PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2M2D-17	A_ARG_139	NH1	A_GLU_136	OE1	2.931
2M2D-17	A_ARG_139	NH2	A_GLU_136	OE1	2.794
2M2D-27	A_ARG_139	NH1	A_GLU_136	OE1	2.983
2M2D-27	A_ARG_139	NH2	A_GLU_136	OE1	2.775
2M2D-31	A_ARG_139	NH2	A_GLU_136	OE1	2.789
2M2D-35	A_ARG_139	NH1	A_GLU_136	OE1	2.862
2M2D-35	A_ARG_139	NH2	A_GLU_136	OE1	2.782
3BIK	A_ARG_113	NH2	B_GLU_136	OE2	3.149
3BIK	A_ARG_125	NH2	B_GLU_136	OE1	3.033
3BIK	A_ARG_125	NH2	B_GLU_136	OE2	3.001
3SBW	B_ARG_114	NH2	A_GLU_136	OE1	3.450
3SBW	C_ARG_113	NH2	B_GLU_136	OE1	3.510
3SBW	C_ARG_125	NH1	B_GLU_136	OE1	3.198
3SBW	C_ARG_125	NH1	B_GLU_136	OE2	2.810
4ZQK	A_ARG_113	NH2	B_GLU_136	OE1	2.645
4ZQK	A_ARG_113	NH2	B_GLU_136	OE2	2.986
5GGR	Y_ARG_139	NH2	Y_GLU_136	OE1	3.539
5GGR	Z_ARG_139	NH1	Z_GLU_136	OE1	3.800
5GGR	Z_ARG_139	NH2	Z_GLU_136	OE1	3.965
5GGR	Z_ARG_139	NH2	Z_GLU_136	OE2	3.968
5GGS	Z_ARG_139	NH2	Z_GLU_136	OE1	3.912

Table 1: Glu136-linked salt bridging networks within the experimentally determined PD-1/PD-L1 structures. In this table, the residue naming scheme is **Chain ID_residue name_residue number**. As PDB ID 2M2D represents an NMR (Nuclear Magnetic Resonance) ensemble, 2M2D-17 represents the 17^{th} structural model of PD-1 experimentally determined by NMR spectroscopy.