

offTarget Native crRNA	peak_score	predicted_gRNA.name	gRNAPlusPAM	offTarget_sequences	guideAlign
chr20:+:32761950:32761972	924	1 293 site4 target	GGCACTGCGGCT	(GGCACTGCGGCT.....	
chrX:-:105602031:10560205	643	0.381818 293 site4 OT1	GGCACTGCGGCT	(AGCTCTGCGGCTA..T.....	
chr10:+:125006289:1250063	171	0.571429 293 site4 OT2	GGCACTGCGGCT	(GGCACGACGGC'.....GA.....	
chr20:+:61435490:61435512	161	0.631579 293 site4 OT3	GGCACTGCGGCT	(TGCACTGCGGCC T.....C...	
chr15:-:40752038:40752060	128	0.3125 293 site4 OT4	GGCACTGCGGCT	(GGCGCTGCGGC'...G.....G..	
chr4:+:55949016:55949038	104	0.244898 293 site4 OT5	GGCACTGCGGCT	(GGCAATGCGGC'.....A.....	
chr7:+:54493728:54493750	80	0.2925 293 site4 OT6	GGCACTGCGGCT	(AGGACTGCGGC' A.G.....	
chr5:-:128925095:12892511	57	0.01634 293 site4	GGCACTGCGGCT	(GGCAATATGGCT'....A.AT.....)	
chr13:+:38688775:38688797	24	0.498462 293 site4	GGCACTGCGGCT	(AGCAGTGCAGGC' A...G.....A	
chr13:-:88248731:88248753	22	0.38854 293 site4	GGCACTGCGGCT	(CACACTGCAGCT CA.....A.....	
chr10:+:75343345:75343367	20	0.578512 293 site4	GGCACTGCGGCT	(GGCATCACGGCT'....TCA.....	
chr17:-:77433192:77433214	15	0.717949 293 site4	GGCACTGCGGCT	(GACACCACGGCT' A...CA.....	
chr19:-:32891169:32891191	15	0.212121 293 site4	GGCACTGCGGCT	(GGCTCTGCGGCT'...T.....	
chr17:-:326505:326527	12	0.816667 293 site4	GGCACTGCGGCT	(TGCACTGTGGCT' T.....T.....	
chr12:-:104694246:1046942	4	0.026886 293 site4	GGCACTGCGGCT	(TGGACTGCGGC' T.G.....	
chr6:-:160096843:16009686	5	0.346667 293 site4	GGCACTGCGGCT	(GGCACTGCTGCT'.....T.....G	
chr4:-:150443895:15044391	6	0 293 site4	GGCACTGCGGCT	(GTCAGTTTGGTT' .T..G.TT..T.	
chr13:-:27055267:27055289	9	0.197802 293 site4	GGCACTGCGGCT	(GGCACTGGGGT'.....G..T....	

offTarget 10DNA	peak_score	predicted_gRNA.name	gRNAPlusPAM	offTarget_sequences	guideAlign
chr20:+:32761950:32761972	518	1 293 site4 target	GGCACTGCGGCT	(GGCACTGCGGCT.....	
chr11:-:125388836:1253888	4	0 293 site4	GGCACTGCGGCT	(GGTGTGTGGG' /..TG...T..G/	

offTargetS	mismatch.	n.PAM.mis	n.guide.mi	PAM.sequ	offTarget_S	offTarget_E	chromoso	inExon	entrez_id
+		0	0	GGG	32761950	32761972	chr20		
-	20,17,3	0	3	GGG	105602031	105602053	chrX		26280
+	15,14	0	2	GGG	125006289	125006311	chr10		1488
+	20,9,3	0	3	TGG	61435490	61435512	chr20		
-	17,9	0	2	AGG	40752038	40752060	chr15	TRUE	55177
+	16,3	0	2	AGG	55949016	55949038	chr4	TRUE	9662
+	20,18,6	0	3	TGG	54493728	54493750	chr7		
-	16,14,13,7	1	6	GAG	128925095	128925117	chr5		28965
+	20,16,8	0	3	TGG	38688775	38688797	chr13	TRUE	341640
-	20,19,12	0	3	TGG	88248731	88248753	chr13		
+	16,15,14	0	3	AGG	75343345	75343367	chr10		84858
-	19,15,14,4	0	4	TGG	77433192	77433214	chr17		10801
-	17,3	0	2	TGG	32891169	32891191	chr19		84902
-	20,13,4	0	3	GGG	326505	326527	chr17		
-	20,18,4,3,2	1	5	GAG	104694246	104694268	chr12		50515
-	12,6	0	2	TGG	160096843	160096865	chr6		3482
-	19,16,14,1	2	5	CTT	150443895	150443917	chr4		987
-	13,10	0	2	GGG	27055267	27055289	chr13		

offTargetS	mismatch.	n.PAM.mis	n.guide.mi	PAM.sequ	offTarget_S	offTarget_E	chromoso	inExon	entrez_id
+		0	0	GGG	32761950	32761972	chr20		
-	18,17,13,1	2	6	CTA	125388836	125388858	chr11		63876

symbol

IL1RAPL2
CTBP2

RMDN3
CEP135

SLC27A6
FREM2

ZNF503
9-Sep
CEP89

CHST11
IGF2R
LRBA

symbol

PKNOX2