Electronic Supplementary Information

Enantiorecognition in a multi-component environment

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Fig. S1. Electronic absorption, ECD and Raman spectra of AXT dissolved in THF in different concentrations for two enantiomeric forms of AXT – (3S,3'S) and (3*R*,3'*R*). Electronic absorption (**A**) and ECD (**B**) spectra were obtained for molar concentrations of AXT equal to 3.33 μ M and 10 μ M. Raman spectra (**C**) were obtained for two molar concentrations of AXT equal to 10 μ M and 30 μ M. Samples for electronic absorption and ECD measurements were diluted threefold in comparison to samples for Raman measurements, to keep absorbance below 1.5.

(3*S*,3'*S*)-AXT:BSA 3:1

(3*R*,3'*R*)-AXT:BSA 3:1



Fig. S2. Room temperature stability of the (3S,3'S)-AXT:BSA and (3R,3'R)-AXT:BSA systems monitored by electronic absorption and ECD in the 300-700 nm range. Electronic absorption (**A**,**B**) and ECD (**C**,**D**) spectra of the AXT:BSA complexes with a molar ratio of AXT to BSA equal to 3:1 were measured for 29 days (C_{AXT} = 30 μ M, C_{BSA} = 10 μ M). A new portion of the sample was measured every time.



Fig. S3. Room temperature stability of the (3S,3'S)-AXT:BSA and (3R,3'R)-AXT:BSA systems monitored by electronic absorption and ECD in the 200-300 nm range. Electronic absorption (**A**) and ECD (**B**) spectra of the AXT:BSA complexes with a molar ratio of AXT to BSA equal to 3:1 were measured for 29 days (C_{AXT} = 1.5 μ M, C_{BSA} = 0.5 μ M). A new portion of the sample was measured every time.



Fig. S4. ECD spectra of AXT:BSA complexes for two enantiomeric forms of AXT – (3S,3'S) and (3R,3'R) as well as for BSA dissolved in PBS. The ECD spectra of AXT:BSA complexes were measured for two molar ratios of AXT to BSA equal to 1:1 and 3:1 (C_{AXT} = 0.5 and 1.5= μ M; C_{BSA} = 0.5 μ M).



Fig. S5. Electronic absorption, ECD and Raman spectra of (*rac*)-AXT dissolved in THF in different concentrations. Electronic absorption (**A**) and ECD (**B**) spectra were obtained for two molar concentrations of AXT equal to 5 μ M and 10 μ M. Raman spectra (**C**) were obtained for two molar concentrations of AXT equal to 10 μ M and 30 μ M. Samples for electronic absorption and ECD measurements were diluted two-fold in comparison to Raman measurements, to keep absorbance below 1.5.* indicates the characteristic band for THF solvent.



Fig. S6. Root mean square displacement (RMSD) of α -carbon atoms (C α) of the BSA binding pocket residues for: (**A-C**) (3*S*,3'*S*)-AXT:BSA; (**E-G**) (3*R*,3'*R*)-AXT:BSA; (**D**) (3*R*,3'*S*)-AXT:BSA; (**H**) (3*S*,3'*R*)-AXT:BSA. For (3*S*,3'*S*)-AXT:BSA and (3*R*,3'*R*)-AXT:BSA, the results of three independent runs are shown.



Fig. S7. Calculated ECD spectra of (3*S*,3'*S*)-AXT dimers based on the structures extracted from the molecular dynamics simulation, compared to the structures of the dimers, their helicity, angles and distances between C14-C14 and C14'-C14' pairs of atoms.



Fig. S8. Coulomb and van der Waals (vdW) interaction energy between AXTi-AXTj and AXTk-BSA for (35,3'S)-AXT:BSA systems (results of 3 runs are presented).



Fig. S9. Coulomb and van der Waals (vdW) interaction energy between AXTi-AXTj and AXTk-BSA for (3*R*,3'*S*)-AXT:BSA and (3*S*,3'*R*)-AXT:BSA systems.



Fig. S10. Number (#) of H-bonds between AXT-AXT and AXT-BSA for (35,3'S)-AXT:BSA system (results of three independent runs are shown).



Fig. S11. Number (#) of H-bonds between AXT-AXT and AXT-BSA for (3R,3'R)-AXT:BSA system (results of three independent runs are shown).



Fig. S12. Number (#) of *H*-bonds between AXT-AXT and AXT-BSA for (3*R*,3'*S*)-AXT:BSA and (3*S*,3'*S*)-AXT:BSA systems.



Fig. S13. Number of *H*-bonds in BSA as a function of physical time for: (**A-C**) (3S,3'S)-AXT:BSA; (**E-G**) (3R,3'R)-AXT:BSA; (**D**) (3R,3'S)-AXT:BSA; (**H**) (3S,3'R)-AXT:BSA. For (3S,3'S)-AXT:BSA and (3R,3'R)-AXT:BSA, the results for the three independent runs are shown.



Fig. S14. Number of salt bridges in BSA as a function of physical time for: **(A-C)** (3S,3'S)-AXT:BSA; **(E-G)** (3R,3'R)-AXT:BSA; **(D)** (3R,3'S)-AXT:BSA; **(H)** (3S,3'R)-AXT:BSA. For (3S,3'S)-AXT:BSA and (3R,3'R)-AXT:BSA, the results for the three independent runs are shown.



Fig. S15. Radius of gyration of BSA as a function of physical time for: (**A-C**) (3S,3'S)-AXT:BSA; (**E-G**) (3R,3'R)-AXT:BSA; (**D**) (3R,3'S)-AXT:BSA; (**H**) (3S,3'R)-AXT:BSA. For (3S,3'S)-AXT:BSA and (3R,3'R)-AXT:BSA, the results for the three independent runs are shown.



Fig. S16. Head-to-tail distance of BSA as a function of physical time for: (**A-C**) (3S,3'S)-AXT:BSA; (**E-G**) (3R,3'R)-AXT:BSA; (**D**) (3R,3'S)-AXT:BSA; (**H**) (3S,3'R)-AXT:BSA. For (3S,3'S)-AXT:BSA and (3R,3'R)-AXT:BSA, the results for the three independent runs are shown.



Fig. S17. Secondary structure of the BSA residues as a function of physical time for (3*S*,3'*S*)-AXT:BSA system (results of three independent runs are shown).



Fig. S18. Secondary structure of the BSA residues as a function of physical time for (3R,3'R)-AXT:BSA system (results of three independent runs are shown).



Fig. S19. Secondary structure of the BSA residues as a function of physical time for (3R,3'S)-AXT:BSA and (3S,3'R)-AXT:BSA systems.



Fig. S20. Secondary structure of the binding pocket residues of the BSA for: (**A-C**) (3S,3'S)-AXT:BSA; (**E-G**) (3R,3'R)-AXT:BSA; (**D**) (3R,3'S)-AXT:BSA; (**H**) (3S,3'R)-AXT:BSA. For (3S,3'S)-AXT:BSA and (3R,3'R)-AXT:BSA, the results of three independent runs are shown.

Table S1. Ratio of integral intensity of 1520 and 1160 cm⁻¹ bands in resonance Raman (RR) and RROA spectra for (3*S*,3'*S*)-AXT:BSA and (3*R*,3'*R*)-AXT:BSA complexes with molar ratio of AXT to BSA equal to 1:1 and 3:1.

	Ratio of integral intensity of bands for		Ratio of integral intensity of bands for	
	(3S,3'S)-AXT		(3R,3'R)-AXT
	I _{RR 3:1} /I _{RR 1:1}	I _{RROA 3:1} /I _{RROA 1:1}	I _{RR 3:1} /I _{RR 1:1}	IRROA 3:1/IRROA 1:1
1520 cm ⁻¹	2.532	9.009	2.457	7.813
1160 cm ⁻¹	2.451	9.524	2.439	7.634

Table S2. The Chemscore docking results for (3R,3'R)-AXT, (3S,3'S)-AXT, *meso* AXT with either S- or Rend in the binding pocket.*

	Chemscore
(3 <i>R,</i> 3' <i>R</i>)-AXT	34,12
(3 <i>S</i> ,3' <i>S</i>)-AXT	34,73
meso AXT (S-end in the pocket)	36,10
meso AXT (R-end in the pocket)	33,59

*The highest binding affinity is found for the *meso* AXT with the S-end in the deep binding site region.