

Figure 1

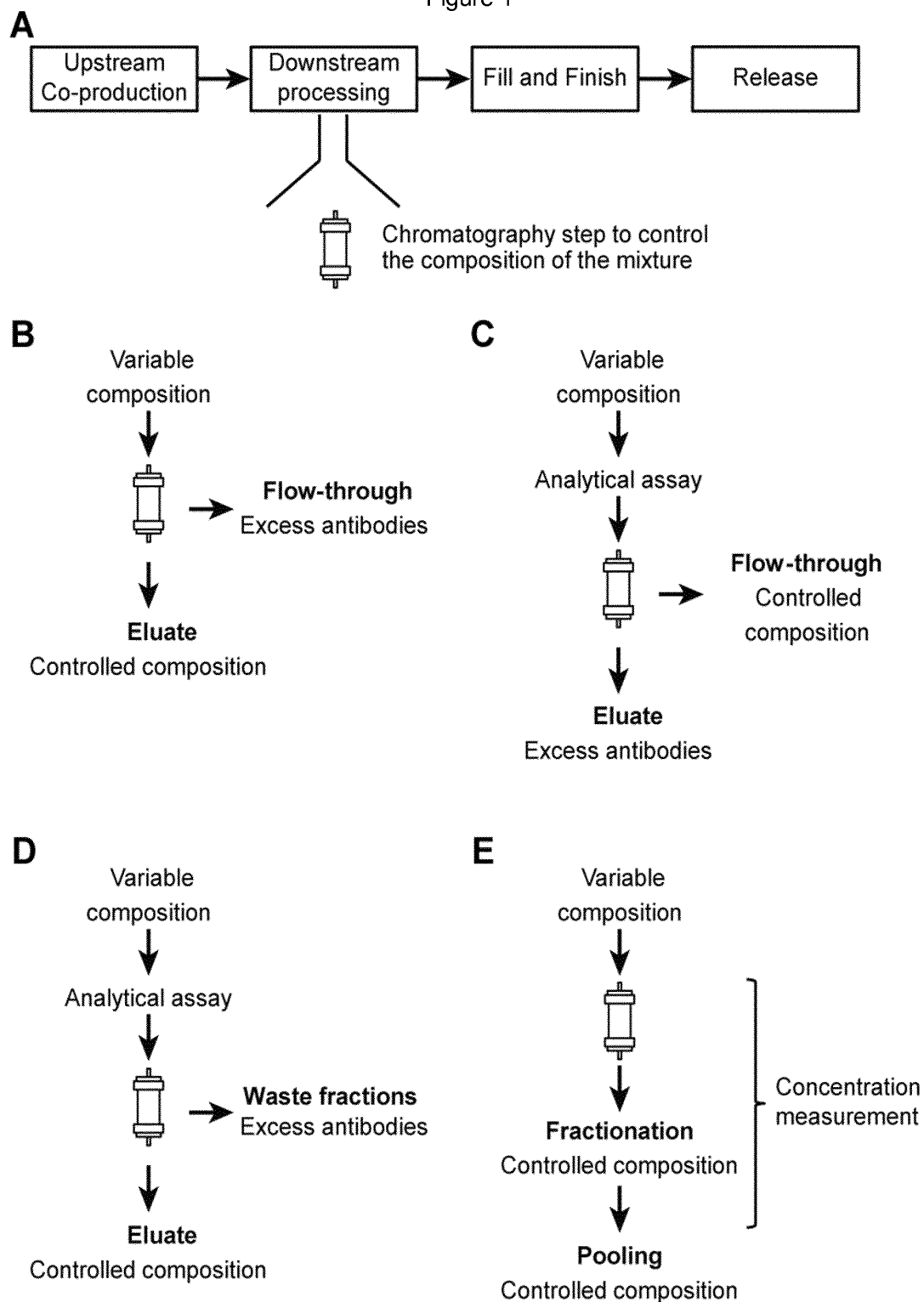


Figure 2

A

[illegible]

Figure 2 (continued)

A (continued)

IMGT numbering	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104
Mutations	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV1-02	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV1-08	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV1-18	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV1-46	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV1-03	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV1-45	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV1-58	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV1-69	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV1-24	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV5-51	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV3-07	M	G	W	I	N	P	-	-	N	S	G	N	T	G	T	N	G	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	A	M	E	L	S	R	L	R	S	E	D	T	A	V	Y	C
hiGHV3-11	V	S	I	S	-	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-21	V	S	I	S	-	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-48	V	S	I	S	-	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-23	V	S	I	S	-	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-64	V	S	I	S	-	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-74	V	S	I	S	-	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-09	V	S	I	S	-	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-20	V	S	I	S	-	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-43	V	S	I	S	-	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-30	V	A	V	I	S	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-33	V	S	V	I	S	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-66	V	S	V	I	S	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-13	V	S	V	I	S	-	-	-	D	S	S	T	I	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-15	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-72	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-73	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV3-49	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV4-04	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV4-59	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV4-61	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV4-31	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV4-39	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV4-28	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV4-34	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV4-28	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV6-01	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV2-05	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV2-70	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
hiGHV2-26	V	G	R	I	K	S	K	T	D	N	S	Y	A	T	A	A	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
2F8HP	V	A	I	F	S	-	-	-	N	D	E	K	S	Y	G	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C			
1014-005HP	M	G	S	I	Y	P	G	-	-	D	S	D	T	R	Y	H	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	C	
1021-511HP	V	S	G	I	S	G	S	-	-	G	G	H	T	Y	H	A	D	S	V	K	G	R	F	T	I	S	R	D	N	A	K	N	S	L																		

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	*		
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q	K	P	G	K
D	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	R	V	V	T	I	C	R	A	S	Q	G	I	I	-	-	-	-	-	-	S	S	W	L	A	W	Y	Q	Q				

[illegible]

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Figure 2 (continued)

D

1014-005HA3	(1)	EVQLVDSGAE	10	VKKPGESLKI	20	SCASGYSFH	30	FYIWGWVRQ	40	PGKLEWVMS	50	IYPGDSSTRY	60	RPSFQGRVTI	70
1014-005HA2	(1)	EVQLVDSGAE	10	VKKPGESLKI	20	SCASGYSFH	30	FYIWGWVRQ	40	PGKLEWVMS	50	IYPGDSSTRY	60	RPSFQGRVTI	70
1014-005HA1	(1)	EVQLVDSGAE	10	VKKPGESLKI	20	SCASGYSFH	30	FYIWGWVRQ	40	PGKLEWVMS	50	IYPGDSSTRY	60	RPSFQGRVTI	70
1014-005HC	(1)	EVQLVDSGAE	10	VKKPGESLKI	20	SCASGYSFH	30	FYIWGWVRQ	40	PGKLEWVMS	50	IYPGDSSTRY	60	RPSFQGRVTI	70
1014-005HP	(1)	EVQLVDSGAE	10	VKKPGESLKI	20	SCASGYSFH	30	FYIWGWVRQ	40	PGKLEWVMS	50	IYPGDSSTRY	60	RPSFQGRVTI	70
1014-005HB1	(1)	EVQLVDSGAE	10	VKKPGESLKI	20	SCASGYSFH	30	FYIWGWVRQ	40	PGKLEWVMS	50	IYPGDSSTRY	60	RPSFQGRVTI	70
1014-005HB2	(1)	EVQLVDSGAE	10	VKKPGESLKI	20	SCASGYSFH	30	FYIWGWVRQ	40	PGKLEWVMS	50	IYPGDSSTRY	60	RPSFQGRVTI	70
1014-005HB3	(1)	EVQLVDSGAE	10	VKKPGESLKI	20	SCASGYSFH	30	FYIWGWVRQ	40	PGKLEWVMS	50	IYPGDSSTRY	60	RPSFQGRVTI	70
IMGT-NR			1		17		24								75
1014-005HA3	(71)	SADKSISTAY	80	LQWTSLKASD	90	TAIYYCARQR	100	GDYYFYFGMD	110	VWGQGTITVTV	120	SS			
1014-005HA2	(71)	SADKSISTAY	80	LQWTSLKASD	90	TAIYYCARQR	100	GDYYFYFGMD	110	VWGQGTITVTV	120	SS			
1014-005HA1	(71)	SADKSISTAY	80	LQWTSLKASD	90	TAIYYCARQR	100	GDYYFYFGMD	110	VWGQGTITVTV	120	SS			
1014-005HC	(71)	SADKSISTAY	80	LQWTSLKASD	90	TAIYYCARQR	100	GDYYFYFGMD	110	VWGQGTITVTV	120	SS			
1014-005HP	(71)	SADKSISTAY	80	LQWTSLKASD	90	TAIYYCARQR	100	GDYYFYFGMD	110	VWGQGTITVTV	120	SS			
1014-005HB1	(71)	SADKSISTAY	80	LQWTSLKASD	90	TAIYYCARQR	100	GDYYFYFGMD	110	VWGQGTITVTV	120	SS			
1014-005HB2	(71)	SADKSISTAY	80	LQWTSLKASD	90	TAIYYCARQR	100	GDYYFYFGMD	110	VWGQGTITVTV	120	SS			
1014-005HB3	(71)	SADKSISTAY	80	LQWTSLKASD	90	TAIYYCARQR	100	GDYYFYFGMD	110	VWGQGTITVTV	120	SS			
IMGT-NR					93		97								
1014-005LB3	(1)	EIVLTQSPGT	10	LSLSPGERAT	20	LSCRASQSVS	30	SSYLAWYQQK	40	FGQVPRLLIY	50	GASSRATGIP	60	DRFSGSGSGT	70
1014-005LB2	(1)	EIVLTQSPGT	10	LSLSPGERAT	20	LSCRASQSVS	30	SSYLAWYQQK	40	FGQVPRLLIY	50	GASSRATGIP	60	DRFSGSGSGT	70
1014-005LB1	(1)	EIVLTQSPGT	10	LSLSPGERAT	20	LSCRASQSVS	30	SSYLAWYQQK	40	FGQVPRLLIY	50	GASSRATGIP	60	DRFSGSGSGT	70
1014-005LC	(1)	EIVLTQSPGT	10	LSLSPGERAT	20	LSCRASQSVS	30	SSYLAWYQQK	40	FGQVPRLLIY	50	GASSRATGIP	60	DRFSGSGSGT	70
1014-005LA1	(1)	EIVLTQSPGT	10	LSLSPGERAT	20	LSCRASQSVS	30	SSYLAWYQQK	40	FGQVPRLLIY	50	GASSRATGIP	60	DRFSGSGSGT	70
1014-005LA2	(1)	EIVLTQSPGT	10	LSLSPGERAT	20	LSCRASQSVS	30	SSYLAWYQQK	40	FGQVPRLLIY	50	GASSRATGIP	60	DRFSGSGSGT	70
1014-005LA3	(1)	EIVLTQSPGT	10	LSLSPGERAT	20	LSCRASQSVS	30	SSYLAWYQQK	40	FGQVPRLLIY	50	GASSRATGIP	60	DRFSGSGSGT	70
IMGT-NR			1												
1014-005LB3	(71)	DFTLKISRLQ	80	PEDFAVYVCQ	90	QYGSLLTFGG	100	GTKVEIK							
1014-005LB2	(71)	DFTLKISRLQ	80	PEDFAVYVCQ	90	QYGSLLTFGG	100	GTKVEIK							
1014-005LB1	(71)	DFTLKISRLQ	80	PEDFAVYVCQ	90	QYGSLLTFGG	100	GTKVEIK							
1014-005LC	(71)	DFTLKISRLQ	80	PEDFAVYVCQ	90	QYGSLLTFGG	100	GTKVEIK							
1014-005LA1	(71)	DFTLKISRLQ	80	PEDFAVYVCQ	90	QYGSLLTFGG	100	GTKVEIK							
1014-005LA2	(71)	DFTLKISRLQ	80	PEDFAVYVCQ	90	QYGSLLTFGG	100	GTKVEIK							
1014-005LA3	(71)	DFTLKISRLQ	80	PEDFAVYVCQ	90	QYGSLLTFGG	100	GTKVEIK							
IMGT-NR					90		9395								

Figure 2 (continued)

1021-511HA3 1021-511HA2 1021-511HA1 1021-511HC 1021-511HP 1021-511HB1 1021-511HB2 1021-511HB3 IMGT-NR	(1)	EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	70
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	60
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	50
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	40
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	30
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	20
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	10
1021-511LB3 1021-511LB2 1021-511LB1 1021-511LC 1021-511LA1 1021-511LA2 1021-511LA3 IMGT-NR	(1)	EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	70
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	60
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	50
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	40
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	30
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	20
		EVQLI	ESGG	LVQPGGSRL	SCA	ASGTF	SYAMNWVRQA	PG	GLEWVSG	ISGSGGHTYH	ADSVKGRFTI	10
1021-511HB3 1021-511HB2 1021-511HB1 1021-511HC 1021-511HP 1021-511HA1 1021-511HA2 1021-511HA3 IMGT-NR	(71)	SRD	NSKNTLY	IQM	NSLR	ED	TAVYYCAKDR	YDIL	TGYN	LDYWGQGT	TVSS	124
		SRD	NSKNTLY	IQM	NSLR	ED	TAVYYCAKDR	YDIL	TGYN	LDYWGQGT	TVSS	120
		SRD	NSKNTLY	IQM	NSLR	ED	TAVYYCAKDR	YDIL	TGYN	LDYWGQGT	TVSS	110
		SRD	NSKNTLY	IQM	NSLR	ED	TAVYYCAKDR	YDIL	TGYN	LDYWGQGT	TVSS	100
		SRD	NSKNTLY	IQM	NSLR	ED	TAVYYCAKDR	YDIL	TGYN	LDYWGQGT	TVSS	90
		SRD	NSKNTLY	IQM	NSLR	ED	TAVYYCAKDR	YDIL	TGYN	LDYWGQGT	TVSS	80
		SRD	NSKNTLY	IQM	NSLR	ED	TAVYYCAKDR	YDIL	TGYN	LDYWGQGT	TVSS	70
1021-511LB3 1021-511LB2 1021-511LB1 1021-511LC 1021-511LA1 1021-511LA2 1021-511LA3 IMGT-NR	(1)	SIQ	ITQSP	SS	LSASV	GD	RV	ITCR	ASQGIS	SWLAWYQ	QKP	60
		SIQ	ITQSP	SS	LSASV	GD	RV	ITCR	ASQGIS	SWLAWYQ	QKP	50
		SIQ	ITQSP	SS	LSASV	GD	RV	ITCR	ASQGIS	SWLAWYQ	QKP	40
		SIQ	ITQSP	SS	LSASV	GD	RV	ITCR	ASQGIS	SWLAWYQ	QKP	30
		SIQ	ITQSP	SS	LSASV	GD	RV	ITCR	ASQGIS	SWLAWYQ	QKP	20
		SIQ	ITQSP	SS	LSASV	GD	RV	ITCR	ASQGIS	SWLAWYQ	QKP	10
		SIQ	ITQSP	SS	LSASV	GD	RV	ITCR	ASQGIS	SWLAWYQ	QKP	0
1021-511HB3 1021-511HB2 1021-511HB1 1021-511HC 1021-511HP 1021-511HA1 1021-511HA2 1021-511HA3 IMGT-NR	(71)	FTLT	ISSI	OP	EDF	ATY	Y	Q	Q	Q	Q	107
		FTLT	ISSI	OP	EDF	ATY	Y	Q	Q	Q	Q	100
		FTLT	ISSI	OP	EDF	ATY	Y	Q	Q	Q	Q	90
		FTLT	ISSI	OP	EDF	ATY	Y	Q	Q	Q	Q	80
		FTLT	ISSI	OP	EDF	ATY	Y	Q	Q	Q	Q	70
		FTLT	ISSI	OP	EDF	ATY	Y	Q	Q	Q	Q	60
		FTLT	ISSI	OP	EDF	ATY	Y	Q	Q	Q	Q	50

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Figure 3

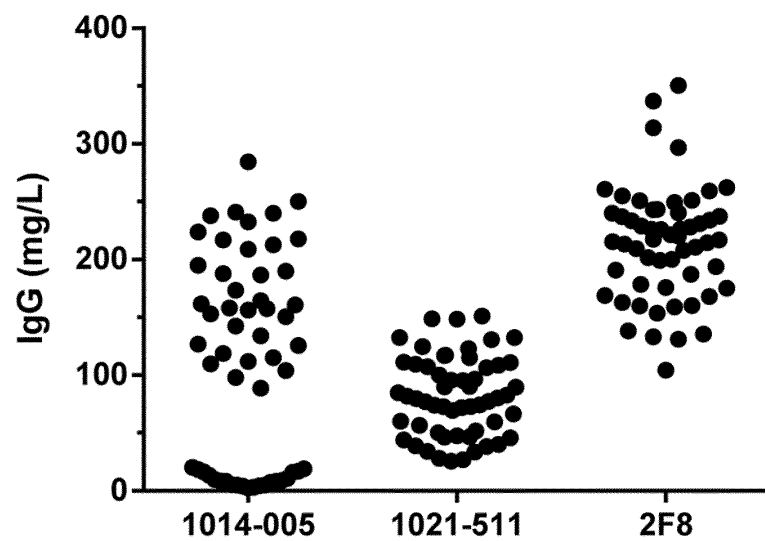


Figure 4

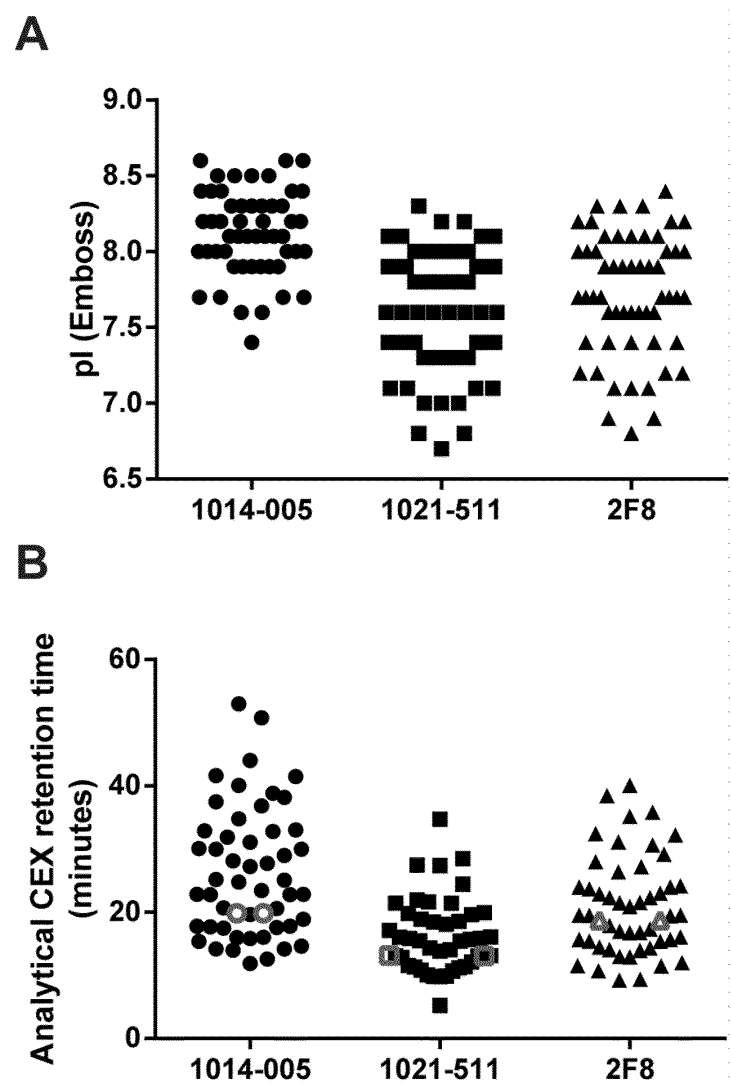


Figure 4 (continued)

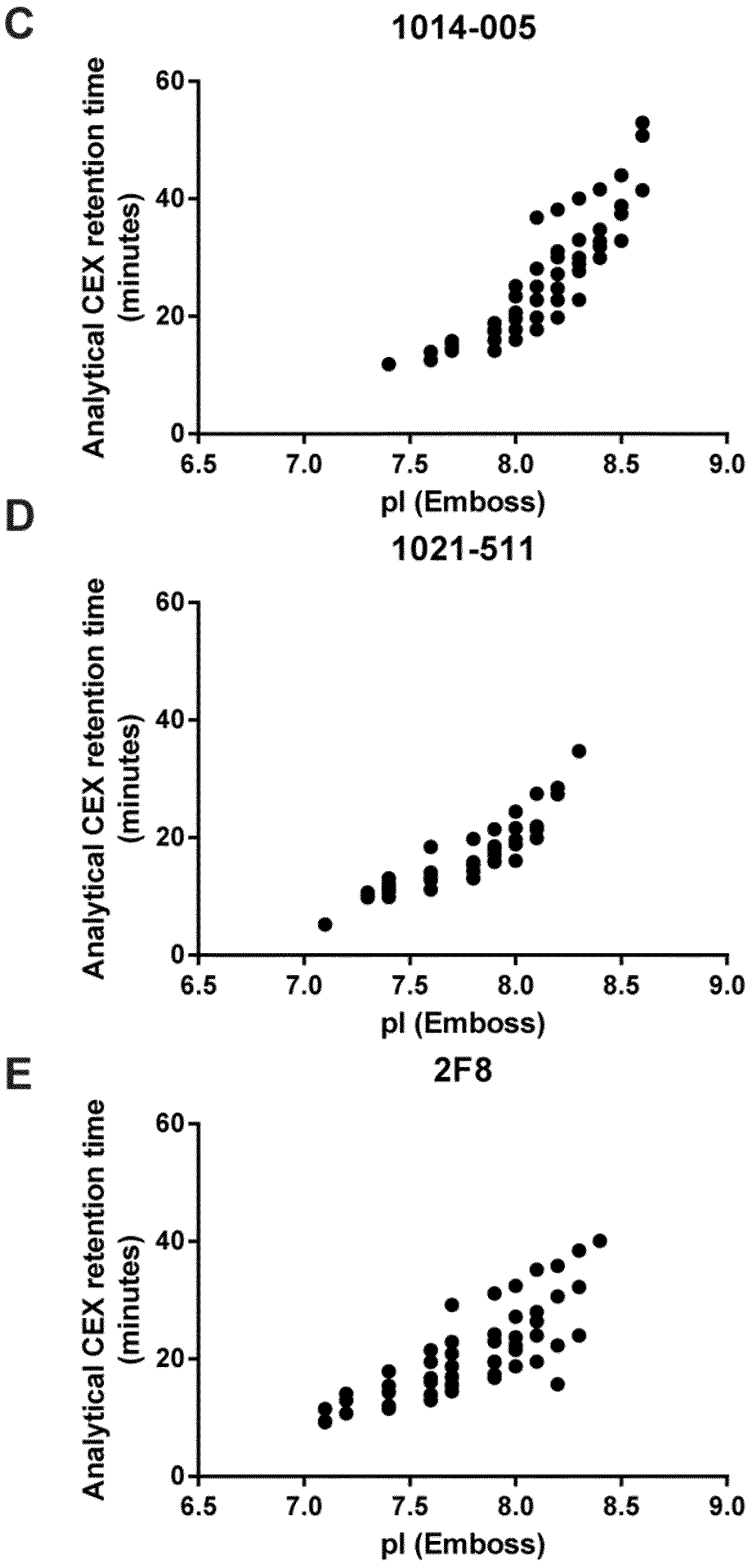
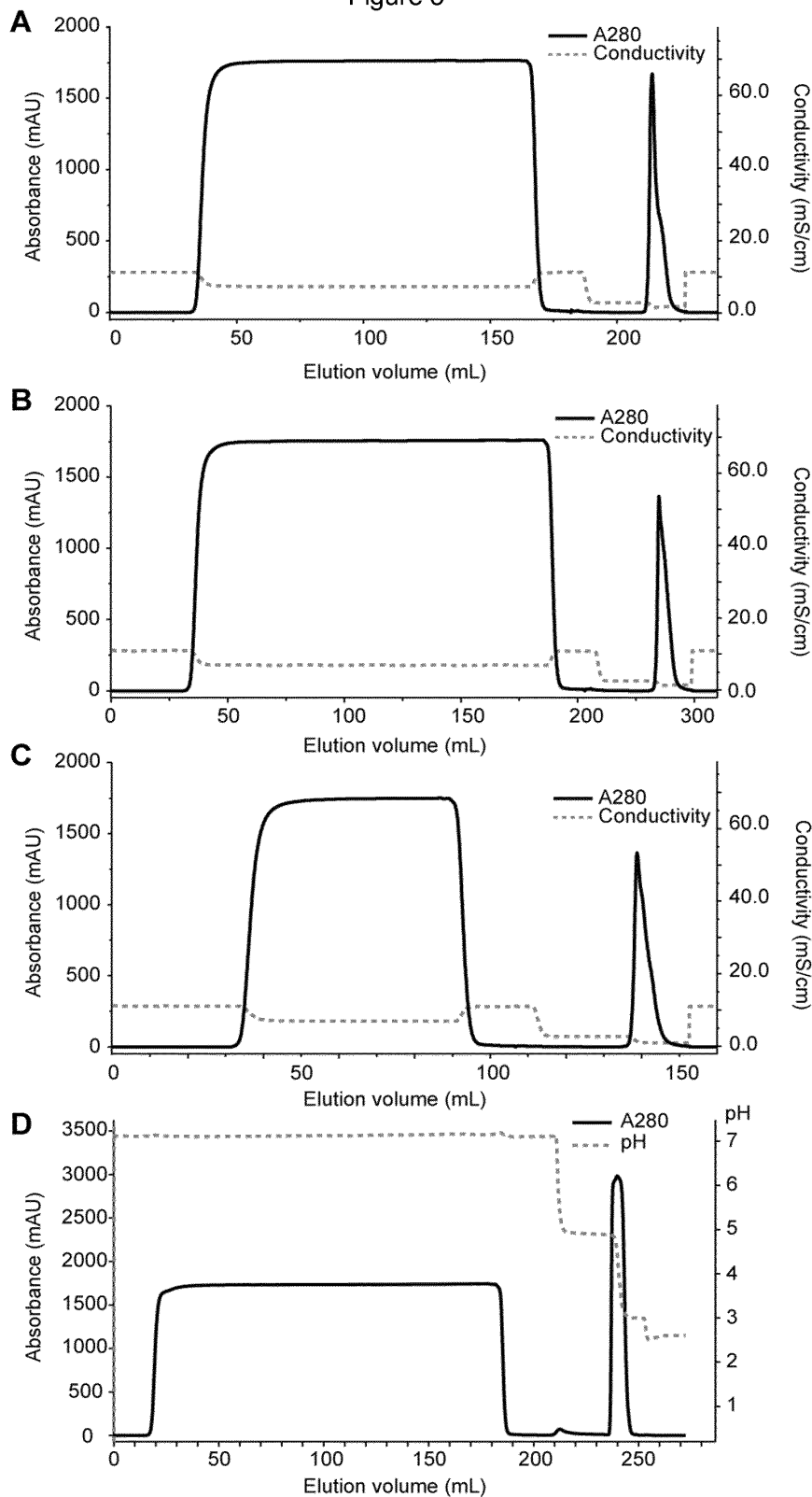


Figure 5



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Figure 5 (continued)

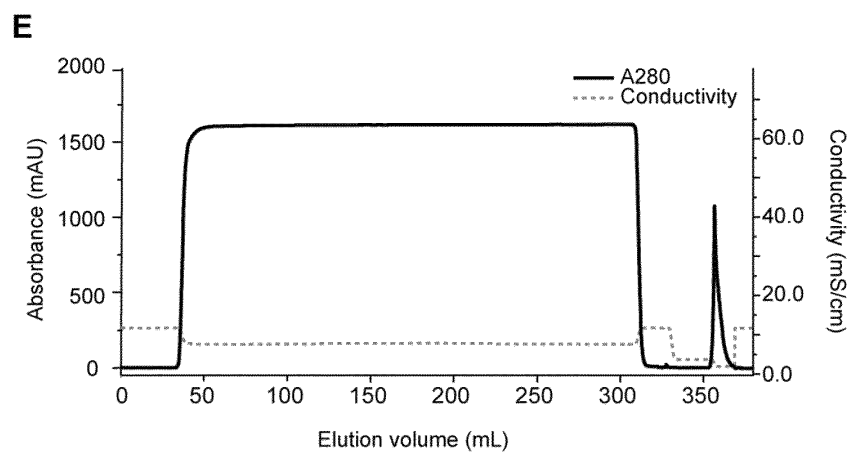


Figure 6

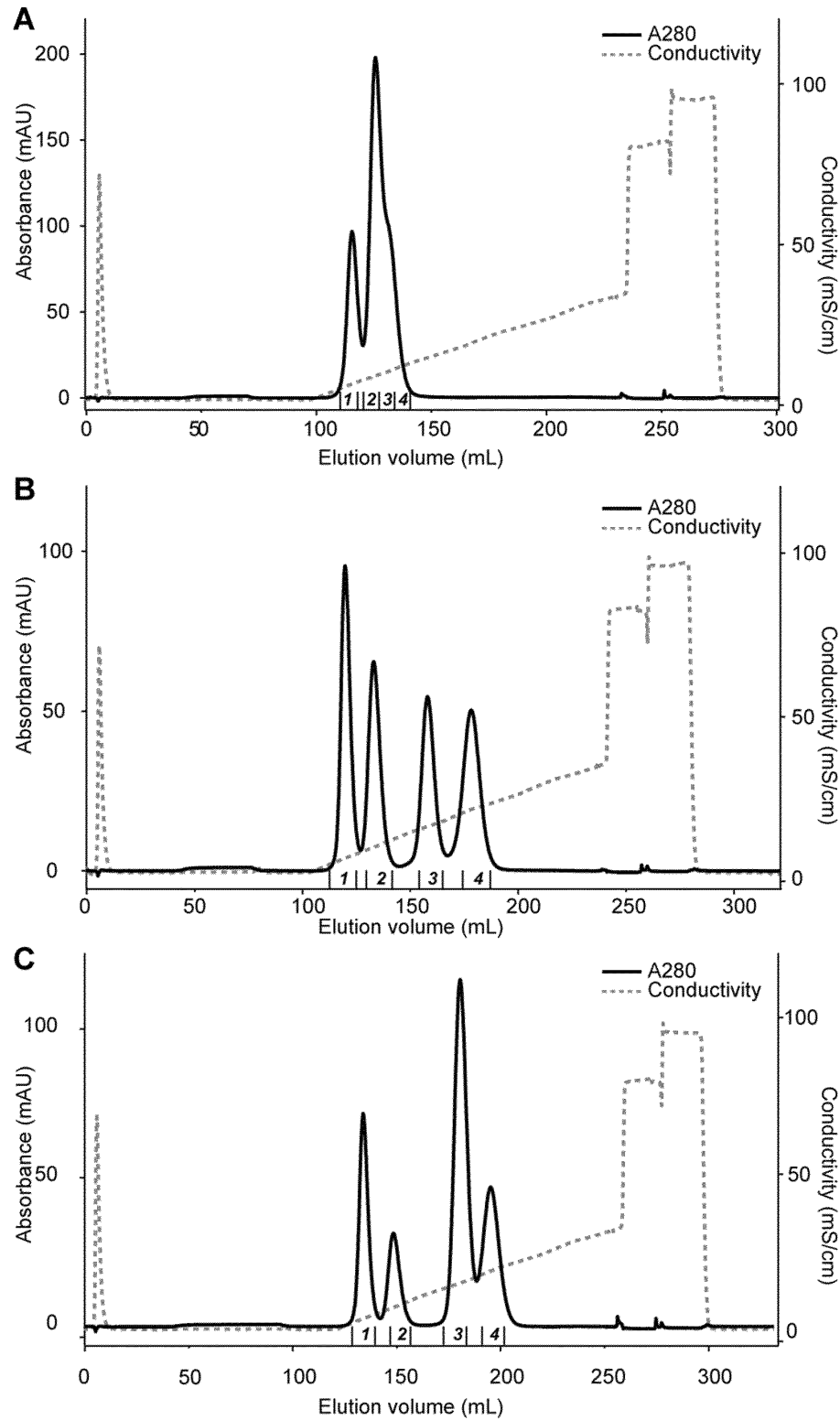
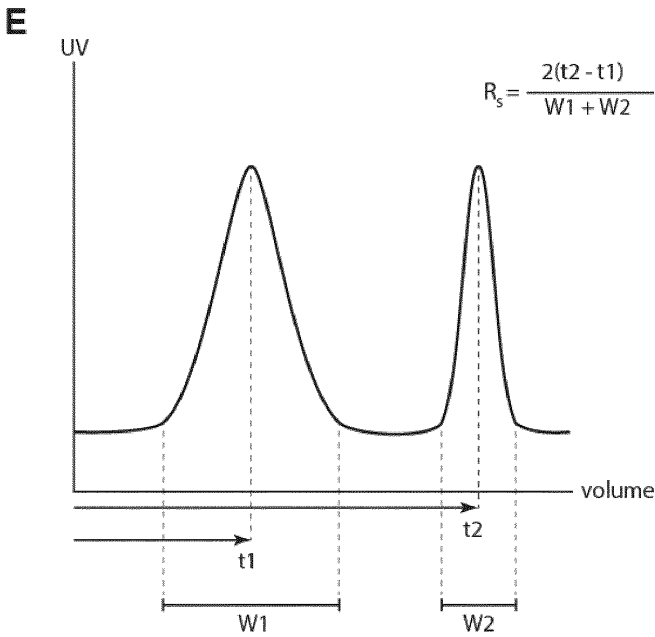
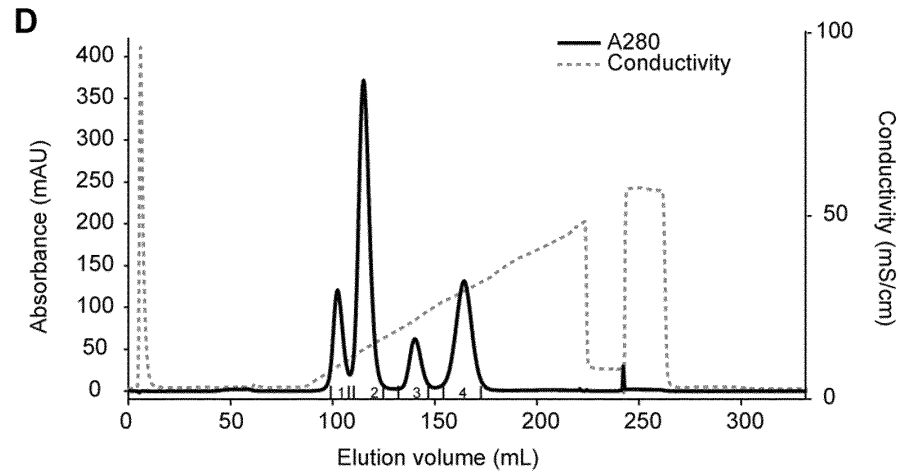


Figure 6 (continued)



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Figure 7

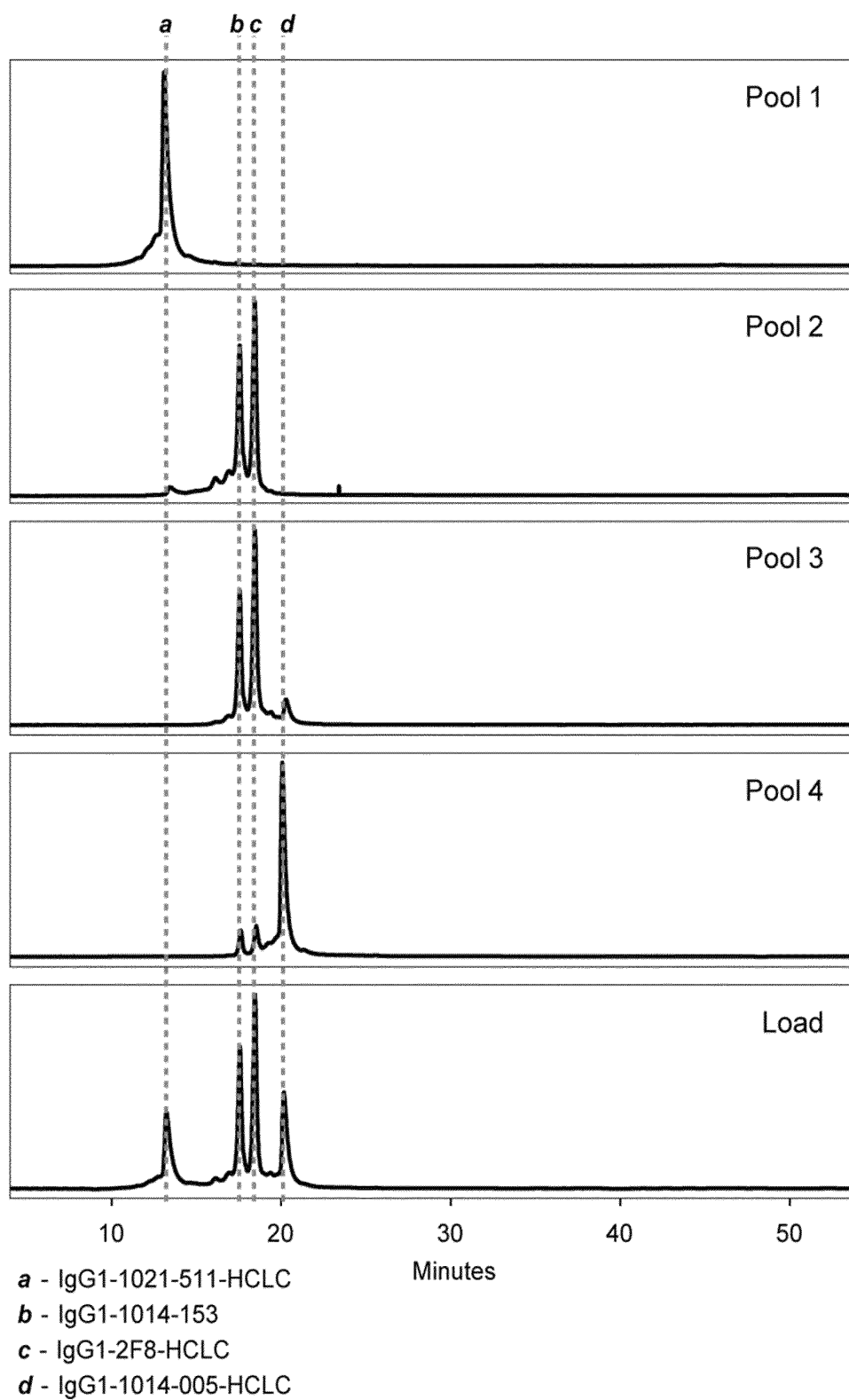
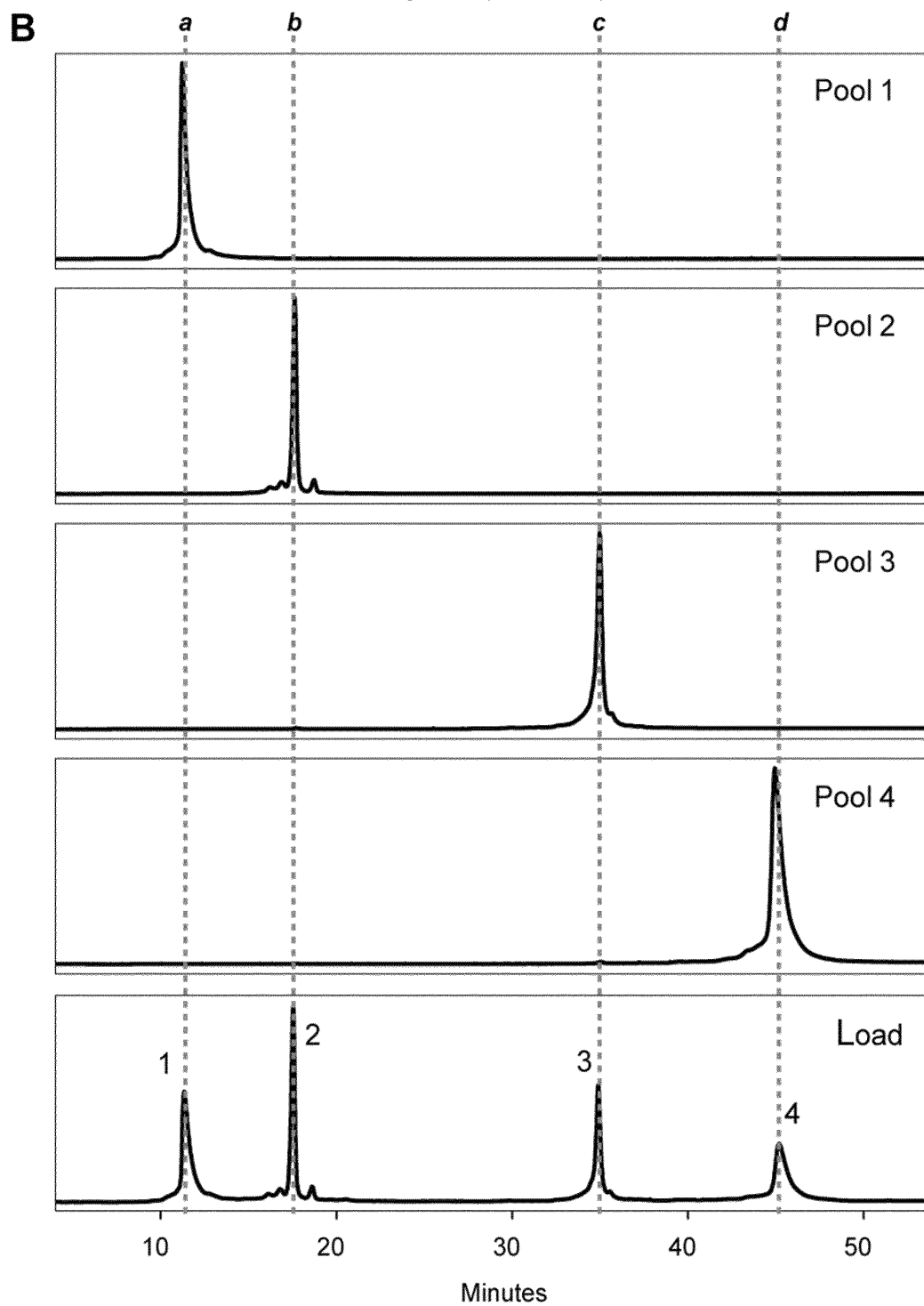
A

Figure 7 (continued)



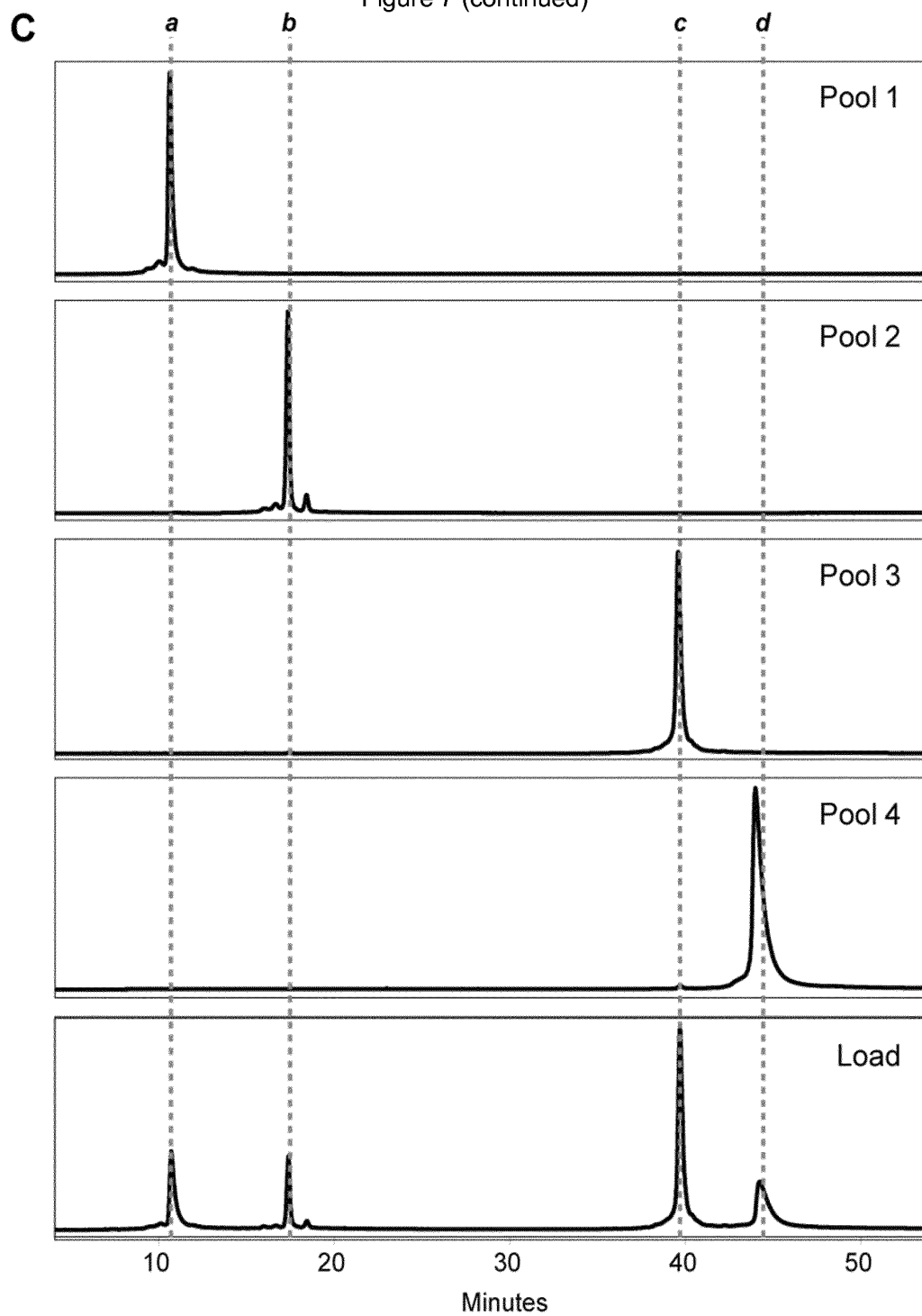
a - IgG1-1021-511-HA3LB2

b - IgG1-1014-153

c - IgG1-2F8-HB3LC

d - IgG1-1014-005-HB3LB1

Figure 7 (continued)



a - IgG1-1021-511-HA3LB2

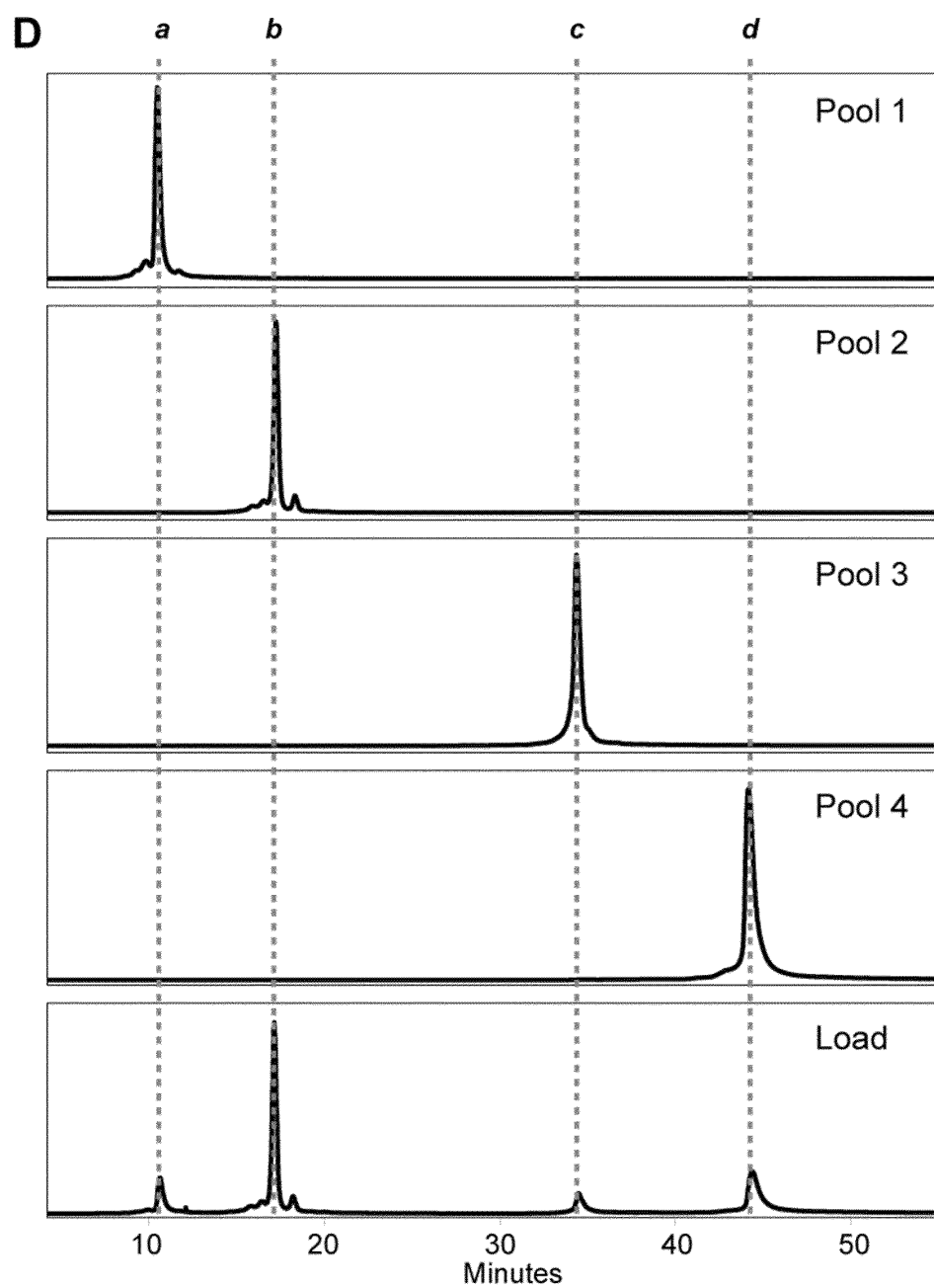
b - IgG1-1014-153

c - IgG1-2F8-HB3LB3

d - IgG1-1014-005-HB3LB1

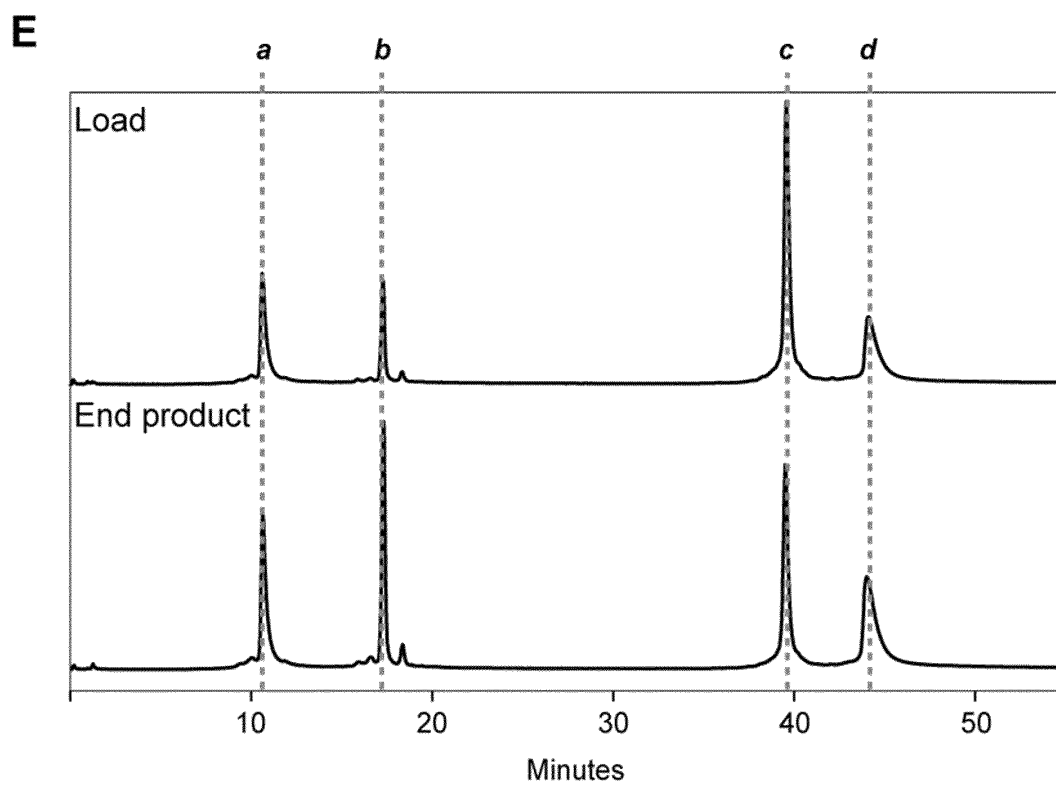
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Figure 7 (continued)

*a* - IgG1-1021-511-HA3LB2*b* - IgG1-1014-153*c* - IgG1-2F8-HB3LC*d* - IgG1-1014-005-HB3LB1

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Figure 7 (continued)



a - IgG1-1021-511-HA3LB2

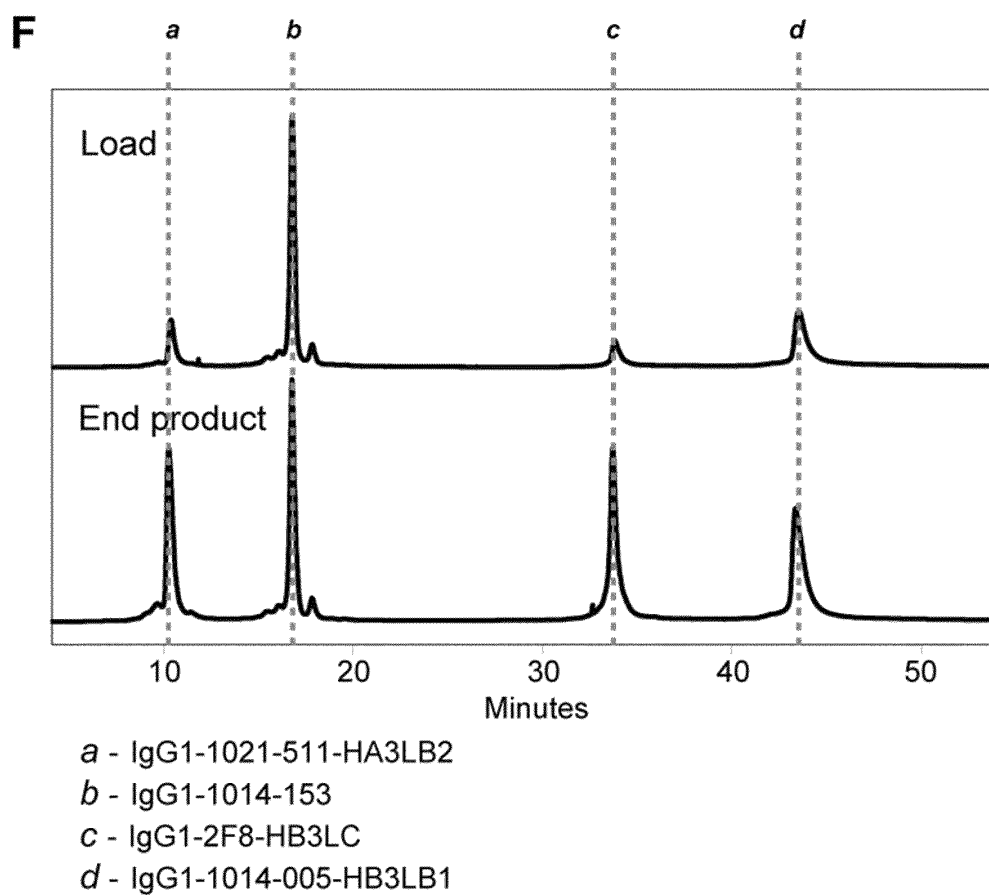
b - IgG1-1014-153

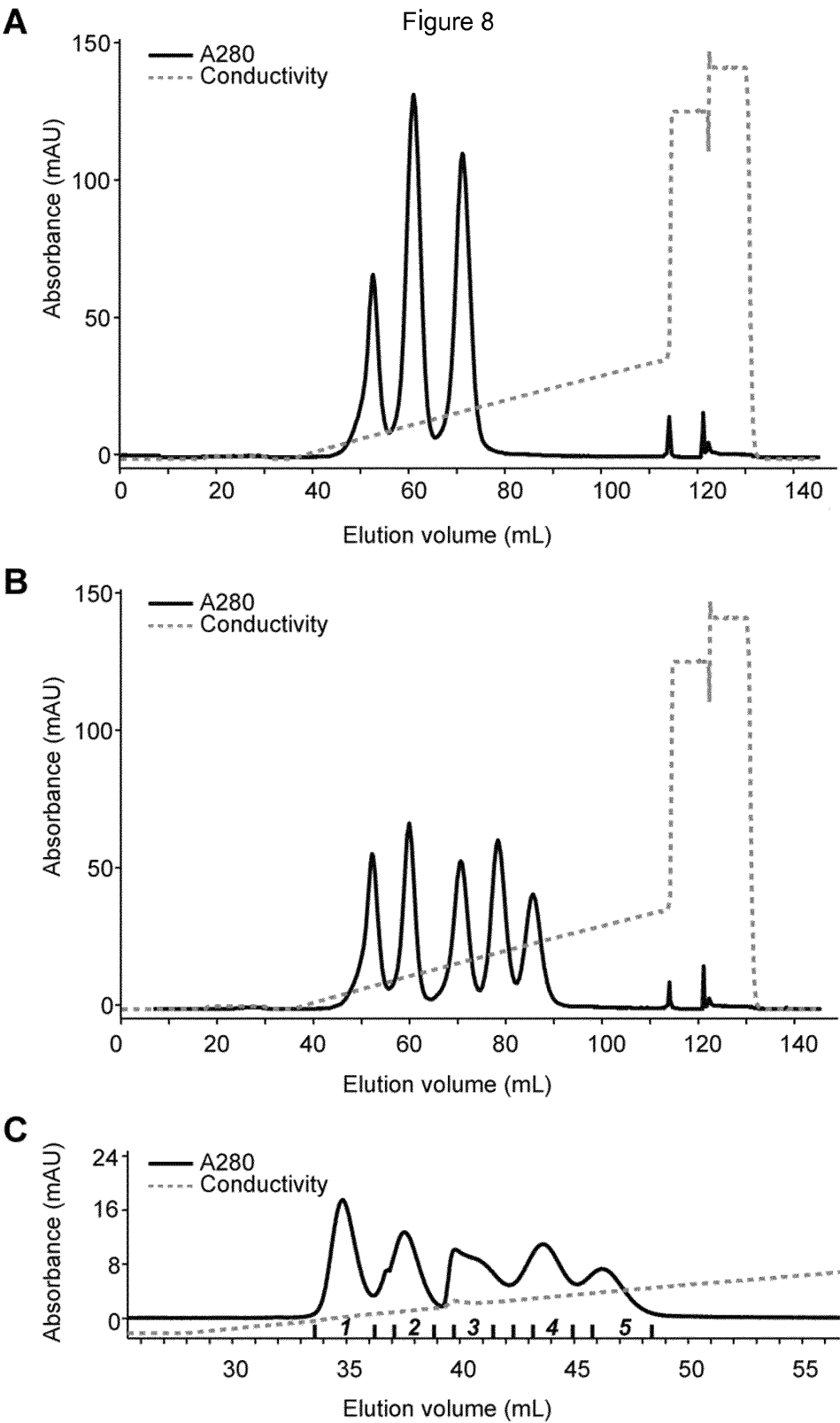
c - IgG1-2F8-HB3LB3

d - IgG1-1014-005-HB3LB1

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Figure 7 (continued)





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Figure 8 (continued)

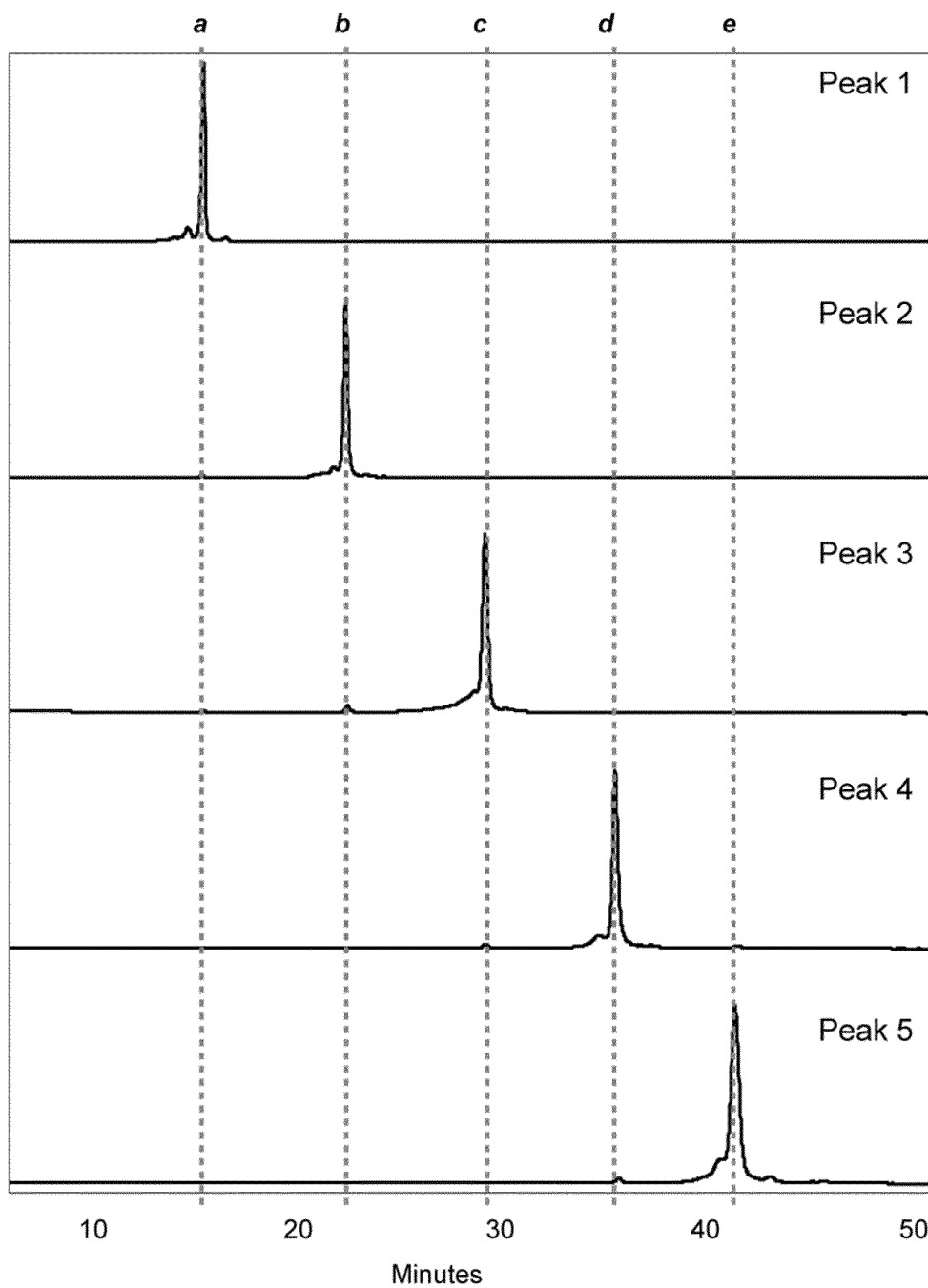
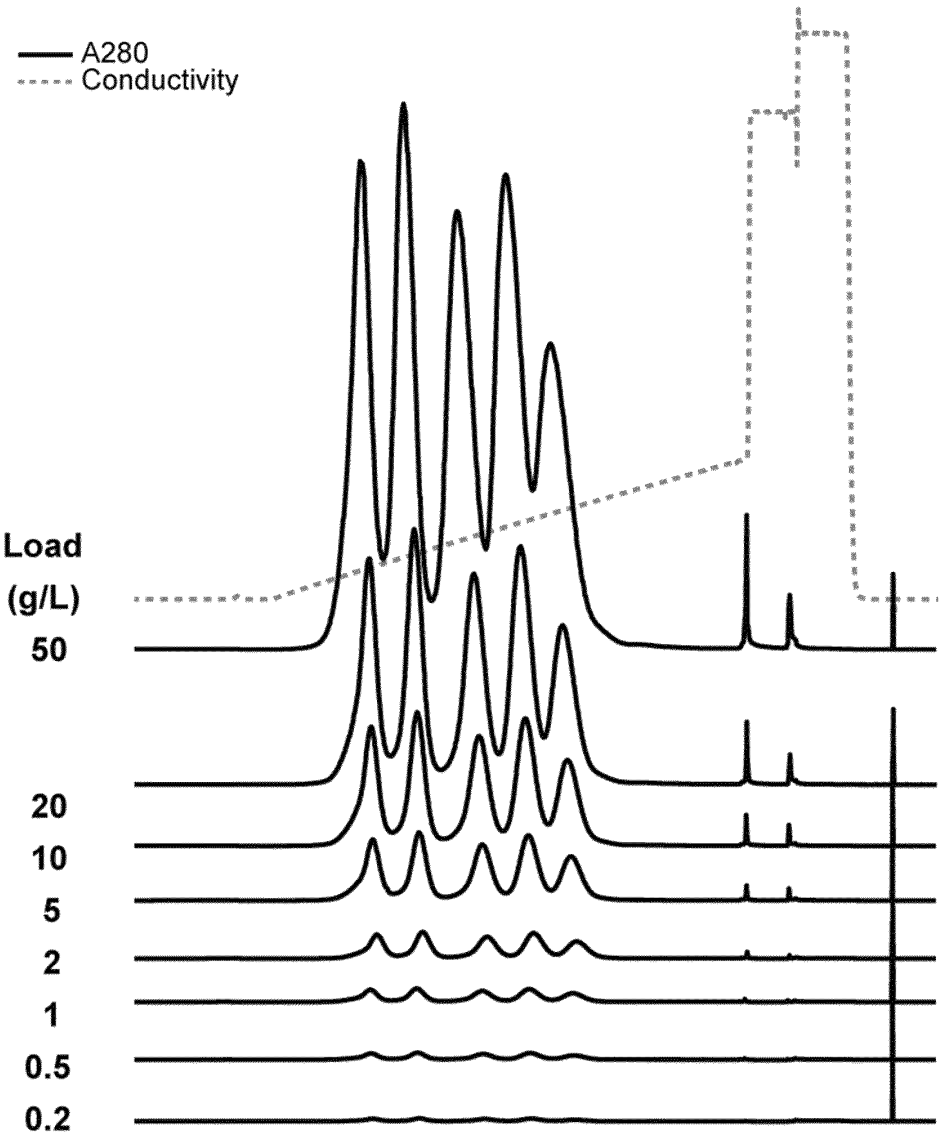
D*a* - IgG1-7D8*b* - IgG1-224*c* - IgG1-CD37-37-3*d* - IgG1-CD19-21D4-E345K*e* - IgG1-CD52-Campath-E345K

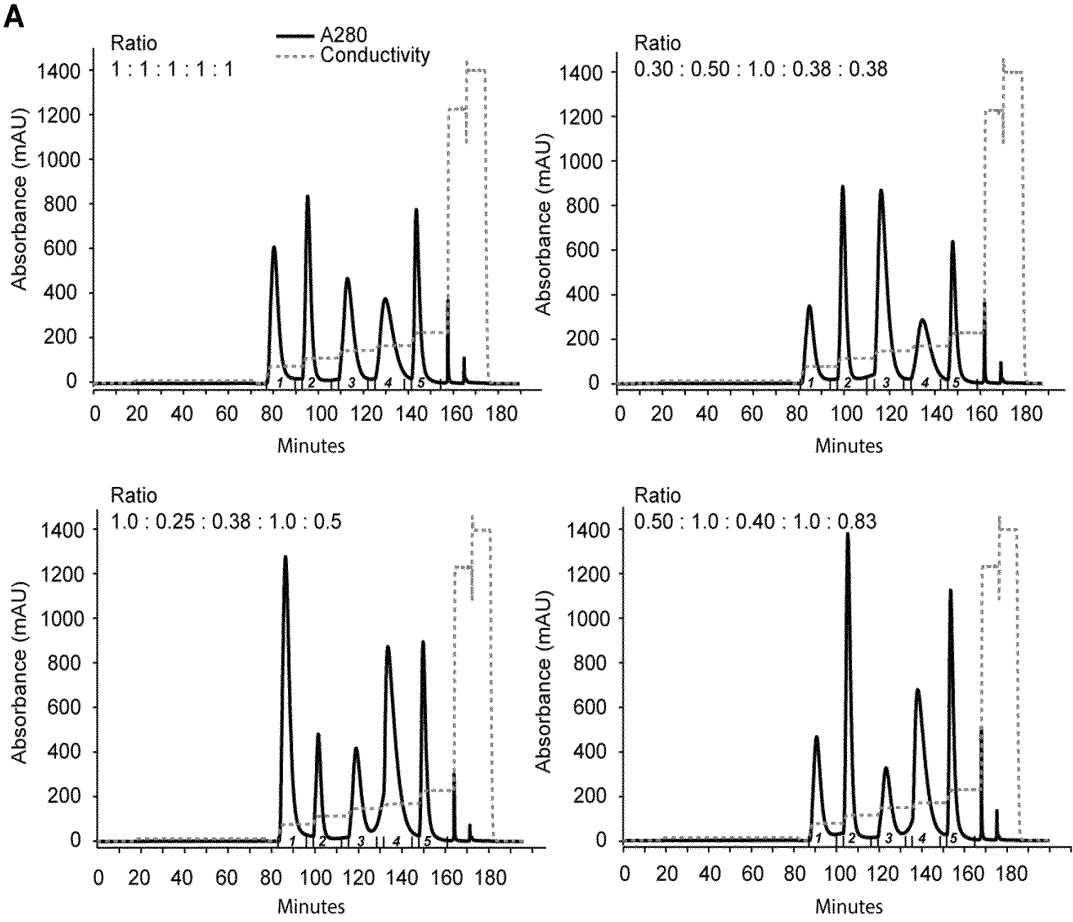
Figure 8 (continued)

E



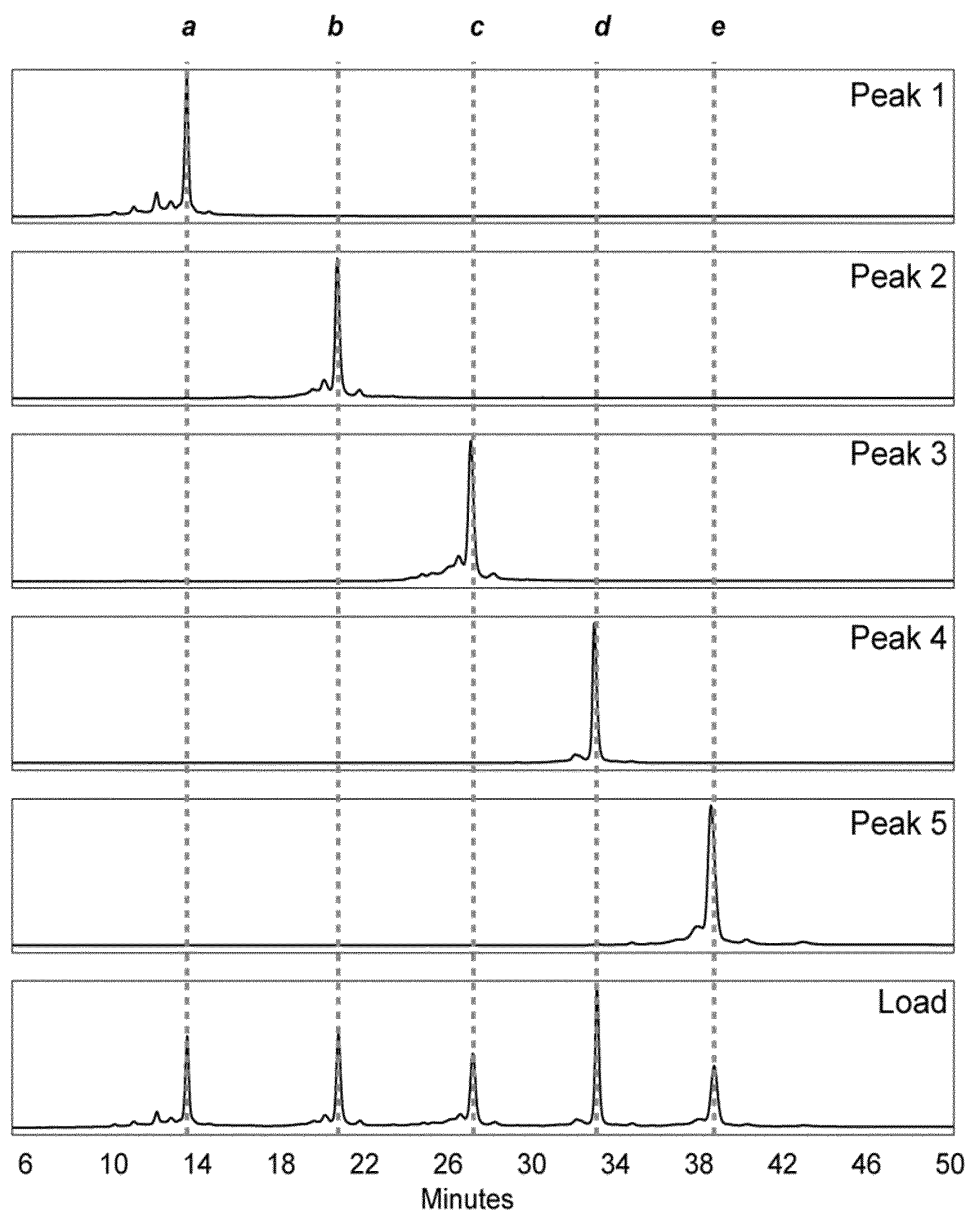
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Figure 9



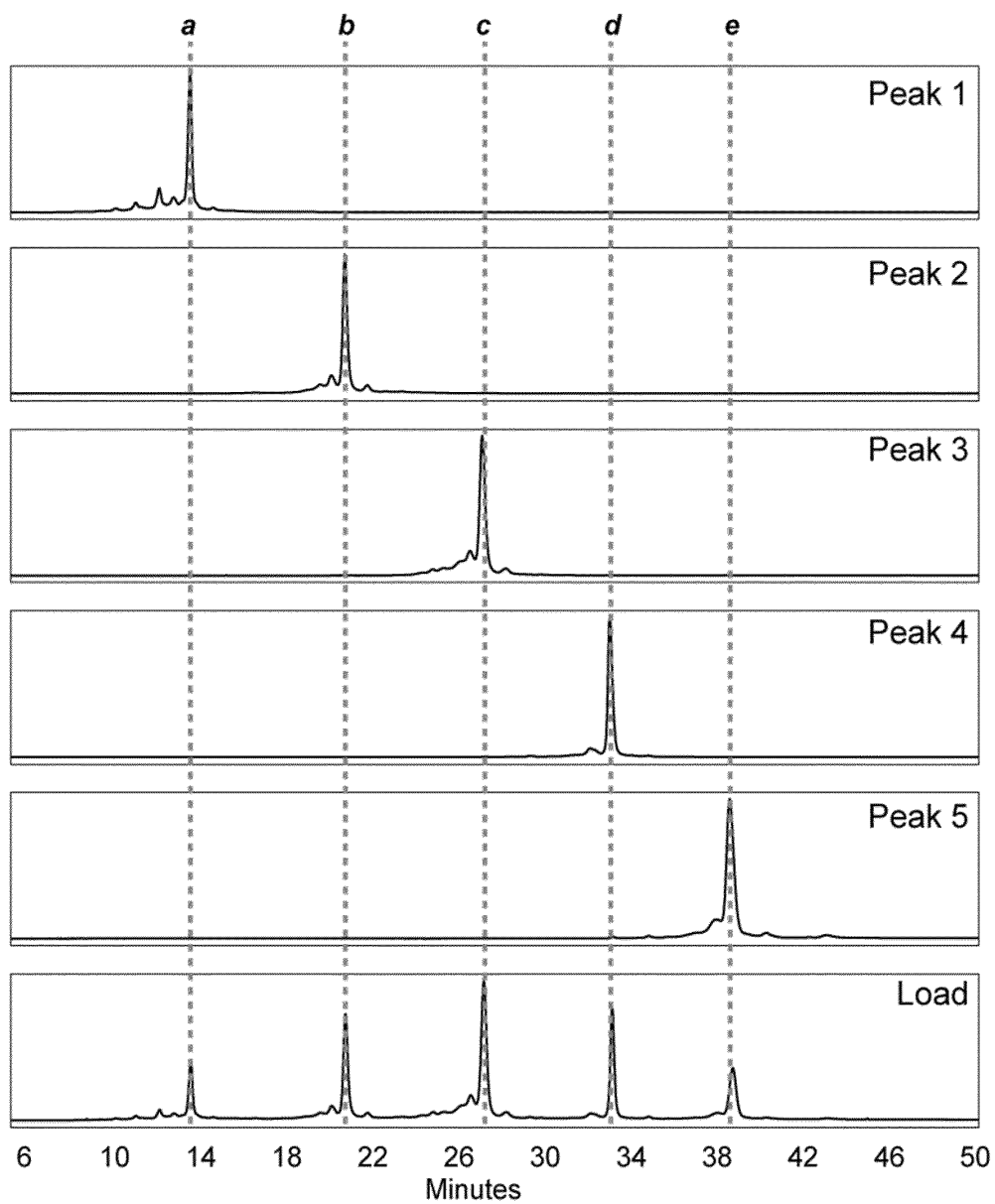
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Figure 9 (continued)

B Ratio 1 : 1 : 1 : 1 : 1

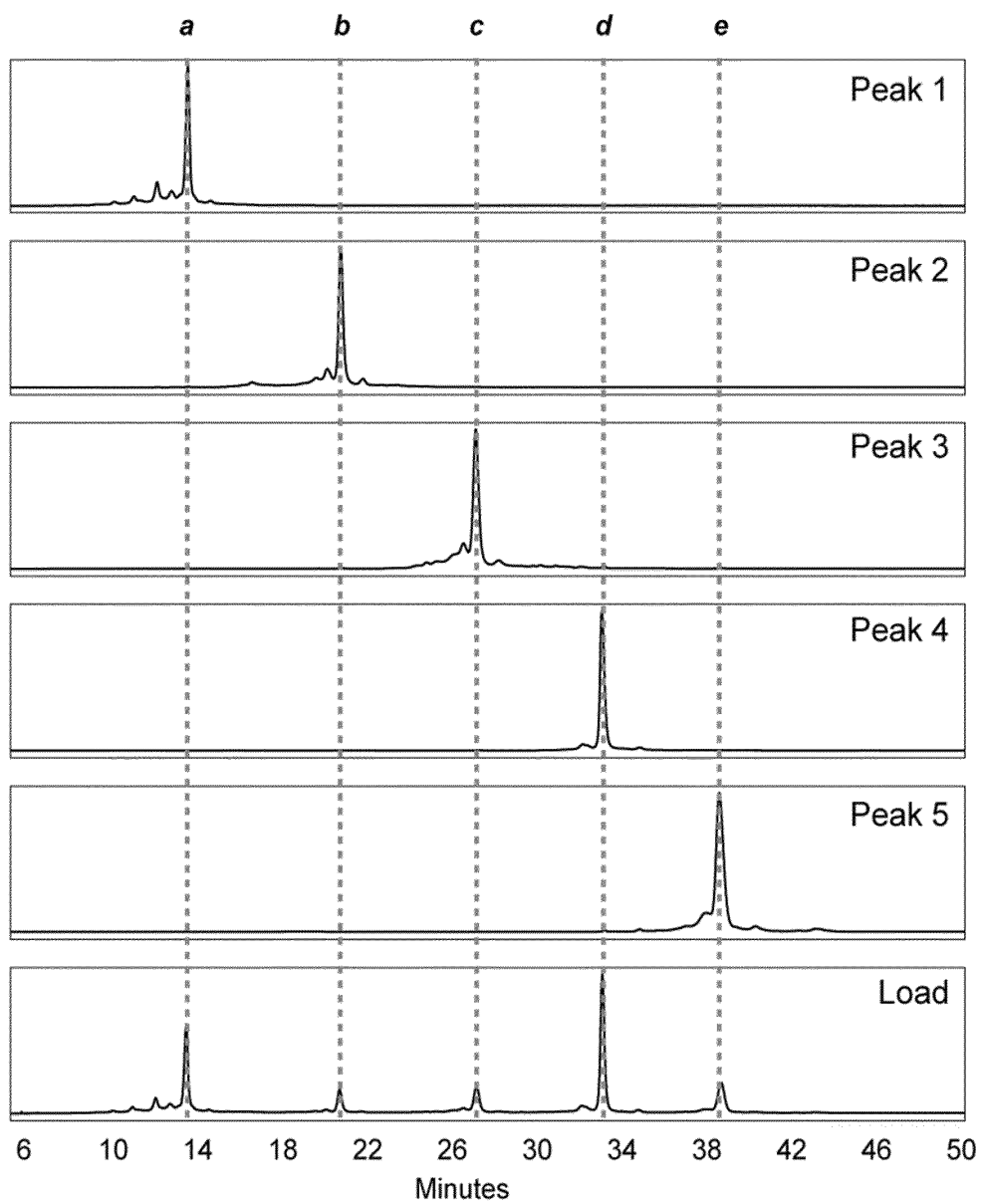
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Figure 9 (continued)

C Ratio 0.30 : 0.50 : 1.0 : 0.38 : 0.38

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Figure 9 (continued)

D Ratio 1.0 : 0.25 : 0.38 : 1.0 : 0.50

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Figure 9 (continued)

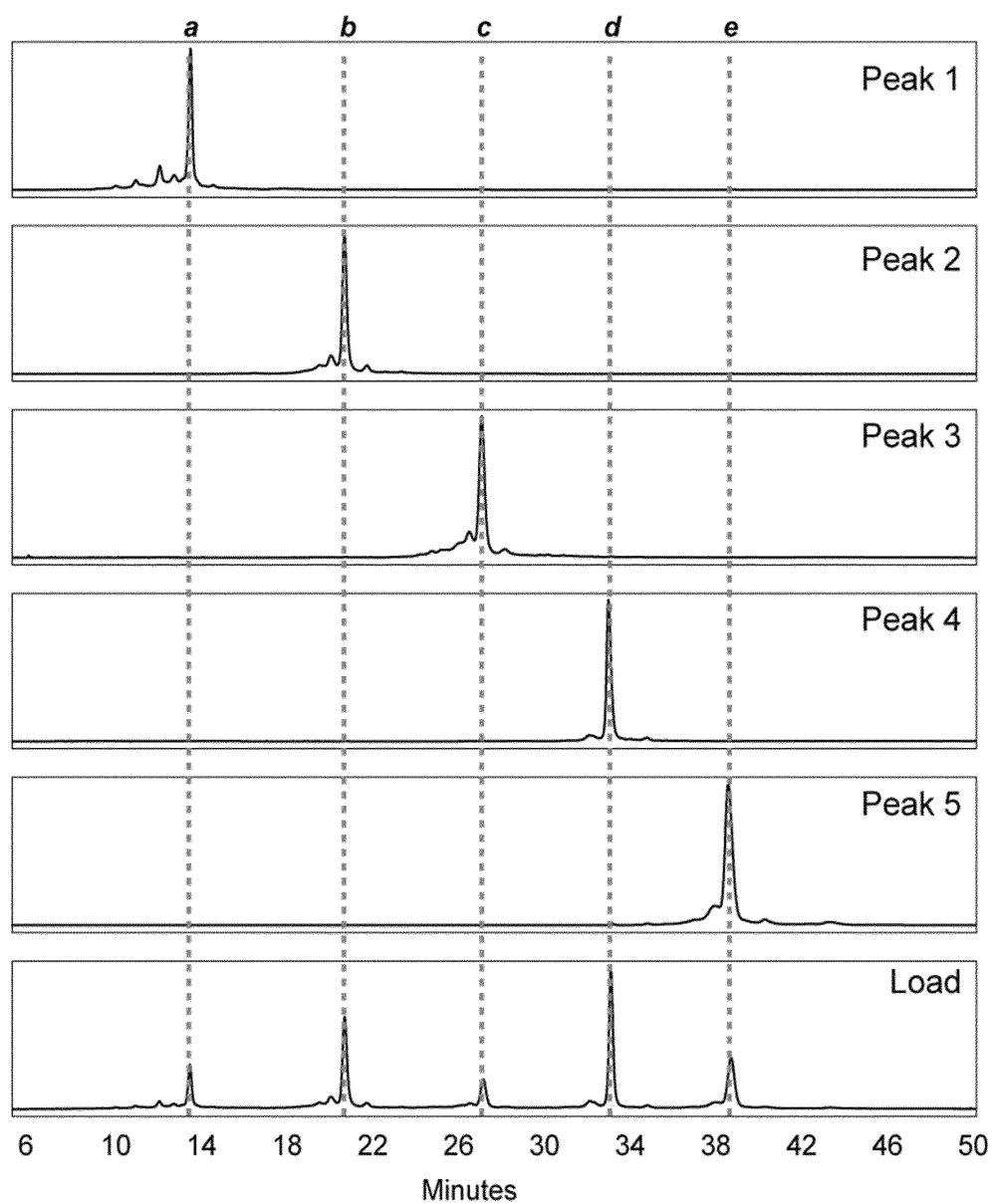
E Ratio 0.50 : 1.0 : 0.40 : 1.0 : 0.83

Figure 10

Figure 10

	1	1	1	1	1	1
	1	2	3	4	5	6
CROSS-REACTIVE	90123456789012345678901234567890123456789012345678	901				
UP P01834 IGKC1_Homsap	TVAAPSVFI	FPPSDEQLKSGTASVVCLLNNFY	PREAKVQWKVDNALQSGN	SQE		
IMGT M11736 IGKC2_Homsap	TVAAPSVFI	FPPSDEQLKSGTASVVCLLNNFY	PREAKVQWKVDNALQSGN	SQE		
IMGT M11737 IGKC3_Homsap	TVAAPSVFI	FPPSDEQLKSGTASVVCLLNNFY	PREAKVQWKVDNALQSGN	SQE		
GB AF017732 IGKC4_Homsap	TVAAPSVFI	FPPSDEQLKSGTASVVCLLNNFY	PREAKVQWKVDNALQSGN	SQE		
GB AF113887 IGKC5_Homsap	TVAAPSVFI	FPPSDEQLKSGTASVVCLLNNFY	PREAKVQWKVDNALQSGN	SQE		
GB AJ619771 IGKC_Macfas	AVAAPSVFI	FPPSEDQVKS	GTVSVVCLLNNFY	PREASVKKVDGAVQTGN	SQE	
GB FJ795855 IGKC_Macmul	AVAAPSVLI	FPPSEDQVKS	GTVSVVCLLNNFY	PREASVKKVDGVLTKGN	SQE	
CONSENSUS +	VAAPSV	IFPPS	Q KSGT	SVVCLLNNFY	PREA V	KVD GN SQE
NON CROSS-REACTIVE						
UP P01837 IGKC_Musmus	ADAAPT	VSIFPPSSEQLTSGGASVVCF	LNNFY	PKDINVKWKIDG	SERQNG	VLN
UP P01844 IGLC2_Musmus	PKSTPT	LTVPFPPSSEELKENKATLVCLIS	NFSPSGVT	VAWKANGT	PITQ	Q VDT
UP P01845 IGLC3_Musmus	PKSTPT	LTMTFPPSPEELQENKATLVCLIS	NFSPSGVT	VAWKANGT	PITQ	Q VDT
UP P0CG04 IGLC1_Homsap	PKANPT	VTFLFPPSSEELQANKATLVCLIS	DFYPGAVT	VAWKADG	SPVKAG	VET
UP P0CG05 IGLC2_Homsap	PKAAPSV	TLFPPSSEELQANKATLVCLIS	DFYPGAVT	VAWKADG	SPVKAG	VET
UP P0CG06 IGLC3_Homsap	PKAAPSV	TLFPPSSEELQANKATLVCLIS	DFYPGAVT	VAWKADG	SPAKAG	VET
UP P0CF74 IGLC6_Homsap	PKAAPSV	TLFPPSSEELQANKATLVCLIS	DFYPGAVK	VAWKADG	SPVNTG	VET
UP A0M8Q6 IGLC7_Homsap	PKAAPSV	TLFPPSSEELQANKATLVCLIS	DFYPGAVT	VAWKADG	SPVKVG	VET
IMGT V01241 IGKC_Ratnor	ADAAPT	VSIFPPSTEQLATGGASVVCLM	NNFY	PRDISVKKIDG	TERRDG	VLD
IMGT K01360 IGKC1_Orycun	DPVAPT	VLIFPPAADQVATGTVTIVC	VANKYFPDVT	VTWEVDG	TTQT	TG IEN
IMGT X00232 IGKC2_Orycun	DPVAPS	VLLFPPSKEELTTGTATIVC	VANKFYPSDIT	VTWKVDG	TTQ	QSG IEN
GB AEM45014 IGKC_Bostau	SDAEP	SVFLFKPSDEQLKTGT	TVSVVCLVNDFY	PKDINVKWKVDG	VTQSSSNFQ	N
CONSENSUS -	V				EA	GN S E
PISA (INTERFACE)		+	++	+	++	+
SELECTED	*				**	** * *
	1	1	1	2	2	
	7	8	9	0	1	
CROSS-REACTIVE	23456789012345678901234567890123456789012345678901234					
UP P01834 IGKC1_Homsap	SVTEQ	DSKDYSL	SLSTLTLSKADYE	KKVYACEVTHQGL	SSPVTKSFNRGEC	
IMGT M11736 IGKC2_Homsap	SVTEQ	ESKDYSL	SLSTLTLSKADYE	KKVYAGEVTHQGL	SSPVTKSFNRGEC	
IMGT M11737 IGKC3_Homsap	SVTEQ	ESKDYSL	SLSTLTLSKADYE	KKVYACEVTHQGL	SSPVTKSFNRGEC	
GB AF017732 IGKC4_Homsap	SVTEQ	DSKDYSL	SLSTLTLSKADYE	KKLYACEVTHQGL	SSPVTKSFNRGEC	
GB AF113887 IGKC5_Homsap	SVTEQ	DSKDYSL	SLSTLTLSKADYE	KKVYACEVTHQGL	SSPVTKSFNRGEC	
GB AJ619771 IGKC_Macfas	SVTEQ	DSKDYSL	SLSTLTLSKADYE	KKVYACEVTHQGL	SSPVTKSFNRGEC	
GB FJ795855 IGKC_Macmul	SVTEQ	DSKDYSL	SLSTLTLSKADYE	SHNVYACEVTHQGL	SSPVTKSFNRGEC	
CONSENSUS +	SVTE	SKD TYSL	SLSTLTLS	DY H	YA EVTHQGL	SSPVTKSFNRGEC
NON CROSS-REACTIVE						
UP P01837 IGKC_Musmus	SWTDQ	DSKDYSL	SMSSLTLT	TKDEYERHNSYTCEATHKT	STSPIVKSFNRNEC	
UP P01844 IGLC2_Musmus	SNPTKE	GN KFMAS	SFLHLTSDQWRSHNSFTCQV	THEGDT	VEKSLSPAEC	L
UP P01845 IGLC3_Musmus	SNPTKE	GN KYMASS	FLHLTSDQWRSHNSFTCQV	THEGDT	VEKSLSPAEC	L
UP P0CG04 IGLC1_Homsap	TKPSKQ	SN NKYA	ASSYLSLTPEQWKSHRSYSCQV	THEGST	VEKTVA	PTPCS
UP P0CG05 IGLC2_Homsap	TTPSKQ	SN NKYA	ASSYLSLTPEQWKSHRSYSCQV	THEGST	VEKTVA	PTPCS
UP P0CG06 IGLC3_Homsap	TTPSKQ	SN NKYA	ASSYLSLTPEQWKSHRSYSCQV	THEGST	VEKTVA	PTPCS
UP P0CF74 IGLC6_Homsap	TTPSKQ	SN NKYA	ASSYLSLTPEQWKSHRSYSCQV	THEGST	VEKTVA	PAECS
UP A0M8Q6 IGLC7_Homsap	TKPSKQ	SN NKYA	ASSYLSLTPEQWKSHRSYSCQV	THEGST	VEKTVA	PAECS
IMGT V01241 IGKC_Ratnor	SVTDQ	DSKDYSL	SMSSLTLT	TKADYESHNL	YTCEVVKTS	SFNRNEC
IMGT K01360 IGKC1_Orycun	SKTPQ	NSADCTYN	LSSTLT	STQYN	SHKEYTCKVT	QGTTS VVQSFNRGDC
IMGT X00232 IGKC2_Orycun	SKTPQ	SPEDNTY	LSSTLT	SLTSAQYN	SHSVYTCEV	QGSASPIVQSFNRGDC
GB AEM45014 IGKC_Bostau	SFTDQ	DSKDYSL	SSILTLPSSEYQ	SHNAYTCEVSHKSL	TALVKS	FSKNEC
CONSENSUS -	E		S	A	T	
PISA (INTERFACE)	+	+	+++	+	+	+
SELECTED	*		*			

Figure 11

	1	2	3	4	5	6
PDB IMHH_A	123456789012345678901234567890123456789012345678901234					
PDB IHEZ_A	DIVMSQSPSSLAVSAGEKVTMSCKSSQSLNSTRKNYLAWYQQKPGQSPKVLIIWA-----					
2F8_VL	DIQMTQSPSSLSASVGDRVTITCRTSQSI-----SSYLNWYQQKPGKAPKLLIYAA-----					
SP P01617 KV204	AIQLTQSPSSLSASVGDRVTITCRASQDI-----SSALVWYQQKPGKAPKLLIYDA-----					
SP P01699 LV101	DIVMTQSPFLSLPVTGPGEPAISCRSSQSLIHS-DGFDYLNWYLQKPGQSPZLLIYAL-----					
PISA (INTERFACE)	QSVLTQPP SASGTPGQRTITSCSGGNFDI-----GRNSVNWYQVHFGTAPRLLIYSS-----					
SELECTED	+++++++ ++++++ +					
	* * * * *					

	7	8	9	1	1	2
PDB IMHH_A	56789012345678901234567890123456789012345678901234567					
PDB IHEZ_A	STRESSGVP-DRFTGRG--SGTDFTLTISSVQAEDQAVYCKQAYI-----PPLTFGAGTKLELK					
2F8_VL	SSLQSGVP-SRFSGSG--SGTDFTLTISSLQPEDFATYCCQSYS----TPRTFGQGTKEIK					
SP P01617 KV204	SSLESGVP-SRFSGSE--SGTDFTLTISSLQPEDFATYCCQFNS-----YPLTFGGGTKEIK					
SP P01699 LV101	SNRASGVP-DRFSGSG--SGTDFTLKISRVEAEDGVYCMZALQ-----APITFGQGTREIK					
PISA (INTERFACE)	DQRSSGVP-DRFSGSK--SGTSASLAISGLQSENEADYFCATWDDS--LDGPVFGGGTKVTVL					
SELECTED	+ +					

Figure 12

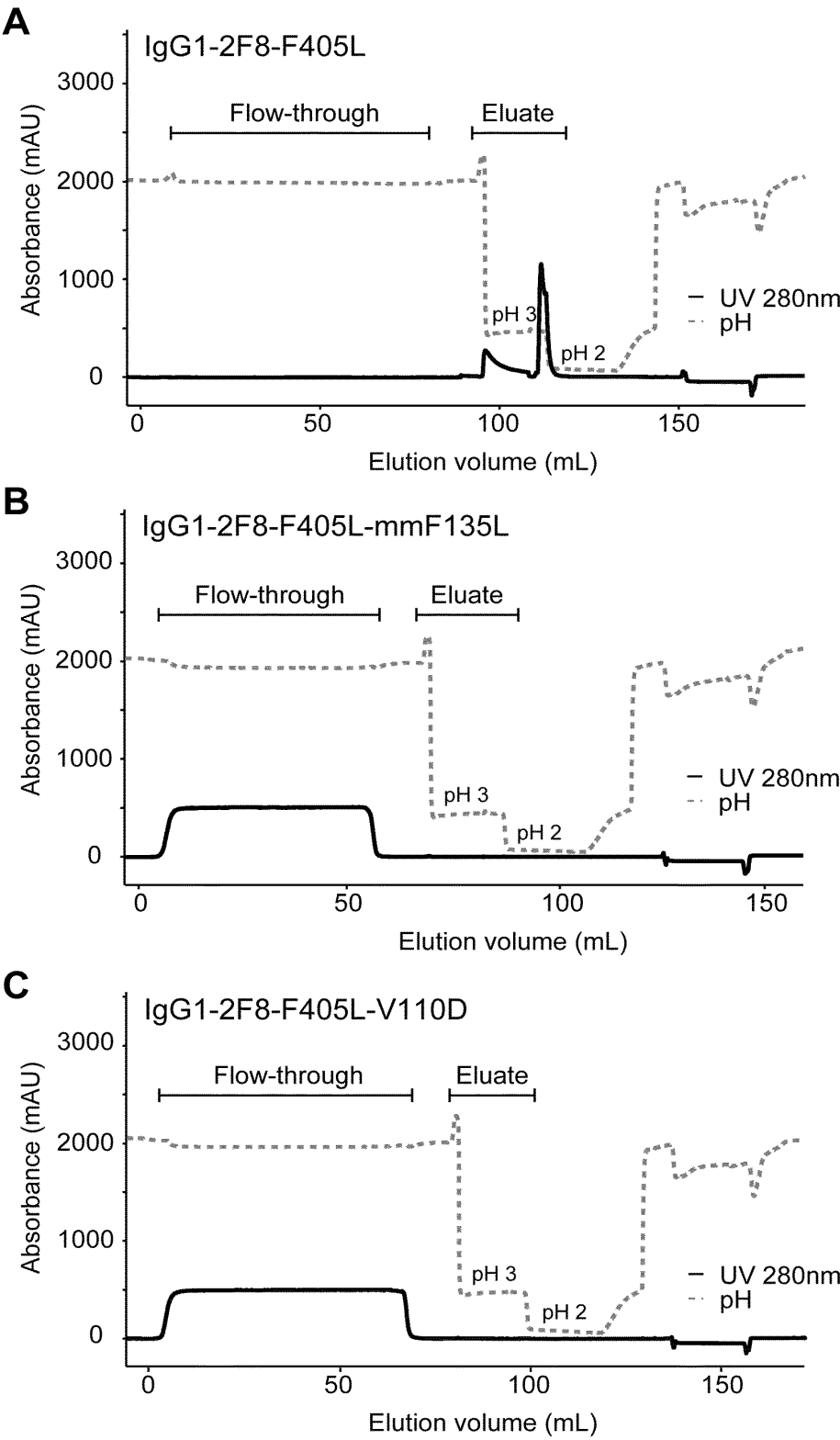


Figure 12 (continued)

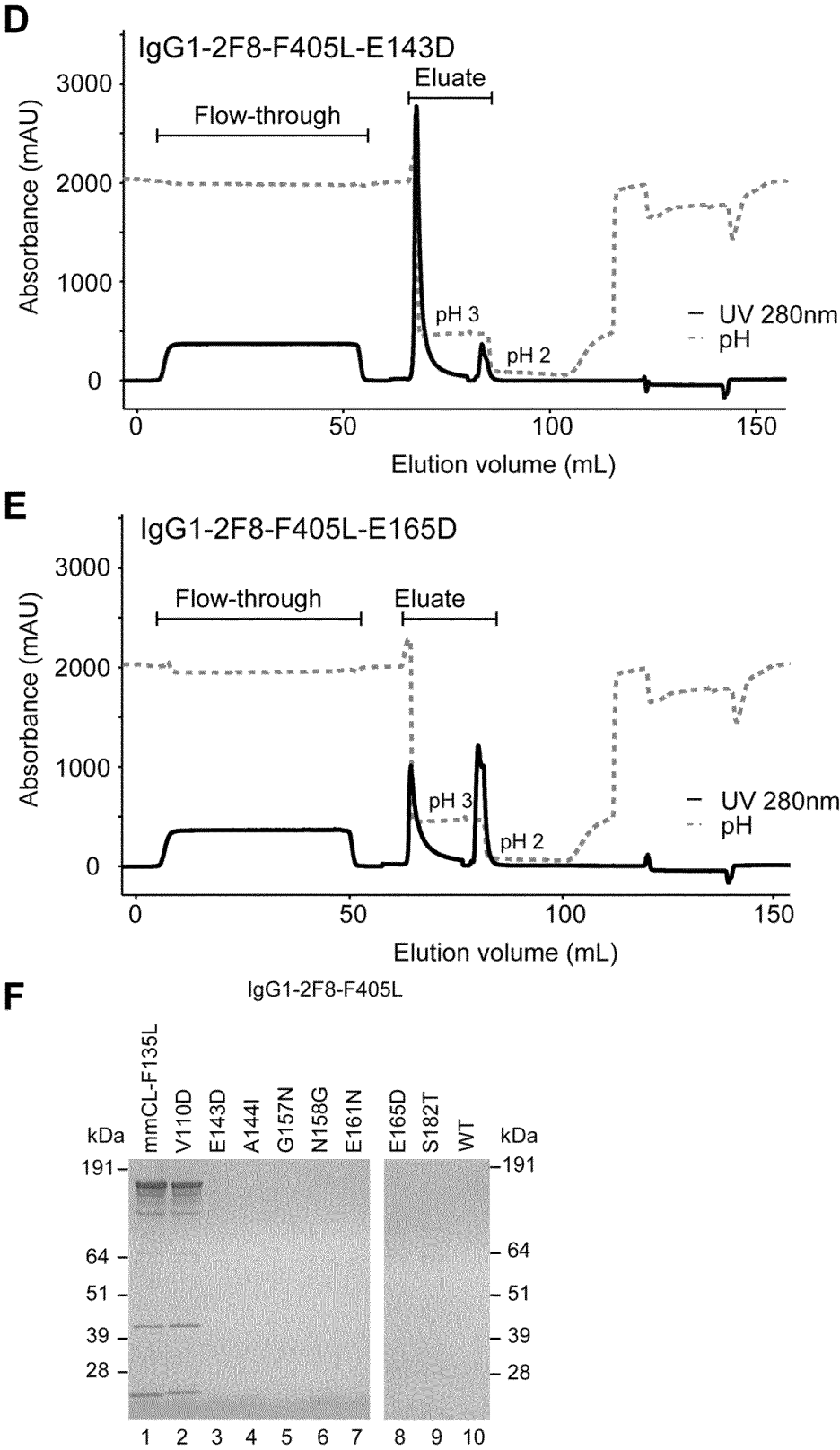


Figure 13

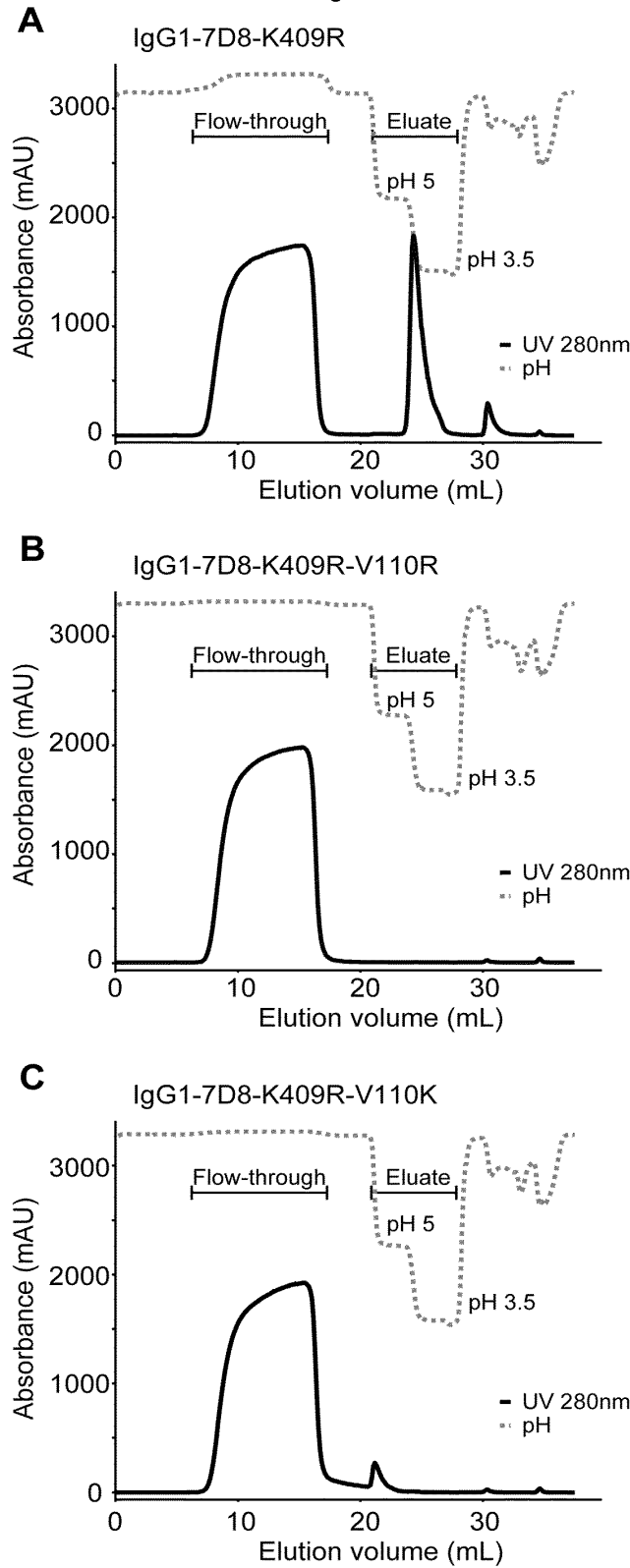


Figure 13 (continued)

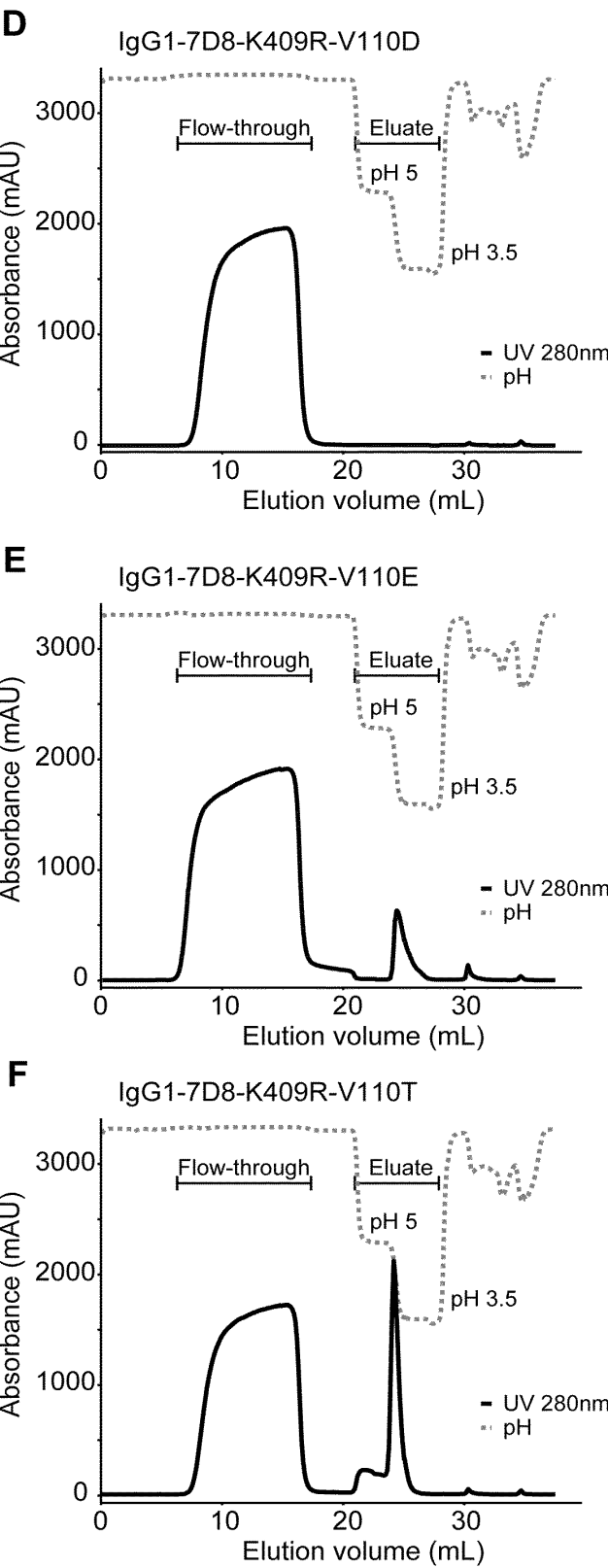


Figure 14

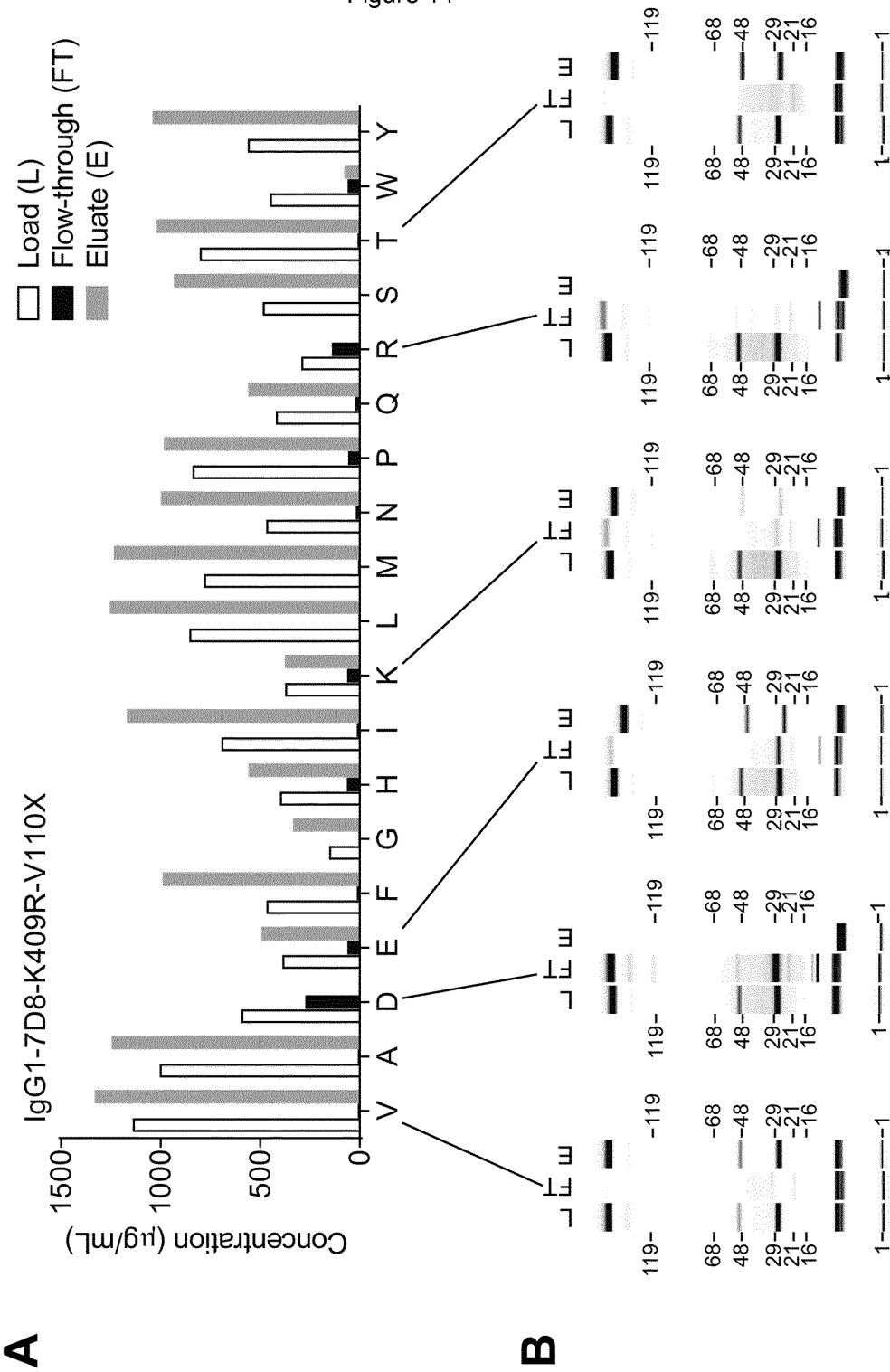


Figure 15

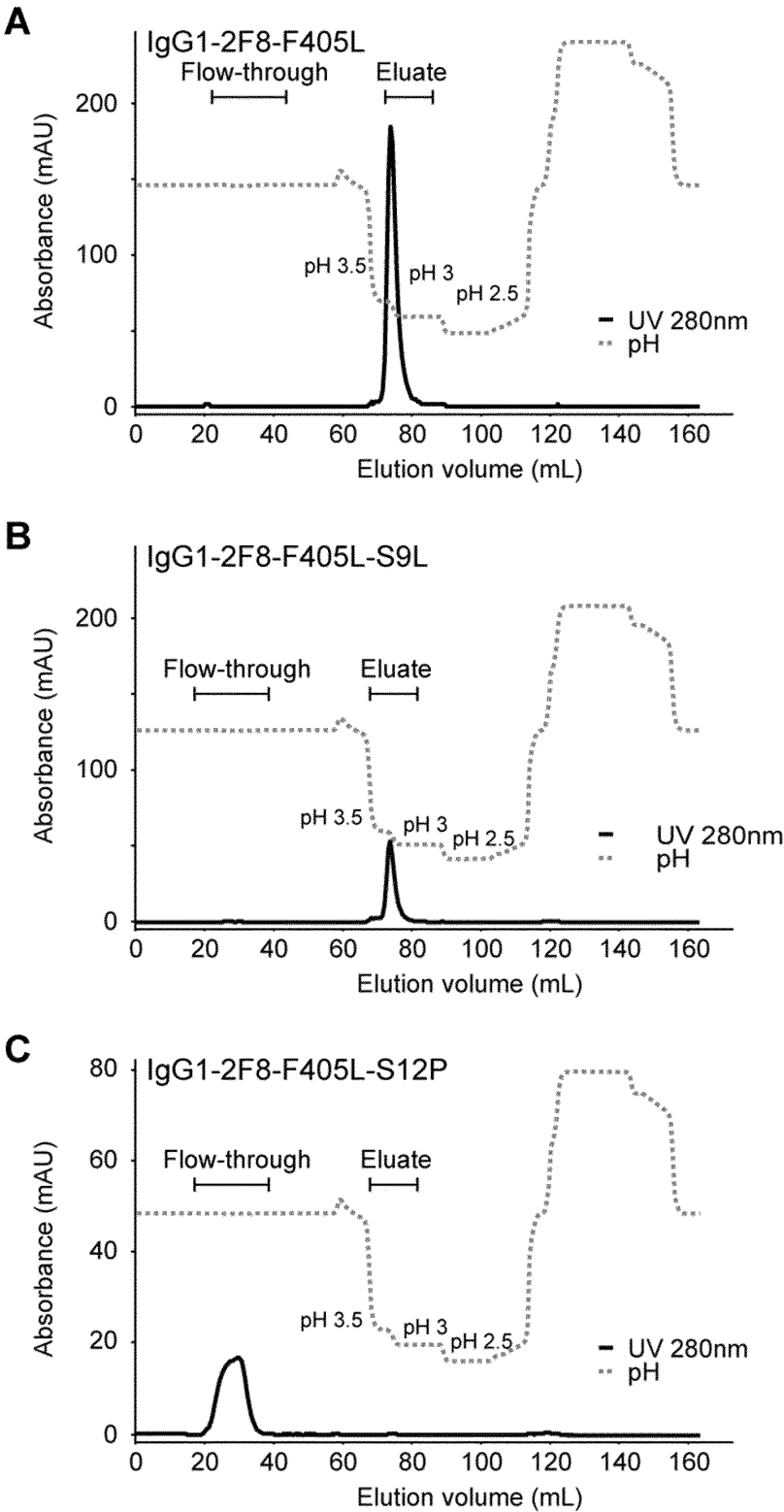


Figure 16

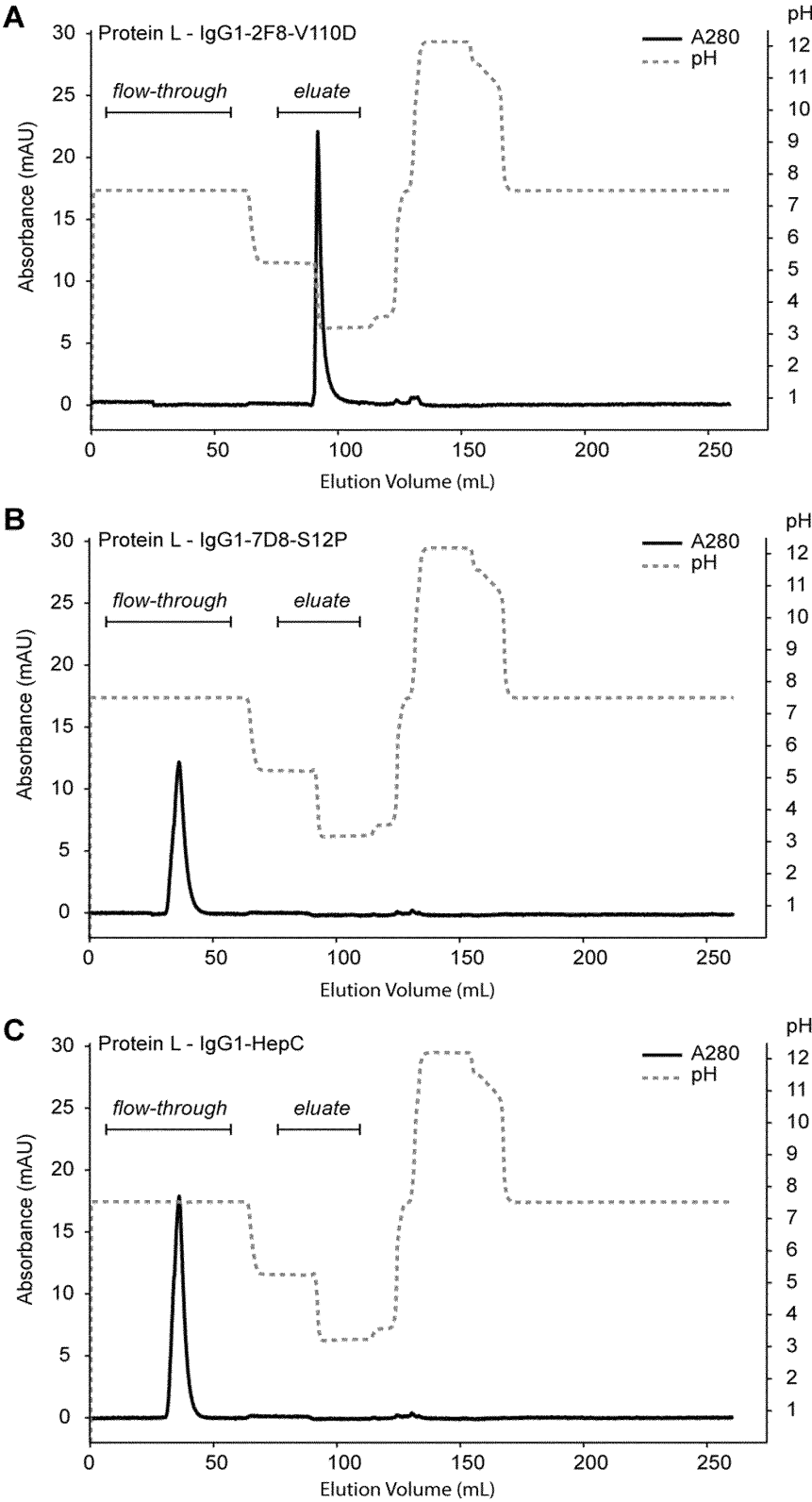


Figure 16 (continued)

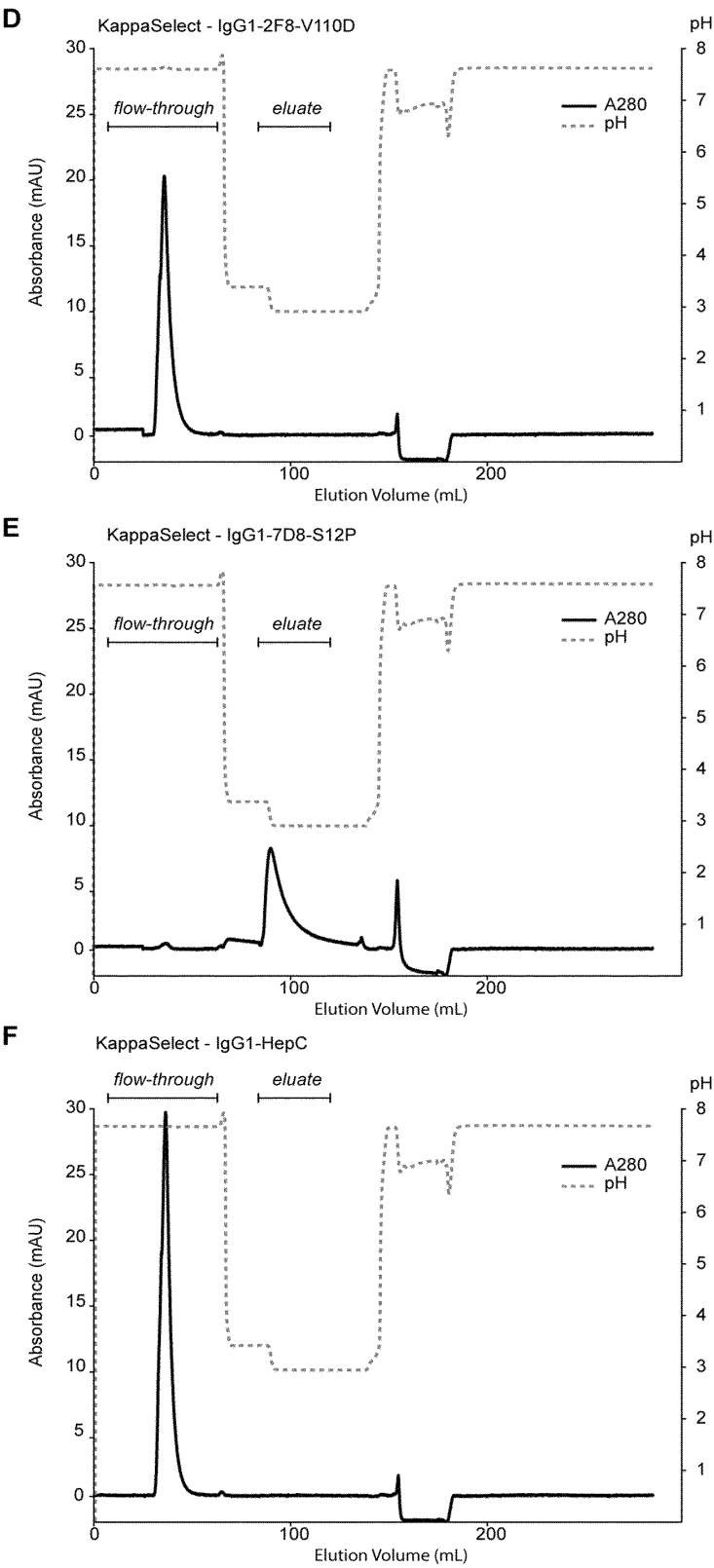


Figure 16 (continued)

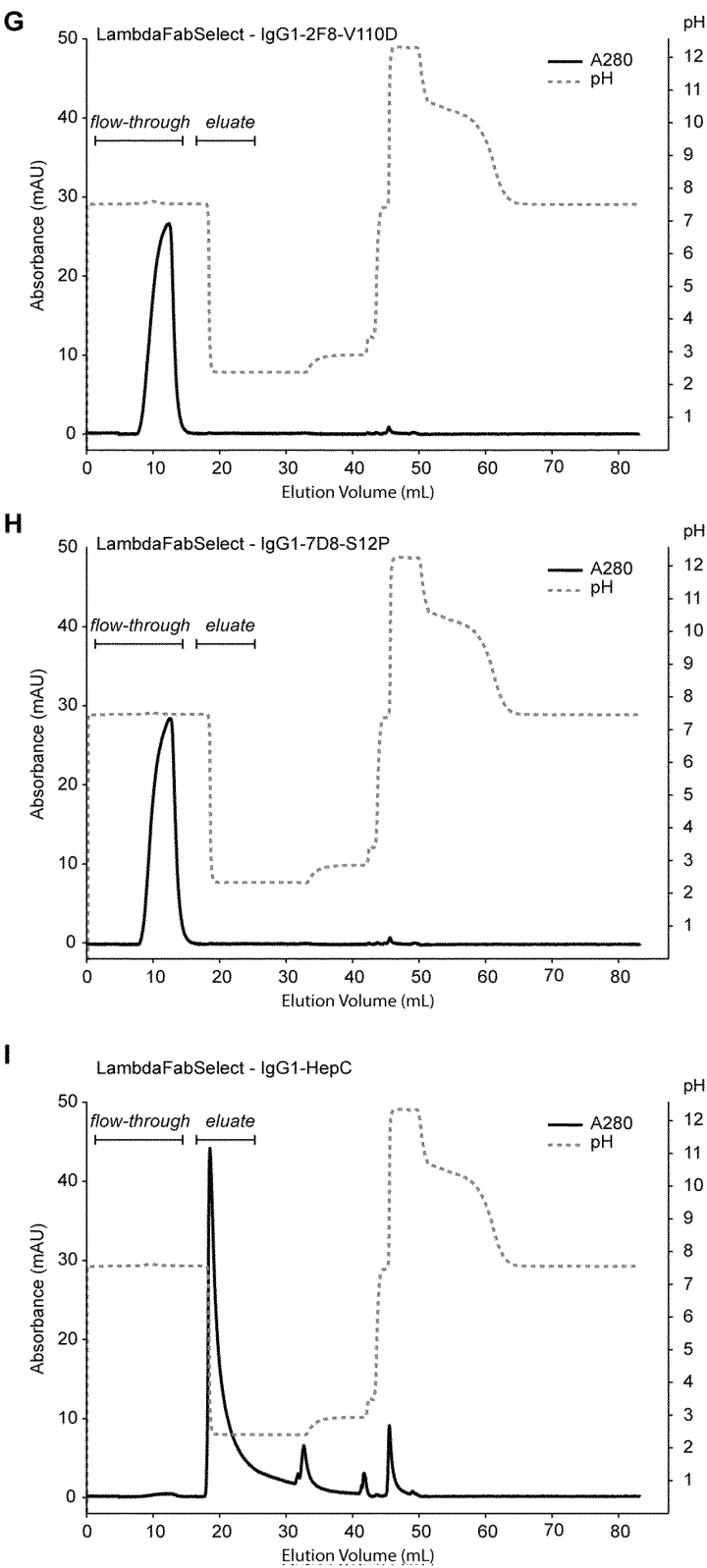
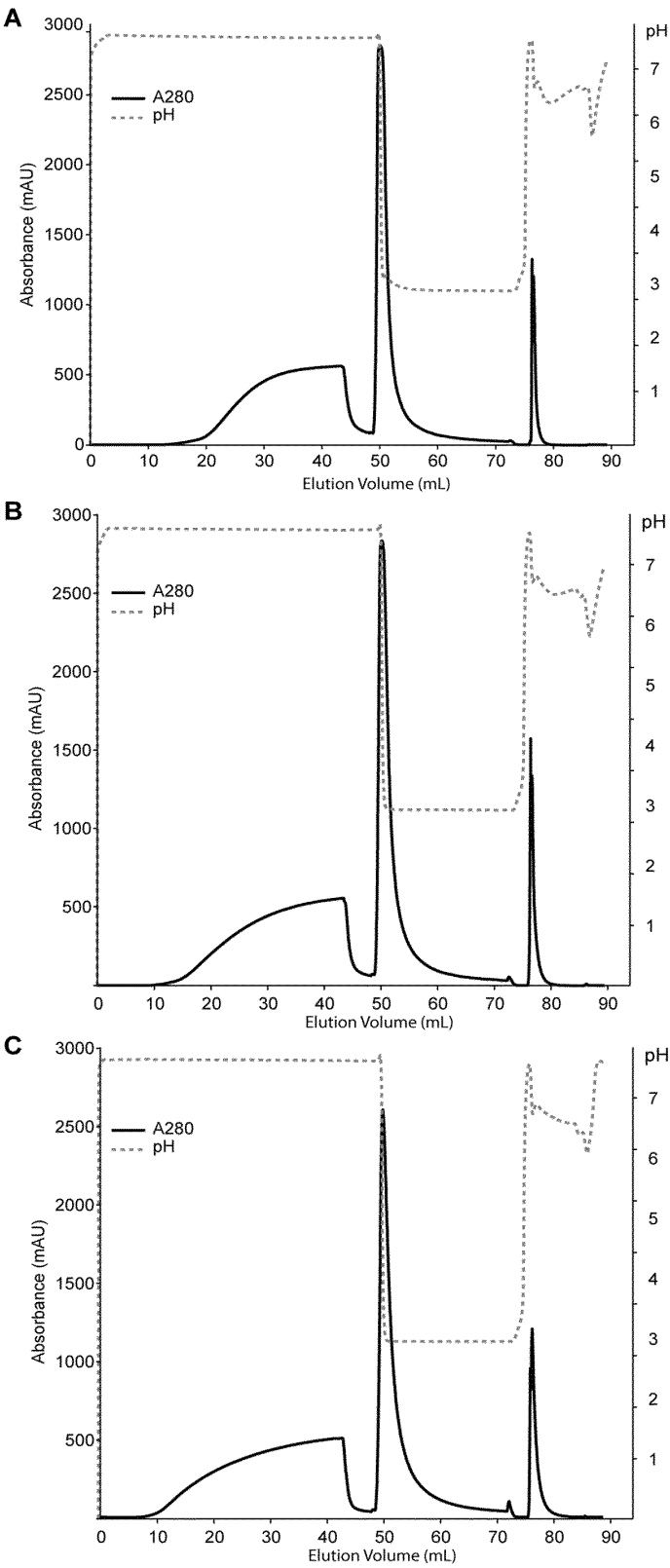


Figure 17



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Figure 18

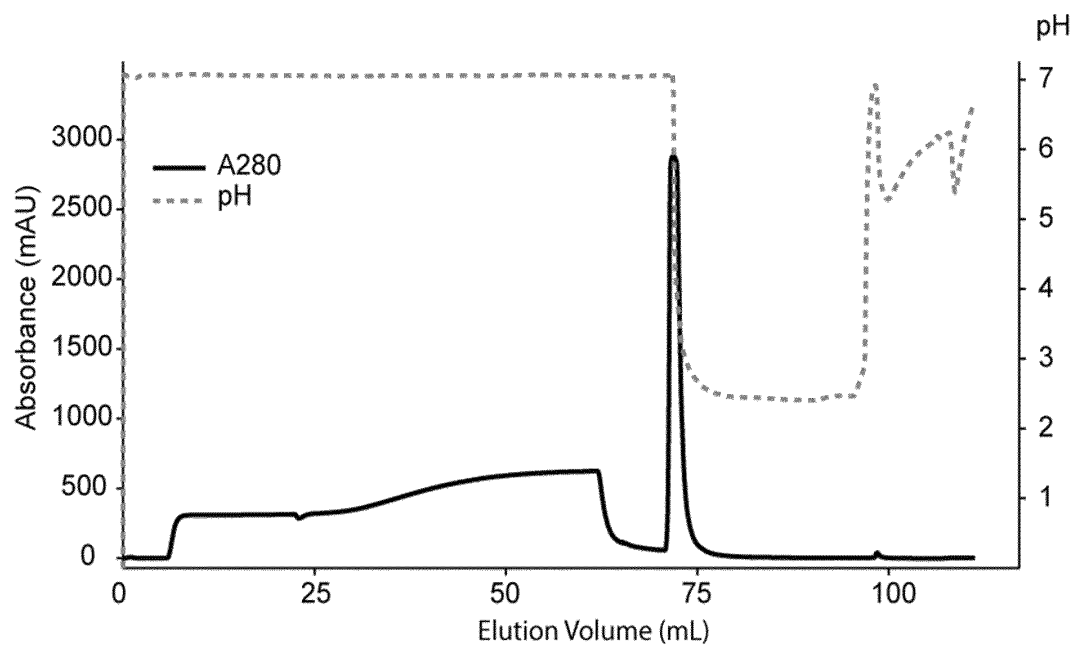
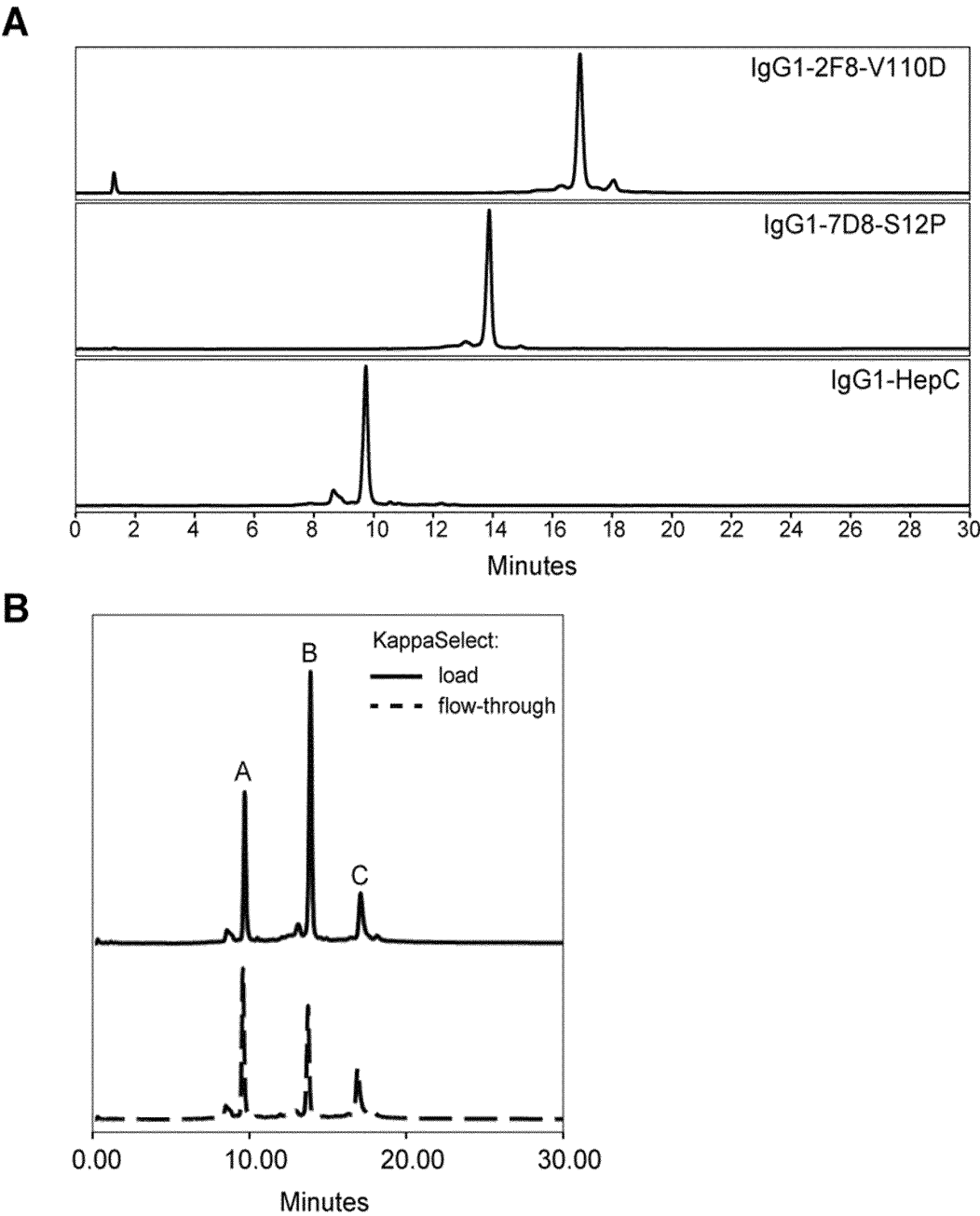


Figure 19



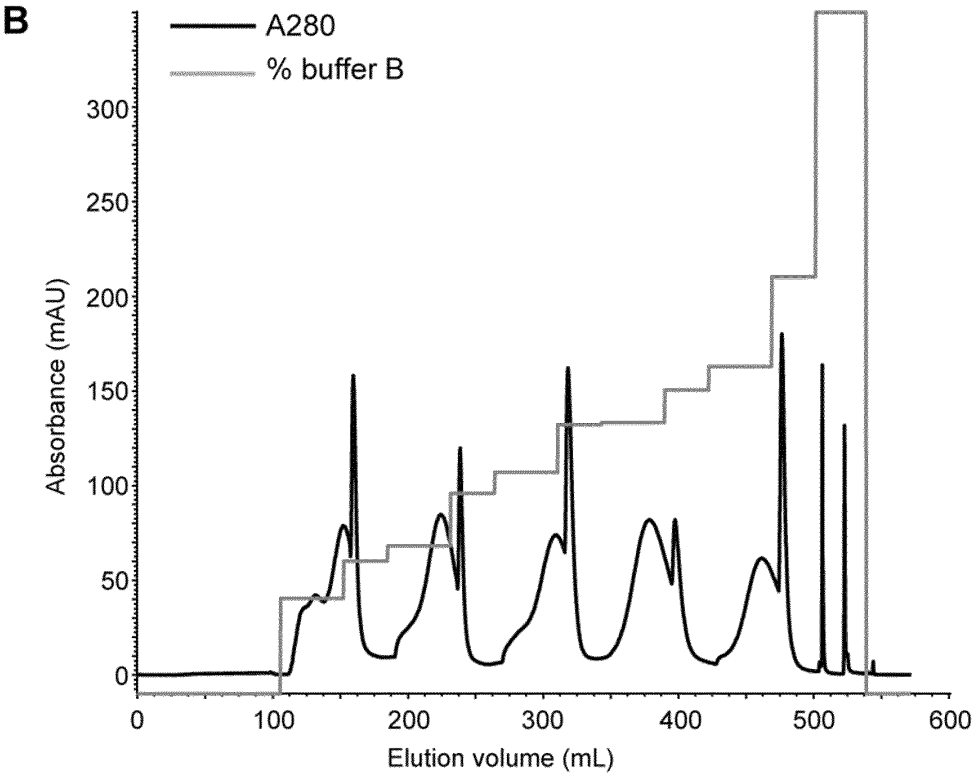
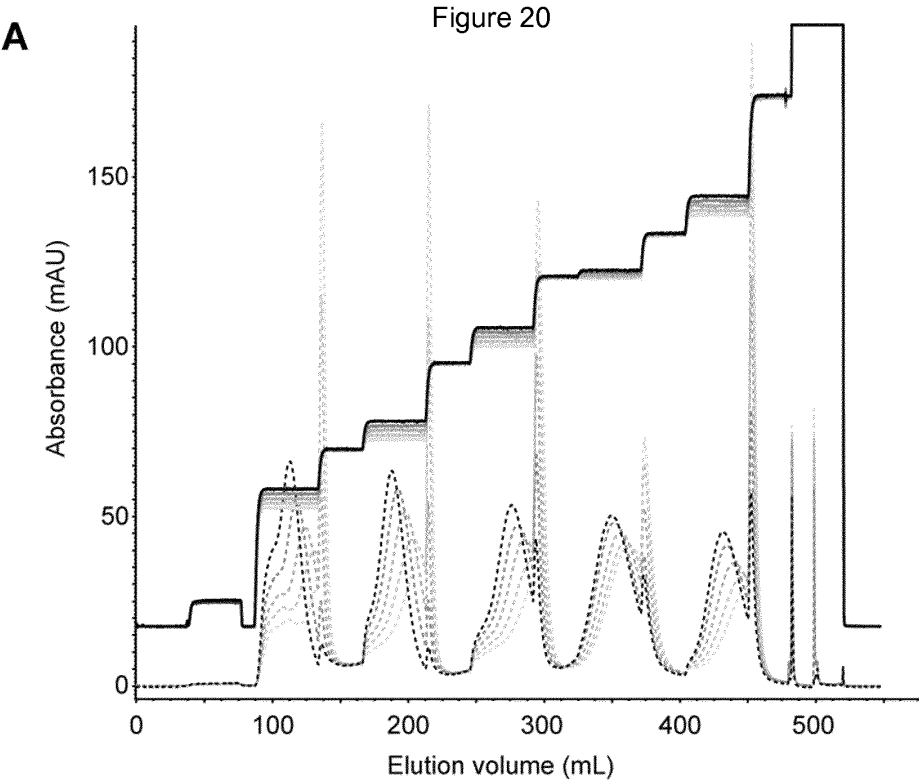


Figure 20 (continued)

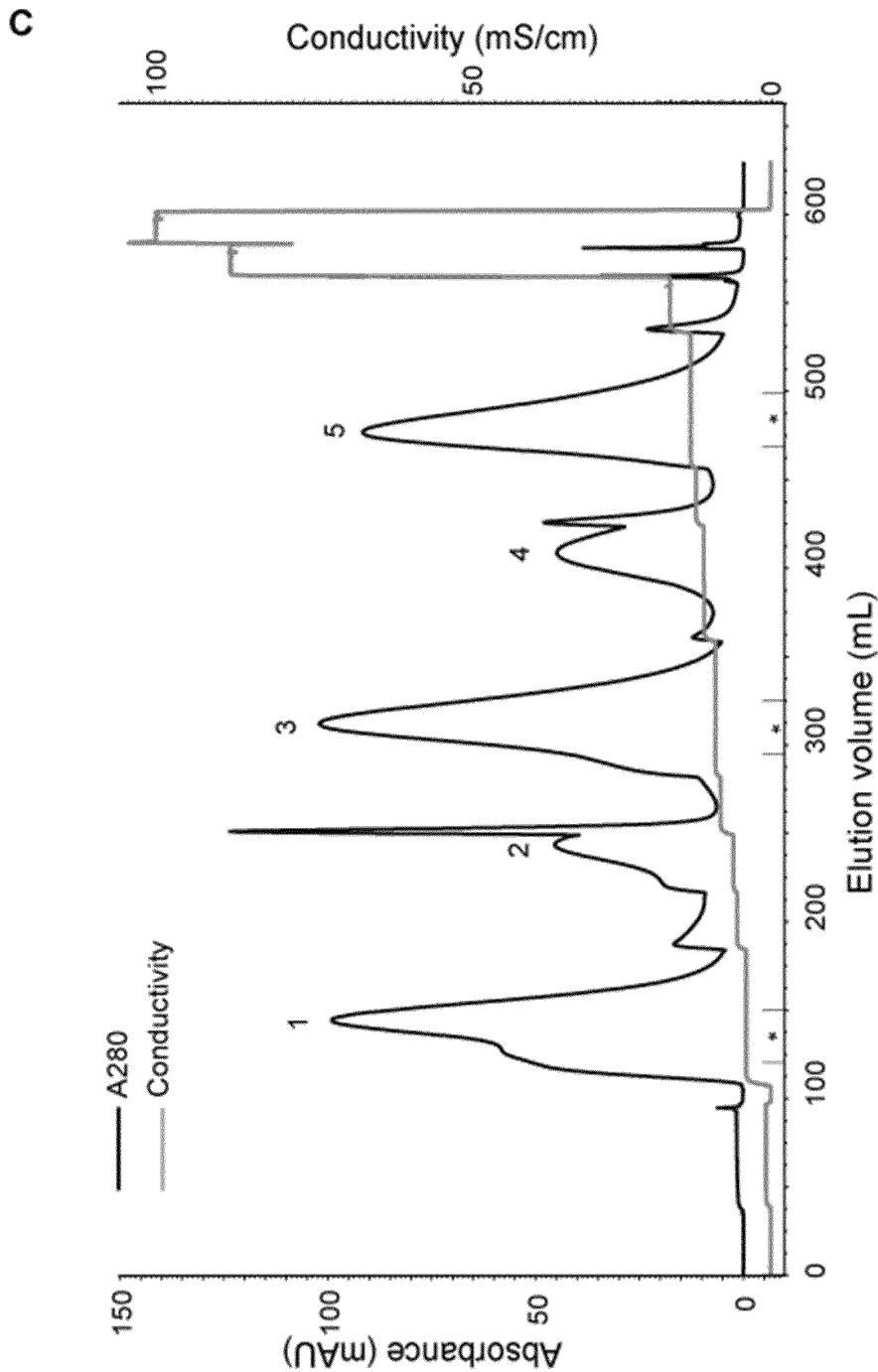


Figure 20 (continued)

D

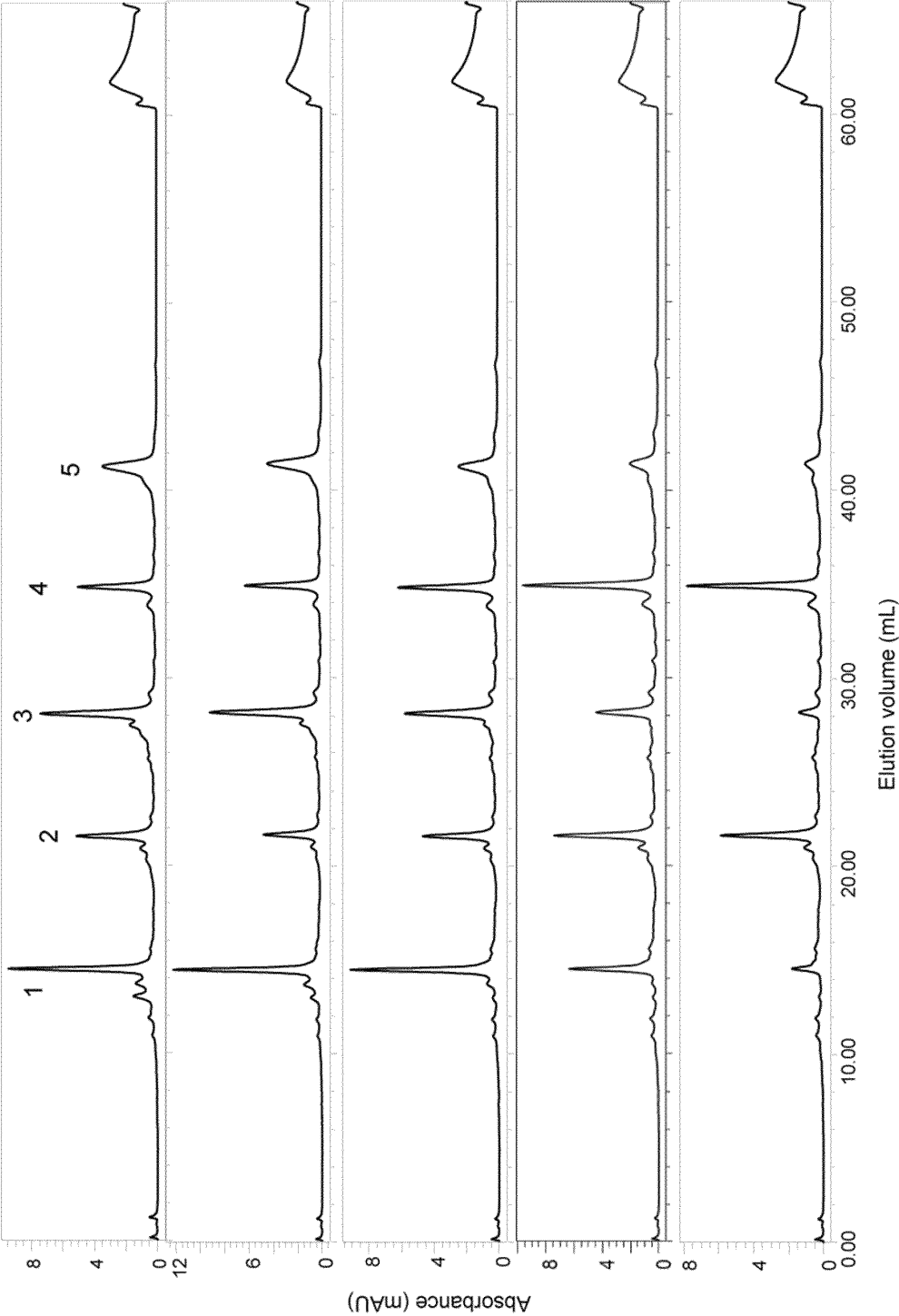


Figure 20 (continued)

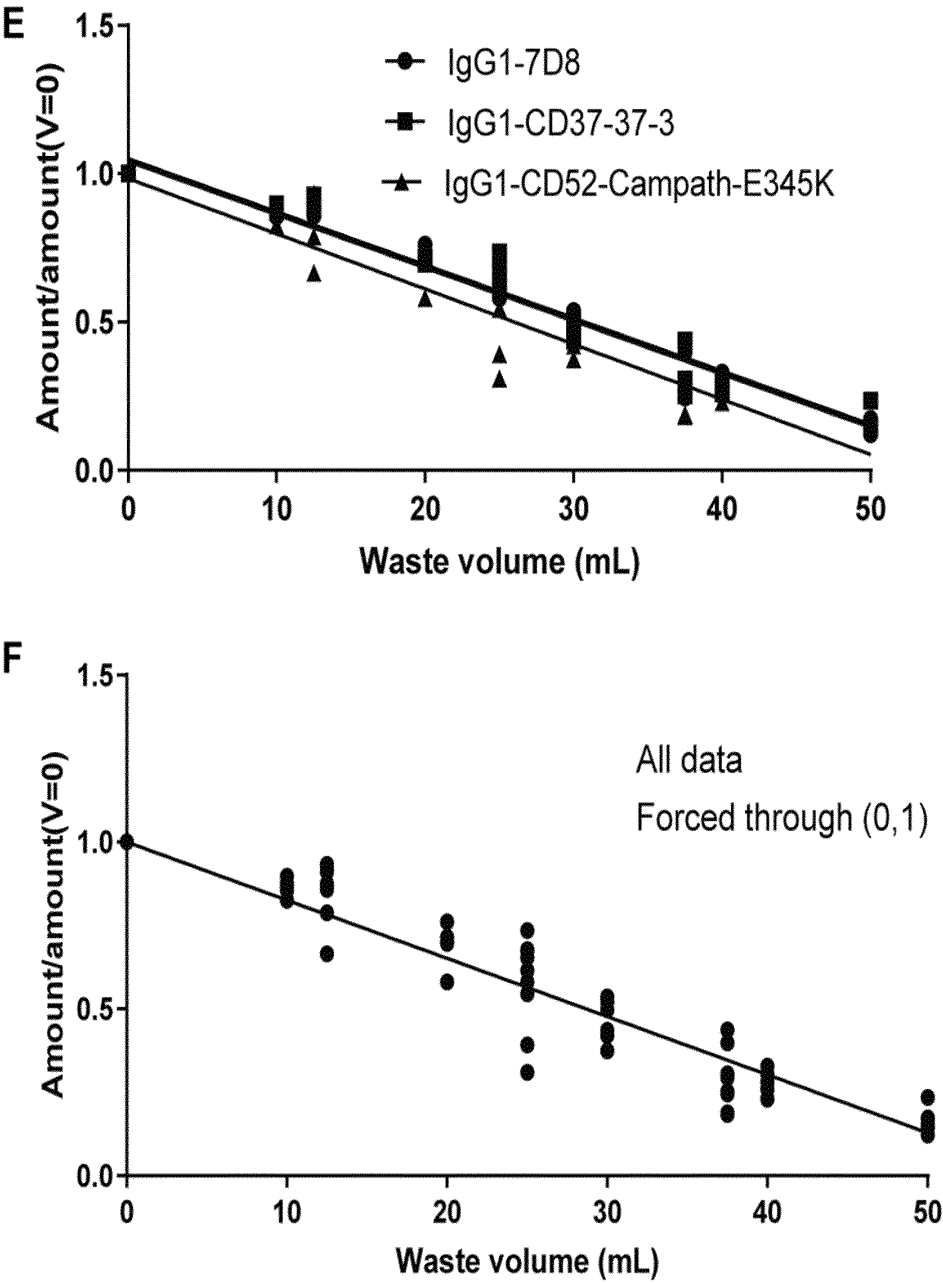
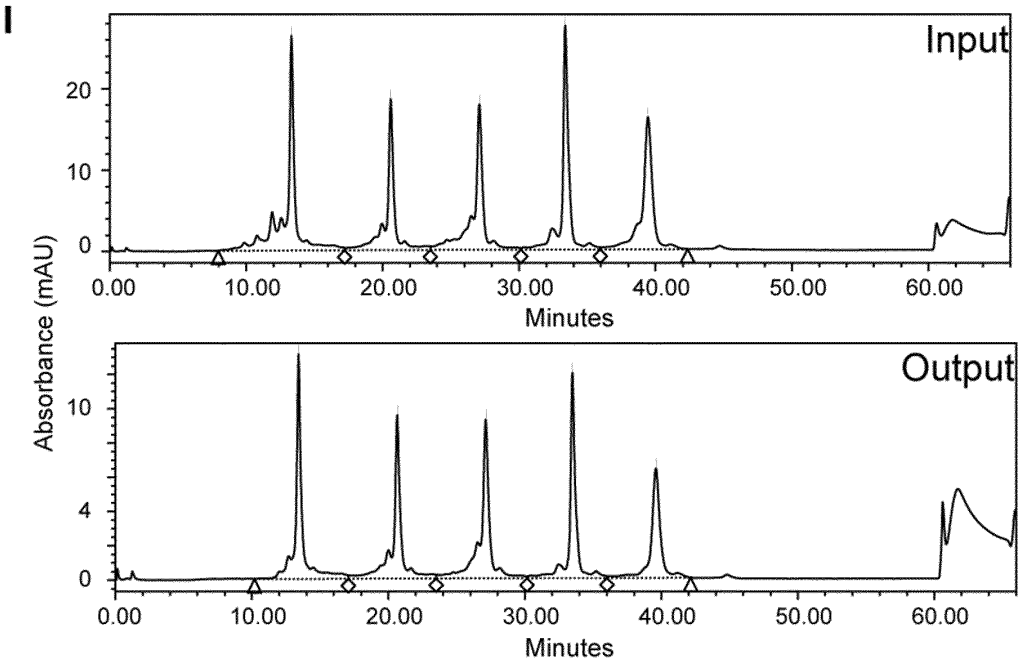
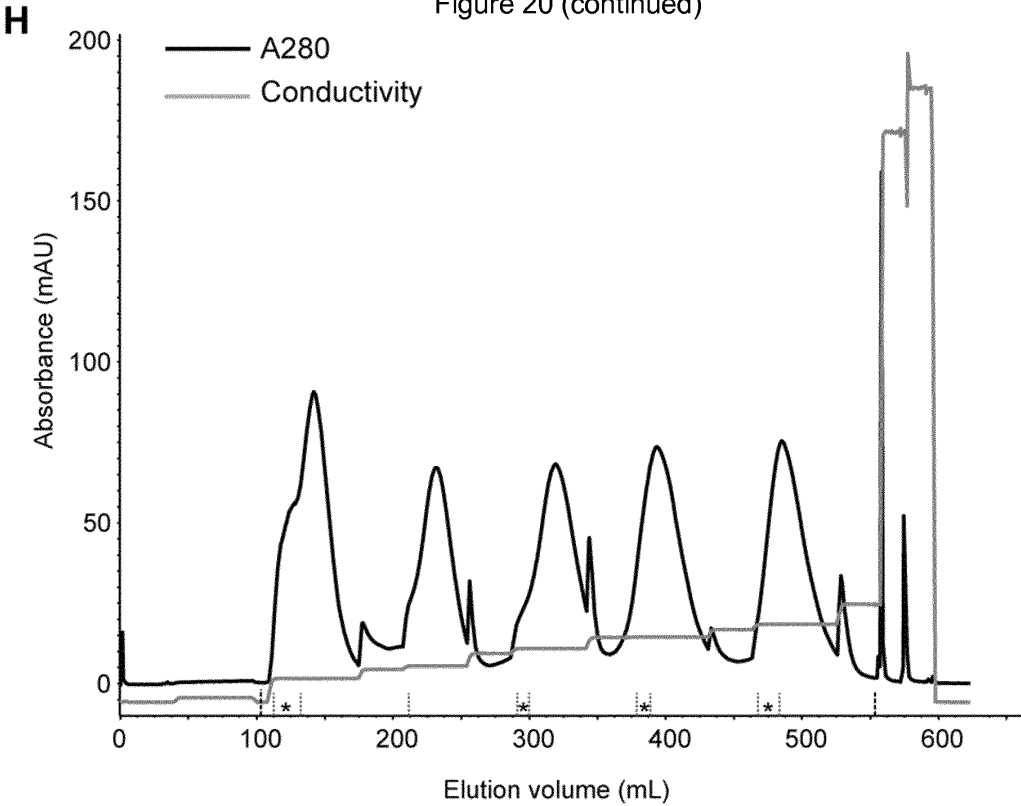


Figure 20 (continued)



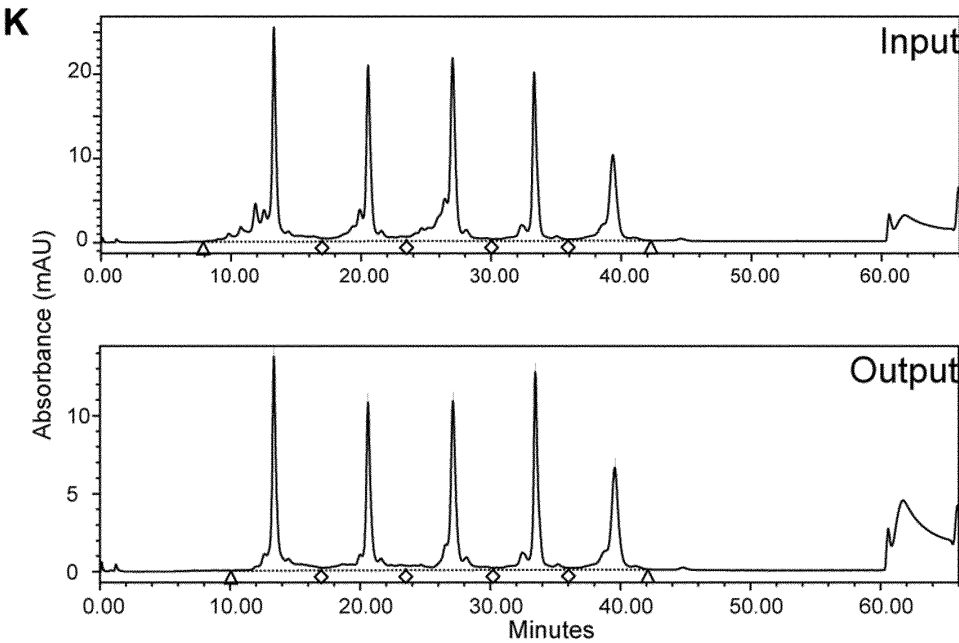
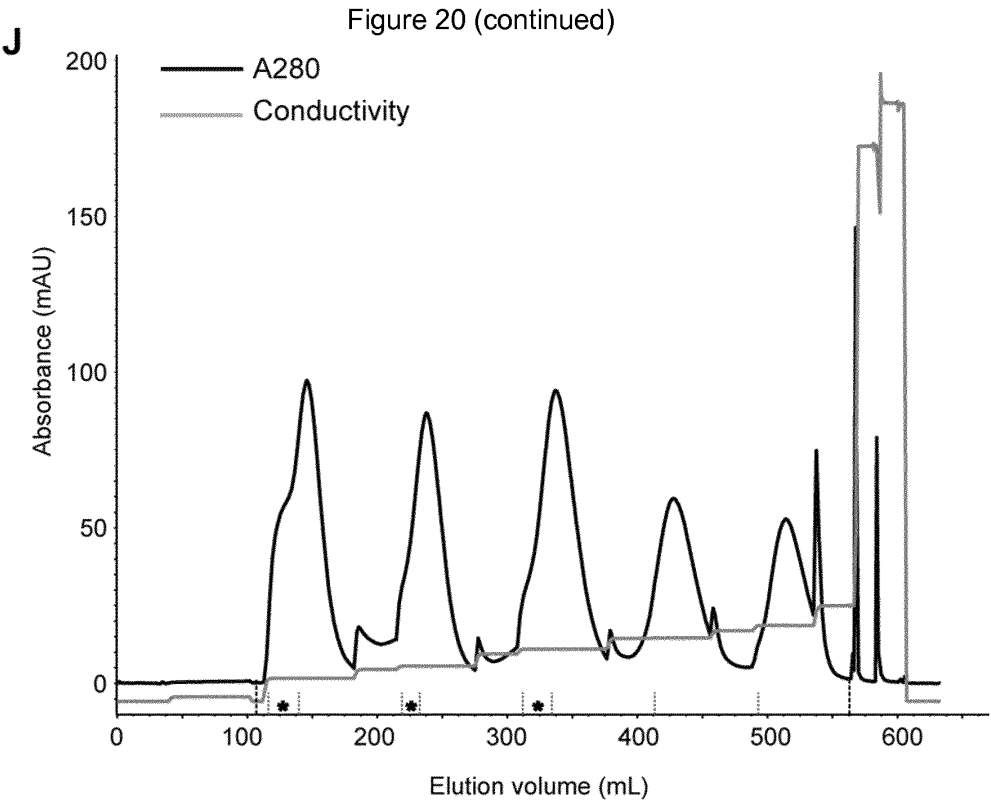


Figure 20 (continued)

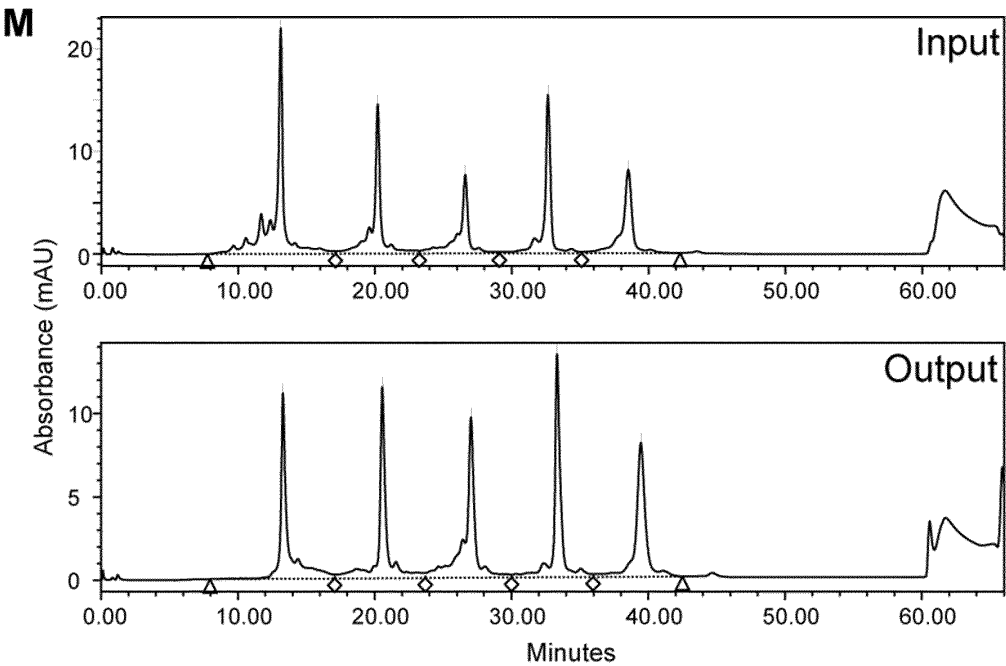
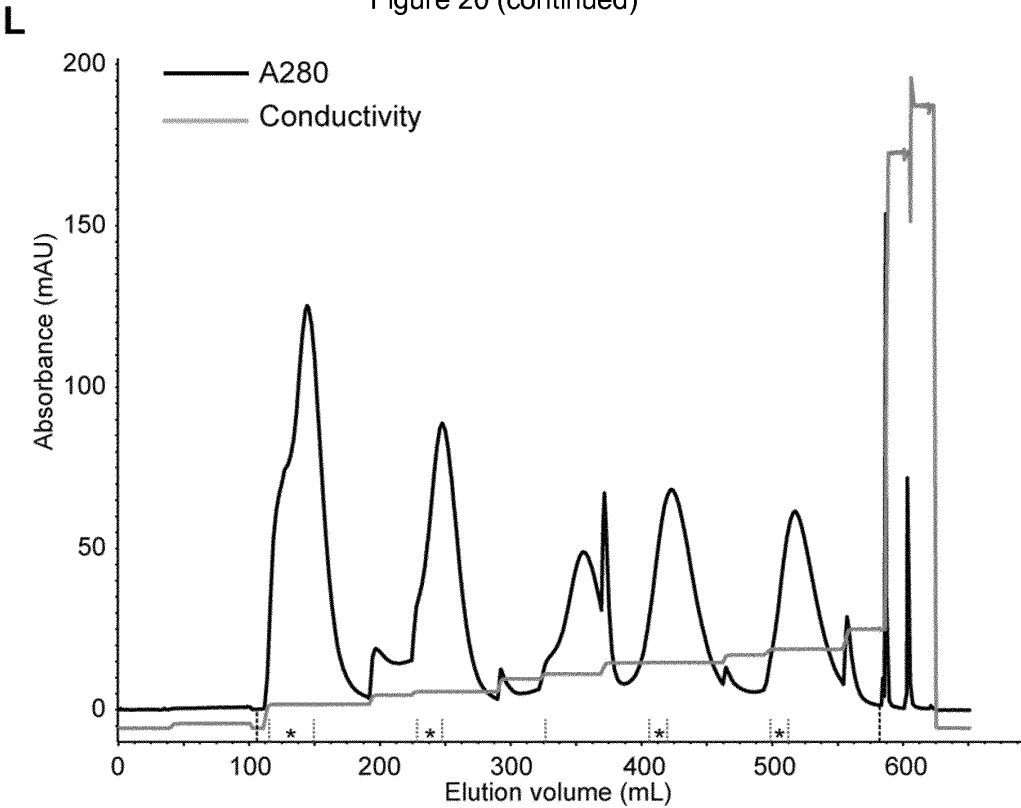


Figure 20 (continued)

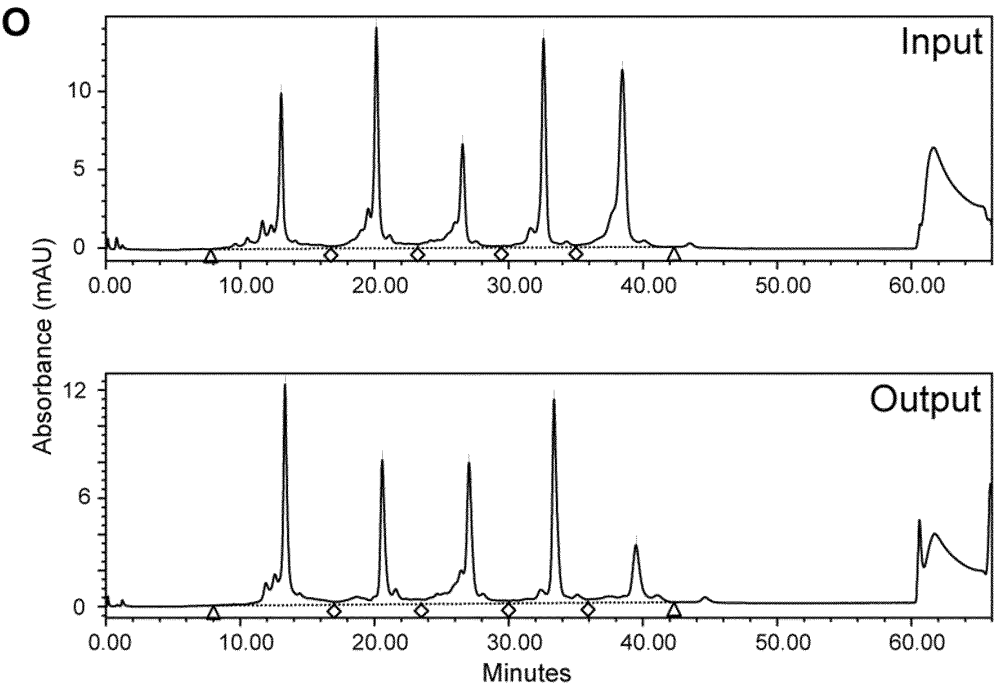
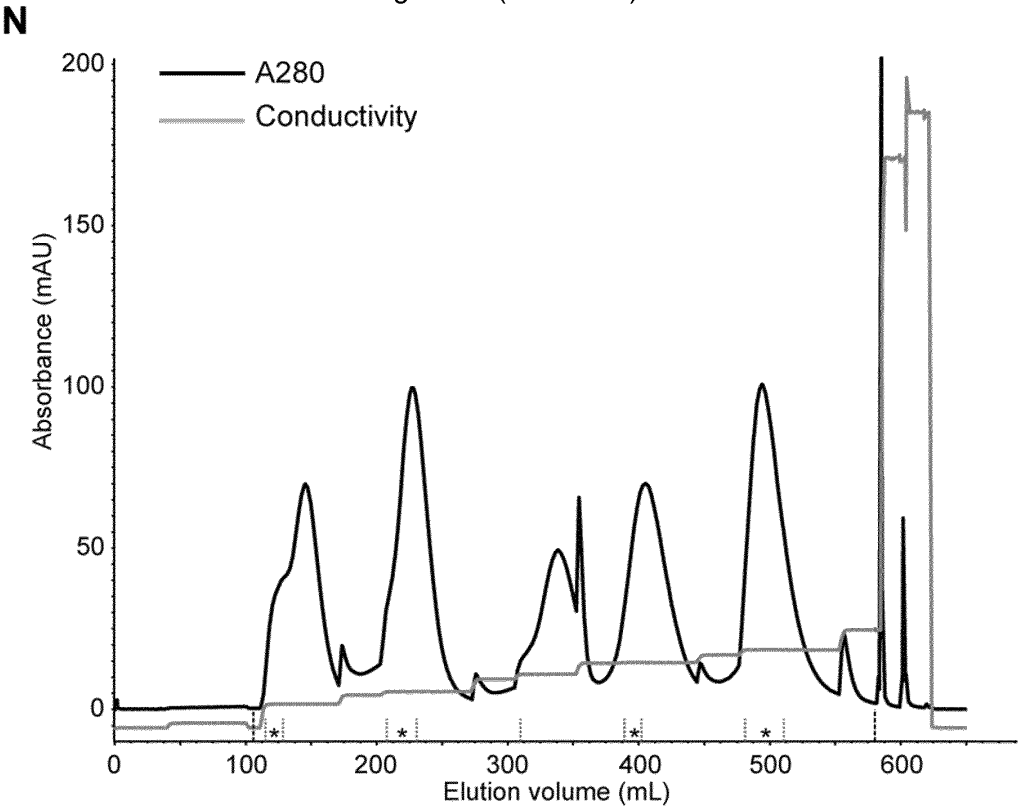


Figure 21

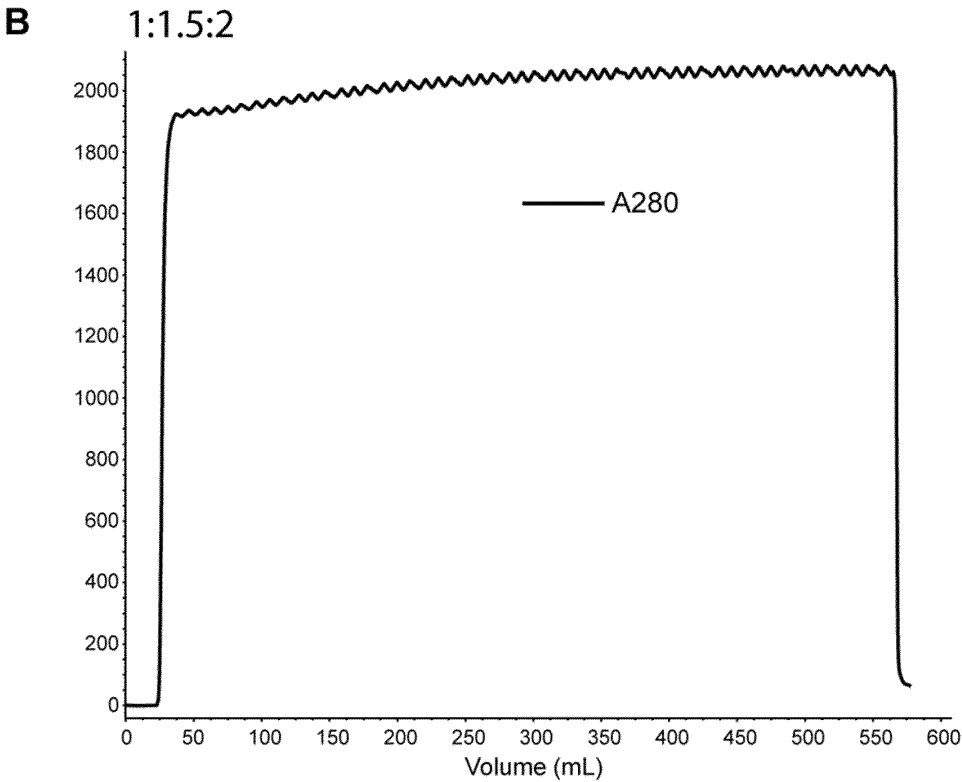
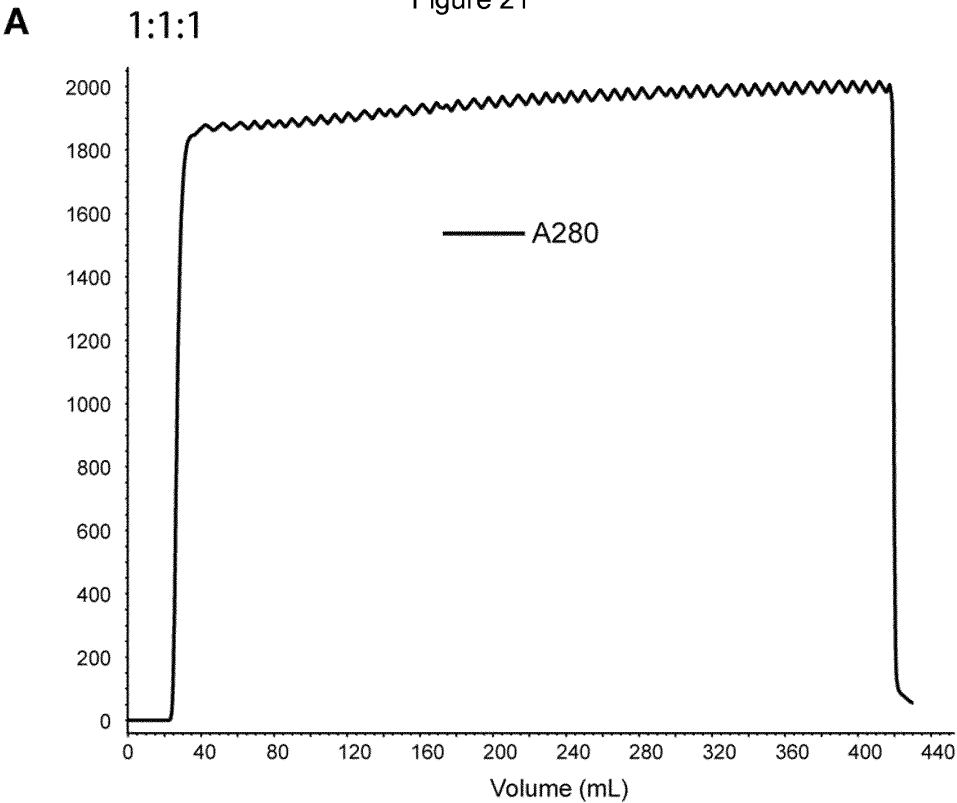


Figure 21 (continued)

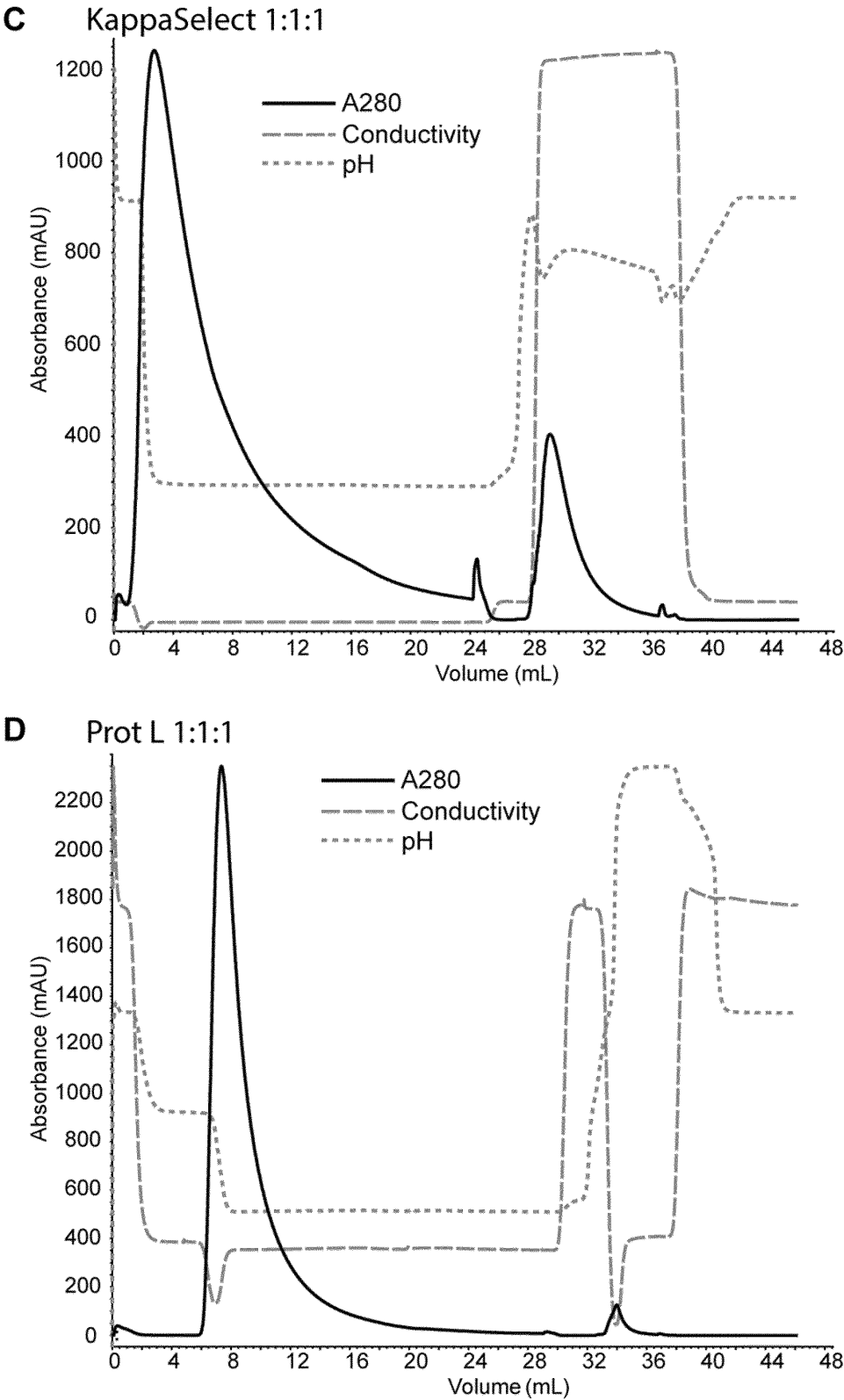
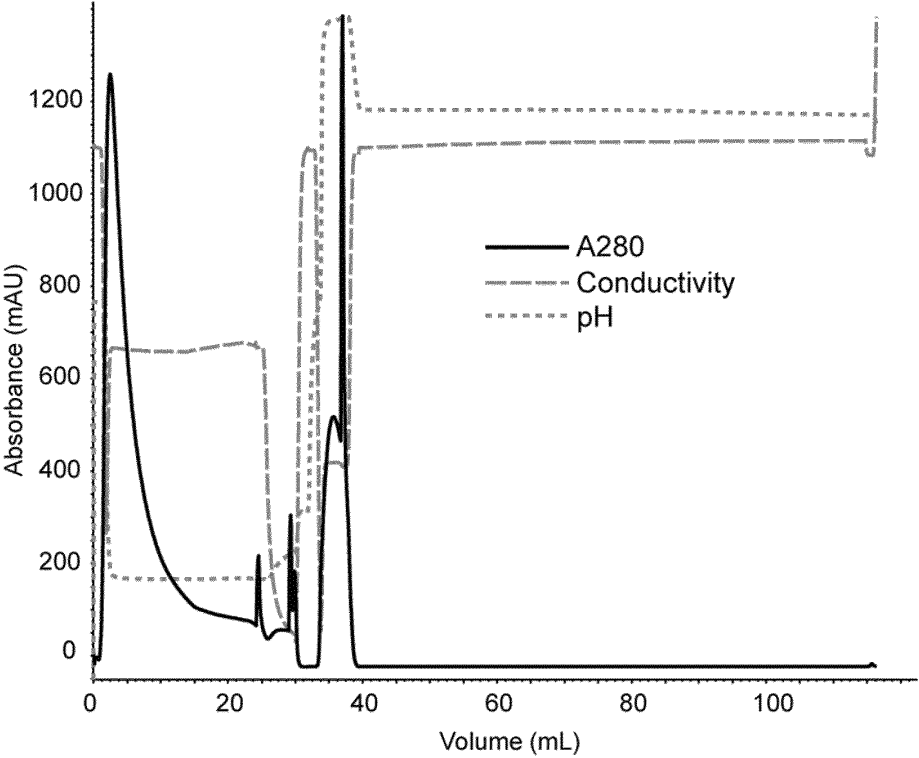


Figure 21 (continued)

E LambdaFabSelect 1:1:1



F Protein A 1:1:1

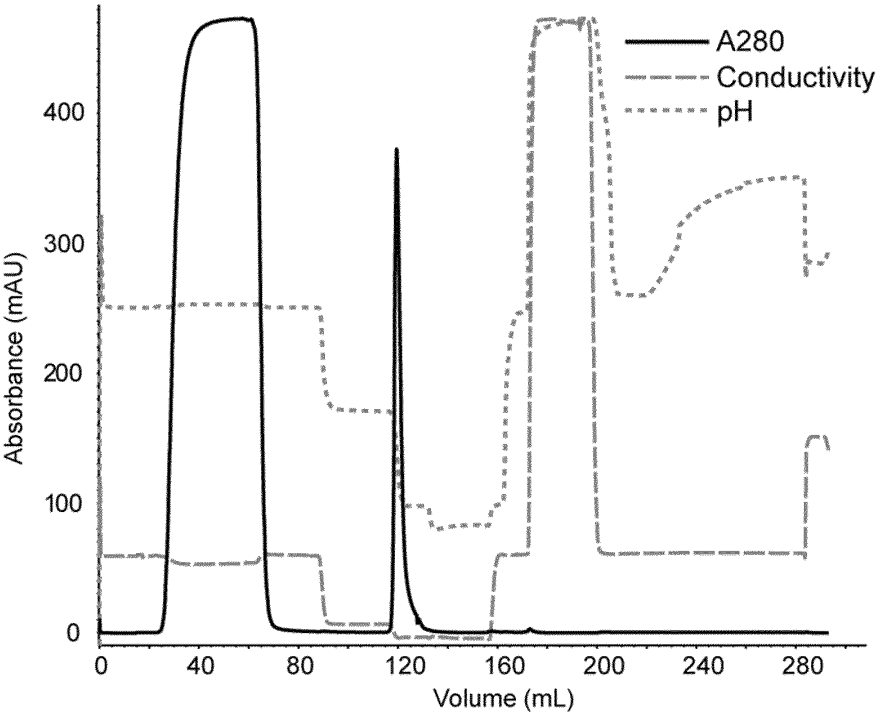


Figure 21 (continued)

G

