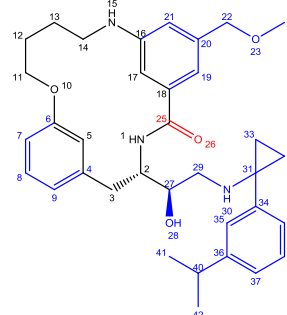
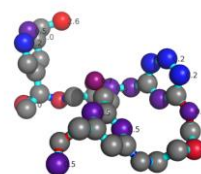


CODE	3K5C (PDB)	Resolution	2.1	
Name		Ring size	16	
Formula	C35H45N3O4	# Ligand atoms	42	
Type	Macrocycle	Scorpion Score	12.5	
Mol. Weight (Da)	571,34	Saturated/ Unsaturated	U	
cLogP	5.8919	Chiral centres.ring	1	
tPSA	91.85	Chiral centres.sub	1	
#HBD's	3			
#HBA's	3			
N _{RB} (RING)	11	N _{RB} (SUBSTITUENT)	8	
Number of substituents	3	P/NP balance, substituents	3/22	
Large (≥5HA)	2	P/NP balance, peripheral groups	1/0	
Small (2-4HA)	1	Degrees of unsaturation ring	15	
Proportion HA in substituents	60%	N:O ratio	3:3	
Number of peripheral groups	1	Chiral centres	2	
Polarity distribution ligand atoms				
	All		Contact	
	Polar	Nonpolar	Polar	Nonpolar
Ring	3	13	1	5
Substituent	3	22	2	10
Peripheral groups	1	-	1	-
Total	7	35	4	15
Protein name	BACE-1			
Organism	Homo sapien			
Classification	Hydrolase/ Hydrolase inhibitor			
Binding mode	Face on			
Receptor secondary structure topology				
Number of residue 'hotspots'	21			
Number of protein-ligand interactions* ('Database link')				
Hydrogen bond	3	Hydrogen donor-π	1	
Ionic interaction	1	π-π	5	
Cation-dipole	-	VdW interaction	17	
Cation-π	-	Unfavourable	6	
Dipolar interaction	1	Poor-angle	2	
Halogen bond		Unclassified	2	
Water-mediated interaction				

2D-STRUCTURE LIGAND



3D-STRUCTURE LIGAND +SCORPIONSORE ('Scorpion link')



Physicochemical properties

['click for publication'](#)

IC50 (nM):

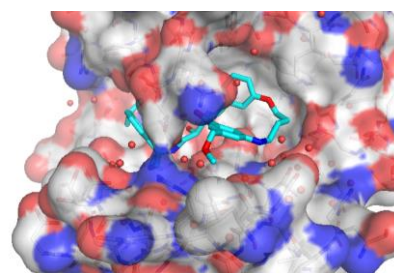
BACE-1 17

CHO 20

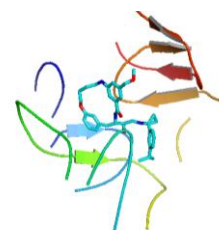
CathD 1

CathE 0.4

LIGAND-PROTEIN COMPLEX (I) (['Pymol link'](#))



LIGAND-PROTEIN COMPLEX (II)



*Based on Scorpion® analysis