

**Figure S1 a,** nAChR is a hetero-pentameric receptor with two ligand binding sites (green) in its extracellular domain (ECD). Regions of ion selectivity are shown in red. A putative gate (purple) is located in the transmembrane domain. **b,** Homomeric AChBP is homolous to the ECD of the nAChR with five ligand binding sites. A, water filled  $Ac_A$ ChBP vestibule is shown with one subunit removed. Vestibule waters are colored in yellow. Ten oxygen atoms at the constriction point are colored red and make a plane of two pentameric rings (108° angles) orthogonal to the five fold axis. **c,** Top view looking down the vestibule of AChBP.

Table S1 Data Collection &	Refinement Statistics
Data collection	SO <sub>4</sub> <sup>2-</sup> /cacodylate
Beamline	ALS/ 8.2.2
Wavelength (Å)	1.00
Space group	P4 <sub>1</sub>
a, b, c (Å)	98.4, 98.4, 265.7
Pentamer / asymmetric unit	2
Resolution range <sup>1</sup>	50 –3.08 (3.19 – 3.08)
R <sub>merge</sub> (%) <sup>1,2</sup>	13.1 (48.8)
Observations	294,191
Unique reflections	46,364
Completeness (%) <sup>1</sup>	100 (100)
Redundancy <sup>1</sup>	6.3 (6.3)
<i σi=""> 1</i>	14.3 (4.0)
B-factor from Wilson plot (Ų)	64.0
Refinement	
Resolution range (Å)	20 – 3.1
Protein atoms	17346
Solvent / PEG atoms	293 / 105
R <sub>cryst</sub> (%) / R <sub>free</sub> (%)	21.2 / 25.0
Free reflections	2,300
R.m.s. 1-2 bond distances (Å)	0.012
R.m.s. 1-3 bond angles (°)	1.441
Mean main / side chain B (Ų)	50.1 /50.8
Mean B solvent /PEG (Ų)	17.5 / 69.9
PDB accession code	Xxxx

Values in parentheses are for the highest resolution shell.

 $<sup>^{2} \; \</sup>mathsf{R}_{\mathsf{merge}} = \Sigma_{\mathit{hkl}} \; \Sigma_{\mathit{i}} \; | \; \mathsf{I}_{\mathit{hkli}} \; - \; <\mathsf{I}_{\mathit{hkli}} > \mathsf{j} / \Sigma_{\mathit{hkl}} \; \Sigma_{\mathit{i}} < \mathsf{I}_{\mathit{hkli}} > \mathsf{;} \; \; R_{\mathit{cryst}} = \; \Sigma || F_{o} | \; - \; | F_{c} || / \Sigma |F_{o} |$