

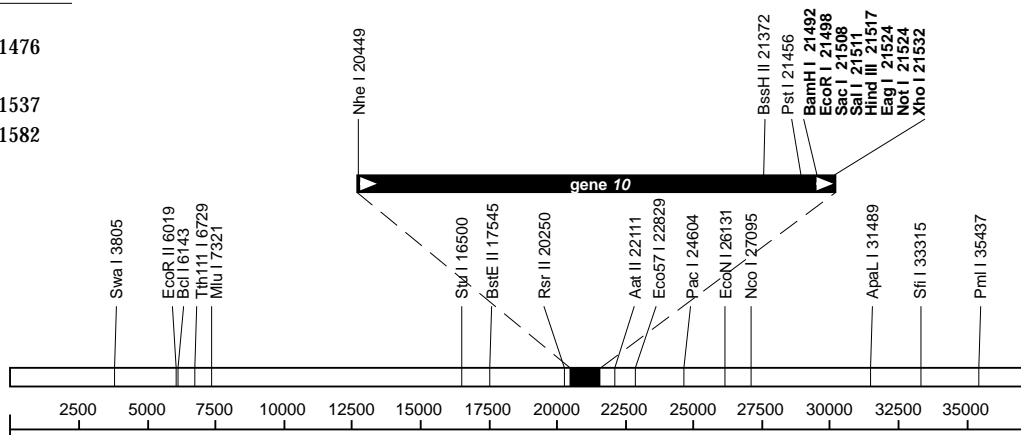
T7Select® 415-1b Vector

The T7Select® 415-1b vector is a protein display vector based on bacteriophage T7. The vector displays 415 copies of peptides up to 50 aa in size on the surface of the T7 capsid. Target sequences are fused to the C-terminus of the 10B capsid protein near amino acid 348. When T7Select415 recombinants are grown on normal T7 hosts such as BL21, the capsid shell is composed entirely of the fusion protein.

The linear genome of T7Select415-1b is 37,314 bp in size. Unique restriction sites are shown on the maps below (cloning sites are shown in **bold** type on the line map).

T7Select415-1b sequence landmarks

10B translation start	20446
T7SelectUP priming site	21457-21476
Multiple cloning region (<i>Bam</i> H I - <i>Xho</i> I)	21492-21537
T7SelectDOWN priming site	21563-21582



T7Select415-1b (37,314bp)

gene 10B @	insert	
left arm...GATCCG	AATTXXXX(N)XXXX	AGCTT...right arm
left arm...CTAGGCTTAA	XXXX(N)XXXXTCGA	A...right arm
...AspPro	AsnPhe...	
	AsnLeu...	
	AsnSer...	
	AsnTyr...	
	AsnCys...	
	AsnTrp...	

Reading frame of inserts cloned into *EcoR* I/*Hind* III T7Select415-1b vector arms.
 The inserts require a 5'-AATT "sticky end" on the top strand (amino terminal side) and a 5'-AGCT "sticky end" on the bottom strand, either created with oligonucleotides or by *EcoR* I/*Hind* III digestion. The reading frame requires the AAT (Asn) initial codon, followed by a TXX codon (possible second amino acids are shown). Use of *EcoR* I cleavage products places C in the second position, resulting in a TCX codon (Ser).

T7SelectUP primer # 70005-3

*Pst*I
*Bam*H I *Eco*R I
Sac I
Sal I
Hind III
Eag I
Not I
Xho I

...GCTGCAGGAGCTGTCGTATTCCAGTCAGGTGTGATGCTCGGGATCCGAAATTCGAGCTCCGTCGACAAGCTTCGCGGCCGCACTCGAGTAAGTTAA
 AlaAlaGlyAlaValValPheGlnSerGlyValMetLeuGlyAspProAsnSerSerSerValAspLysLeuAlaAlaAlaLeuGluEnd
 aa335 aa348 aa363

CCCCTTGGGGCCTCTAAACGGGTCTTGAGGGTTTTTTG
 T7SelectDOWN primer # 70006-3

T7Select415-1b cloning region

T7Select® 415-1b Restriction Sites

Enzyme	# Sites	Locations	Enzyme	# Sites	Locations	Enzyme	# Sites	Locations		
AatII	1	22111	DrdI	10	538 4041 4796 14682 15067 15534 29537 30387 32124 32298	SapI	4	7063 12268 17626 34432		
AccI	31		DsaI	25		Sau3AI	7	6143 6246 8994 11833 21492 33061 33464		
AcII	180		EaeI	3	21524 32915 33316	Sau96I	78			
AflIII	16		EagI	1	21524	Scal	4	12996 31479 36229 36371		
AflIII	21		EarI	44		ScrFI	8	537 6021 12178 13153 19319 20672 25739 35099		
AhdI	12		Eco57I	1	22829	SfaNI	84			
AluI	135		EcoNI	1	26131	Sfcl	46			
AlwI	3	21487 21500 33472	EcoO109I	22		Sfil	1	33315		
Alw26I	91		EcoRI	1	21498	SnaBI	13			
AlwNI	16		EcoRII	1	6019	SpeI	3	5526 14758 21540		
ApaLI	1	31489	FauI	21		Sspl	6	7446 24609 29908 32867 33332 33611		
ApoI	14		Fnu4HI	142		StuI	1	16500		
AvaI	6	8344 13381 21487 21532 23496 27459	FokI	88		StyI	35			
Avall	54		FspI	6	1970 13144 22831 26243 27181 32692	Swal	1	3805		
AvrII	3	17483 28940 30599	HaeII	25		Tal	162			
BamHI	1	21492	HaeIII	65		TaqI	103			
BanI	32		HgaI	62		TfiI	99			
BanII	2	17085 21508	HhaI	94		Thal	63			
BbsI	35		HincII	59		Tsel	105			
BbvI	105		HindIII	1	21517	Tsp45I	102			
BcgI	19		HinfI	210		Tsp509I	75			
BcgI'	19		HpaI	18		TspRI	85			
BclI	1	6143	HphI	94		Tth111I	1	6729		
Bfal	51		KpnI	5	41 3449 7024 21224 37195	UbaEI	5	1780 6602 7218 7787 15214		
BglI	2	11002 33315	MaeIII	202		VspI	11			
Bpml	23		MbolI	133		XbaI	3	10309 20404 31671		
Bpu10I	38		MluI	1	7321	XcmI	8	11613 14869 18274 18436 26672 26747 27093 27714		
Bpu1102I	19		MnlI	316		XhoI	1	21532		
BsaI	28		MscI	2	32917 33318	XmnI	12			
BsaAI	35		MseI	193		Enzymes that do not cut pT7Select415-1b:				
BsaBI	7	870 1015 4982 8993 16383 17468 34999	MslI	38		ApaI	Ascl	BglII	BspEI	Eco47III
BsaHI	7	339 8773 8916 21668 22108 23033 32882	MspI	55		EcoRV	FseI	NgoAIV	PvuI	SacII
BsaJI	82		MspA1I	31		SexAI	SgfI	SgrAI	SmaI	SphI
BsaWI	32		MunI	8	3571 12057 15218 18907 19013 31539 32824 33764	SrfI	Sse8387I	SunI		
BseRI	10	10085 10097 14985 17441 19897 28383 28812 36461 36625 36771	MwoI	155						
BsgI	18		NarI	2	8916 32882					
BsiEI	17		NciI	7	537 12178 13153 19319 20672 25739 35099					
BsiHKAI	25		NcoI	1	27095					
BsII	89		NdeI	7	3507 4195 11786 17434 20444 25103 31108					
BsmI	13		NheI	1	20449					
BsmBI	14		NlaIII	133						
BsmFI	44		NlaIV	96						
Bsp1286I	39		NotI	1	21524					
BspLU111	6	799 12821 16621 16742 16788 34948	NruI	3	1103 24943 26096					
BspMI	17		NsiI	7	6585 17469 19458 27378 35702 36515 36674					
BsrI	116		NspI	21						
BsrBI	15		NspV	6	3849 9639 16694 20341 20359 28814					
BsrDI	15		Pacl	1	24604					
BsrFI	3	20872 33087 34842	PfIMI	8	7148 10863 16245 23234 32202 33406 33769 35411					
BsrGI	11		PinAI	2	33087 34842					
BssHII	1	21372	PleI	111						
BssSI	30		PmeI	2	276 8555					
Bst1107I	8	5511 16992 20810 21841 24516 25868 26148 37006	PmlI	1	35437					
BstEII	1	17545	PshAI	4	13548 26381 27110 35995					
BstXI	11		Psp1406I	18						
BstYI	2	21492 33464	Psp5II	12						
Bsu36I	28		PstI	1	21456					
Cac8I	98		PvuII	2	11102 21650					
Clal	3	20336 24477 34457	Rcal	12						
CviJI	537		Rsal	159						
Ddel	272		RsrII	1	20250					
DpnI	7	6145 6248 8996 11835 21494 33063 33466	SacI	1	21508					
Dral	9	276 441 3805 4333 8555 14350 17777 28748 37125	Sall	1	21511					
Drall	16		SanDI	3	12884 23772 25970					