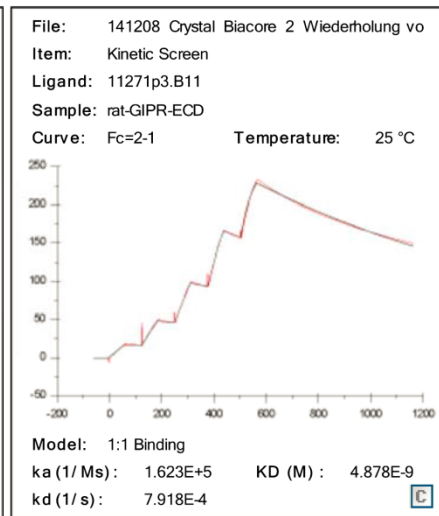
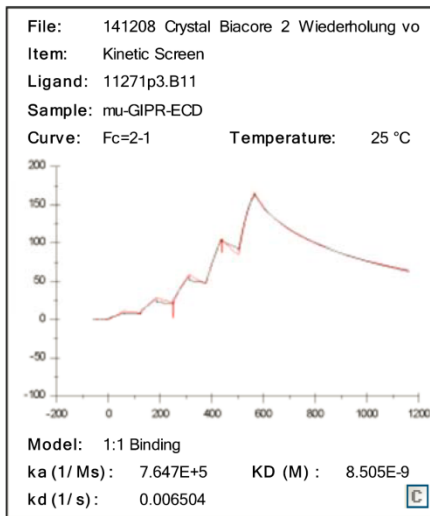
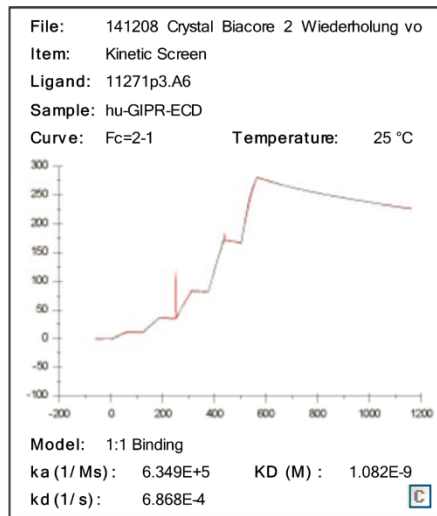
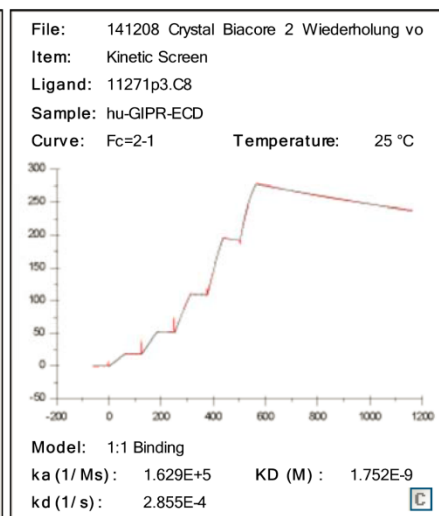
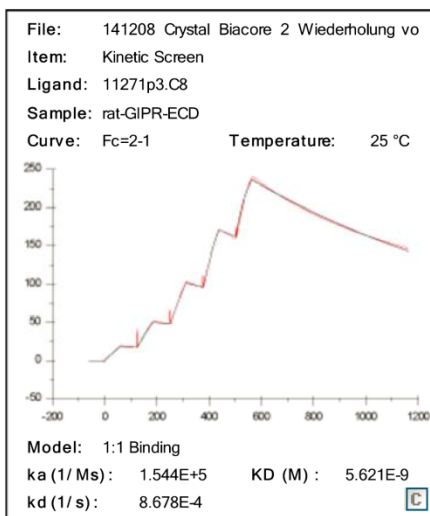
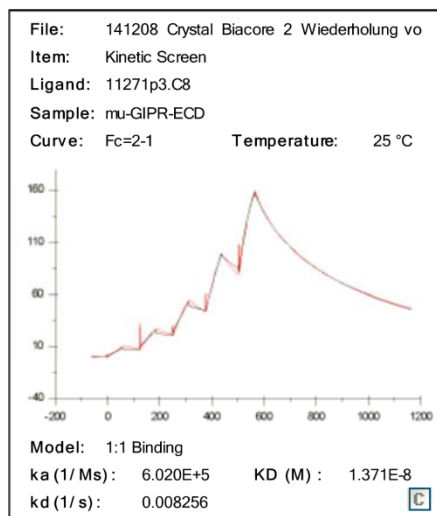
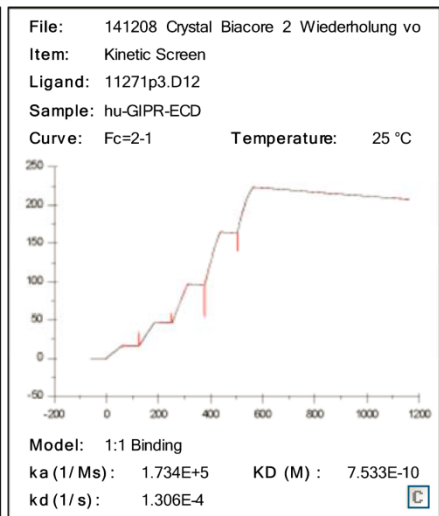
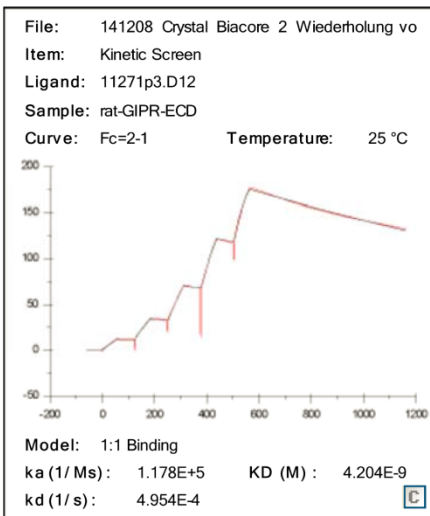
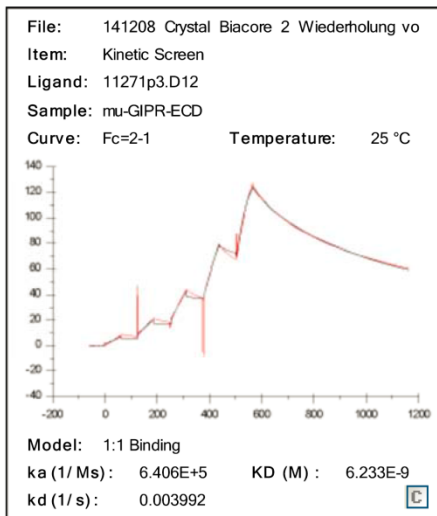


		Section 1																																																																				
		1	10	20	30	40	50	60	76																																																													
GIPR_human_NP_000155.gp	(1)	MTTS	FTLQ	LLLR	LSLC	GLLQ	RAET	GS	KG	-QT	AGELY	QRWE	HY	RR	EC	QET	LA	AA	EP	PS	GL	AC	NG	SF	DM	YV	CW	DY	AA																																									
GIPR_mouse_NP_001074284.gp	(1)	---	MLRL	LLLL	LLWL	WG--	LQWA	ET	DS	EG	QT	TGELY	QRWE	HY	GQ	EC	QK	ML	ET	EP	PS	GL	AC	NG	SF	DM	YV	AC	WY	TA																																								
GIPR_rat_NP_036846.gp	(1)	---	MLRL	LLLL	LLWL	WGLS	LQRA	ET	DS	EG	-QT	TGELY	QRWE	HY	GW	EC	QNT	LE	AT	EP	PS	GL	AC	NG	SF	DM	YV	AC	WY	TA																																								
		Section 2																																																																				
		77	80	90	100	110	120	130	152																																																													
GIPR_human_NP_000155.gp	(76)	PN	A	TAR	AS	CP	WY	LP	W	H	H	V	A	A	G	F	V	L	R	Q	C	G	S	D	G	Q	W	G	L	W	R	D	H	T	Q	C	E	N	P	E	K	N	E	A	F	L	D	Q	E	L	I	L	E	R	L	Q	V	V	Y	T	V	G	Y	S	L	S	L	A	T	
GIPR_mouse_NP_001074284.gp	(72)	AN	T	TAR	V	S	CP	WY	LP	W	F	R	Q	V	S	A	G	F	V	E	R	Q	C	G	S	D	G	Q	W	G	S	W	R	D	H	T	Q	C	E	N	P	E	K	N	G	A	F	D	Q	T	L	I	L	E	R	L	Q	V	V	Y	T	V	G	Y	S	L	S	L	A	T
GIPR_rat_NP_036846.gp	(73)	AN	T	TAR	V	S	CP	WY	LP	W	F	R	Q	V	S	A	G	F	V	E	R	Q	C	G	S	D	G	Q	W	G	S	W	R	D	H	T	Q	C	E	N	P	E	K	N	G	A	F	D	Q	T	L	I	L	E	R	L	Q	V	V	Y	T	V	G	Y	S	L	S	L	A	T

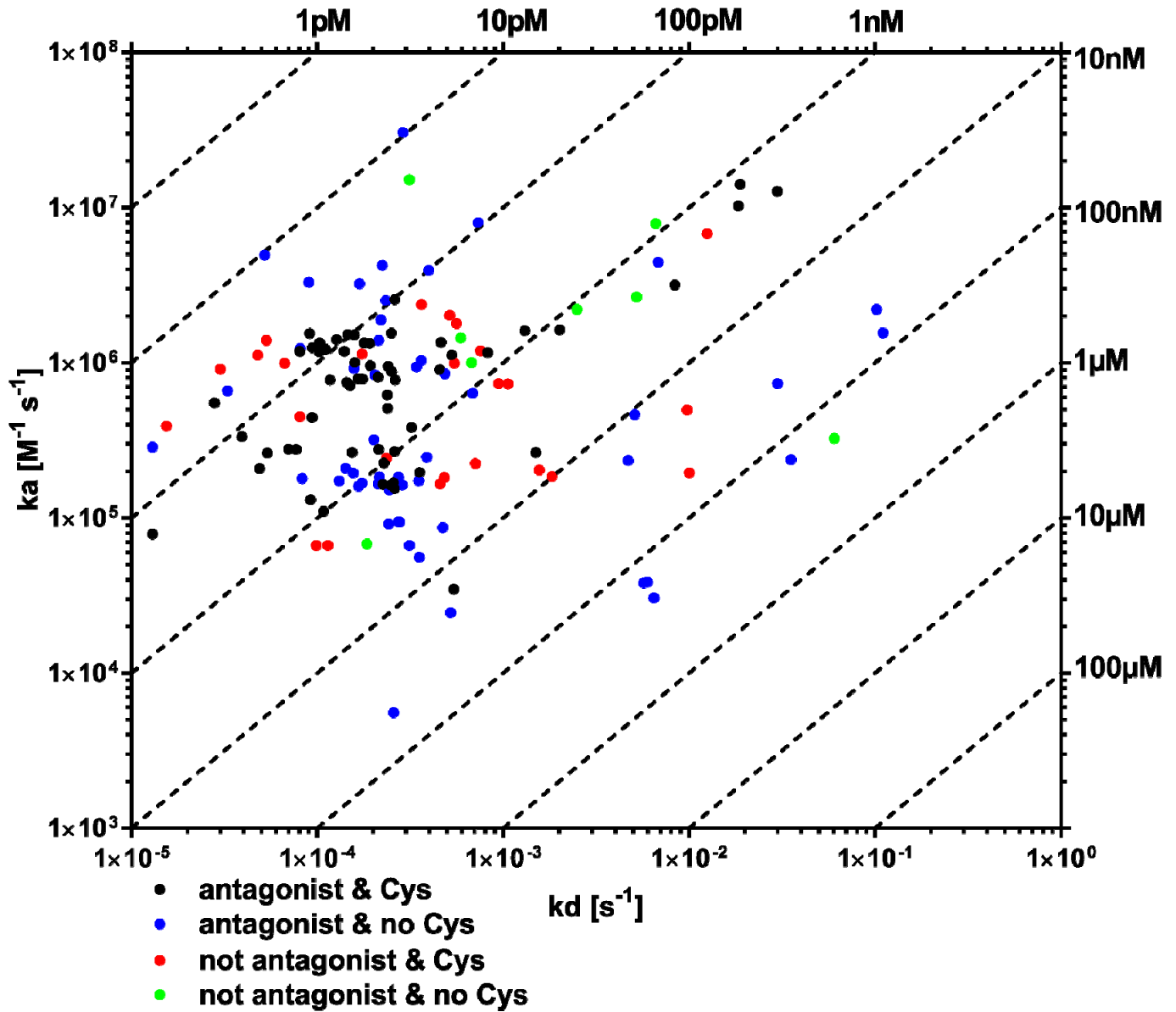
**Supplement 1: GIPR-N terminal extracellular domain sequences.**

Shown are the human, mouse and rat extracellular domain amino acids (22-139) that were used to generate recombinant rabbit (for biophysical analyses) or human (as antigen for immunization) Fc fusion proteins respectively.



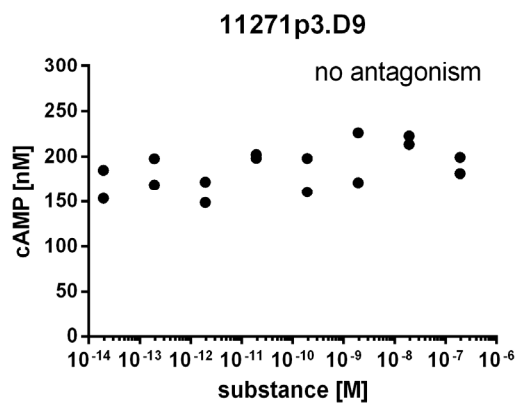
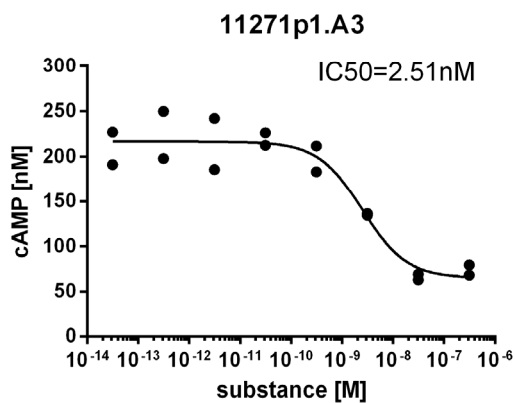
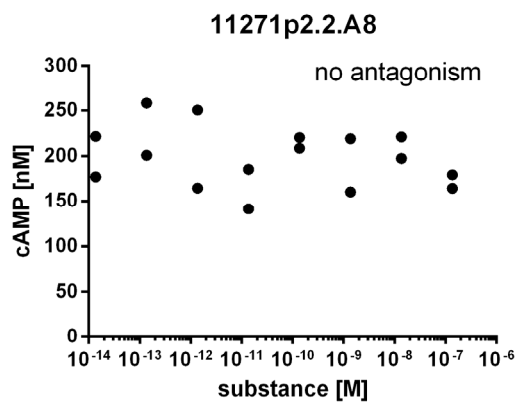
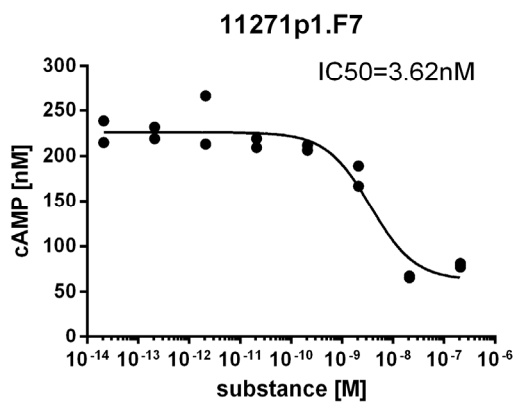
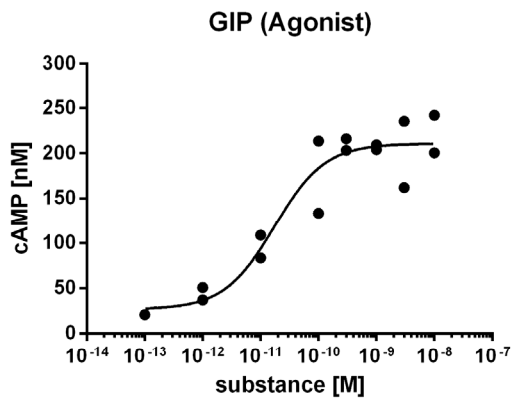
### Supplement 2: Biacore Single Cycle Kinetics Data

Shown are exemplary Biacore derived Single Cycle Kinetics binding curves for three representative antibodies (top: 11271p3.D12, middle 11271p3.C8, bottom 11271p3.A6) and human, mouse or rat derived GIPR-ECD. 5 concentrations were tested for each antibody. KD values were calculated by fitting a 1:1 binding model.



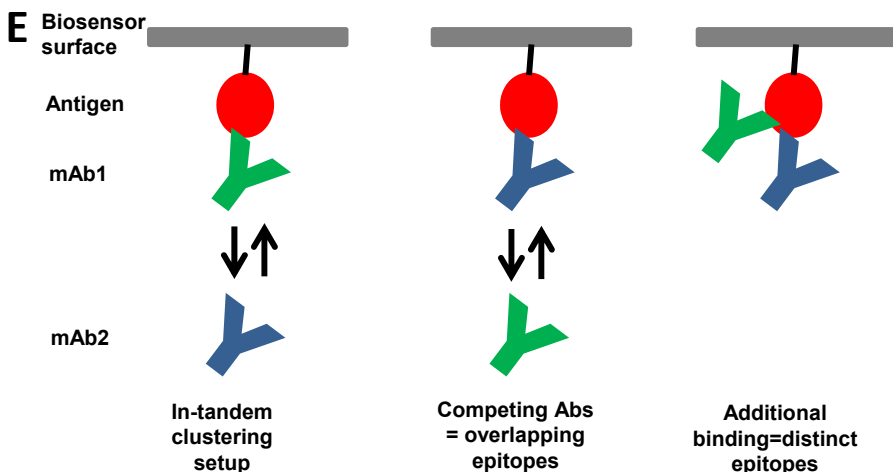
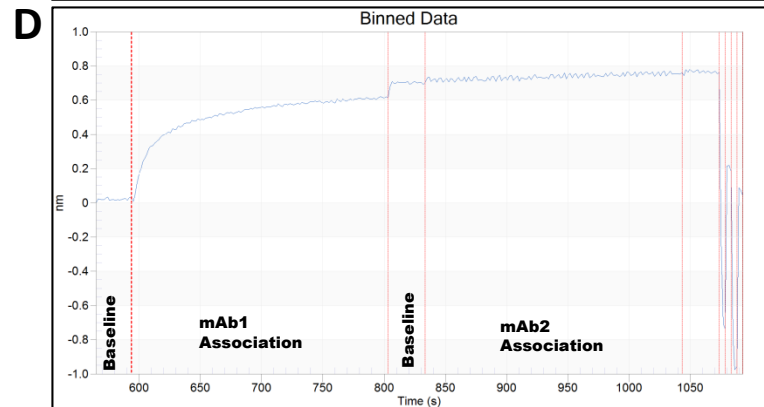
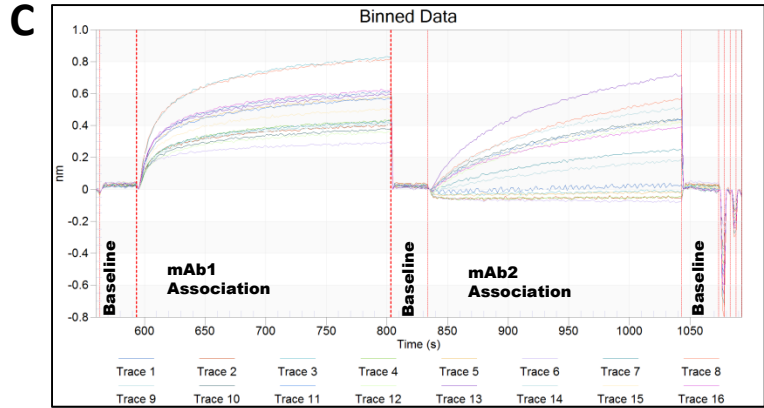
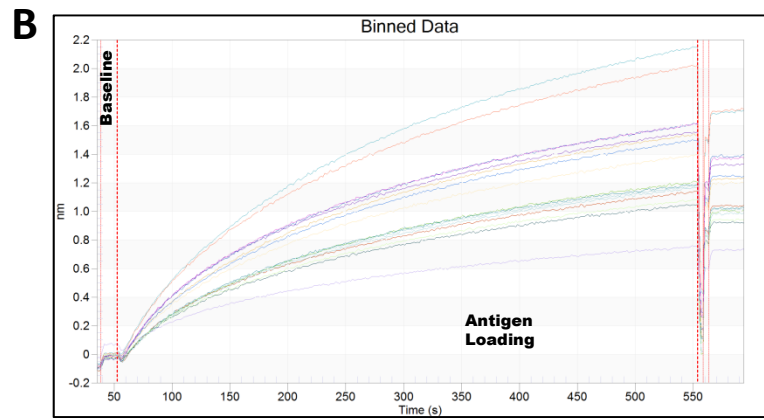
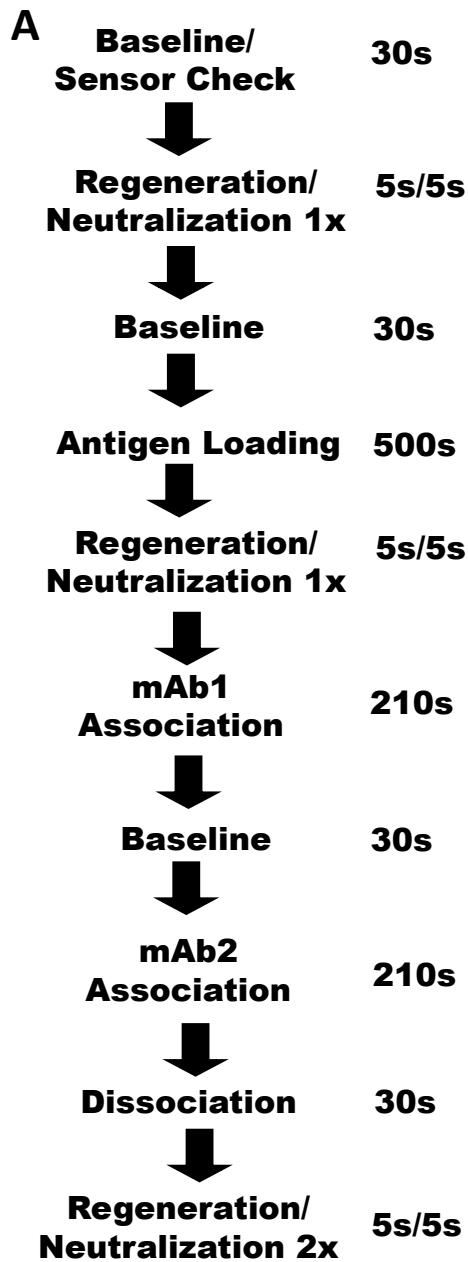
**Supplement 2: Isoaffinity plot for Biacore rate constants**

Shown are the on-rate ( $k_a$ ) and off-rate ( $k_d$ ) constants derived from measuring the binding of all chicken derived antibodies against the human GIPR-ECD. The diagonals indicate the  $K_D$  values and the antibody populations are color coded by their ability to antagonize GIPR signaling and cysteine content.



#### Supplement 4: Alphascreen cAMP functional assay data

Shown are representative activity data from the Alphascreen cAMP assay. The natural agonist of the GIPR GIP (top row, left) was used as a positive control. As expected, it increases the cAMP signal in a concentration dependent manner. Antagonistic antibodies are able to reduce the cAMP production stimulated by GIP (11271p1.F1, 11271p1.A3), whereas non-antagonists (11271p2.2.A8, 11271p3.D9) have no impact on the amount of cAMP.



#### Supplement 5: Epitope Clustering by BLI

In A, the measurement step and cycling times used for BLI clustering on the Fortebio Octet HTX are shown. Antigen and test antibodies were diluted in PBS. Baseline, dissociation and neutralization steps were also performed in PBS. For Regeneration, 10mM Glycine pH 3 was used. B shows exemplary antigen immobilization data for 8 biosensors. Biotinylated human GIPR-ECD-rbFc antigen was loaded onto streptavidin biosensors. The step is sandwiched between two baselines and followed by one regeneration cycle before Ab1 and Ab2 binding are performed. In C, example data for the immobilization of Ab1 versus 16 different Ab2 is illustrated. D shows the self-binding of the primary antibody – no additional binding occurs highlighting that the sensor surface is saturated. The absence of self-binding is essential in obtaining clean epitope clustering data. In C and D, all steps are aligned to the baseline. E gives an overview of the in-tandem epitope clustering setup. An immobilized antigen is saturated with a primary antibody and then incubated with a secondary antibody. If the secondary Ab competes with the first, no additional binding (=nm shift) occurs. An addition binding signal indicates the secondary Ab recognizing a distinct epitope.