

Table 2. Binding parameters of GIP and GLP-1 variants

Peptide	K_d (μM)		Stoichiometry	ΔH (kJ mol^{-1})	$-\Delta\Delta H^*$ (kJ mol^{-1})	$-T\Delta S^{**}$ (kJ mol^{-1})	$-T\Delta\Delta S^{a,b}$ (kJ mol^{-1})
GIP ₁₋₄₂	1.1 ± 0.1	0.1	1.0 ± 0.1	-92.7 ± 0.4	-	59.2 ± 1.2	-
GIP ₁₋₄₂ D15A	1.4 ± 0.1	0.1	1.1 ± 0.1	-83.8 ± 0.4	8.9	50.9 ± 1.7	8.3
GIP ₁₋₄₂ Q19A	1.5 ± 0.2	0.2	1.0 ± 0.1	-85.4 ± 1.3	7.3	52.6 ± 5.8	6.6
GIP ₁₋₄₂ Q20A	2.2 ± 0.1	0.1	1.0 ± 0.1	-79.0 ± 0.3	13.7	47.2 ± 1.9	12.0
GIP ₁₋₄₂ F22A	210.5 ± 21.6	21.6	1.3 ± 0.1	-73.6 ± 11.3	19.1	53.0 ± 13.4	6.2
GIP ₁₋₄₂ V23A	139.1 ± 10.0	10.0	0.6 ± 0.1	-58.6 ± 10.4	34.1	36.9 ± 11.9	22.3
GIP ₁₋₄₂ L26A	5.5 ± 0.2	0.2	1.1 ± 0.1	-97.6 ± 1.2	-4.9	68.1 ± 2.3	-8.9
GIP ₁₋₄₂ L27A	104.7 ± 3.6	3.6	1.1 ± 0.1	-58.7 ± 2.3	34.0	36.3 ± 3.1	22.9
GIP ₁₋₄₂ K30A	0.7 ± 0.1	0.1	1.1 ± 0.1	-86.4 ± 0.2	6.3	51.9 ± 5.1	7.3
GIP ₁₃₋₄₂	6.8 ± 0.2	0.2	1.1 ± 0.1	-77.3 ± 0.6	15.4	48.2 ± 1.7	11.0
GIP ₁₅₋₄₂	11.9 ± 0.5	0.5	1.1 ± 0.1	-78.7 ± 1.1	14.0	51.0 ± 2.4	8.2
GIP ₁₇₋₄₂	15.2 ± 0.5	0.5	1.1 ± 0.1	-67.6 ± 0.7	25.1	40.5 ± 1.5	18.7
GIP ₁₉₋₄₂	34.5 ± 0.9	0.9	1.1 ± 0.1	-58.7 ± 0.8	34.0	33.6 ± 1.4	25.6
GIP ₂₁₋₄₂	105.6 ± 4.8	4.8	0.9 ± 0.1	-52.3 ± 3.7	40.4	29.9 ± 4.7	29.3
GIP ₂₃₋₄₂	n.d.		n.d.	n.d.	-	n.d.	-
GIP ₁₋₄₂ + 9% MCD***	5.4 ± 0.1	0.1	1.1 ± 0.1	-109.4 ± 0.2	-16.7	79.7 ± 0.5	-20.5
GLP-1 ₇₋₃₆	13.5 ± 0.8	0.8	1.2 ± 0.1	-39.5 ± 0.8	53.2	12.1 ± 2.3	47.1
GLP-1 ₇₋₃₆ E15D	18.2 ± 0.8	0.8	1.4 ± 0.1	-45.7 ± 0.5	47.0	19.0 ± 1.6	40.2
GLP-1 ₇₋₃₆ A19Q	24.1 ± 1.1	1.1	1.2 ± 0.1	-39.0 ± 0.7	53.7	13.1 ± 1.9	46.1
GLP-1 ₇₋₃₆ E15D/A19Q	19.9 ± 0.8	0.8	1.3 ± 0.1	-48.9 ± 0.7	43.8	22.4 ± 1.8	36.8
GLP-1 ₇₋₃₆ K20Q	12.0 ± 0.7	0.7	1.3 ± 0.1	-38.9 ± 0.9	53.8	11.3 ± 2.5	47.9

Errors correspond to standard deviation of non-linear least-squares fit of the data points in the titration curve. n.d., not determined.

* Relative to binding of GIP₁₋₄₂.

** T = 293 K.

*** 9% Methyl- β -Cyclodextrin being present in titrand (GIP₁₋₄₂) and analyte (GIPR ECD) solution.