Table S2. Formation of ligand binding sites.

	Cm	Dxc	LDAO
Y30$^{TM1.3}$	3.4	4.0	3.9
N33$^{TM1.2}$	2.8	3.9	3.2
D34$^{TM1.2}$	2.4	2.4	3.2
M58$^{TM2.1}$	3.6	3.7	3.5
L62$^{TM2.2}$	3.7	3.4	3.9
L119$^{TM4.3}$	3.9		
A150$^{TM5.3}$	3.2		
L151$^{TM5.3}$	3.4		
P154$^{TM5.2}$		3.4	
S232$^{TM7.4}$			3.8
L235$^{TM7.3}$	3.7		
L236$^{TM7.3}$	3.6	3.7	3.8
I239$^{TM7.2}$	3.5		3.9
L268$^{TM8.3}$	3.9		
S350$^{TM11.5}$		3.9	
G354$^{TM11.4}$		3.7	
Q357$^{TM11.4}$		3.3	
M358$^{TM11.3}$		3.5	
F361$^{TM11.3}$			3.9

Closest distances (within 4.0 Å) between non-hydrogen atoms of the ligand and individual amino acid residues are reported. Colour code: green indicates short distances and red long distances. In the first column, residues from the N- and C-domains are highlighted in cyan and yellow, respectively.