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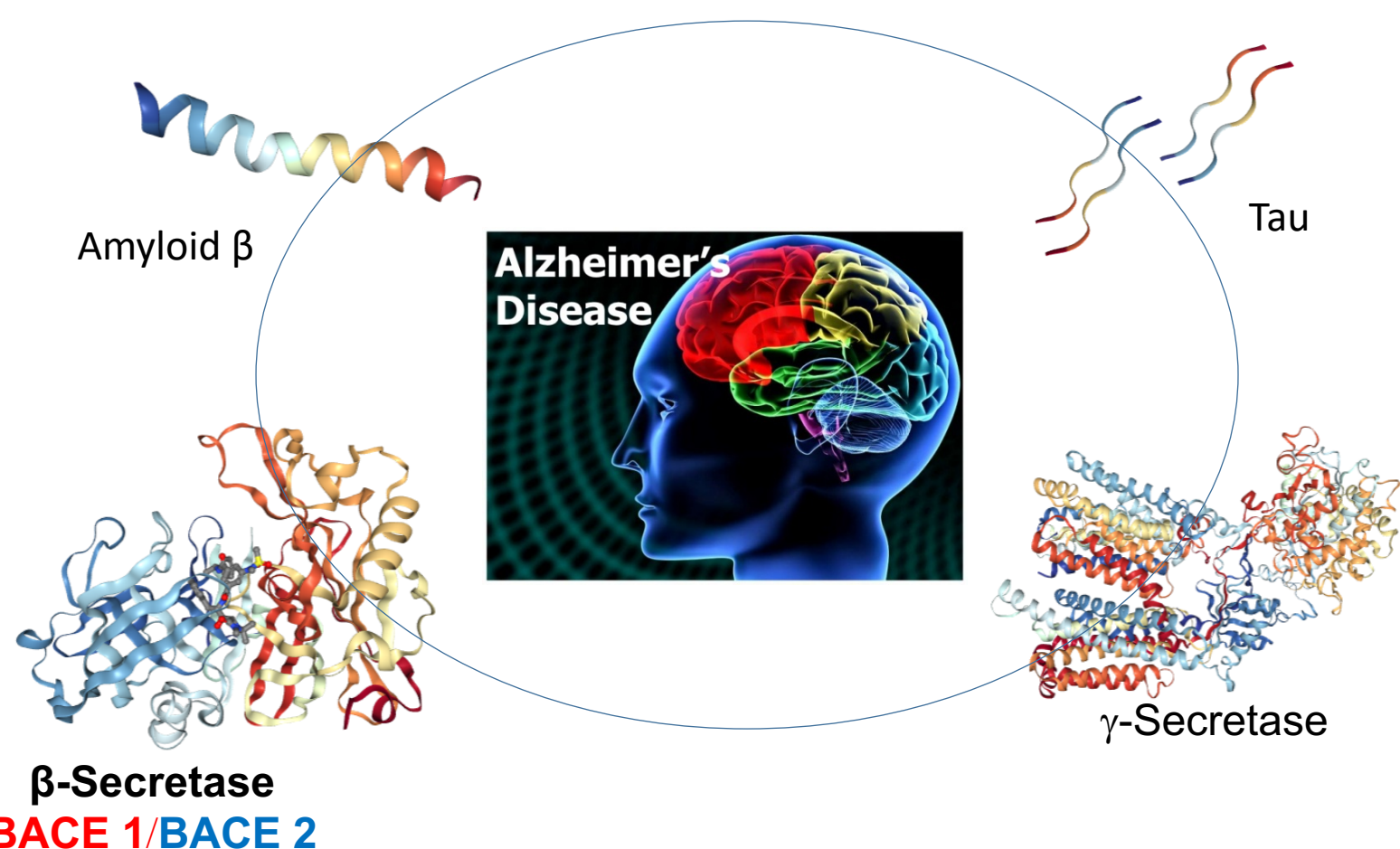
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Identification of selective inhibitors against BACE 1 over BACE 2 in Alzheimer's disease by Quantitative Structure-Activity Relationship (QSAR)

Strategy for Diagnosis & Treatment in Alzheimer's diseases (AD)

Molecular Targets



Attractive drug target for AD

Selective inhibitors against BACE 1/ BACE 2

Modern drug discovery strategies

Ligand Based (LB) (Information of Ligands Required)

- QSAR
- Pharmacophore modeling

Structure-Based (SB) (3D Structure of Target Required)

- Docking
- Molecular Dynamics
- Pharmacophore modeling

To find/develop a hit or lead compound as drug candidate

Some steps of the drug discovery process require the use of **Machine Learning** techniques to construct statistically validated models

Machine Learning

Supervised

- ✓ Multiple Linear Regression Analysis

Unsupervised

- ✓ k-means clustering
- ✓ Hierarchical clustering

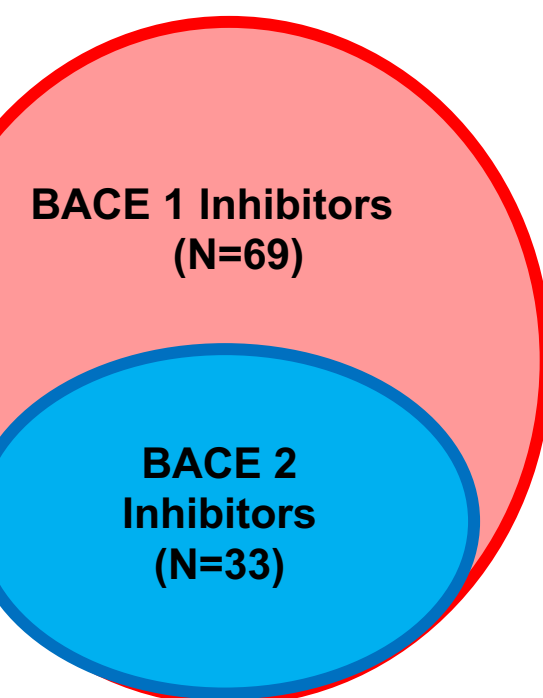
We aim to develop Quantitative Structure-Activity Relationship (QSAR) models to Identification of selective inhibitors against BACE 1/ BACE 2 in Alzheimer's disease for a data set of N-Phenylpicolinamide derivatives

Input Data Set

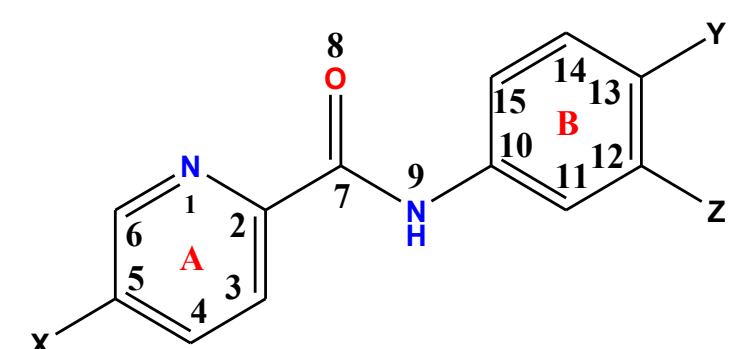
Pharmacophore Derivatives

Estimation of molecular properties (descriptors)

Selection of training and test sets using Cluster Analysis



N-Phenylpicolinamide

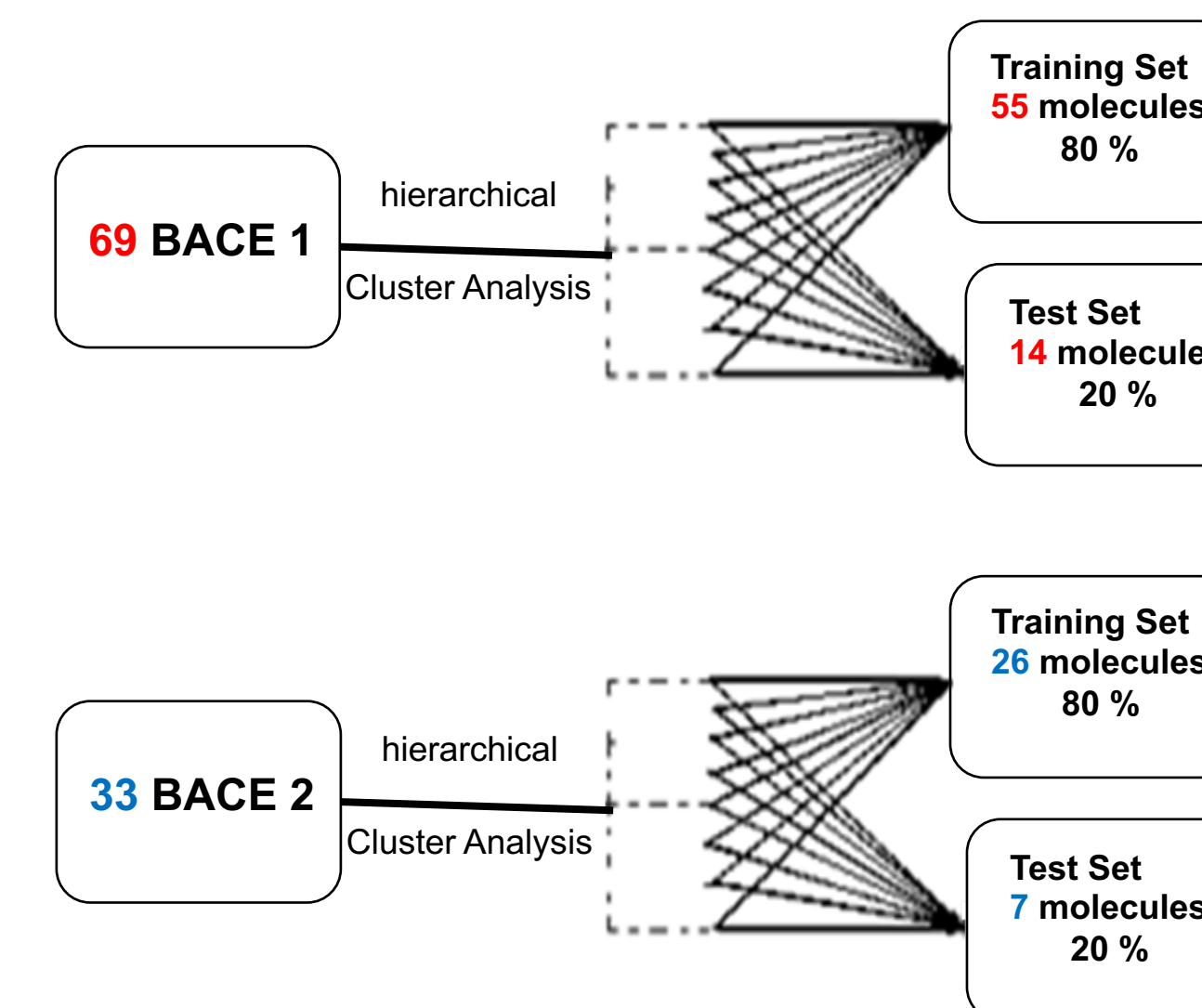
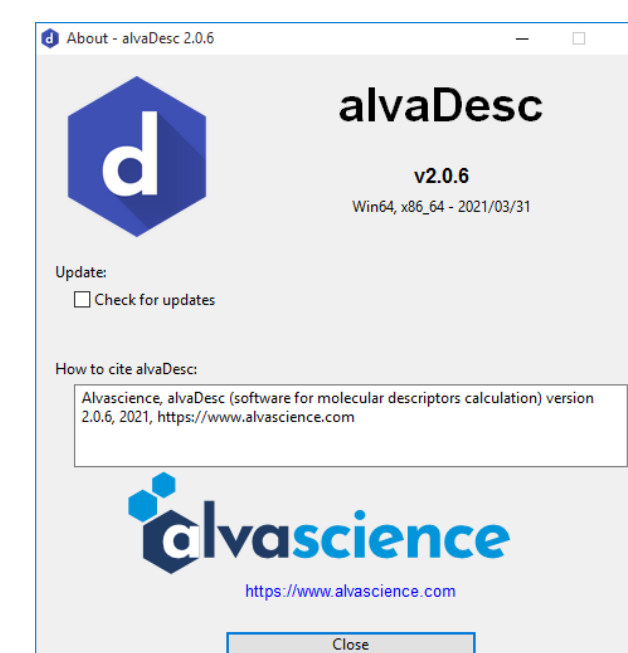


A: an (hetero)aromatic ring, B: an (hetero)aromatic ring and an amide linker is installed between A- and B-rings allowing the B-ring to enter deep into the pocket. X, Y, Z: Substituent groups, Position 4: C or N atom

BLOCK	TOTAL	SELECTION	EXCLUDE
1. Constitutional indices	50	14	36
2. Ring descriptors	35	5	30
3. Geometrical descriptors	38	0	38
4. Randic molecular profiles	41	0	41
5. Functional group counts	154	1	153
6. Pharmacophore descriptors	165	3	162
7. 2D Atom Pairs	1596	4	1592
8 3D Atom Pairs	36	0	36
9. Charge descriptors	15	0	15
10. Molecular properties	27	11	16
11. Drug-like indices	30	6	24
12. Chirality descriptors	70	0	70
TOTAL	2257	44	2213

Exclusion criteria:

- At least one value as zero
- Constant values
- Not applicable



Cluster analysis is used in QSAR models to build the training and test sets as well as to determine the structural diversity of the dataset

- ✓ Compounds with biochemical activity below 1 μM were selected for further inhibition assay
- ✓ The IC_{50} value is the concentration of compound which inhibits BACE 1 and BACE 2 binding by 50 %
- ✓ In our study, the negative logarithm of the biological activity, pIC_{50} , was used as the dependent variable to determine QSAR correlation equations
- ✓ Active molecule (pIC_{50} greater or similar than 6) and inactive molecule (pIC_{50} lower than 6)

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- The two-dimensional (2D) chemical structures of the inhibitors were generated using ChemDraw Ultra and saved in mol format.
- The 3D structure of each inhibitors were obtained by the geometrical optimization of each molecule using Kohn-Sham's DFT B3LYP/6-31G method included in Gaussian 09 program routines

Significant and Predictive QSAR model of BACE 1 inhibitors

$$PIC_{50} = -0.44 \text{ F03[C-C]} + 0.60 \text{ MR99} + 0.19 \text{ TPSA(Tot)} + 0.45 \text{ LOGP} + 2.78 \text{ LLS_02} - 3.13$$

Training sets : n=55; R=0.90; R² = 0.81; s=0.26; F=42.71; Q2=0.76; P=0.00

Test sets: n=14; R=0.80; R² =0.64; s=0.70; F=21.43

F03[C-C]	MR	TPSA	LOGP	LLS_02: A lead-like score (8 rules)
Frequency of C - C at topological distance 3	Molar Refractivity	Topological polar surface area using N,O,S,P polar contributions	Octanol/Water partition coefficient	$LS = \frac{nRules}{tRules}$ nRules: number of satisfied rules. tRules: total number of rules
Electronic	Steric	Electronic	Lypophilicity	Lypophilicity-Steric-Electronic rules
(-)	(+)	(+)	(+)	(+)

Significant and Predictive QSAR model of BACE 2 inhibitors

$$PIC_{50} = -2.05 \text{ SCBO} + 1.29 \text{ D/Dtr06} + 8.94 \text{ DLS_cons} + 7.07 \text{ LLS_01} - 10.85 \text{ QEDu} + 9.53$$

Training sets: n=28; R=0.91; R² = 0.83; s=0.42; F=22.47; Q2=0.75; P=0.00

Test sets: n=6; R=0.92; R² = 0.85; s=0.48; F=22.98

SCBO: Sum of Conventional Bond Orders (H-depleted)	D/Dtr06: Distance/Detour ring index of order 6	DLS_cons: DRAGON consensus Drug-Like Score (7 rules)	LLS_01: modified Lead-Like Score (6 rules)	QEDu: Quantitative Estimation of Drug-likeness (unweighted) (8 rules)
$LS = \frac{nRules}{tRules}$ nRules: number of satisfied rules tRules: total number of rules				
Steric	Steric	Lypophilicity-Steric-Electronic	Lypophilicity-Steric-Electronic	Lypophilicity-Steric-Electronic
(-)	(+)	(+)	(+)	(-)

➤ Challenges for BACE1 inhibitors, notably achieving central penetration and avoiding toxicity, been progressively overcome in the past 10 years

➤ The most recent progress was made in getting high BACE1/BACE2 selectivity, which further reduces the toxicity risk.

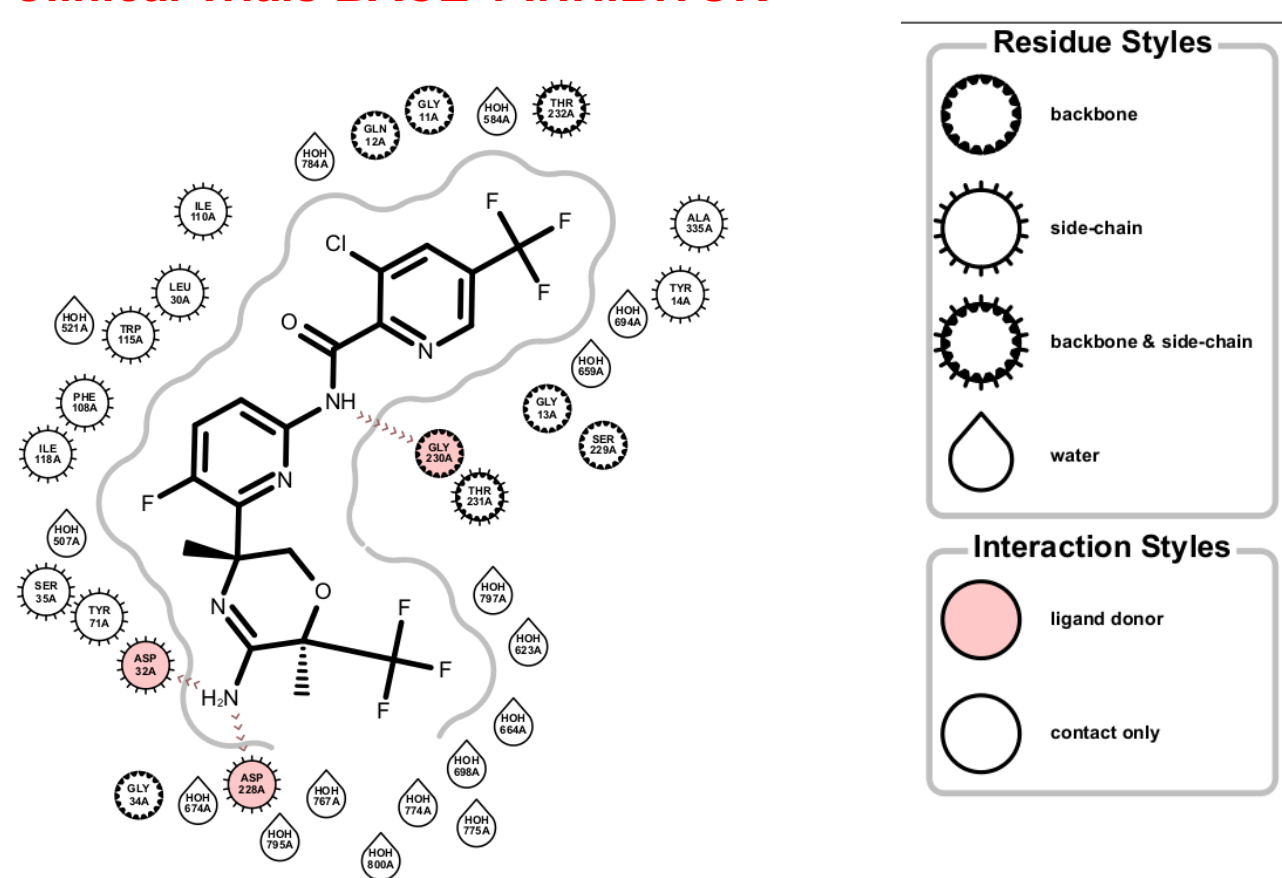
157
Modified
Ribonucleotides



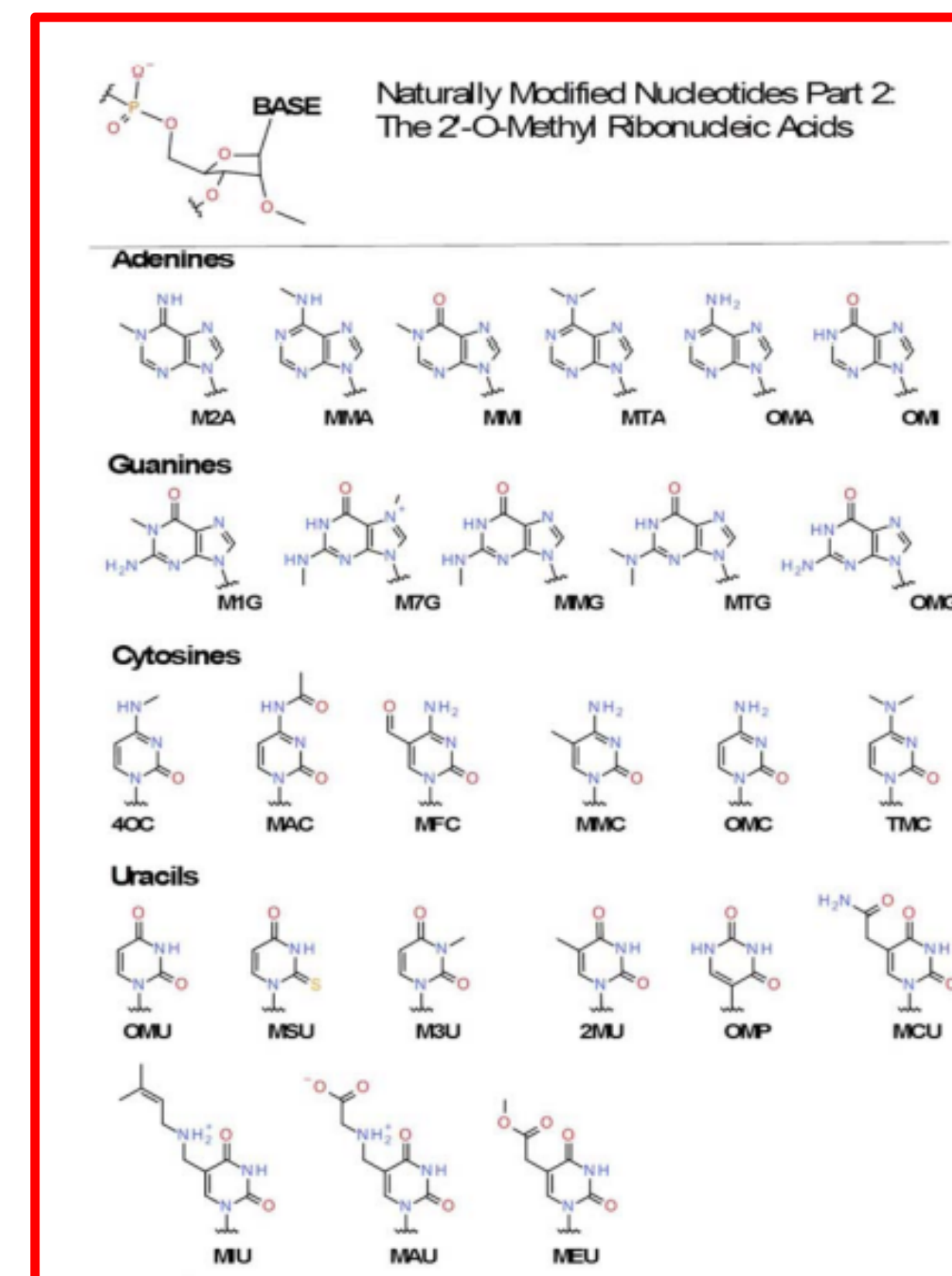
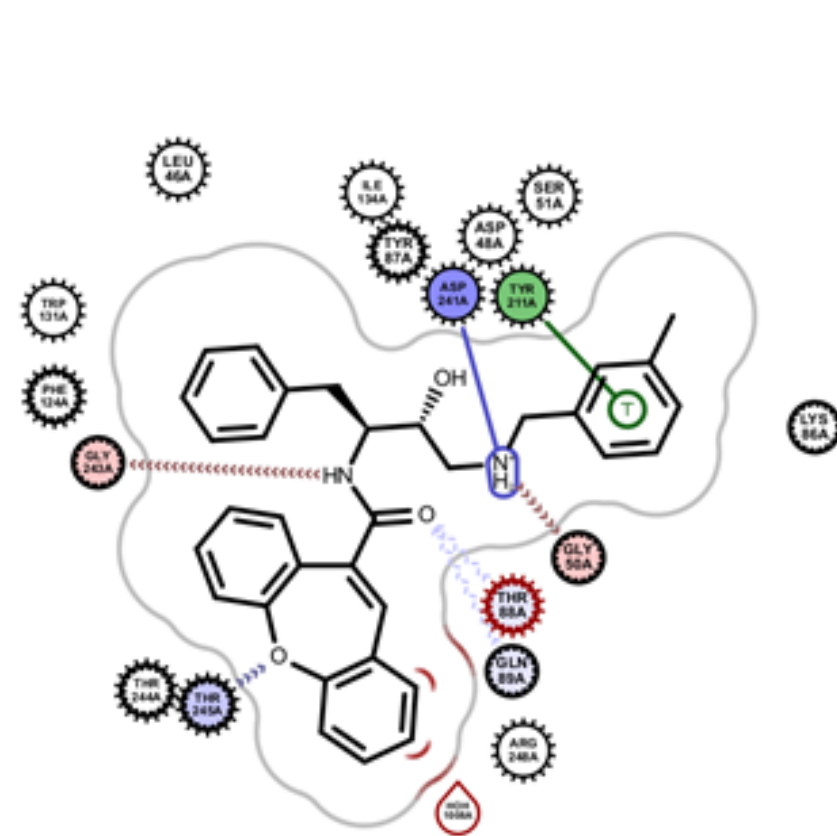
Five Selective
β-Secretase (BACE1)
Inhibitors over
BACE2

Several BACE1/BACE 2 inhibitors have been progressed into clinical trials

Clinical Trials BACE 1 INHIBITOR



Clinical Trials BACE 2 INHIBITOR



Example of Selective β -Secretase (**BACE1**) Inhibitors over **BACE2**

BACE 1_{Cal.} = 10.00

F03[C-C]/10 = 2

MR99/10 = 13.06

TPSA(Tot)/10 = 24.80

MLOGP = - 0.60

LLS_02 = 0.63

BACE 1_{Cal.} = 8.50

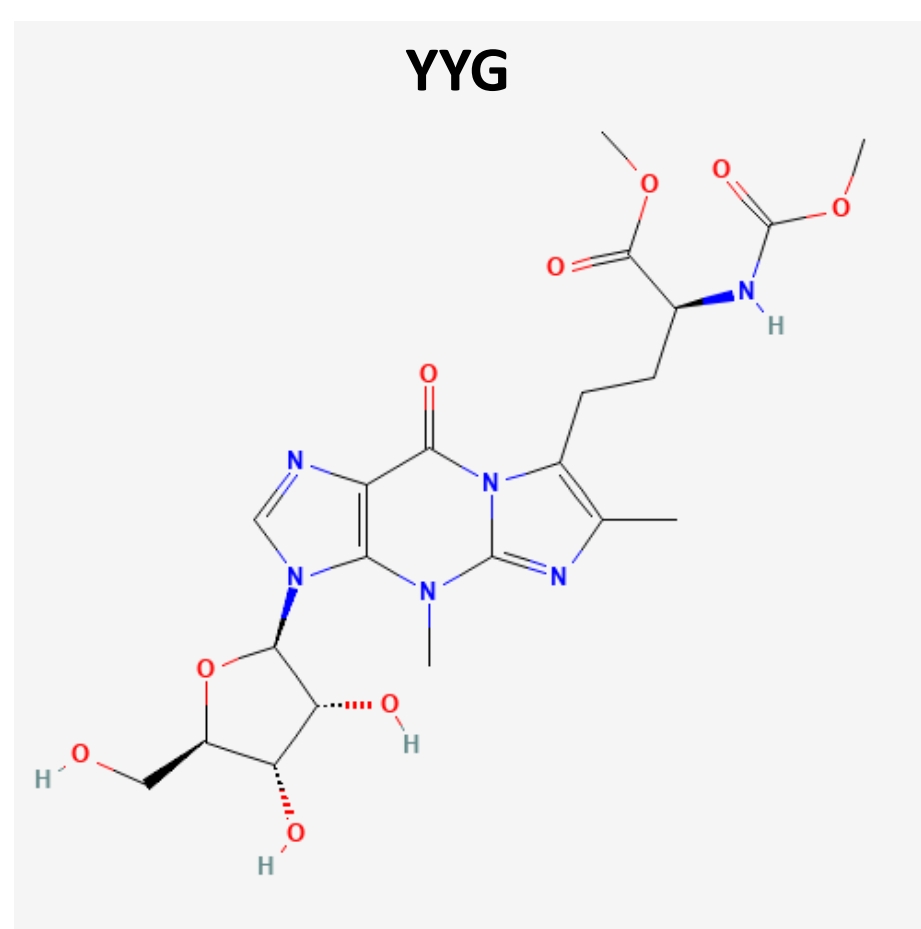
F03[C-C]/10 = 2

MR99/10 = 11.97

TPSA(Tot)/10 = 19.17

MLOGP = - 0.89

LLS_02 = 0.75



BACE 2_{Cal.} = 4.65

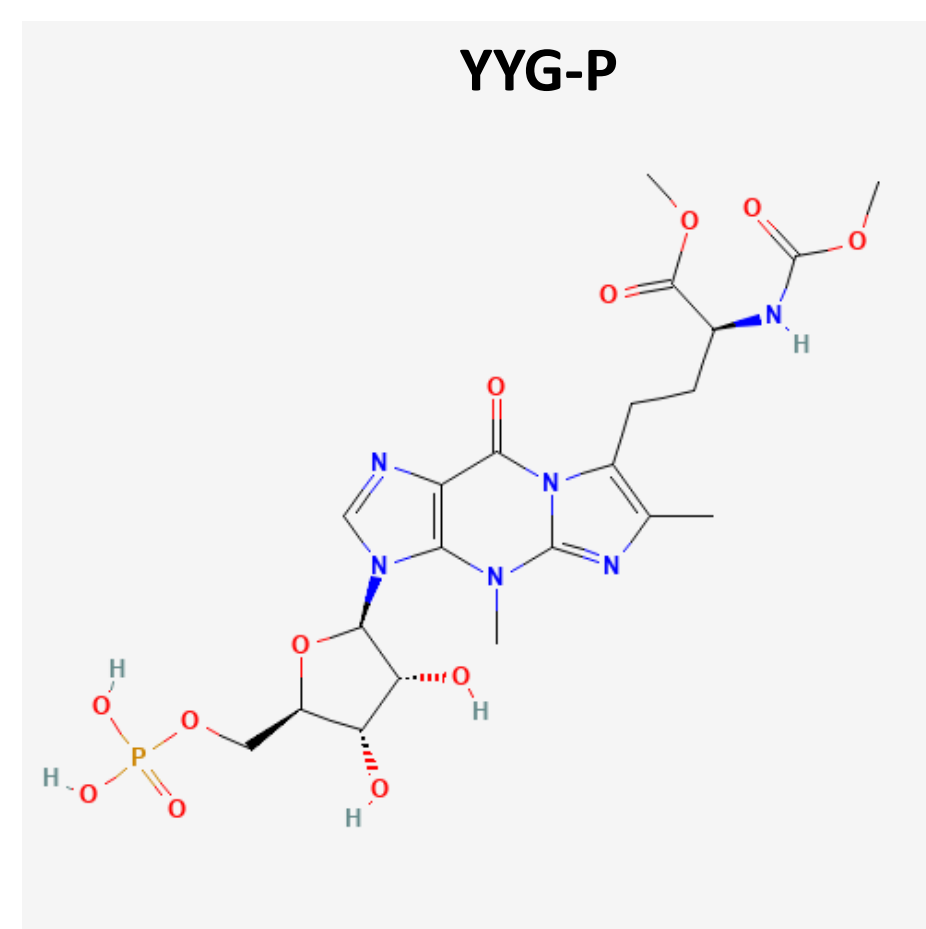
SCBO/10 = 5.20

D/Dtr06/100 = 0.92

DLS_cons = 0.50

LLS_01 = 0.17

QEDu = 0.10



BACE 2_{Cal.} = 5.75

SCBO/10 = 4.70

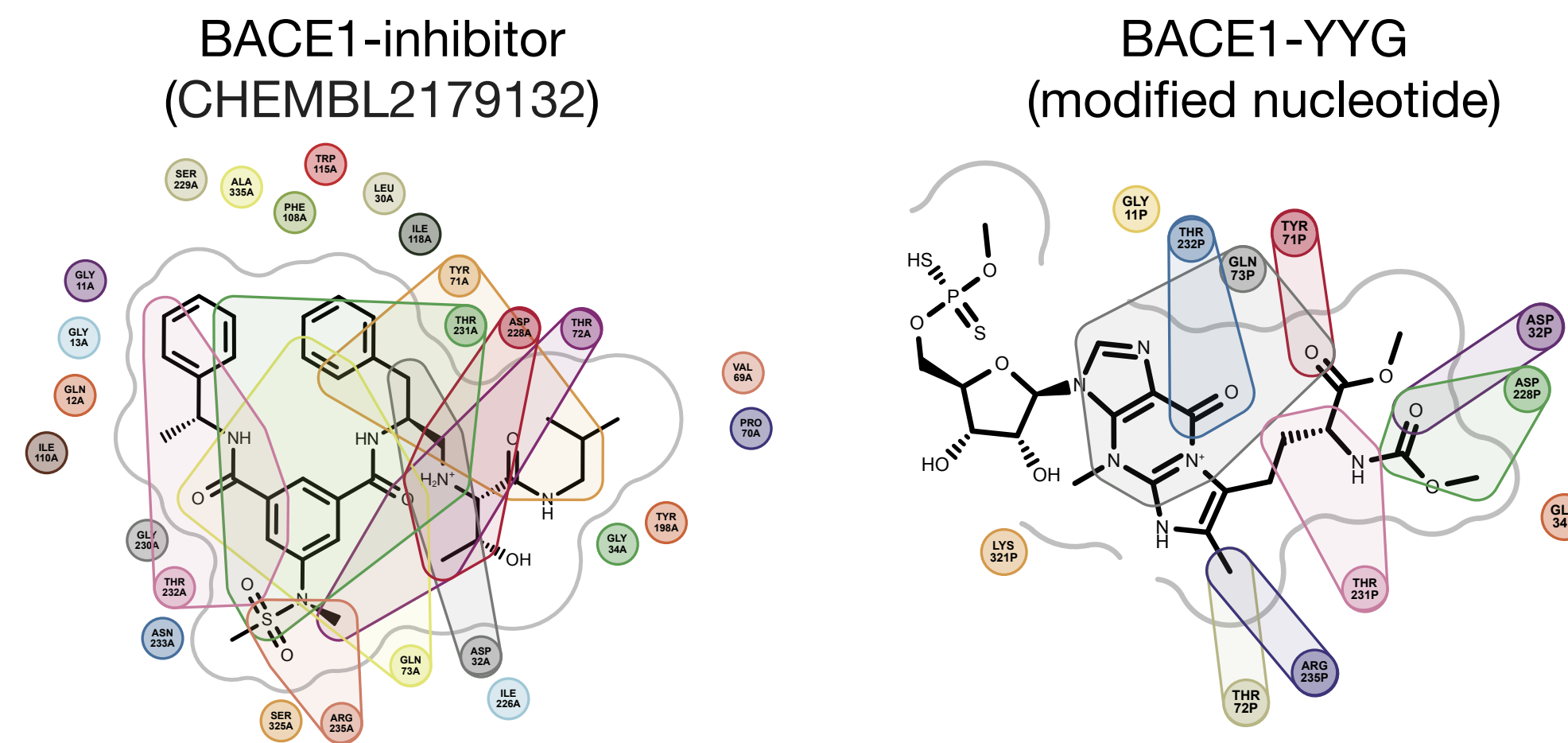
D/Dtr06/100 = 0.80

DLS_cons = 0.62

LLS_01 = 0.17

QEDu = 0.18

Possible binding mode of YYG modified nucleotide at the β -Secretase (**BACE1**) active site: common contacted residues



Conclusions

- 1) The combined possibilities of quantum and physicochemicals MD's, together with the Machine Learning techniques, allowed us to generate QSAR models, capable of discriminating between Selective β -Secretase (BACE 1) Inhibitors over BACE 2.
- 2) Hydrophobic, Steric and Electronic significant molecular descriptors included in the predictive QSAR model of BACE 1 and BACE 2 inhibitors allow the structural interpretation of the biological process, evidencing the main role of the shape of molecules, its hydrophobicity and its electronic properties in the transport and the Ligand–Receptor interaction.
- 3) QSAR models allowed the identification of five modified nucleotides as selective inhibitors against BACE 1/ BACE 2 in Alzheimer's disease. Phosphate group in the selective modified nucleotides have a positive impact in the inhibitor's activity. According the value of the significant molecular descriptors include in the QSAR models of BACE 1, a Phosphate group increases the MR, TPSA and LOG P values with a positive contribution to the BACE 1 inhibitor activity.

Perspectives

1. Integrative model QSAR/structural data of BACE1(BACE2)-ligand complexes
2. MCSS calculations on BACE1 with modified nucleotides (in progress)