

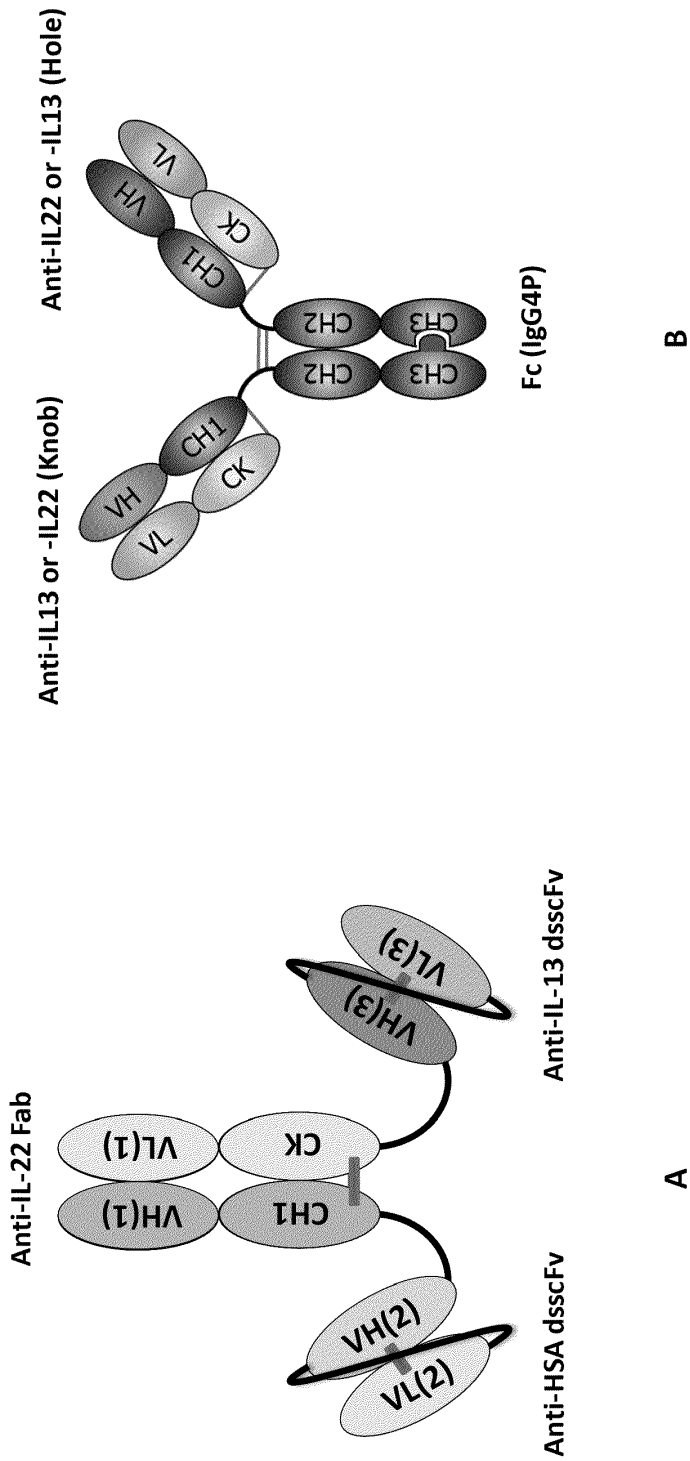
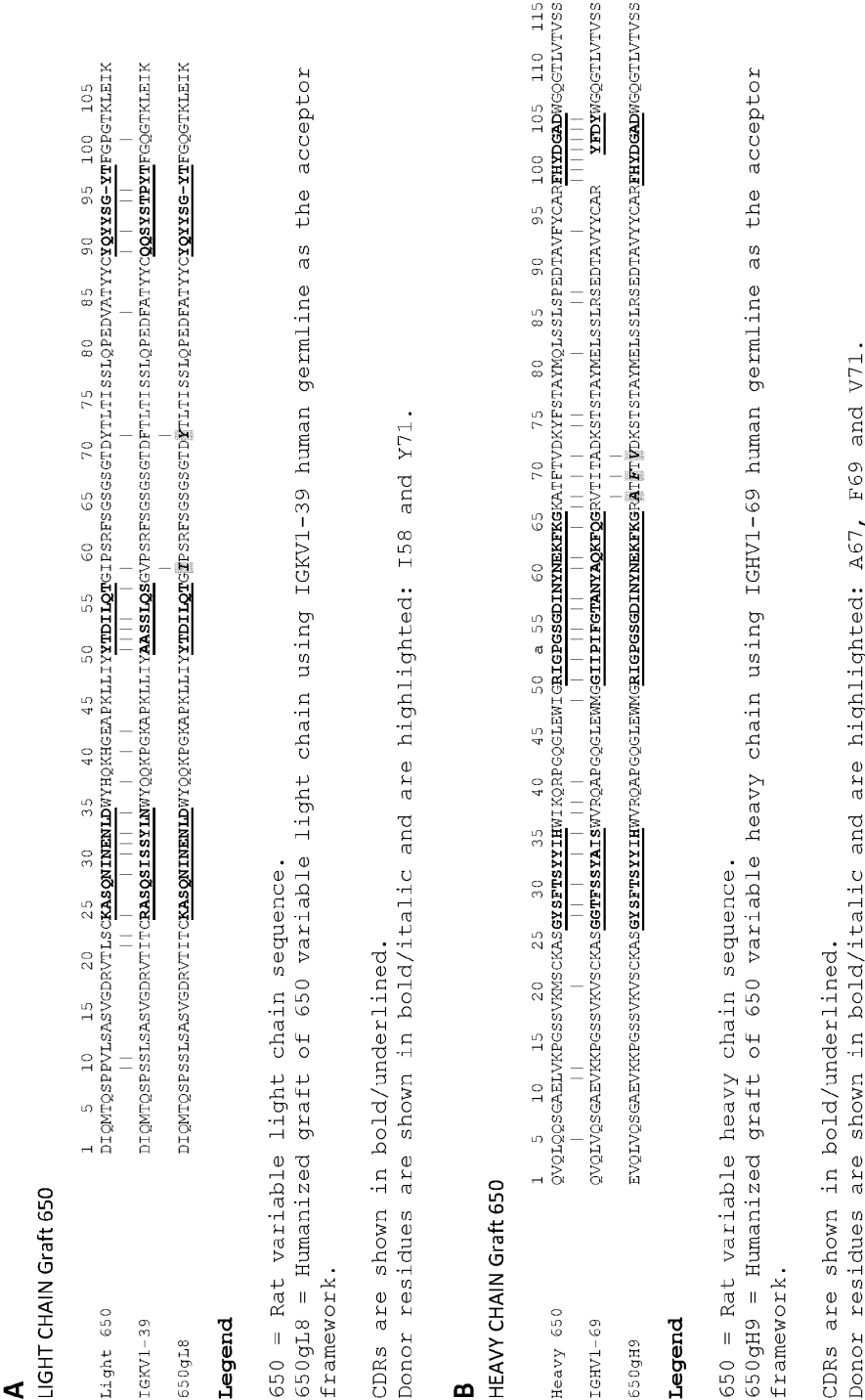


Figure 1



LIGHT CHAIN Graft 11041

Light 11041	1	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100	105	110	
	AV	VL	LT	QT	AS	PV	SA	PG	VT	IK	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>	
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	
IGKV1D-13	AI	QL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL1	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL1 (C91S)	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL1 (C91V)	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL6	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL7	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL1 (N95D)	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL1 (S96A)	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL1 (C91S, S96)	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL6 (C91S)	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL7 (C91S)	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL6 (C91S, S96)	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II
11041gL7 (C91S, S96)	AV	VL	TQ	SP	SS	LS	AS	VG	DR	VT	IT	<u>CA</u>	<u>SE</u>	<u>DI</u>	<u>Y</u>	<u>T</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>
	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II	II

Legend

11041 = Rabbit variable light chain sequence.
11041gL1, gL6 and gL7 = Humanized grafts of 11041 variable light chain using IGKV1D-13 human germline as the acceptor framework.
CDRs are shown in bold/underlined.
Donor residues are shown in bold/italic and are highlighted: V2 and V3.
Mutations in CDRL3 to replace a free Cysteine residue (C91S and C91V) or to modify a potential Asparagine deamidation site (N95D or S96A) are shown in bold/underlined and are highlighted.

Figure 3

A
LIGHT CHAIN Graft 11070

Light 11070
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105
 DIVTQTPNIIAAGPSVSINCRASNTISKYLAQQQPKAKMLIYSGSTLOSQTPSRFSGSGSSTFTTITRIIEPEDFGIYVCOQHNEYPLTSGGKTKLEIK
 DTQMTQPSVASGDRVTITCRASGCSISHLAAQQQPKAPKLLIYAASLSQSGVPSRFSGSGSSTFTTITSIISQPEDFATVYCOQANSFFYTGCGTKLEIK
 DIVTQTPSASVASGDRVTITCRASNTISKYLAQQQPKAKMLIYSGSTLOSQGT-SRFSGSGSSTFTTITSIISQPEDFATVYCOQHNEYPLTGGGKTKLEIK
 DTQMTQPSASVASGDRVTITCRASNTISKYLAQQQPKAKMLIYSGSTLOSQGT-SRFSGSGSSTFTTITSIISQPEDFATVYCOQHNEYPLTGGGKTKLEIK
 DIVTQTPSASVASGDRVTITCRASNTISKYLAQQQPKAKMLIYSGSTLOSQGT-SRFSGSGSSTFTTITSIISQPEDFATVYCOQHNEYPLTGGGKTKLEIK
 DTQMTQPSASVASGDRVTITCRASGCSISHLAAQQQPKAPKLLIYAASLSQSGVPSRFSGSGSSTFTTITSIISQPEDFATVYCOQANSFFYTGCGTKLEIK

Legend

11070 = Rat variable light chain sequence.
11070gL1 and gL7 = Humanized grafts of 11070 variable light chain using IGV1-12 human germline as the acceptor framework.

CDRs are shown in bold/underlined.

Donor residues are shown in bold/italic and are highlighted: V3, N44, T58 and S68.

B
HEAVY CHAIN Graft 11070

[illegible]

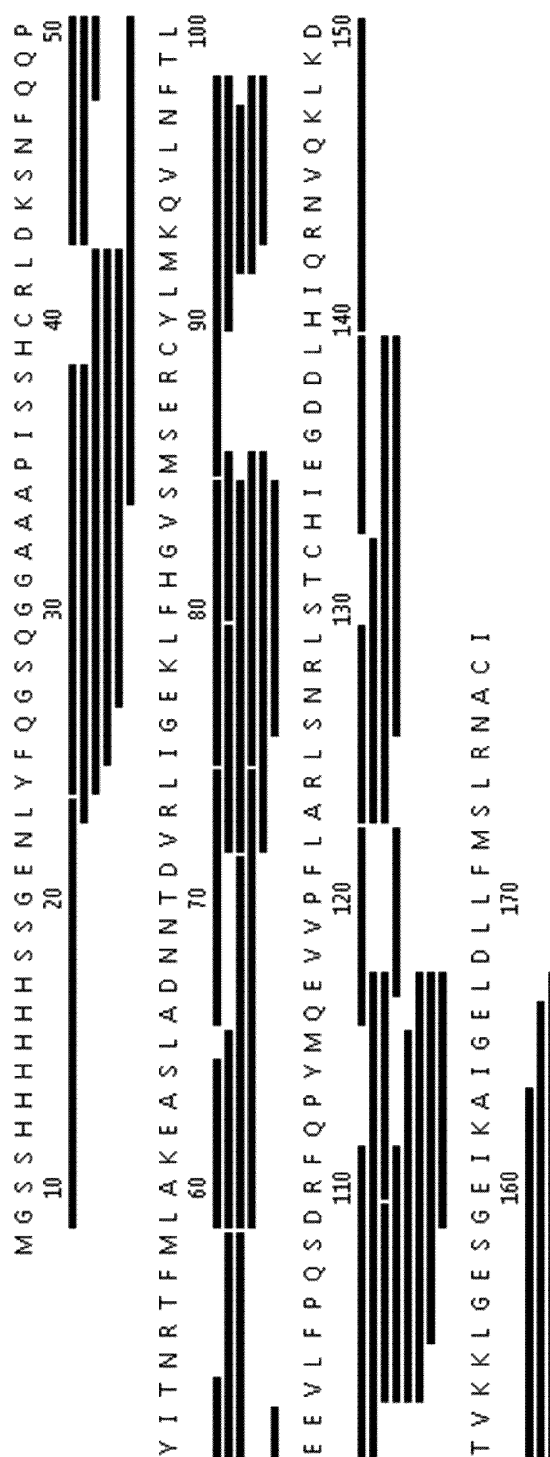
Legend

11070 = Rat variable heavy chain sequence.

11070 variable heavy chain using IGHV4-31 human germline as the acceptor framework.

CDRs are shown in bold/underlined.

Donor residues are shown in bold/italic and are highlighted: E1, V37, S41, M48, L67, R71, S76 and V78. Mutation in CDRH2 to modify a potential Asparagine deamidation site (S61T) is shown in bold/underlined highlighted.



Total: 47 Peptides, 91.3% Coverage, 3.48 Redundancy

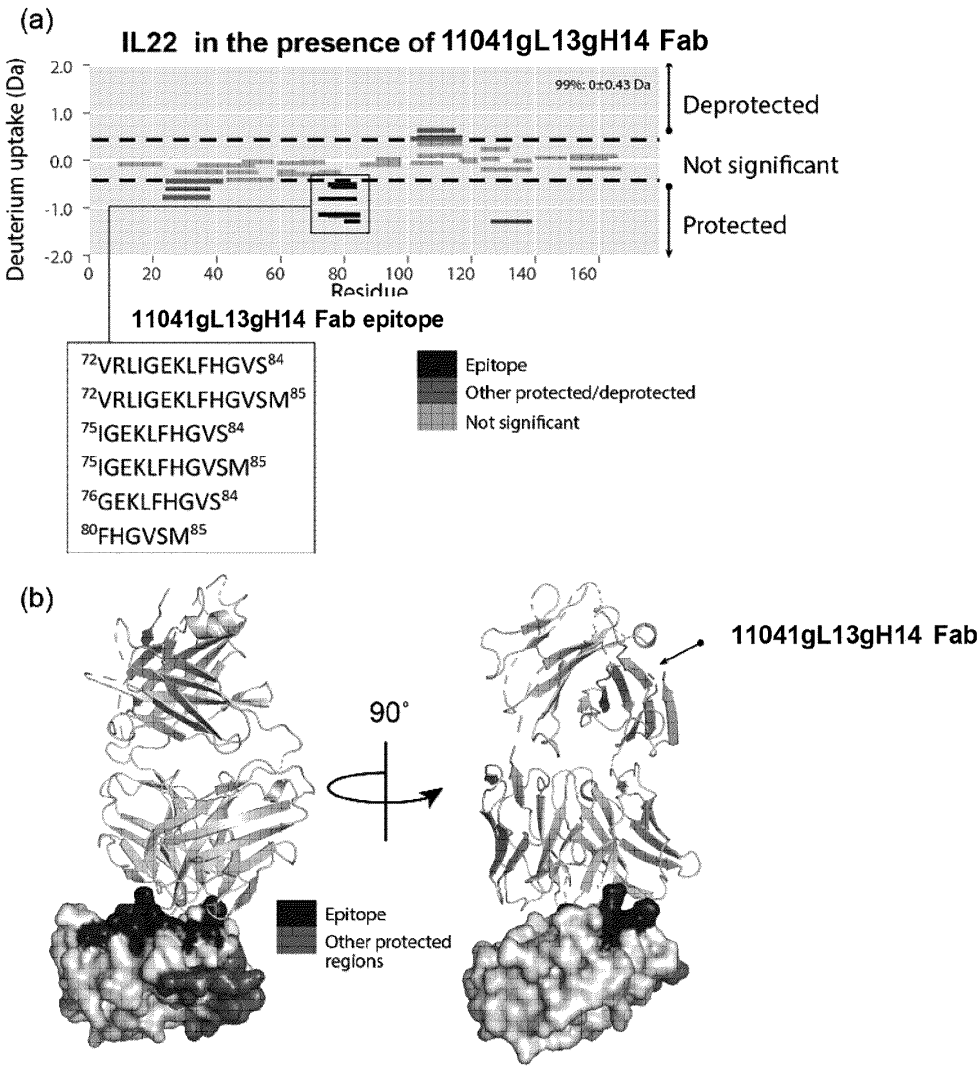


Figure 7

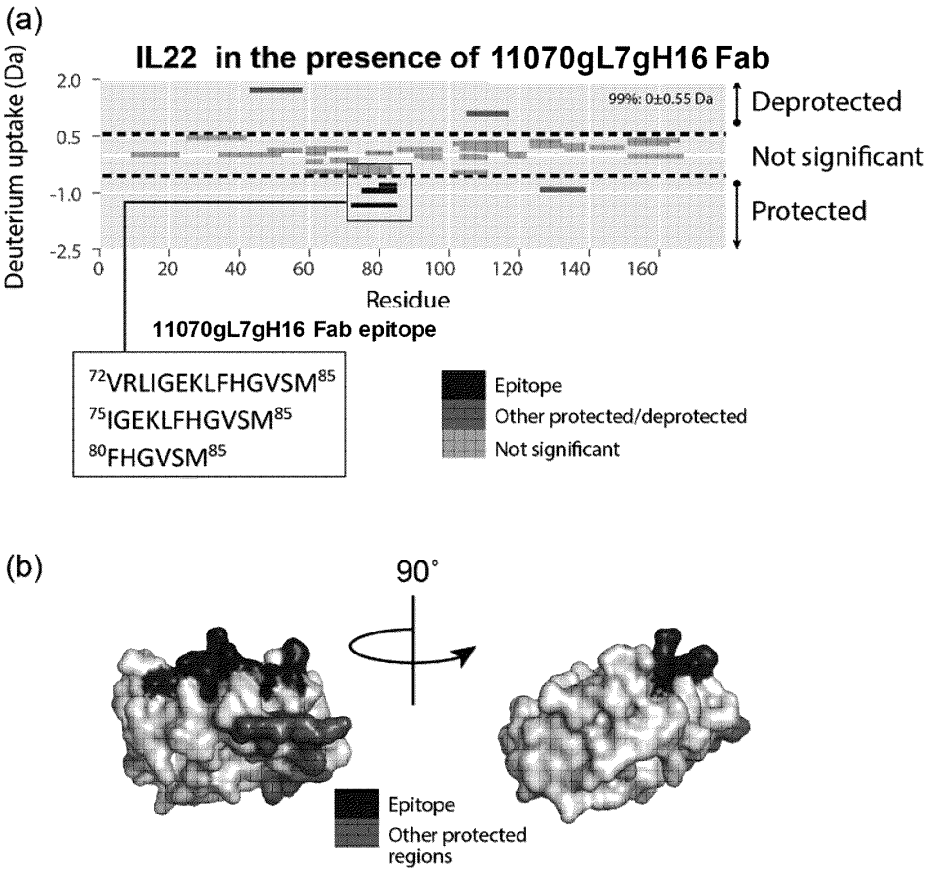


Figure 8

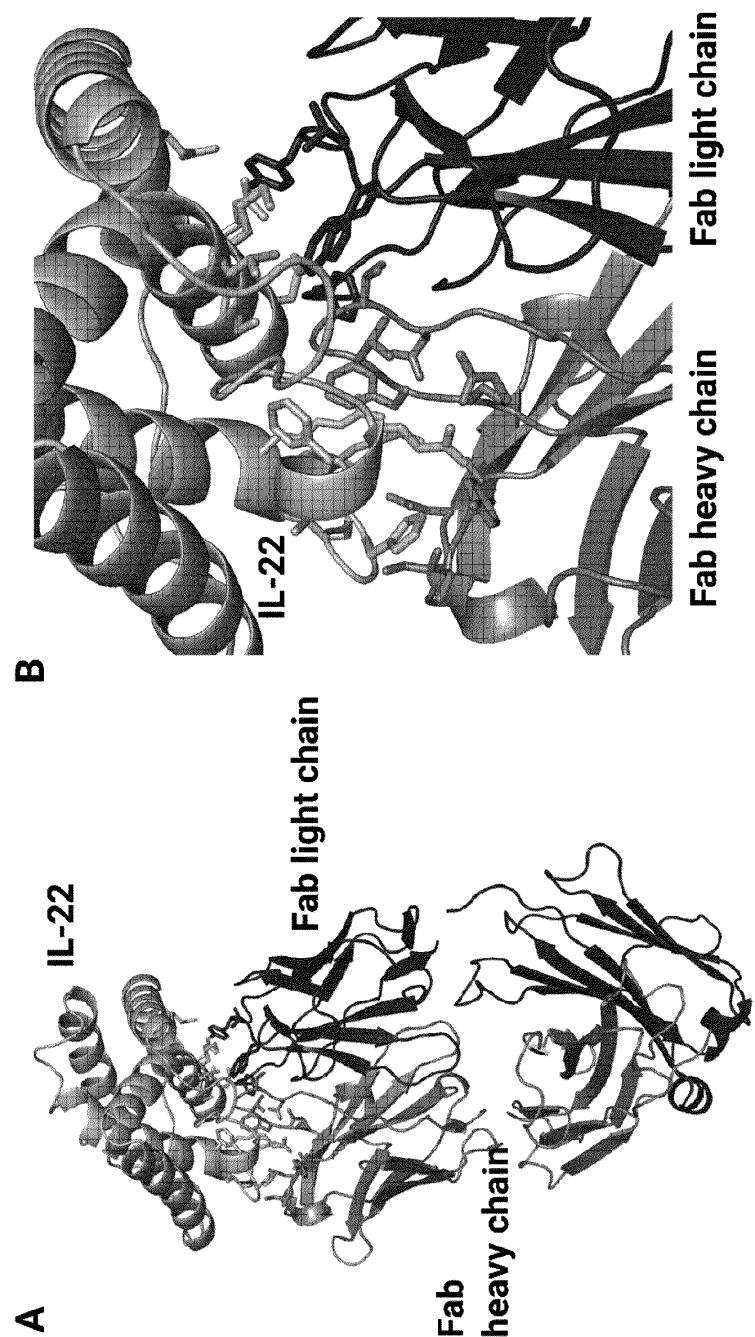


Figure 9

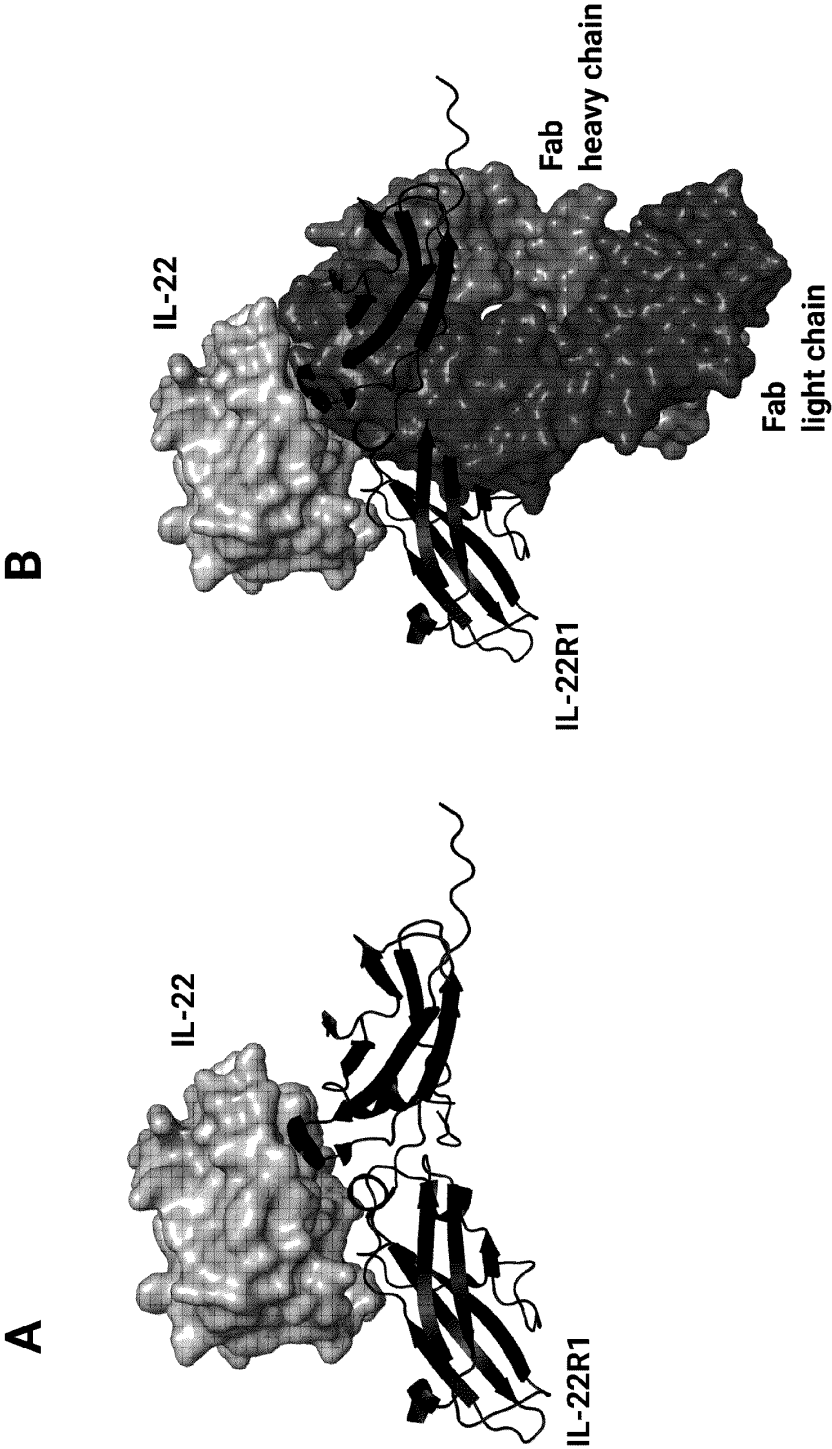


Figure 10

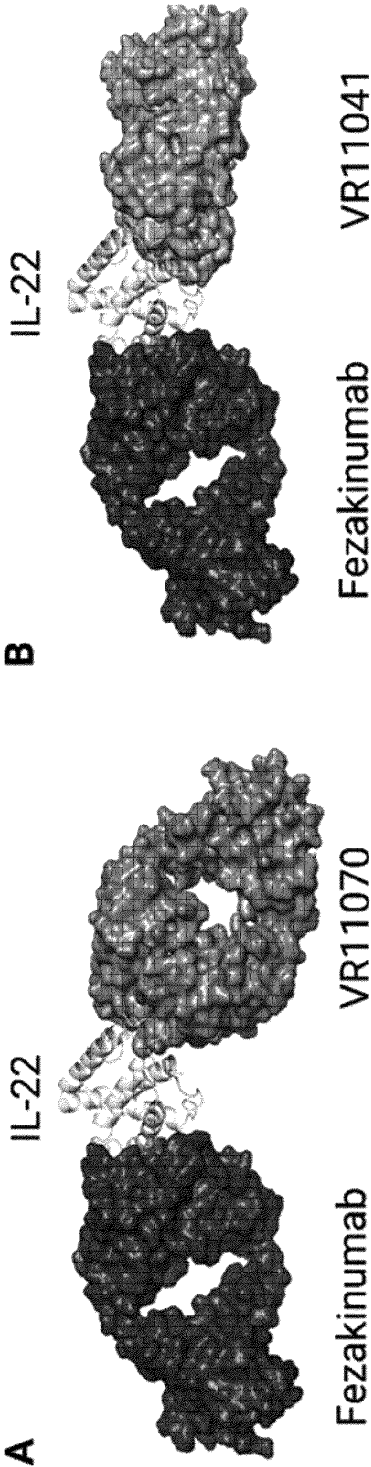


Figure 11

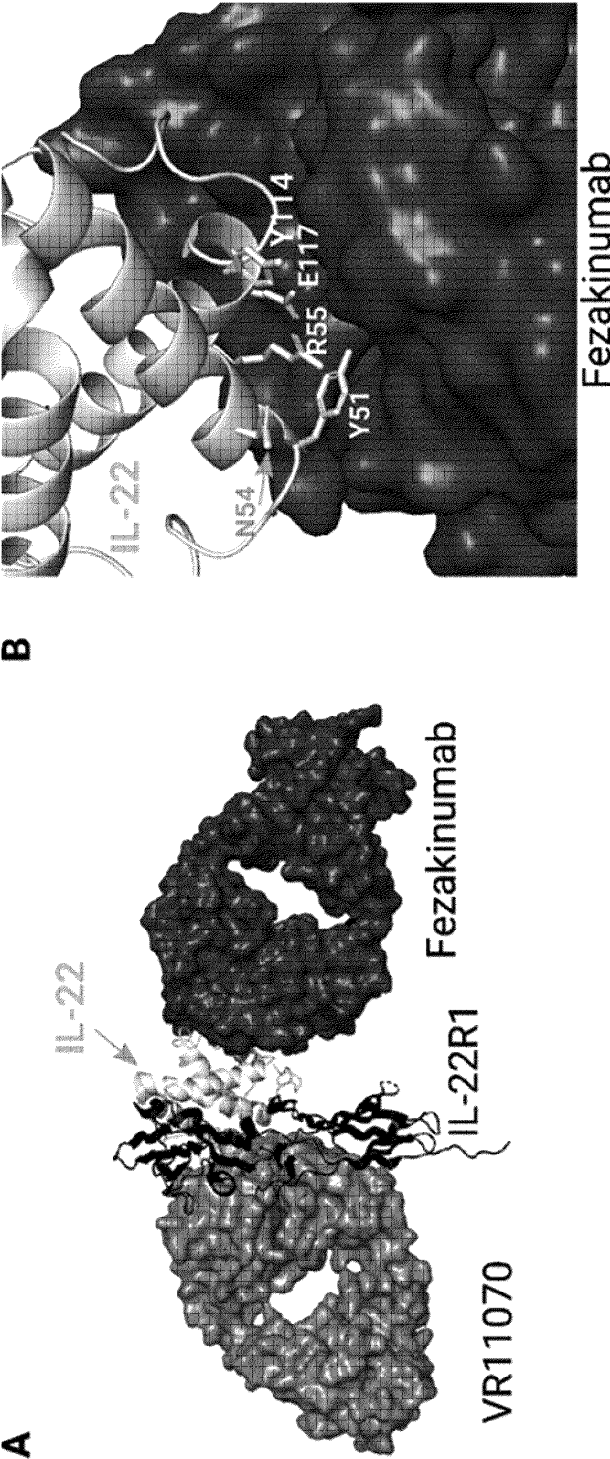


Figure 12

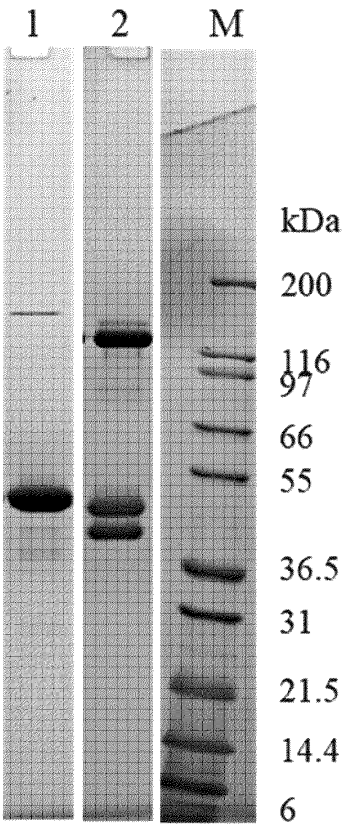
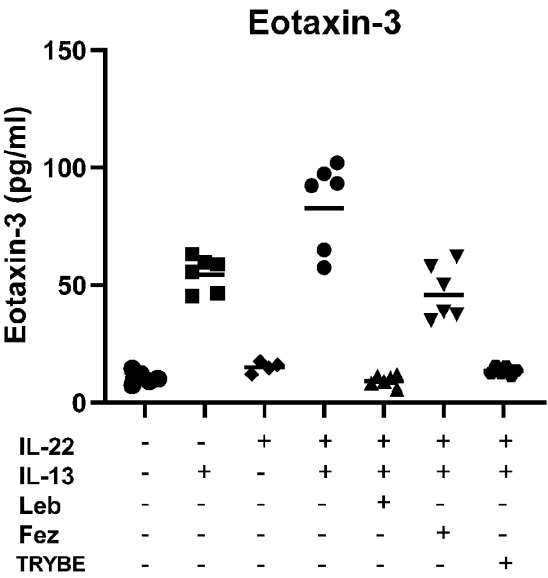


Figure 13

A



B

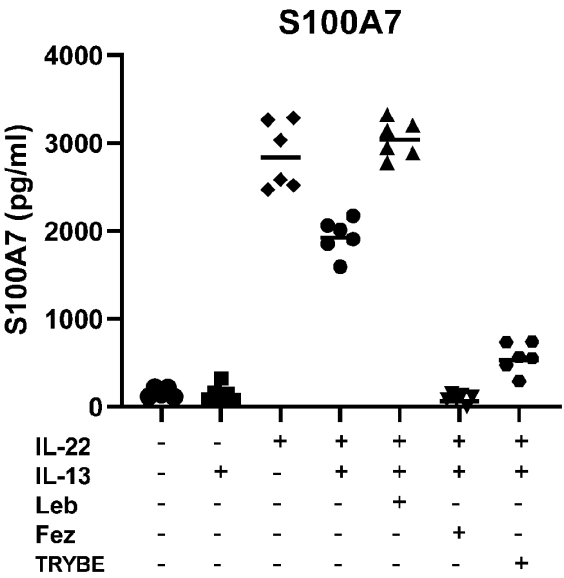
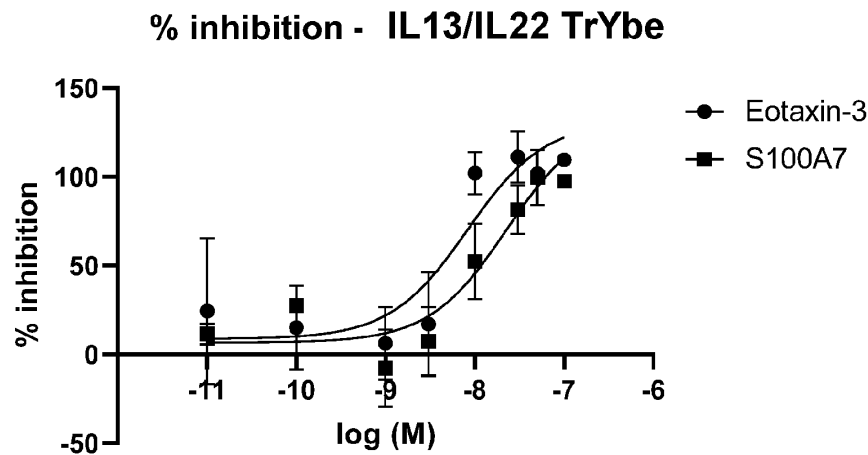


Figure 14

A



B

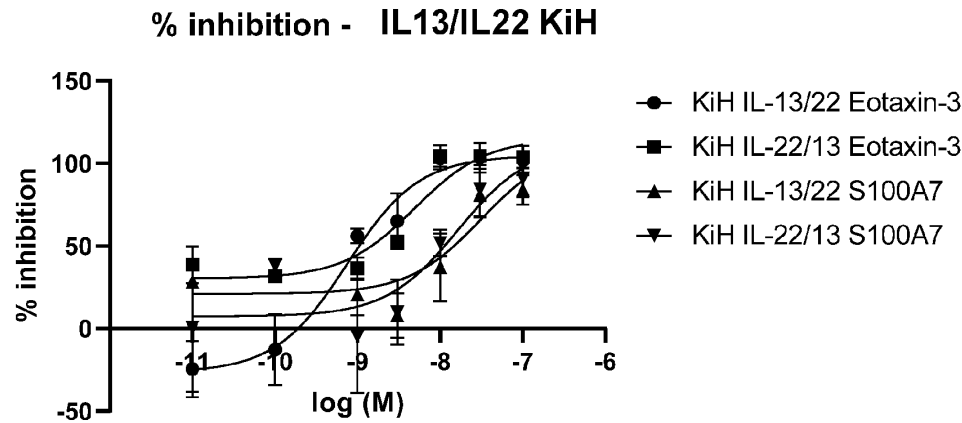


Figure 15

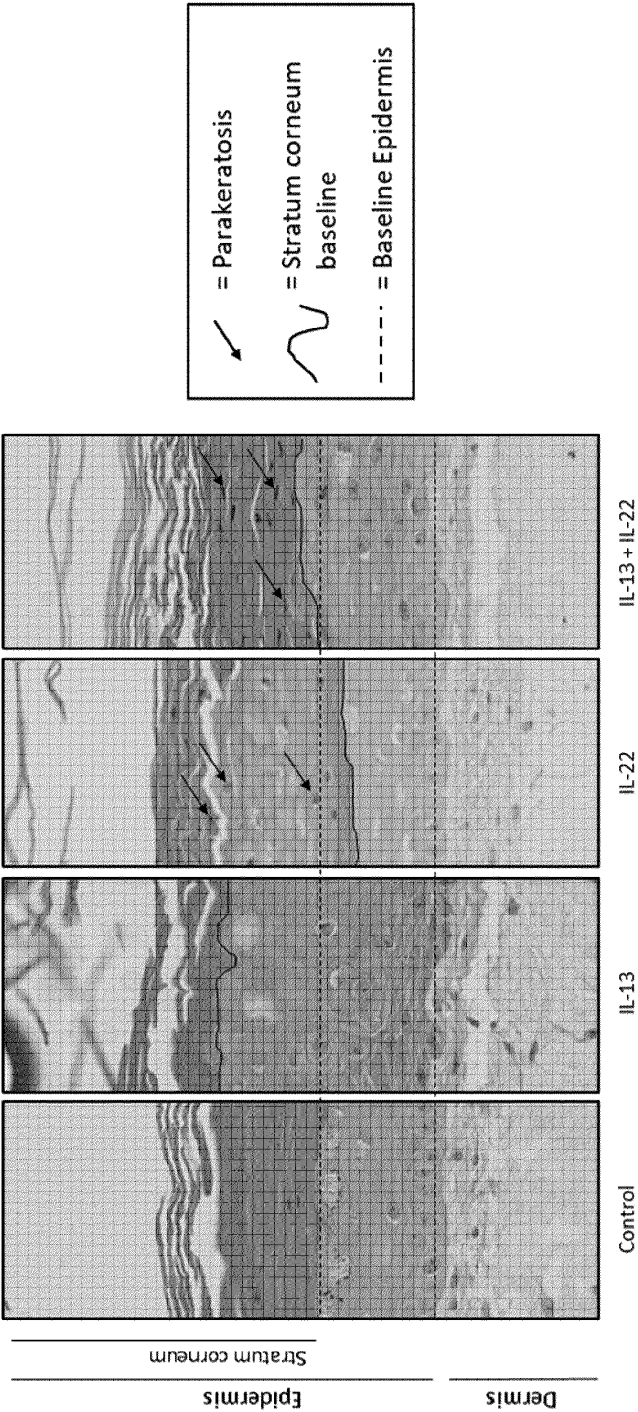


Figure 16

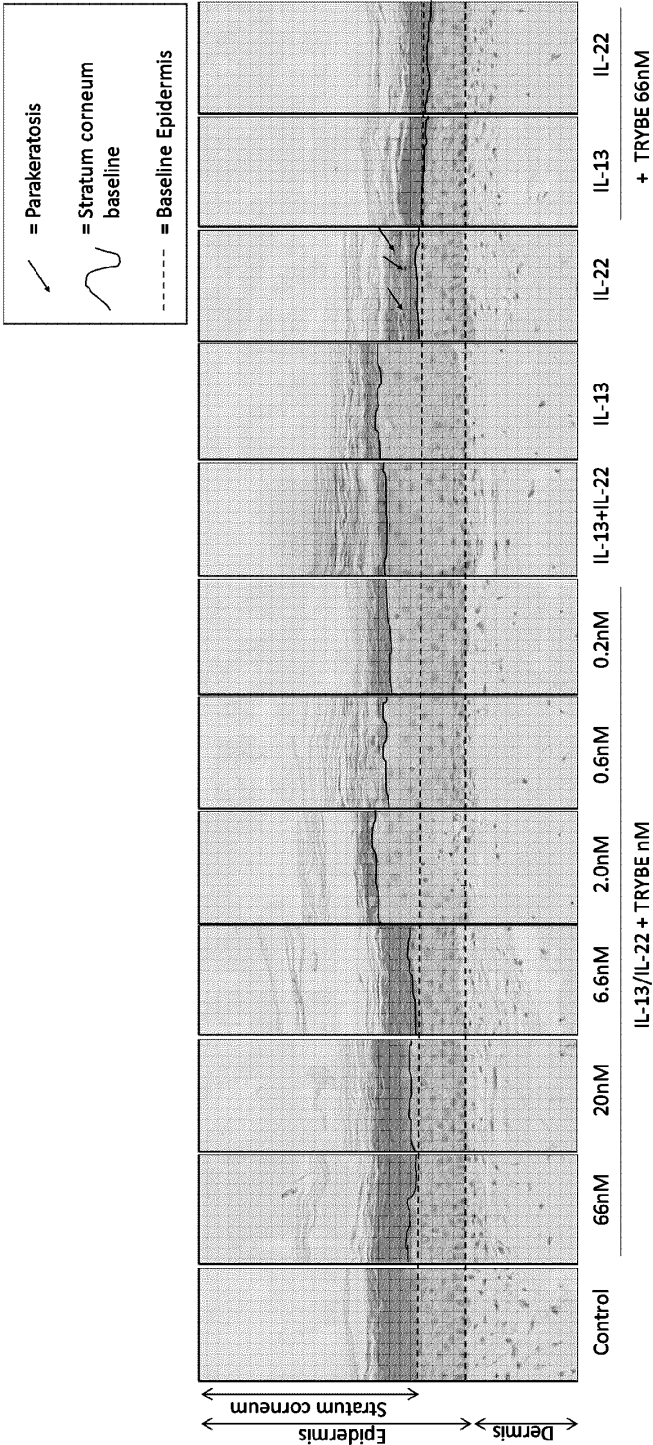


Figure 17

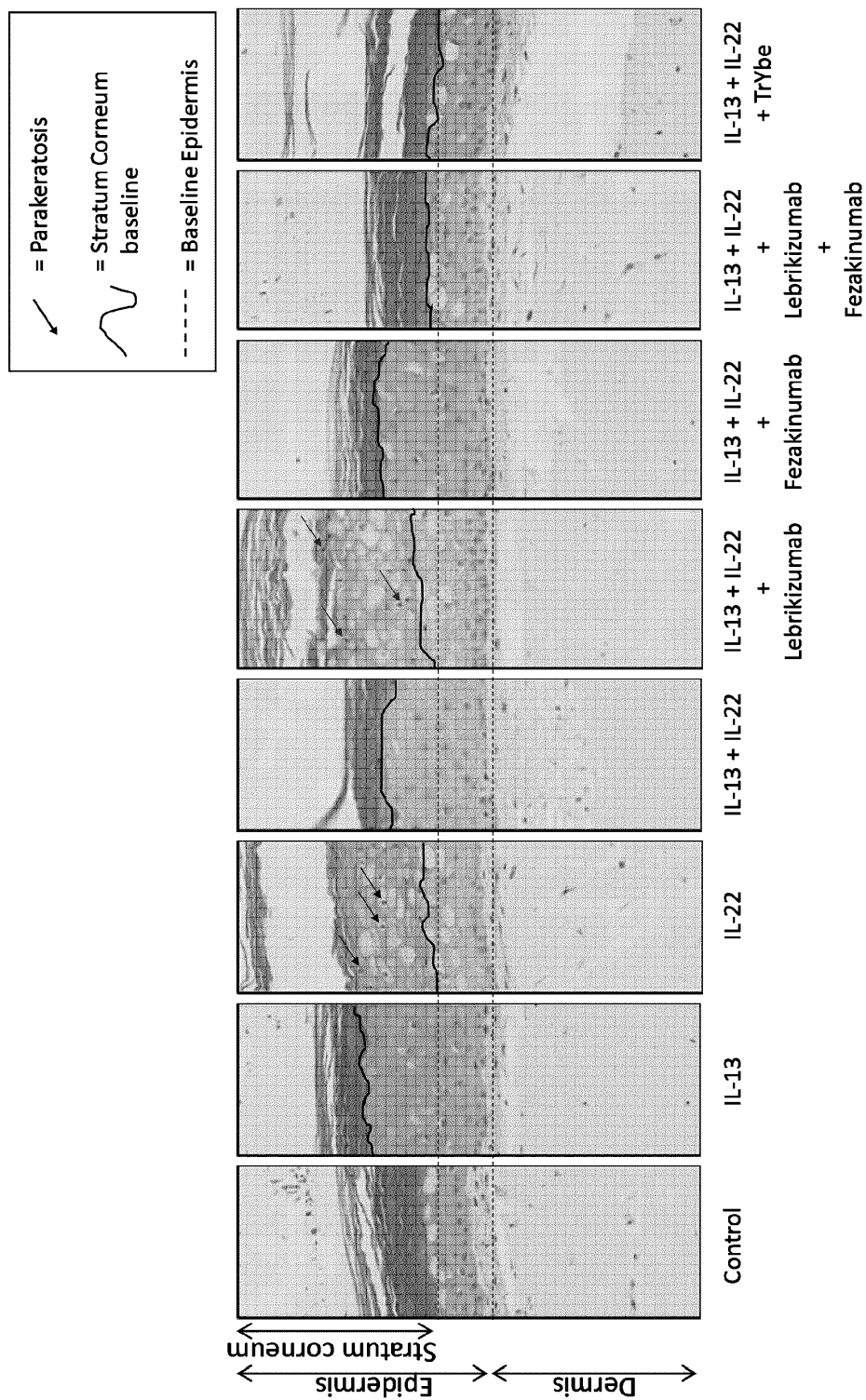


Figure 18