

Pharmacological characterisation of the highly Nav1.7 selective spider venom peptide Pn3a

Jennifer R. Deuis,¹ Zoltan Dekan,¹ Joshua S. Wingerd,¹ Jennifer J. Smith,¹ Nehan R. Munasinghe,² Rebecca F. Bhola,² Wendy L. Imlach,² Volker Herzig,¹ David A. Armstrong,³ K. Johan Rosengren,³ Frank Bosmans,⁴ Stephen G. Waxman,⁵ Sulayman D. Dib-Hajj,⁵ Pierre Escoubas,⁶ Michael S. Minett,⁷ Macdonald J. Christie,² Glenn F. King,¹ Paul F. Alewood,¹ Richard J. Lewis,¹ John N. Wood,⁷ Irina Vetter^{1,8*}

Supplementary Table 1: Energy and structural statistics of the 20 lowest energy structures of μ -TRTX-Pn3a calculated using a simulated annealing procedure with CNS

	μ -TRTX-Pn3a	STDEV
Energies:		
Overall (kcal/mol)	-1344	39.9
Bonds (kcal/mol)	22.6	1.48
Angles (kcal/mol)	58.6	4.08
Improper (kcal/mol)	20.6	2.70
Dihedral (kcal/mol)	169	2.99
Van Der Wall (kcal/mol)	-154	6.18
NOE (kcal/mol)	0.33	0.03
cDih (kcal/mol)	0.29	0.19
Electrostatic	-1461	45.8
RMSD:		
Bonds (Å)	1.28e-2	4.53e-4
Angles (°)	1.375	0.0436
Improper (Å)	1.43	0.1166
Dihedral (Å)	41.3	0.199
NOE (Å)	2.53e-2	1.15e-3
cDih (Å)	0.189	0.0671
Pairwise RMSD (Residues 2-31)		
Backbone atoms (Å)	0.33	0.07
Heavy atoms (Å)	116	0.12
Experimental Data:		
Distance Restraints:		
Intra-residue (i- j=0)	111	
Sequential (i-j = 1)	160	
Medium range (i-j <5)	67	

Long range (i-j \geq 5)	149
Dihedral restraints	43 backbone / 19 side chain
Hydrogen bond restraints	34 (for 17 hbonds)
NOE violations $>0.3 \text{ \AA}$	0
cDih violations $> 3.0^\circ$	1
Ramachandran statistics	
Residues in most favoured regions (%)	92
Residues in additionally allowed regions (%)	8
