

Start	End	Sequence	Charge	1E2	2G10	9G3	3E3	5G10	7E6	9D3	4E7
				$\Delta\%D$	$\Delta\%D$	$\Delta\%D$	$\Delta\%D$	$\Delta\%D$	$\Delta\%D$	$\Delta\%D$	
145	151	IQRRTL	1	2.2	1.4	4.2	4.9	4	-2.4	3.4	3.1
154	185	CGIKRKSIVKWCRENSEKITVCPDRKIQLCI	5	0	1.7	1.3	5.9	3.8	2.8	1.5	2.2
184	189	CIANFL	1	0.6	0.4	2.9	2.8	2.9	2.7	13.8	0.6
184	195	CIANFLNSRLET	2	1.5	-1.3	3.1	0.2	-	7.1	-1.6	1.6
188	195	FLNSRLET	2	2.6	3.3	6.4	9.7	8.8	8.6	-	1.8
196	204	MEKFKEIFL	2	0.2	0.6	2.5	3	2.9	2.6	0.2	1.2
205	213	ISVNTAKL	1	1.9	-2.6	-1.2	-1.4	-1.9	-0.2	-3.5	-2.4
214	226	LYNKNEGKDPSIF	2	-2.9	2.8	5.9	8	6.7	6.5	12.5	3.3
227	237	CNELRNSFSDF	2	-0.2	0	1.7	2.5	-0.3	-0.3	0	0.2
238	266	RNSFIGDDMDFGGNTDRVKGYNKKFSDY	4	-0.1	0.5	1.9	2.3	2.4	1.3	2.2	0.9
267	277	YKEKNVEKLNN	2	2	2	2	3.8	3.6	12.8	3.4	2.8
278	290	IKKEWWEKNKANL	2	-0.4	0.5	1.9	1.9	0.5	1.6	1.4	0.4
291	305	WNHMIVNHKGNIKE	2	2.7	2.3	3.2	4.7	4.1	2.1	-3.3	3
306	318	CAIHPAEEPQINL	2	1.5	1.3	4.4	4.4	4.6	4.4	3.4	1.8
319	326	WIKEWNEN	2	-1.6	0.7	-1.1	1.4	-0.6	-0.1	0.1	0.4
319	327	WIKEWNENF	2	-1.5	0.5	-0.6	1.3	0.4	0.5	0.8	0.3
328	336	LMEKKRFL	2	-1.7	-6.7	-1.2	-7.8	-10.1	0.2	0.6	0.3
337	351	NIKDKCVENKYEAC	3	0.9	-7.8	42	-4.8	-4.5	0.1	1	1.6
352	365	FGGCRPCSSYTSF	2	0.9	-1.5	6.6	4.7	-	6.8	-	2.3
366	376	MKKSQTQMEVL	2	-1.8	-3.1	-6.7	3.4	-1.6	-1.2	0.3	-1.2
374	379	EVLTNL	1	-5.8	-1.3	-6.5	-0.6	-1.2	-0.7	1.2	-0.2
380	396	YKKKNSGVDKNNFLNDL	2	-22.4	1.7	-17.9	6.3	4.9	8.4	6.5	2.8
397	407	FKKNNKNDLDD	3	-11.8	2.7	-9.9	5.1	4.5	4.7	5	2.8
408	418	FFKNEKEYDDL	3	0.9	-14.9	4	-10.1	-14.2	7.8	6.6	3.7
409	418	FKNEKEYDDL	2	0.1	-19.4	2.9	-15.2	-18.1	5.5	5.1	3.3
409	420	FKNEKEYDDLCD	2	0.2	-15.6	2.3	-13.1	-16.9	-	6.6	3.2
427	441	IISFLNGPAKNDVD	2	-1.5	-0.1	0.9	2.4	2.8	2.9	2.3	1.3
442	457	IASQINVNDLRGFGCN	2	1.2	2.5	6.2	8.3	8.9	6.9	-	4.5
445	457	QINVNDLRGFGCN	2	0.5	0.5	2.5	2.7	6.2	3.7	3.9	3.4
458	472	YKSNNEKSWNCAGTF	2	-1.5	-1.4	2.9	1.8	-0.3	4.8	3.9	-0.5
473	490	TNKFPGTCEPRRQTLCL	3	-0.1	0.7	1.9	3.4	8.8	4.6	4.2	5.7
491	503	GRTYLLHRGHEED	3	2.4	1.4	2	5	0.4	4.3	-4.5	2.2
504	512	YKEHLLGAS	2	0.6	0.7	0.4	1	1.1	0.7	-0.2	9.2
513	518	IYEAQL	1	-0.5	0.9	0.9	-12.9	2.8	0.9	3.1	17.4
519	533	LKYKYKEDENALCS	3	3.3	3.2	4.5	5.2	4	6	1.6	7.5
532	542	CSIIQNSYADL	2	-0.5	7.6	-2.8	0.1	-3.7	0.7	4.1	28.1
543	550	ADHKGSD	1	0.8	0.7	0.4	1.3	1.2	0.4	1	14.1
551	564	IIKDYYGKKMEENL	3	-1.5	1.8	4	4.6	5.1	5.7	5.5	8.2
565	578	NKVNKDKKRNEESL	2	4	2.1	4.5	5.6	3.5	3.1	2.8	3.3
579	585	KIFREKW	2	2.4	1.1	3.1	3	3.5	3.1	-	11.1
581	594	FREKWWDENKENVW	2	1.4	2	7.7	4.7	6	5.5	-1.1	9.5
595	601	KVMSAVL	1	0.4	-0.2	-	-0.3	1.5	-	-	19.3
599	619	AVLKNKETCKDYDKFQKIPQF	3	2.9	2.2	6.3	5.7	5.5	6.4	6	6.2
610	619	YDKFQKIPQF	2	1.5	1.8	5	5.4	6.8	6	7.3	6.1
620	629	LRWFKEWGDD	2	0.4	4.1	1.3	5.4	1.2	1.5	6.7	9.4
630	641	FCEKRKEKIYSF	3	1.4	1.8	2.9	4.1	3	2.5	2.6	3.4
645	664	KVECKKKDCDENTCKNKCS	3/4*	2.5	1.4	5.7	3.3	3.6	4	*2.4	2
665	671	YKKWIDL	2	1.3	1.2	1.3	1.9	1.4	-	-	2.2
672	697	KKSEYEKQVDKYTKDKNKMYDNIDE	3	-0.2	1.2	3	4	4.2	3.1	3.8	5
676	705	YEKQVDKYTKDKNKMYDNIDEVKNKEANV	4	0.6	0.2	-0.4	0.9	1.3	-0.5	1	2.9
705	719	VYLKEKSKECKDVF	3	1.2	-1.6	1.8	3.9	1.7	3	2.4	0.7
720	734	DDKIFNEAPNEYEDM	2	2.6	2.8	7.1	7	7.4	10.4	9.4	3.1
735	746	CKKCDEIKYLNE	2	4.1	3.2	3.3	5.6	5.5	5.7	2.7	3.8
747	755	IKYPKTKHD	2	2.5	2.2	3.5	4.5	4.3	2.3	3.9	3.4

**Table S2:** The  $\Delta D\%$  values represent the average difference of deuterium incorporation between PfEBA140 alone and the corresponding PfEBA140-antibody complex states across all six time points. Negative values of  $\Delta D\%$  indicate less deuterium incorporation in the PfEBA140-antibody state. Peptides for regions showing significantly less HDX upon binding to different mAbs are highlighted in green.