Table 2: Thermodynamic parameters for PSGL1-VISTA interactions determined by ITC

Syringe	[Syringe] (μM)	Cell	[Cell] (μM)	Temperature (°C)	pH	n	K_A (M^{-1})	KD (μM)	ΔG (kcal/mol)	ΔH (kcal/mol)	TΔS (kcal/mol)	ΔS (cal/mol/K)
PSGL1-Fc	200	VISTA-His	10	25	6.0	1.58 ± 0.05	(3.66 ± 0.54) x 10^5	2.73 ± 0.41	-7.6	-14.4 ± 0.6	-6.8	-22.9
PSGL1-Fc	200	VISTA-Fc	10	25	6.0	1.20 ± 0.04	(1.53 ± 0.40) x 10^6	0.65 ± 0.17	-8.4	-14.3 ± 0.6	-5.9	-19.8
PSGL1-Fc	130	VISTA-Fc	10	25	6.0	1.10 ± 0.02	(1.19 ± 0.15) x 10^6	0.84 ± 0.11	-8.3	-14.8 ± 0.4	-6.5	-22
PSGL1-Fc	130	VISTA-Fc	10	37	6.0	1.19 ± 0.04	(3.44 ± 0.53) x 10^5	2.91 ± 0.45	-7.9	-16.0 ± 0.8	-8.1	-26.4
PSGL1-Fc	130	VISTA-Fc	10	25	7.4	no detectable binding						
PSGL1-Fc	130	VISTA-Fc	10	37	7.4	no detectable binding						
VISTA-Fc	352	PSGL1-Fc	45	25	7.4	no detectable binding						

The dissociation constant K_D was calculated using the equation $K_D=1/K_A$ (K_A: Association constant). ΔG and TΔS were calculated using the relationships $\Delta G = -RT \ln K_A$ and $\Delta G=\Delta H-T\Delta S$, respectively. The data are representative of one experiment. The listed errors indicate the error of the fit to the "one set of sites" binding model.