

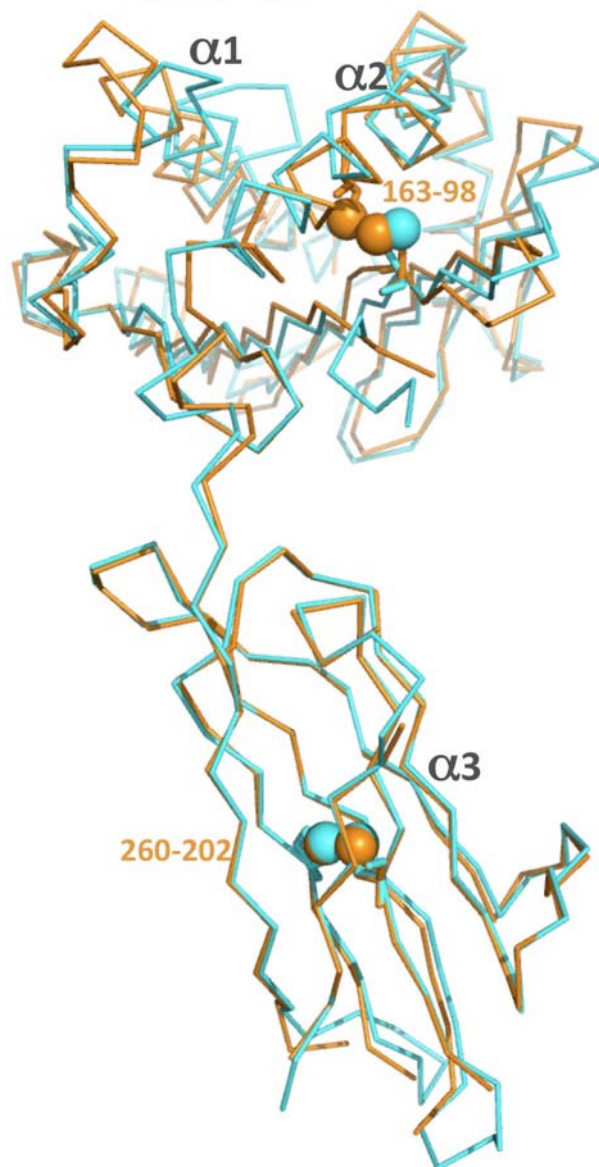
Supplemental Legends:

Figure S1. Disulfide bonds on chicken CD1 structures. The structure of the heavy chain of chCD1-1 (orange) is superimposed on chCD1-2 structure (cyan). Both possess the conserved disulfide bond (ball-and-stick format) on the $\alpha 3$ domain, however, chCD1-2 lacks the other conserved disulfide bond on the antigen binding domain.

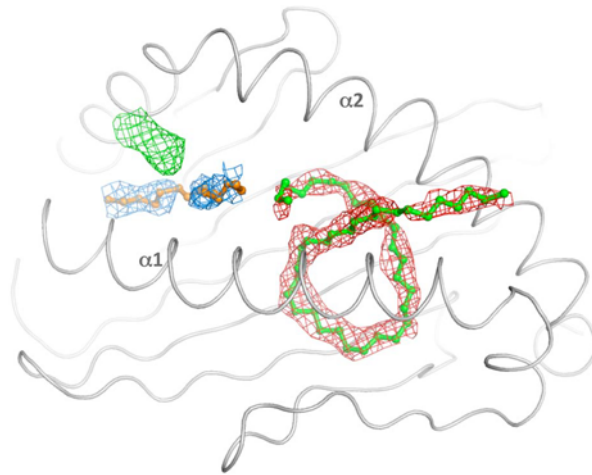
Figure S2. Composite omit map around the refined ligands. The structure of the chCD1-1 binding groove is shown with a similar view as in Figure 3a. The ligands are drawn as balls and sticks, green in the A' pocket and orange in the F' pocket. Composite omit map was calculated in Phenix (45) using the refined coordinates of the structure excluding the ligands. The map is contoured at 1 and 0.9 σ in the A' and F', respectively.

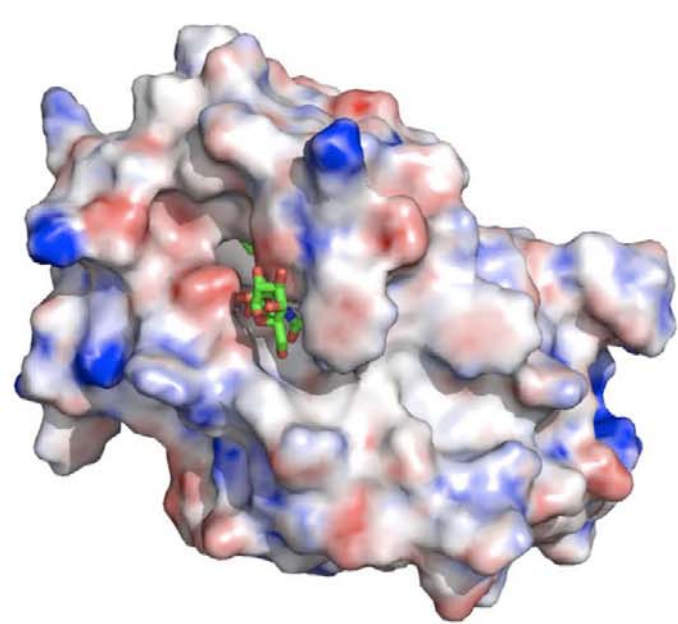
Figure S3. Electrostatic surfaces of CD1 lipid-binding domains. Atomic charge values were calculated using PDB2PQR (46) based on the coordinates for $\alpha 1$ - $\alpha 2$ superdomain of hCD1a (1ONQ), hCD1b (1UQS), hCD1d (1ZT4), chCD1-2 (3DBX) and of chCD1-1 reported here (3JVG). The electrostatic properties were then evaluated using APBS (47) and displayed in PyMol (32).

Zajonc, Figure -S1

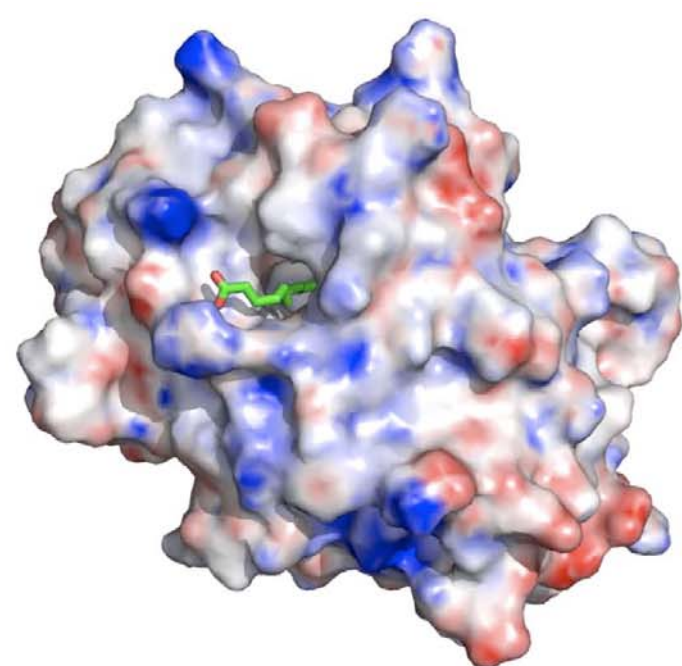


Zajonc, Supplementary Figure 2

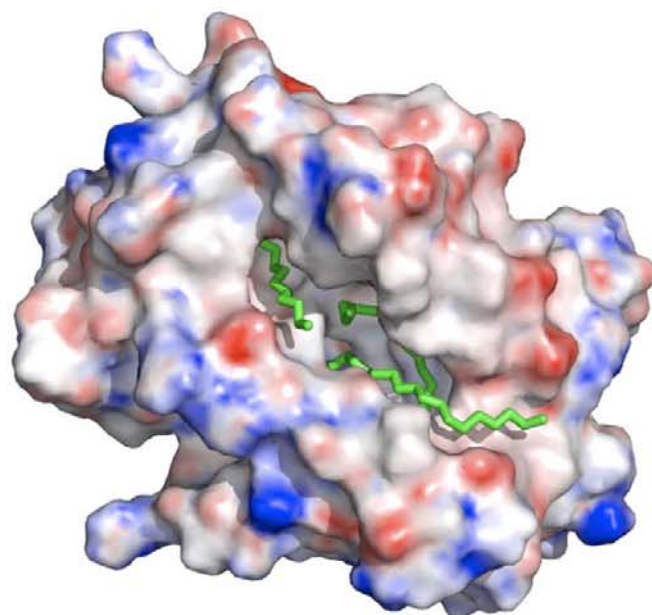




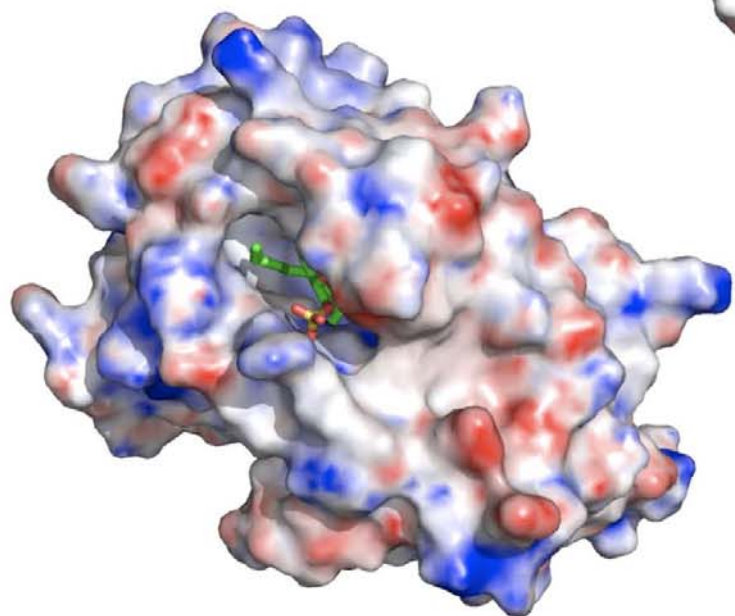
hCD1D



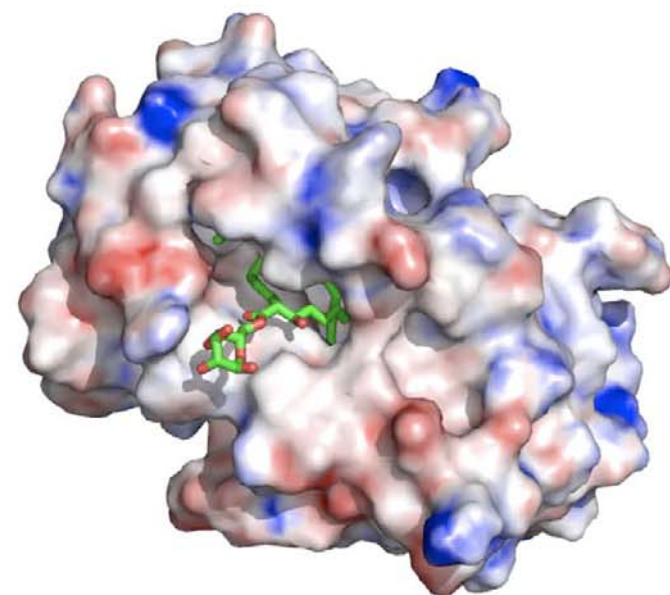
chCD1-2



chCD1-1



CD1a



hCD1B

Supplementary Table 1. Identity and similarity scores for sequence alignments of CD1 antigen binding domains.

Identity Scores (%)

	chCD1-1	chCD1-2	hCD1a	hCD1b	hCD1c	hCD1d	hCD1e	mCD1d1
chCD1-1	100	24.2	24.7	27.5	22	24.2	25.3	23.9
chCD1-2	45.1	100	17	19.8	16.5	14.3	19.2	17.9
hCD1a	44.5	40.1	100	49.2	50.5	37.6	47.5	38.3
hCD1b	49.5	42.9	63.5	100	57.1	40.9	48.1	38.3
hCD1c	42.9	42.9	68.1	72	100	40.7	45.6	38
hCD1d	50	40.7	60.8	63	62.1	100	44.8	61.2
hCD1e	47.8	41.2	66.3	68	69.8	67.4	100	42.6
mCD1d1	45.1	41.8	57.4	56.8	59.2	74.3	58.5	100

Similarity Scores (%)