

Conformation of the Tripeptide Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ Deduced from Two-dimensional ¹H-NMR and Conformational Energy Calculations is Related to its Affinity for NK₁-Receptor

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Abstract: Chemical modifications of dual NK₁/NK₂ ligand Cbz-Gly-Leu-Trp-OBzl(CF₃)₂ (**1**) enabled us to create a high NK₁ selective ligand Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ (**2**). A determination of the conformational behavior of tripeptide **2** in solution is described. The 1D and 2D ¹H-NMR techniques (COSY and ROESY) were used to assign resonances. Observed interproton distance restraints were considered to characterize conformational behavior. Spectral data indicate that tripeptide **2** presents a rigidified structure in DMSO stabilized by H-bond in two γ -turns. Agreement with experimental data was obtained by averaging the ¹H-NMR parameters over several combinations of low-energy conformations. Copyright © 2001 European Peptide Society and John Wiley & Sons, Ltd.

Keywords: conformational analysis; neurokinin A; NMR; substance P

INTRODUCTION

Sensory neuropeptides (tachykinins) including substance P (SP: Arg-Pro-Lys-Pro-Gln-Gln-Phe-Phe-Gly-Leu-Met-NH₂) and neurokinin A (NKA: His-Lys-Thr-Asp-Ser-Phe-Val-Gly-Leu-Met-NH₂) are co-released from capsaicin-sensitive primary afferent nerves by a variety of chemical, physical and pharmacological stimuli [1].

The central and peripheral actions of the mammalian tachykinin substance P (SP) have been associated with numerous diseases including migraine [2–5], rheumatoid arthritis [6–8], asthma [9,10] inflammatory bowel disease as well as with mediation of the emetic reflex [11,12], and with the modulation of central nervous system disorders such as Parkinson's disease [13] and depression [14,15].

Several NK₁ receptor antagonists, coming essentially from screening and optimization programs, have been described in recent years and some of them are being clinically developed [16–18].

We recently described [19] a potent NK₁/NK₂ ligand and Cbz-Gly-Leu-Trp-OBzl(CF₃)₂ (**1**) whose peptidic structure was inspired from the C-terminal SP sequence. In order to optimize the affinity and the selectivity for NK₁ receptor, we replaced Gly by Pro since Pro is often observed at (*i* + 1) position of β -turn [20,21] and imposes strong restraints on the peptide conformation.

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Evaluation of NK₁/NK₂ receptor binding affinity (Table 1) revealed tripeptide Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ (**2**) as a new selective NK₁ ligand with high affinity. For a better understanding of the interaction of **2** with its NK₁ receptor, we decided to determine its conformational behavior in DMSO-*d*₆ using the rotating frame Overhauser effect (ROESY) and molecular modeling.

MATERIALS AND METHODS

Peptide Synthesis

Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ was obtained (Figure 1) according to a previously described synthetic peptidic method in solution [22]. The cesium salt of *N*-Boc-Trp-OH was alkylated in DMF with 3,5-bis(trifluoromethyl)benzyl bromide. Removal of the Boc group of compound **3** in a methanolic HCl solution gave amine **4** which was reacted with Boc-Leu-OH using PyBOP as coupling agent to afford **5**. Deprotection of the Boc group using standard methodology resulted in amine **6**. Condensation

Table 1 NK₁ and NK₂ Receptor Binding Affinity

Compound	hNK ₁ K _i ^a (nM)	hNK ₂ K _i ^a (nM)
1	40	250
2	1.3	> 10 000
SP	0.16	139

^a Inhibition of [³H]SP or [³H]NKA specific binding to NK₁ or NK₂ receptors expressed in CHO cell lines. Data represents the mean of triplicate determination (S.E. ± 10%).

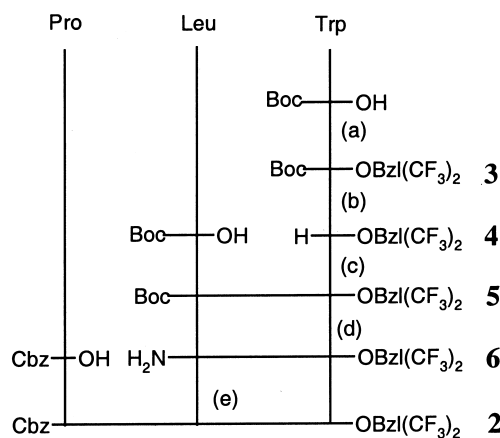


Figure 1 Reagents and conditions: (a) Cs₂CO₃, BrBzl(CF₃)₂, DMF; (b) MeOH, HCl; (c) PyBOP, DIEA, CH₂Cl₂; (d) MeOH, HCl; (e) PyBOP, DIEA, CH₂Cl₂.

with Cbz-Pro-OH gave the tripeptide Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ (**2**).

Chemistry

Column chromatography was performed on silica gel 60 230–400 mesh purchased from Merck. Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ was characterized by MS, HPLC, elemental analysis, IR and NMR. Melting points were determined on a Büchi 535 capillary melting point apparatus and were uncorrected. Mass spectra were recorded on a Finnigan Mat SSQ 710 instrument in the electronic impact mode. HPLC analyses were performed on a Hewlett-Packard 1090 liquid chromatograph, using a Licrospher 60 RP-select B C8 5 μm 250 × 4.6 mm column (inverse phase) to determine the purity of the products. Elution was performed with the following two systems: solution A (80% water, 5% PIC[®] B-8 low UV reagent (Waters Part No. Wat084283), 15% methanol) and solution B (10% water, 5% PIC[®] B-8, 85% methanol). Elemental analyses for C, H, N were performed by the 'Service Central d'Analyses' at the CNRS, Vernaison, France, and were within 0.4% of theoretical values for the proposed structures. The IR spectra were determined as potassium bromide discs with a Perkin-Elmer 1310 spectrophotometer, absorbances were reported in ν (cm⁻¹). The spectra confirmed the proposed structures.

N-α-Cbz-Pro-Leu-Trp 3,5-Bis(trifluoromethyl)benzyl ester (**2**). Commercial Cbz-Pro-OH (249 mg, 1.0 mmol), *N,N*-diisopropylethylamine (0.51 ml, 3.0 mmol) and PyBOP (572 mg, 1.1 mmol) were added to a solution of H-Leu-Trp-OBzl(CF₃)₂. HCl [22] (543 mg, 1.0 mmol) in dichloromethane (40 ml). The reaction was stirred for 48 h. The solution was partitioned between dichloromethane and 1 N hydrochloric acid. The organic extract was dried (magnesium sulfate) and evaporated to yield an oil which was purified by column chromatography on silica gel using hexane/ethyl acetate (5/5). The precipitate thus obtained was recrystallized from dichloromethane/hexane (1/9) to give **2** as a white solid (55%); m.p. 65–67°C; IR (KBr) ν: 3380–3280 cm⁻¹ (NH), 1750 cm⁻¹ (CO), 1690 cm⁻¹ (CO), 1645 cm⁻¹ (CO); MS (electronic impact) *m/z* 774 (M), 666, 413, 130, 91; HPLC: (isocratic 10% A, 90% B), λ = 220, 230, 254 and 280 nm, R_t = 11.25 min, 100% purity. Anal. Calc. for C₃₉H₄₀F₆N₄O₆: C, 60.46; H, 5.20; N, 7.23; Found: C, 60.31; H, 5.25; N, 7.09%.

Pharmacology

Binding experiments were performed according to standard techniques [23] using clones of Chinese hamster ovary (CHO) as the receptor source for both NK₁ and NK₂ subtypes. Crude membranes were prepared and stored in 20 mM Tris, 250 mM sucrose medium, pH 7.4, at -70°C. Both tritiated radioligands were used with specific activities of # 170 Ci/mmol (Amersham). Incubation conditions were the following: 50 mM Tris, 2 mM Mg (final concentrations), pH 7.4 and additional 160 µg/ml Bacitracine at 25°C for 60 min. The reaction was terminated by rapid vacuum filtration onto glass fiber filters (GF/C Whatman presoaked 2 h in 0.1% PEI); after four 2-ml washes with 50 mM Tris at 4°C, pH 7.4, the radioactivity trapped onto the filters was counted and the binding was calculated. Non-specific binding was determined with additional non-radioactive substance P (1 µM). Competition curves were fitted according to the Cheng and Prusoff equation [24] (Kaleidagraph software, Microsoft for Macintosh).

Structure Calculations

Molecular modeling studies were performed using SYBYL [25] software version 6.4 running on a Silicon Graphics Indigo 2 R4600 workstation. Amides were considered in *trans* geometry. Three-dimensional models of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ were built from a library of standard fragments and their geometry was subsequently optimized using the Tripos force field [26] including the electrostatic term calculated from Gasteiger and Hückel atomic charges. The method of Powell available in the Maximin2 procedure was used for energy minimization until the gradient value was smaller than 0.001 kcal/mol/Å².

NMR Experiments

Peptides were dissolved in DMSO-*d*₆. ¹H-chemical shifts were given in parts per million (δ ppm) using tetramethylsilane as an internal standard. The ¹H-NMR spectra were recorded on a Bruker DPX 300 spectrometer equipped with a probe head broad band inverse, operating in the Fourier transform mode with quadrature detection at 300 MHz for protons. For ¹H-NMR spectra, typical acquisition parameters were 4000 Hz spectral width, 3.05 µs pulse width ($\pi/2 = 6.1$ µs) and 16 K time domain addresses. Assignments of the amino acid residues resonance were established by two-dimensional (2D) correlated spectroscopy using the pulse se-

quence D₁-90°-D₂-90° acquisition (COSY). ROESY experiments enabled us to show preferential conformational distance by constraints between pairs of protons. The pulse sequence was D₁-90°-D₂-(180°-180°)_n. Acquisition in the phase sensitive mode was used with a mixing time of 1 s through 320 experiments.

RESULTS AND DISCUSSION

Assignment Resonance of Amino Acid Residues of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂

All ¹H-NMR assignments for Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ in DMSO-*d*₆ at 293 K are reported in Table 2 including chemical shifts and ³J(NH-C^αH).

The COSY spectrum disclosed cross-peaks between δ and γ protons allowing for the unambiguous attribution of the protons of Leu and then Pro. Additional through-space sequential (NH_{*i*}-C^αH_{*i-1*}) connectivities resulted in complete resonance assignments. The ROESY spectrum (Figure 2) used to obtain distance constraints between pairs of protons gave the assignments of the aromatic protons of Trp via the cross-peaks between H₄ and β protons (Figure 3). The assignments of the other protons (3,5-bis(trifluoromethyl)benzyl and *N*-benzyloxycarbonyl) did not present any particular problem.

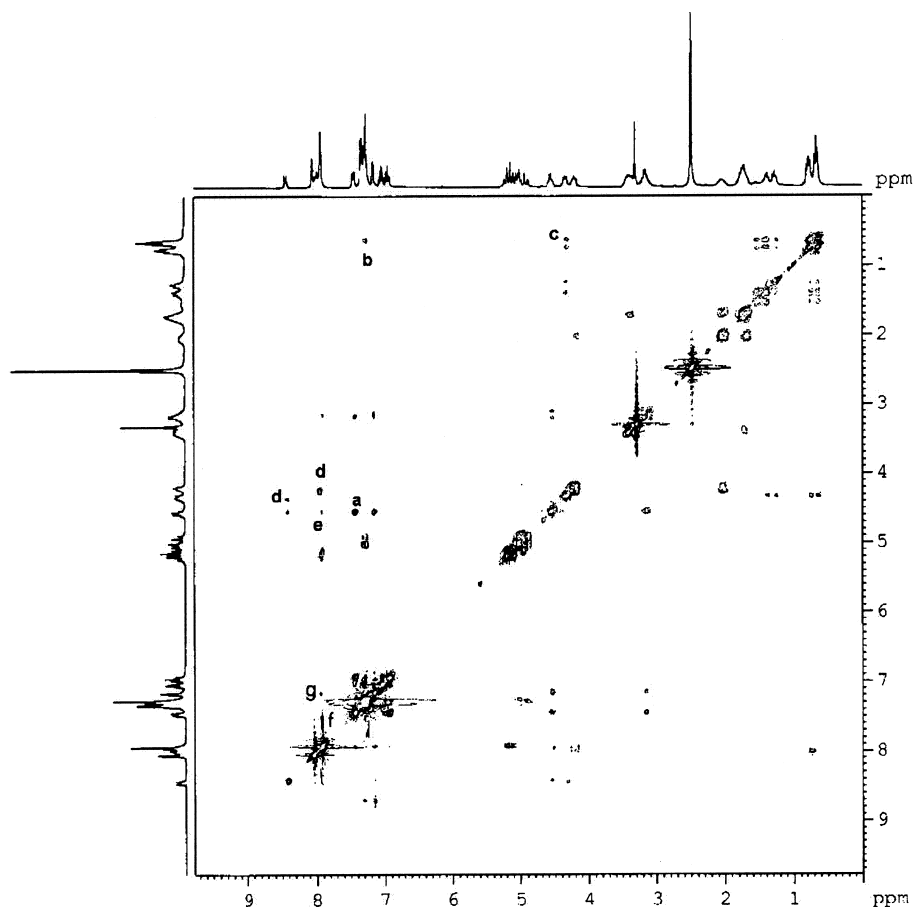
Conformational Behavior of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂

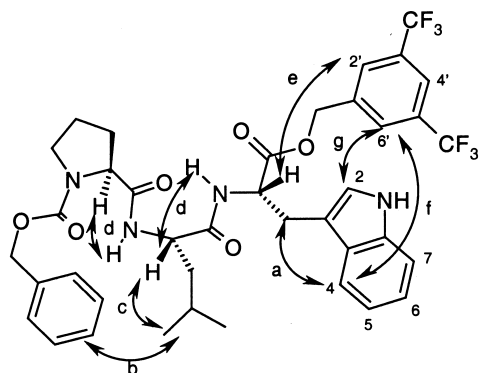
The combined ROESY and molecular mechanics study was performed to characterize the bioactive putative conformation of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂. The results led to three significant observations that enabled us to propose a conformational behavior of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂.

Firstly, the presence of interresidue cross-peaks between aromatic ring protons of Cbz and C^αH (Leu) was detected (Figure 3). Conformational analysis of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ using molecular modeling studies revealed precisely that it was not possible to have a β-turn structure if such a connectivity cross-peaks is observed (Figure 4). Moreover, no cross-peaks connectivity between NH (Trp) and NH (Leu) were observed, while it is generally present in a β-turn arrangement [21]. These observations suggested that the peptide adopted an extended structure instead of a β-turn conformation. To verify these assumptions, the data derived

Table 2 ^1H Chemical Shifts of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ in DMSO-*d*₆ at 293 K (10 mg/ml)

Residue	δ (ppm)							$^3J(\text{NH-C}^\alpha\text{H})$ (Hz)
	NH	$\Delta\delta/\Delta T$ (ppb/K)	α	β	γ	δ	Other	
Pro			4.20–4.24	1.61–1.81, 2.00–2.10	1.61–1.84	3.24–3.48		
Leu	8.04	-2.1	4.32	1.22–1.40	1.44–1.53	0.64–0.82		8.7
Trp	8.46	-2.8	4.53	3.11–3.20			(ring) NH 10.91; H ₂ 7.18; H ₄ 7.46; H ₅ 6.96; H ₆ 7.05; H ₇ 7.33	7.0
Cbz							4.90–5.06; (ring) 7.28–7.32	
Bzl(CF ₃) ₂							5.16–5.25; (ring) H _{2'} and H _{6'} 7.94; H _{4'} 8.06	

Figure 2 ROESY connectivity diagram recorded at 300 MHz of a 10 mg/ml Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ solution in DMSO-*d*₆ showing selected interesidue cross-peaks a, b, c, d, e, f, g (for signification, see Figure 3).



Cbz-Pro-Leu-Trp-OBzl(CF ₃) ₂	
a	H ₄ - C ^β H (Trp)
b	Cbz (ring) - C ^δ H (Leu)
c	C ^α H (Leu) - C ^δ H (Leu)
d	C ^α H (Pro) - NH (Leu) C ^α H (Leu) - NH (Trp)
e	C ^α H (Trp) - H ₂ ' and / or H ₆ '
f	H ₄ - H ₂ ' and / or H ₆ '
g	H ₂ - H ₂ ' and / or H ₆ '

Figure 3 Representation of selected ROESY connectivities observed for Cbz-Pro-Leu-Trp-OBzl(CF₃)₂. The arrows indicate connectivities observed in the ROESY spectrum.

from ROESY was used to build models or to serve as inputs in constraint molecular dynamic studies. The NMR constraints previously obtained were employed for the selection of the tripeptide starting conformations. For this purpose, we used the information on the connectivity between the protons of the Cbz ring with that of the C^δH (Leu). The interaction between C^δH (Leu) and C^αH (Leu) was also considered. These elements reduced the number of *N*-terminal sequence conformations. Thus, an ordered γ -turn structure consisting of a folded segment stabilized by a putative hydrogen bond between NH (Leu) and the CO of Cbz was postulated. Energy minimization of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ allowed the next NH (Trp) to form a second γ -turn via an hydrogen bond with Leu. Interestingly, the conformation obtained after energy minimization positioned Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ into a rigidified *N*-terminal structure with two intramolecular hydrogen bonds. There was no evidence of any other stable structural features (Figure 5) in the Cbz-Pro-Leu-Trp segment.

The dual γ -turn structure proposition was de-

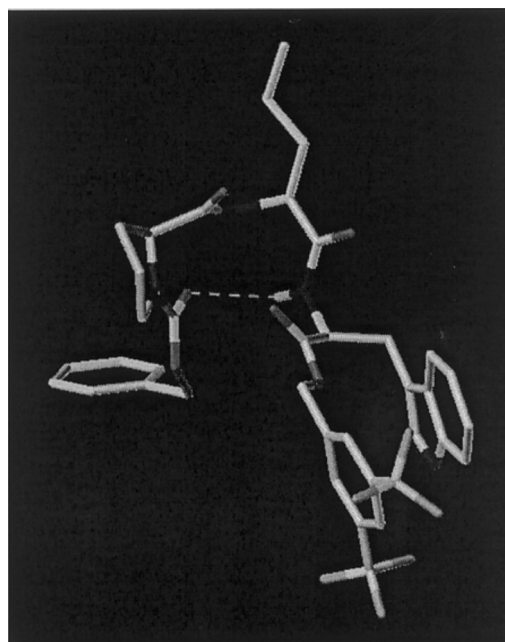


Figure 4 Stereoviews of a simulated β -turn Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ conformation.

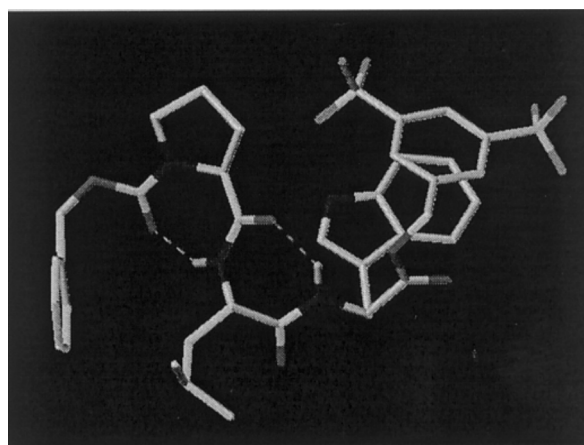


Figure 5 Stereoviews of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ calculated from simulated annealing and according to the ROESY connectivity data. H-bond and putative aromatic interactions are noted.

duced using amide chemical shift dependence on temperature: $\Delta\delta/\Delta T$. Both Leu and Trp had a low value temperature coefficient (> -3.0 ppb/K) in DMSO-*d*₆ at 298–338 K, which strongly supported the dual γ -turn suggestion.

Secondly, ROESY cross-peaks between C^αH (Pro)-NH (Leu) and C^αH (Leu)-NH (Trp) (Figure 3) were observed. Both elements concurred with the proposition of two γ -turns in the *N*-terminal moiety and allowed a trans conformation of Leu and Trp.

Thirdly, the results showed that the C-terminal sequence exhibited an intramolecular π - π interaction between the 3,5-bis(trifluoromethyl)benzyl group and indole moiety. Interresidue cross-peaks displayed connectivities between H₂ (indole), H₄ (indole), and C^oH (Trp) with H₂ and/or H₆. These observations indicated clearly that these two aromatic moieties, which are essential for NK₁ affinity [19], represent a global U-shaped pharmacophore. Moreover, as regards the aromatic interactions between the 3,5-bis(trifluoromethyl)benzyl group and indole moiety, the lowest energy calculation fitted with a face-to-face π - π interaction instead of an edge-to-face interaction. The orientation of the C-terminal sequence was in accordance with all observed ROESY connectivities.

The energy conformation between putative bioactive conformation (Figure 5) and a β -turn simulated conformation (Figure 4) was next compared. It was observed that the supposed conformation had lower energy ($\Delta E = 3.78$ kcal/mol) than the β -turn conformation ($\Delta E = 13.5$ kcal/mol).

Finally, to validate this study, a representative sample of the conformational space was generated by a 100-cycle simulated annealing experiment. Computation begun at 900 K and the system was held at that temperature for 2000 fs. The temperature was then reduced with exponential ramping until 300 K was reached. At this point, the conformation was noted for energy minimization. Ten conformations of Cbz-Pro-Leu-Trp-OBz(CF₃)₂ with an acceptable energy conformation ($\Delta E < 10$ kcal/mol) were selected. Conformation diversity was considerable, but only one structure concurred with the ROESY connectivities observed, which proved to be the conformation previously calculated (Figure 5).

Structure-Activity Relationships

Evaluation of NK₁/NK₂ receptor binding affinity (Table 1) revealed that the replacement of a Gly residue by Pro in the Cbz-Pro-Leu-Trp-OBz(CF₃)₂ (**2**) increased affinity and selectivity for NK₁ receptor. Conformational analysis of the tripeptide Cbz-Pro-Leu-Trp-OBz(CF₃)₂ deduced from combined NMR spectroscopy and molecular mechanics calculations enabled us to discuss the structure-function relationship with the NK₁ receptor.

In a previous report [19] concerning the 3,5-bis(trifluoromethyl)benzyl ester of tryptophan (L-732 138), a competitive and selective NK₁ antagonist (IC₅₀ = 1.6 nM for NK₁), we reported a

putative three-point pharmacophoric interaction between the NK₁ receptor and the antagonist. This interaction was imposed by indole residue, benzyl group and ester linkage via the carbonyl group (Figure 6). These elements established a global U-shaped pharmacophore favored by a face-to-face π - π interaction between the 3,5-bis(trifluoromethyl)benzyl group and indole moiety, which were both implicated in the interaction with two residues His²⁶⁵ and His¹⁹⁷ of the NK₁ receptor [27,28].

All the results obtained concerning the C-terminal sequence of Cbz-Pro-Leu-Trp-OBz(CF₃)₂ were in total agreement with those observed and led to the postulation that the C-terminal sequence was responsible for NK₁ affinity. The direct influence of the N-terminal sequence on the increased affinity for the NK₁ receptor seemed difficult to correlate with the structure of tripeptide **1**. The identification of Cbz-Gly-Leu-Trp-OBz(CF₃)₂ (**1**) as a lead compound [22] in the conception of dual NK₁/NK₂ ligand led us to explore the effect of chemical modifications in the amino acid side-chain and proved that the indolylmethyl and the Cbz carbamate groups were essential for NK₂ affinity. Replacement of a Gly residue by Pro in **1** made it possible to obtain a high selective NK₁ ligand. The suppression of NK₂ affinity seems to be related to the fact that N-terminal sequence was arranged in a rigid structure and that the Cbz ring interacted with C^oH (Leu), thus impeding any interaction.

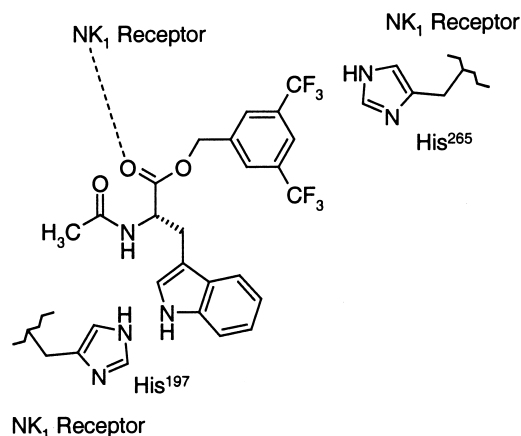


Figure 6 Representation of a proposed pharmacophoric receptor interaction of tryptophan ester NK₁ antagonist L-732 138 based on SAR data obtained from site-directed mutagenesis of the NK₁ receptor.

CONCLUSION

The synthesis of a suitable NK₁ ligand has been described and characterized. The three-dimensional structure of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ was studied by one and two-dimensional 300 MHz NMR experiments in DMSO and by molecular modeling. The results indicate that peptide **2** did not adopt a β -turn arrangement as expected on the basis of a previous report [21], but an extended conformation stabilized by a H-bond in two γ -turns. Together, the results show that the C-terminal architecture was stabilized by a face-to-face interaction between the 3,5-bis(trifluoromethyl)benzyl group and indole moiety. These two elements, which are essential for NK₁ affinity, concurred with our previous work and with results reported by other researchers [27–29]. The determination of the three-dimensional bioactive conformation of Cbz-Pro-Leu-Trp-OBzl(CF₃)₂ could be applied in the conception of non-peptidic NK₁ antagonists of direct therapeutic interest.

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