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## Supplementary Material

Determination of  $pK_a$  values of carboxyl groups in the N-terminal domain of rat CD2: anomalous  $pK_a$  of a glutamate on the ligand binding surface

Ho Ann Chen<sup>‡</sup>, Mark Pfuhl<sup>‡</sup>, Mark S. B. McAlister<sup>‡,§</sup>, Paul C. Driscoll<sup>‡,1,\*</sup>

<sup>‡</sup> Department of Biochemistry and Molecular Biology, University College London, Gower Street, London WC1E 6BT, U. K.

§ Present Address: Department of Crystallography, Birkbeck College, Malet Street, London WC1E 7HX., U. K.

<sup>1</sup> Ludwig Institute for Cancer Research, 91 Riding House Street, London W1P 8BT, U. K.

\* To whom correspondence should be addressed:

Dr. Paul C. Driscoll

Department of Biochemistry and Molecular Biology,

University College London,

Gower Street,

London WC1E 6BT.

E-mail: driscoll@biochem.ucl.ac.uk

Tel. +44-20 7679 7035

Fax. +44-20 7679 7193

Figure S1. Regions of the 2D H(C)CO spectra from the pH titration of rat CD2d1 showing glutamic acid and aspartic acid cross peaks at pH 8, pH 5 and pH 3. The spectra were recorded at 25°C at a protein concentration of 1.2 mM, in 20 mM phosphate buffer.

Figure S2. pH dependence of chemical shift of protons adjacent to the carboxyl groups  $(H^{\gamma})$  for Glu,  $H^{\beta}$  for Asp) in CD2d1. Both of the chemical shift profiles for the two methylene protons of selected carboxyl groups are shown. The chemical shift profiles were fit to a multi-component Henderson-Hasselbalch equation as described in the text.

**Table S1.** Acidity constants (p $K_a$  values) determined from the pH titration of rat CD2d1 monitored by 2D [ $^{15}$ N, $^{1}$ H]-HSQC experiments.

Residue	Ionising	$pK_a$ value <sup>c</sup>							
(nucleus) <sup>a</sup>	group <sup>b</sup>						<b>.</b>		
		No	100 mM	300 mM	Bis-tris	E41Q	E29Q		
		NaCl	NaCl	NaCl					
Asp2 (N)	Asp2	3.6	3.7	3.5	3.5	3.3	3.2		
: :	$\alpha$ -NH <sub>2</sub>	7.1	7.4	<sup>d</sup>	7.0	6.9	7.2		
His12 (N)	His12	6.8	6.9	6.9	6.7	6.5	6.8		
	Glu99	4.3	4.1	4.1	4.4	4.3	3.6		
Ile18 (H <sup>N</sup> )	Asp62	4.4	4.3	4.3	4.2	4.1	4.0		
Asp25 (N)	Asp25	3.7	3.6	3.5	3.6	3.4	3.3		
Asp26 (N)	Asp26	3.7	3.7	3.5	3.6	3.5	3.1		
Asp28 (H <sup>N</sup> )	Asp28	3.4	3.4	3.3	3.3	3.5	3.2		
	Glu41	7.1	6.9	6.9	7.0	-	5.0		
Glu29 (H <sup>N</sup> )	Glu41	6.6	6.6	6.6	6.8	-	5.0		
Glu29 (N)	Glu41	6.6	5.8	5.2	6.4	-	4.9		
	Asp28	3.4	3.1	3.3	3.5	3.1	2.9		
Glu33 (N)	Glu33	4.3	4.2	4.1	4.1	4.3	3.6		
Glu41 (H <sup>N</sup> )	Glu41	6.9	6.8	6.7	6.8	-	5.1		

	Glu29	4.9	4.9	4.6	4.8	4.6	- ;
Lys43 (N)	Glu41	6.7	6.6	6.8	6.7	-	5.1
	Glu29	4.9	4.8	4.7	4.5	4.4	<u>-</u>
Ser52 (N)	Glu41	6.8	6.7	6.7	6.7	-	-
Glu56 (H <sup>N</sup> )	Glu56	4.0	4.0	4.0	3.9	3.7	3.8
Asn60 (H <sup>N</sup> )	Asp62	4.4	4.3	4.0	4.2	4.1	4.0
Asp62 (H <sup>N</sup> )	Asp62	4.2	4.2	4.0	4.1	4.0	4.0
Thr69 (H <sup>N</sup> )	Asp72	4.3	4.3	4.3	4.1	4.4	3.6
Arg70 (N)	Asp71	3.1	3.3	2.9	3.4	3.0	3.1
Asp71 (H <sup>N</sup> )	Asp72	4.5	4.5	4.5	4.3	4.2	4.2
Asp72 (N)	Asp72	4.5	4.5	4.6	4.2	4.2	4.1
Thr79 (N)	Glu41	6.7	6.6	6.6	6.7	_ ` `;	. <b>-</b>
Asp94 (N)	Asp94	4.1	4.0	4.0	4.0	3.8	3.7
Glu99 (N)	Glu99	4.6	4.9	5.0	4.7	4.4	4.4
	α-СООН	3.3	3.5	3.3	3.4	3.1	3.1

## Notes

<sup>&</sup>lt;sup>a</sup> Residue identification and nucleus (in brackets) giving rise to the resonance for which the chemical shift variation was monitored as a function of pH. Chemical shift pH profiles were fit to the Henderson-Hasselbalch equation as described in the text.

<sup>&</sup>lt;sup>b</sup> The ionisable groups identified to be responsible for the  $pK_a$  values derived from fitting. If more than one  $pK_a$  is apparent in the chemical shift pH profile, only those

values which give rise to changes in chemical shift  $\Delta\delta > 0.05$  ppm for  $H^N$  protons and  $\Delta\delta > 0.5$  ppm for  $^{15}N$  chemical shifts are listed.

 $^{\circ}$  p $K_{\rm a}$  values were determined for wild-type CD2d1 at varying salt and buffer conditions as indicated, and separately for the E41Q and E29Q CD2d1 mutants at low ionic strength. All titrations were performed in 20 mM phosphate except for the experiment for wild-type CD2d1 in 10 mM Bis-tris buffer.

<sup>&</sup>lt;sup>d</sup> pK<sub>a</sub> value not determined due to increased amide proton exchange at higher salt concentration.

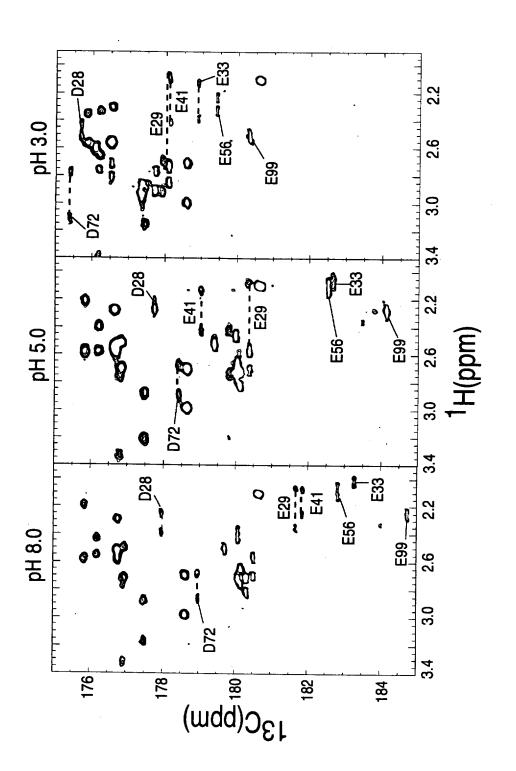


Figure S

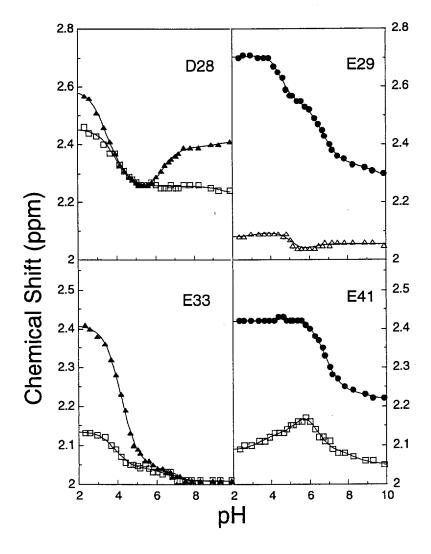


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