



STRUCTURAL BIOLOGY  
COMMUNICATIONS

**Volume 73 (2017)**

**Supporting information for article:**

**Crystal structure of an anti-idiotypic variable lymphocyte receptor**

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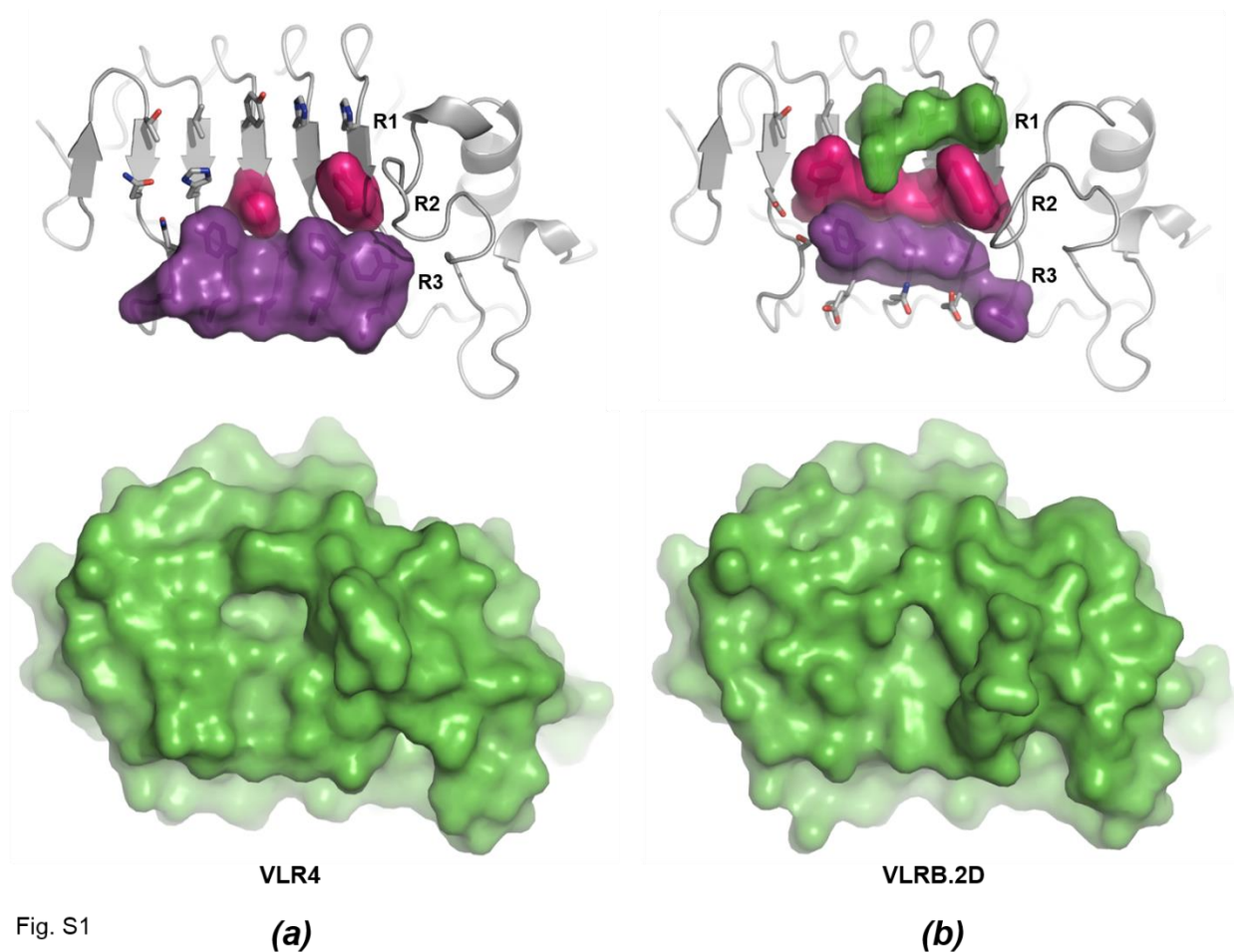


Fig. S1

**Figure S1** Antigen binding surfaces of protein binding VLRs. Concave face of VLR4 (a) and VLRB.2D (b) shown as cartoon representation with upward-facing side chains shown as sticks (top). Side chains involved in interactions with antigen that comprise the three “ridges” (R1, R2, R3) on the concave face, as described in (Deng *et al.*, 2013), are shown as a surface representation. Residues that do not interact with antigen are shown only as sticks. The VLR4 R1 ridge does not interact with antigen and the R3 ridge is comprised of residues that interact with antigen but are not part of the concave face. (Bottom) Surface representation of the concave face of each VLR.

**Table S1** Selected X-ray data collection statistics by resolution shell

<b>Resolution Limit</b>	<b>Observed</b>	<b>Unique</b>	<b>Possible</b>	<b>Completeness</b>	<b>Rmerge</b>	<b>Rmeas</b>	<b>I/sigma</b>	<b>CC<sub>1/2</sub></b>
4.47	21281	5937	6439	92.2%	4.2%	4.9%	26.15	99.7
3.17	36175	10439	11588	90.1%	4.8%	5.6%	24.67	99.5
2.59	47010	13420	15015	89.4%	5.6%	6.6%	20.93	99.4
2.25	59095	16297	17729	91.9%	7.0%	8.2%	17.44	99.2
2.01	64617	17736	20123	88.1%	9.3%	10.9%	13.24	98.8
1.83	76974	20394	22233	91.7%	14.0%	16.3%	9.01	98.1
1.70	79834	21151	24182	87.5%	22.8%	26.6%	5.20	95.2
1.59	89681	23444	25922	90.4%	38.5%	44.7%	3.06	87.9
1.50	61883	16525	27660	59.7%	62.0%	72.3%	1.74	94.2
Total	536550	145343	170891	85.1%	6.4%	7.5%	11.06	99.7