Supporting Information

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Table S1. Data collection and refinement statistics (SAD)

	CDH23 EC1–EC2	CDH23 EC1–EC2 (Eu peak L3)
Data collection		
Space group	P21	P21
Cell dimensions		
a, *b*, *c* (Å)	38.37, 64.20, 47.85	38.38, 64.60, 47.94
α, β, γ (°)	90, 110.89, 90	90, 110.50, 90
Resolution (Å)	23–1.1	44–2.5
R_{sym} or R_{merge}	0.08 (0.49)	0.188 (0.33)
$I/\sigma I$	11.49 (1.51)	11.0 (9.63)
Completeness (%)	92.3 (75.2)	96.6 (94.3)
Redundancy	3.4	7.3
Figure of merit (RESOLVE)		0.76
Refinement		
Resolution (Å)	23–1.1	44–2.5
No. reflections	277,629	55,283
R_{work}/R_{free}	0.163/0.187	0.169/0.223
No. atoms		
Protein	1,667	1,580
Ligand/ion	28	6
Water	279	68
Avg. *B*-factors		
Protein	12.4	12.6
Water	27.8	13.0
R.m.s. deviations		
Bond lengths (Å)	0.0095	0.0198
Bond angles (°)	1.354	1.760

Values in parentheses are for highest-resolution shell. A single crystal was used to collect each data set.