT
TEMPLATES	5-HT _{1B}	Leucine transporter
	5-HT _{2B}	
	A _{2A}	
	beta1	
	beta2	Dopamine transporter
	CXCR4	
	D ₃	
	H ₁	
	M ₂	
	M ₃	

The compounds purchasing was supported by the docking results. To make them independent from the template used for modeling, the docking to 5 best performing models indicated in Table 3 were taken into account. For each compound, the consensus docking score was calculated, taking into account the docking score function and the quality of the homology model constructed. It was expressed as the weighted average of absolute values of the docking score with weights being the AUROC obtained during the homology models evaluation step. At the end, 100 compounds were selected for purchasing and their activity towards all considered serotonin receptors and SERT will be examined in *in vitro* experiments.



References

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