

Supplementary table S5: BlastP analysis of each epitope.

Protein	Epitope Sequence	Amino acid position	BLAST Total score	BLAST alignment score
>borr H7C7L6	GEESKEDEEENEQAV	106	53.0	<40
	EEKKRKKQEQQEEKK	174	114	<40
	KTWGDLEDEEGEGLG	254	29.1	<40
	QEQRKERRAKNKKK	192	30.3	<40
	KDATGKDATGKDATG	32	24.0	<40
	EEDKKVVNLEEKELE	128	57.9	<40
	HENEPPLKENVDVSE	295	57.1	<40
	EKVKEYLKDNSKFEE	322	29.5	<40
	DPVKDKIASNGPIAD	66	22.3	<40
	KKYYAHENEPPLKEN	290	23.5	<40
	ILDPVKDKIASNGPI	64	24.0	<40
	QEEKVNNNGEEENDK	87	44.5	<40
	DKAVFLGEESKEDEE	100	28.2	<40
	KKETEDEDKEEIEK	144	138.0	<40
	NKKYYAHENEPPLKE	289	23.5	<40
	VKEYLKDNSKFEEIK	324	44.5	<40
>borr H7C7M3	LAKKKGERKKALQEA	131	25.7	<40
	NLKNSEQNLESSEQN	28	27.4	<40
	KLDEKDTKEIEKQIQ	68	29.1	<40
	EEYKKQVDSTGKTQ	150	28.6	<40
	KKTEQEIKKQVEGFL	44	45.8	<40
	NRGGVGVQAWQCANE	170	23.1	<40
	SYSNGGSDNSNTDEL	190	22.3	<40
	DTSTGKTQGDRSKNR	157	22.3	<40
>borr Q9S0D9	LKKKKKEERKKALQEA	128	156	<40
	KNMTSGNNTSDMTNE	185	23.5	<40
	VKDLESSEQNVKKTE	33	28.2	<40
	GVTHGSQVQRQGGVG	158	23.5	<40
	LNGKGLEDKLNELSE	112	26.1	<40
	ETYSGYEEKINKIKE	96	29.1	<40
	SLKKKKKEERKKALQE	127	135.0	<40
	KTAAWNSGTSTLTIT	212	25.7	<40
>borr P0CL66	KNISKSGEVSVELND	189	24.0	<40
	EYTGIKSDGSGKAKE	146	26.5	<40
	SSTEKFNEKGEVSE	120	39.0	<40
	VLVSKEKNKDGYDL	40	26.5	<40
	VQQYDSNGTKLEGSA	245	32.0	<40
	GTSDKNNGSGVLEGV	65	38.6	<40
	TITVQQYDSNGTKLEG	142	32.0	<40
	KSDGSGKAKEVLKGY	151	23.5	<40
	IFIYKEDLKEDVKIG	320	28.6	<40

	LDLGGGINNLFKTAT	174	23.5	<40
>borr O51039	RYKVDSSVINDVNFS	117	22.7	<40
	VIVDNVSWLKSFSVF	328	37.3	<40
>borr G5IXI6	SDISSTTGKPDSTGS	98	26.1	<40
	AAEQDGKKPEEAKNP	243	37.3	<40
	AKLEKTKTDLNSLPK	81	24.8	<40
	KSDPKKSDVKTYFTT	64	24.4	<40
	NCKSQVADKDDPTNK	20	24.8	<40
>borr Q9S036	GDLVVRKEENGIDTG	74	25.2	<40
	HTLYDEQSNGLKLLK	36	26.1	<40
	NNGVGGDKTAEYAIP	163	24.8	<40
	CKIHTSYDEQSSGEI	20	24.0	<40
	TVKIKNKDNNSNWD	58	43.3	<40
	KYEQSSANGIQNKEI	128	29.1	<40
	GHSATFFSLKESEVN	93	25.7	<40
	KINNGVGGDKTAEYA	161	22.7	<40
>borr Q07337	KELTSPVVAESPKKP	196	25.2	<40
	NNSGKDGNTSANSAD	20	24.0	<40
	NNGLDTENNHNGSLL	84	22.7	<40
	KLKEKHTDLGKEGVT	137	56.2	<40
	KEAILKTNGTKTKGA	156	24.8	<40
	TFTNKLKEKHTDLGK	133	59.6	<40
	TNGTKTKGAEEELGKL	162	22.3	<40
>borr O50889	NNQNLNESQNSKSS	72	25.7	<40
	KDLEAQKKEKDTQIE	104	26.5	<40
	NLKKTNSHTNSENSA	56	23.1	<40
	CAPFGNVNPNKLKNP	25	27.4	<40
	IQDTLQTLSKEKAE	205	25.7	<40
	SSDAQYDFLENFKLH	121	28.6	<40
	TLKEILEKLDTEDNN	165	27.8	<40
	KEILEKLDTEDNNRR	167	27.4	<40
>borr H7C7N5	HSATFFSLEEEEINN	81	26.1	<40
	GDLVVRKEKDIETG	61	26.9	<40
	INNSAGGDKIAEYAI	149	25.7	<40
	IHTSYDEQSNGEVKV	22	26.1	<40
	SLYYGYNDEESDKNV	109	26.9	<40
	NKEIKTKIEKINDTE	126	41.6	<40
	TVKIKNKNNNSNNWAD	45	24.2	<40
>borr O50957	NFEDKSGDLSTSDEK	53	81.7	<40
	LKVYNQNTQDNEKIL	218	42.0	<40
	NKYKDFDTLKPAFY	237	26.9	<40
	GKELEDQKKEENIQI	80	26.9	<40
>borr O51272	DEIFIDSVKEPDLVA	709	26.5	<40
	IAPIPGREAVGIEIP	411	25.7	<40
	KVYGDSVDDLKDSQV	183	26.9	<40
	KGPVVTMYAVRPDKG	372	24.4	<40

	DENVDEIDESCEYKY	260	25.2	<40
	EISGENIVFDLVNSP	456	71.7	<40
	GYVGPVNGSKPREVL	772	24.0	<40
	GPSDEPMFDEALEIV	725	26.9	<40
	RNNKKPSNINLDKTI	221	24.4	<40
	KVKACEIRTKGIISQ	288	24.0	<40
	LEIVKTTRKASASYL	736	24.4	<40
	DMGYVGPVNGSKPREV	770	24.0	<40
	LRNNKKPSNINLDKT	220	24.8	<40
	SVDDLKDSQVFDEKK	188	24.0	<40
>borr Q44767	SGASRPTDARGGTNP	50	24.8	<40
	AKSGDTNFBVETSNSG	365	24.8	<40
	FDVDSDRHLVNPANG	118	24.0	<40
	STKNVTFACNLDKRL	170	23.5	<40
	IQGWMARDLEGEKVI	135	24.8	<40
	NVASIDTIHTQGAFQ	72	23.1	<40
>borr O50835	YYLDEYDEEDEEEIR	190	103.0	<40
	NSISYTDEIEEEDYD	174	29.5	<40
	MNKKGKGKIARKKGK	54	41.1	<40
	LFDKGNSILETSEES	35	29.1	<40
	SGESGELEEPISNE	138	25.2	<40
	LDNFAKAKAKEEAAK	249	71.7	<40
	LKEQSETRKEKIQKQ	108	95.2	<40
	KVSRKEPYIHSLKRD	70	24.8	<40