Antibody Design LABORATORIES

fADL-1 Phage Vector

INSTRUCTION MANUAL

fADL™-1 Phage Vector for Phage Display

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Description

Introduction

The fADL™-1 vector is a type 3 phage display vector (Smith 1997) with a cloning site for display on the N-terminal side of the full-length gene III protein. Secretion in the periplasm of the fusion protein is driven by the PelB leader peptide, in place of the wild-type gene III protein leader sequence.

fADL™-1 derives from the phage vector fd-kan, a vector analogous to fd-tet (Smith 1990) where the tetracycline resistance genes derived from Tn10 have been replaced by the kanamycin resistance determinant of Tn903. It has a smaller size (7982 bp), making cloning easier. Like fd-tet, the number of double-stranded RF copy number is relatively low, about 60 copies in stationary-phase cells. Therefore fADL-1 is well tolerated by the host, giving large colonies and small plaques. Yield of physical particles is about $5x10^{11}$ virions/ml, similar to fd-tet; infectivity of the virions is around 5%, depending on the insert sequence. Display is usually multivalent with limited polyphage production, even in the case of large polypeptides such as scFvs.

Content, Shipping & Storage

Content

VECTOR	COMPOSITION	AMOUNT
fADL™-1	20 µl at 0.5 µg/µl of DNA vector in DNA Conservation Buffer (Tris-HCL 5 mM, EDTA 0.1 mM, pH 8.5)	10 µg

Shipping & Storage

fADL™-1 phage vector is shipped on wet ice. Upon receipt, store the vector at -20ºC.

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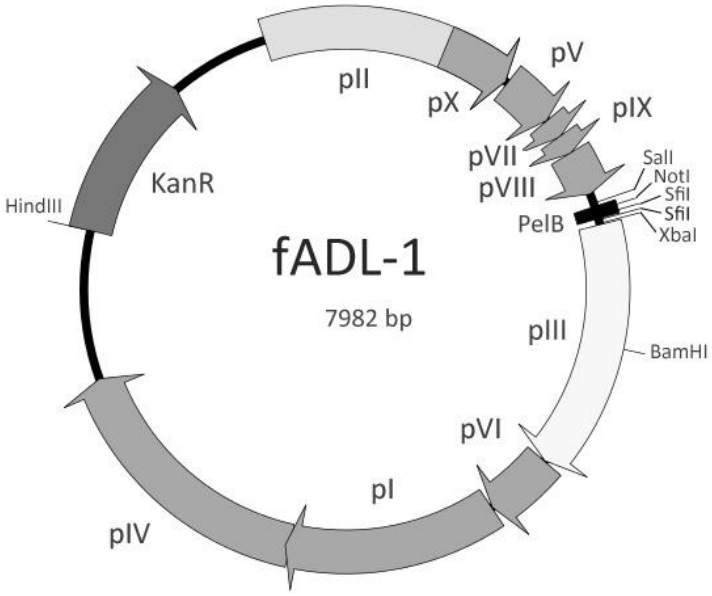
Vector Map

The figure below illustrates the main features of fADL™-1 vector. The full vector sequence is available online for download in varied formats on the product web page; the total length of the vector is 7982 bp.



Cloning Site

Following is an illustration of fADL-1 cloning site from the end of the gene VIII sequence to the gene III sequence. The PelB peptide leader sequence (translation *MKYLLPTAAAGLLLLAAQPAMA*) is missing the two last amino acids MA, which will have to be re-introduced during cloning to insure proper reading frame and cleavage (on the C-terminal side of the terminal Alanine).

```
        pVIII terminator                          SalI                          PelB
        ──────────────────────────────────────┐   |                            MetL
1540    AGGCTCCTTT TGGAGCCTTT TTTTTGTCGA CTAACGAGGG CAAATCATGA

                                 NotI                                  SfiI/BglI
        leader peptide            |                                     |
        ysTyrLeuLe uProThrAla AlaAlaGlyL euLeuLeuLe uAlaAlaGln
1590    AATACCTATT GCCTACGGCG GCCGCTGGAT TGTTATTACT CGCGGCCCAG

                          Sfi I/BglI                  XbaI        g3p full length
                              |                         |        ┌──────────────...
        ProAlaMet       GlyPro GlyGlyLeuS erLeuGluAl aGluThrVal
1640    CCGGCCATGC TAGTGGCCCG GGAGGCCTGT CTCTAGAAGC CGAAACTGTT
```

Feature Table

The main features of fADL™-1 vector are highlighted in the following table.

FEATURE	LOCATION	HEADING 5
Protein VIII terminator	1538-1564	Transcriptional terminator.
PelB leader sequence	1586-1648	PelB leader sequence for export in the periplasm of the host bacteria. The missing terminal methionine and alanine will have to be added during the cloning to obtain a complete leader peptide (MKYLLPTAAAGLLLLAAQPAMA) necessary for proper removal of the leader during the export process.
g3p fusion coding sequence	1678-2898	Full-length gene III fusion protein coding sequence; the fd g3p protein is fused on its N-terminal side to the linker GPGGLSLE; the exact final sequence of the fusion depends on the cloning strategy (see cloning site).
Kan^R	7089-6274	Kanamycin resistance gene

Restriction Site Summary

Enzyme	Site	Nb	Position	Strand	Isoschizomers
AjuI	(7/12)GAANNNNNNNTTGG(11/6)	1	6609	-	
AloI	(7/12)GAACNNNNNNTCC(12/7)	1	7340	-	
BalI	TGG^CCA	1	5126		MlsI MluNI MscI Msp20I
BamHI	G^GATCC	1	2265		
BseRI	GAGGAG(10/8)	1	2053		
Bsp1407I	T^GTACA	1	1021		BsrGI BstAUI
BstAPI	GCANNNN^NTGC	1	6076		
BstEII	G^GTNACC	1	5709		BstPI Eco91I EcoO65I PspEI
BstXI	CCANNNNN^NTGG	1	1644		
CspCI	(11/13)CAANNNNNGTGG(12/10)	1	3055		
DrdI	GACNNNN^NNGTC	1	7334		AasI DseDI
EagI	C^GGCCG	1	1608		BseX3I BstZI EclXI Eco52I
EciI	GGCGGA(11/9)	1	2007	-	
FalI	(8/13)AAGNNNNNCTT(13/8)	1	2531		
GsuI	CTGGAG(16/14)	1	7631	-	BpmI
MfeI	C^AATTG	1	715		MunI
NaeI	GCC^GGC	1	1639		PdiI NgoMIV MroNI
NmeAIII	GCCGAG(21/19)	1	7400	-	
NotI	GC^GGCCGC	1	1607		CciNI
NruI	TCG^CGA	1	6998		Bsp68I BtuMI RruI
PacI	TTAAT^TAA	1	4178		
PflMI	CCANNNN^NTGG	1	6391		AccB7I BasI Van91I
PpiI	(7/12)GAACNNNNNCTC(13/8)	1	7341	-	
PshAI	GACNN^NNGTC	1	990		BoxI BstPAI
PspXI	VC^TCGAGB	1	7054		
PvuI	CGAT^CG	1	6656		Ple19I BpvUI MvrI
SacII	CCGC^GG	1	6138		Sfr303I KspI SgrBI Cfr42I SstII
SalI	G^TCGAC	1	1565		
SgfI	GCGAT^CGC	1	6655		AsiSI RgaI SfaAI
SnaBI	TAC^GTA	1	1268		BstSNI Eco105I
StuI	AGG^CCT	1	1662		AatI Eco147I PceI SseBI

SwaI	ATTT^AAAT	1	7515		SmiI
XbaI	T^CTAGA	1	1671		
XhoI	C^TCGAG	1	7055		StrI TliI Sfr274I PaeR7I SlaI
AclI	AA^CGTT	2	4680		Psp1406I
		2	7505		
AlfI	(10/12)GCANNNNNNTGC(12/10)	2	4889		
		2	6977		
BaeI	(10/15)ACNNNNGTAYC(12/7)	2	1840	-	
		2	2182		
BbvCI	CCTCAGC(-5/-2)	2	1370	-	
		2	1416		
BglI	GCCNNNN^NGGC	2	1634		
		2	1655		
BsaXI	(9/12)ACNNNNNCTCC(10/7)	2	1936		
		2	7340		
BspMI	ACCTGC(4/8)	2	1113	-	Acc36I BfuAI BveI
		2	2303		
BsrBI	CCGCTC(-3/-3)	2	4615		AccBSI MbiI
		2	5618		
BtsI	GCAGTG(2/0)	2	6712	-	
		2	6791		
DraIII	CACNNN^GTG	2	7186		AdeI
		2	7291		
Eam1104I	CTCTTC(1/4)	2	4120		Bst6I EarI
		2	6846		
EcoNI	CCTNN^NNNAGG	2	2984		BstENI XagI
		2	6740		
EcoP15I	CAGCAG(25/27)	2	1368	-	
		2	4918		
Esp3I	CGTCTC(1/5)	2	865		BsmBI
		2	6643		
HindIII	A^AGCTT	2	6020		
		2	6535		
PscI	A^CATGT	2	195		PciI
		2	3763		
PsiI	TTA^TAA	2	5769		AanI
		2	7419		
SfiI	GGCCNNNN^NGGCC	2	1633		
		2	1654		
SmaI	CCC^GGG	2	1656		Cfr9I TspMI XmaI
		2	6781		
TaqII	GACCGA(11/9)CACCCA(11/9)	2	3325	-	
		2	7279		
XmnI	GAANN^NNTTC	2	357		Asp700I MroXI PdmI
		2	2691		

Absent Sites:
AarI, AatII, AbsI, AflII, AgeI, ApaI, ApaLI, AscI, AsuII, AviII, AvrII, BarI, BauI, BcgI, BciVI, BclI, BfiI, BglII, BpiI, BplI, BsePI, BsgI, BsiWI, Bsp1720I, BssNAI, Bsu36I, BtrI, Eam1105I, Eco31I, Eco47III, Eco57I, EcoRI, EcoRV, FseI, FspAI, HpaI, KflI, KpnI, MauBI, MluI, MreI, MroI, NarI, NcoI, NheI, OliI, PasI, PfoI, PmaCI, PmeI, PsrI, PstI, PvuII, RsrII, SacI, SapI, ScaI, SexAI, SgrAI, SgrDI, SpeI, SphI, SrfI, Sse8387I, TstI, Tth111I, XcmI.

Experimental Procedures

Working with fADL-1

General Molecular Biology Techniques

Molecular cloning and phage display should be conducted under the supervision of a qualified instructor trained to standard safety practice in a molecular biology laboratory environment. Standard molecular biology procedures can be found in a general molecular biology handbook such as Sambrook (1989).

Working with Filamentous Phage

Keep the bench clean and regularly wiped with 2% bleach to limit phage cross-contamination and only use filtered tips to prevent aerosol contaminations. Phages are known to survive standard autoclaving conditions and are not removed by 0.22 µm filtration. Phages are either killed by heat-treating dry, autoclaved materials in an oven for 4 hours at 105ºC (Phage Display 2001) or by incubation in 2% bleach for at least 1 hour. We recommend to extensively wash with hot water all glass and plastic-ware, then submerge (tubes) or incubate (flasks) with a 2% solution of bleach for at least one hour. Heat-resistant glassware can then be autoclaved in an autoclave that is never used for biological waste while sensitive plastic-ware can be used directly or at best heat-treated as described above.

Bacterial Strains

In theory, any K12 F^+ *E. coli* strain is suitable for phage display using fADL-1. Practically we recommend the strain SS320 with which fADL-1 gives large colonies. SS320 which has been widely used for phage display, is well-documented in the literature and has been extensively tested with fADL-1. SS320 derives from MC1061 by introduction of a tet^R F' episome (Sidhu 2000). Like most derivatives of MC1061, SS320 can be made highly competent for transformation by electroporation. We also recommend using the parent strain MC1061 for building libraries to limit contaminations by exogenous filamentous bacteriophage in original library stocks.

MC1061 and SS320 phenotypes are highlighted below:

SS320 *hsdR2 mcrA0 araD139 Δ(araA-leu)*7697 Δ*lac*X74 *galK16 galE15(GalS) λe14⁻ rpsL150(*Str^R*) spoT1 thi F'[proAB+lacIqlacZΔM15 Tn10 (*tet^r*)]*

MC1061 *F⁻ hsdR2 mcrA0 araD139 Δ(araA-leu)*7697 Δ*lac*X74 *galK16 galE15(GalS) λe14⁻ rpsL150(*Str^R*) spoT1 thi*

Plasmid Maintenance

Propagation and maintenance of fADL-1 is obtained on any F^-, *recA1, endA1 E. coli* strain using kanamycin 50 µg/ml as a selection marker. The use of an F^+ male strain may select for in-frame mutants that can take over the bacterial culture. We routinely isolate fADL-1 RF dsDNA using DH10B™ from Life Technologies with yields up to 2 mg/l and more.

Cloning into fADL-1

Primer Design and PelB Leader Sequence

A complete PelB leader sequence *MKYLLPTAAAGLLLLAAQPAMA* is necessary for export in the periplasm and proper removal of the leader peptide by host proteases. In the following schema, where [NNN] represents the insert sequence and [Xxx] the translated amino acid sequence, the short hexanucleotide ATGGCN must be appended immediately to the first *SfiI* site to obtain a complete PelB leader encoding sequence; cleavage will occur on the C-terminal side of the terminal alanine (codon GCN):

Cloning in fADL-1 Using SfiI/BglI Sites

Large libraries in the 1 x 10^9 range and above can easily be constructed using the double BglI/SfiI cloning site.

The *SfiI* restriction enzyme recognizes rare 8-base-long interrupted palindromes GGCCNNNN/NGGCC and leaves 3-nucleotide-long overhangs after digestion. The fADL-1 cloning site contains one *SfiI* site close to the end of the PelB leader sequence and a second *SfiI* site 8 nucleotides apart from the first site. The PelB sequence of the empty vector has an early termination by an ochre stop codon and no gene III protein is produced by the vector alone.

The *SfiI* restriction enzyme requires two copies of its recognition sequence for cleavage to occur; cleavage of the two sites happens simultaneously through interaction of two *SfiI* tetramers (Wertzell 1995). Vectors bearing two sites very close to each other are cut in trans and digestion might not complete. Therefore we strongly recommend opening fADL-1 with the alternative *BglI* restriction enzyme, which cuts the shorter 6-base-long interrupted palindromes GCCNNNN/NGGC and generates identical overhangs.

Sites open with BglI will re-ligate with sites open with SfiI as long as overhangs are complementary. Practically, the pentanucleotide NNNNN must be identical to the original vector sequence to handle both ligation of the complementary overhangs and conservation of the amino acid sequence (PelB sequence and linker to protein III).

PREPARATION OF VECTOR DNA FOR CLONING

1. On ice add successively water, *BglI* buffer (1x final), fADL-1 vector and *BglI* enzyme 5 units/µg DNA; make sure the enzyme volume does not to exceed 1/10 of the total reaction volume.
2. Incubate 4 h to overnight at 37ºC.
3. Inactivate for 20 min at 70ºC.
4. Confirm the digestion by DNA analysis on a minigel.
5. Purify the cut vector.

For routine cloning, a standard DNA purification kit can be used directly after the digestion to remove the excess of buffer, the small DNA stuffer and leftover restriction enzyme. For library construction, phenol/chloroform extraction and/or gel purification may be required.

PREPARATION OF INSERTS

SfiI digestion should be rapid and complete in 4 hours especially for fragments longer or equal to 200 bp where sites are cut in *cis*. *BglI* may be used when the insert sequence is known to be free of *BglI* site and therefore is not recommended for building antibody libraries.

Sequencing of Inserts

The following primers give both strong PCR amplification and sequencing traces.

Forward or Sense Primers

phi8S3 5'- CTCGAAAGCAAGCTGATAAACC

phiS2 5'-ATGAAATACCTATTGCCTACGG

Backward, Antisense or Reverse Primers

psiR2 5'-CGTTAGTAAATGAATTTTCTGTATGAGG

psiR3 5'-GCGTAACGATCTAAAGTTTTGTCG

Nested Sequencing

Often it is easier to sequence an insert by PCR on the bacterial culture supernatant or directly from a colony rather than on tediously isolated plasmids. Use the outward primers phi8S3 and psiR3 together with a DNA polymerase not inhibited by bacterial cultures such as TAQ polymerase for the PCR and sequence the insert with the nested reverse primer psiR2. Use less than 1 µl of bacterial culture supernatant per 50 µl-PCR reaction or the touch of a toothpick on a colony as DNA template.

Counting & Amplifying fADL-1 Virions

Preparation of bacterial cells

1. Peak a single colony from a SS320 agar plate supplemented with tetracycline 20 µg/ml and inoculate a 3-ml culture of 2xYT medium.
2. Incubate overnight at 37ºC with agitation at 250 rpm.
3. Dilute an aliquot of the culture 1:10 v/v with fresh 2xYT medium in a new culture tube and incubate for one hour at 37ºC with agitation at 250 rpm.
4. Take a small aliquot in sterile conditions and measure the absorbance at 600 nm of a 1:10 dilution in 2xYT medium (A_{600}). Absorbance corrected for dilution should be between 0.5 OD and 1.0 OD and cells are ready to be transduced. If necessary adjust the length of incubation to your conditions.
5. Keep the cells at room temperature on the bench and proceed to the transduction within the hour.

Transduction step

1. Dilute the phage with TBS is necessary.
2. Mix gently an aliquot of the phage dilution with an equal volume or more of bacterial culture.
3. Incubate at 37ºC with agitation at 250 rpm for 30 min.
4. Dilute the culture if necessary with fresh 2xYT medium.
5. Plate immediately on 2xYT/agar plates supplemented with kanamycin 50 µg/ml and incubate o/n at 37ºC.
6. In parallel add kanamycin 50 µg/ml final to the culture and pursue the incubation o/n at 37ºC to amplify the phage if necessary.

Counting transducing units (TU)

The day after count the number of colonies, adjust for dilution and express the results indistinctively as either cfu/ml (colony forming unit) or TU/ml (transducing unit). If you know the infectivity of your virions (normally around 5% for small peptide inserts but sometimes much lower for larger inserts), you can deduce the number of virion particles per ml (v/ml) and verify retrospectively than your multiplicity of infection (MOI) at the time of transduction was less than 0.1 (less than one virion particle per 10 bacteria) counting 1.4E9 bacteria/ml at A_{600} of 1.0 OD.

Systematically add controls to your experiments. Plating the bacterial culture on a plate supplemented with kanamycin 50 µg/ml will insure the absence of contamination by one of your phage prior to transduction; plating dilutions of the bacterial culture will count bacteria and help measure the MOI at the time of transduction. Finally always plate in duplicate and repeat the experiment on a different day with a new batch of bacteria and new phage dilutions for accuracy.

Working with fADL-1 Virions

Phage Production

The phage vector fADL-1 does not require a helper phage to produce virions. Cultures can be seeded directly from colonies obtained on kanamycin plates. For optimal conditions of growth and virion production, we recommend a rich medium such as 2xYT medium supplemented with kanamycin 50 µg/ml; incubate overnight at 37ºC and 250 rpm.

Phage Purification

For most applications, including screening of phage libraries, a single PEG precipitation is sufficient as a purification step. Please, consult **Antibody Design Labs** online technical resources at http://www.abdesignlabs.com/technical-resources/ for a purification protocol using PEG precipitation. Sometime, especially when working with large libraries, a second PEG precipitation is indicated to achieve concentrated phage preparations. Note that multiple steps of PEG precipitation will be useful for concentration purposes but will unlikely improve purity; other purification methods beyond the scope of this manual such as purification over a cesium chloride gradient may be necessary. Phages are usually re-suspended in TBS or in PBS; conservatives are not necessary.

Phage Quantification

The two main methods to quantify phages are transduction and spectrophotometry.

Transduction is a functional assay that measures a number of transducing units and is the recommended method to follow a biopanning experiment (the number of eluted TU normally increased rapidly when selection occurs). A detailed protocol is given in the above paragraph Counting & Amplifying fADL-1 Virions.

Since virions are exclusively made of protein and DNA in a precise ratio, a formula has been devised to convert U.V spectrophometry absorption readings into virion concentrations. Please, consult **Antibody Design Labs** online technical resources at http://www.abdesignlabs.com/technical-resources/ for a protocol for phage concentration determination using spectrophotometry. Using this method, phage concentrations can be expressed in OD using $A_{269-320}$ data. Spectrophotometry is the recommend method to quantify purified phages. For most phages a 10x concentration factor is sufficient during purification; some clones that do not produce a lot of virions may require a 20x or more concentration factor to yield phage concentrated enough for assay purpose. Note that below 0.1 OD (as equivalent phage OD taken in the original bacterial culture), results are usually biased and the concentration of phages is most likely overestimated.

Storage

Phage are extremely resistant particles that will survive almost indefinitely once frozen. On the other hand, peptides and large inserts are more fragile and should not be stored more than a few days in the original culture supernatant at 4ºC, or immediately frozen after purification and stored up to a few weeks at -20ºC or at -80ºC for longer term storage.

Phage preparations can be frozen directly without conservative although some people recommend adding 10% or 15% v/v glycerol. In our hands, in absence of glycerol, TU determination can tolerate up to 2 freeze-thaw cycles and binding assays such as ELISA and Western blots up to 4 freeze-thaw cycles without apparent changes. We normally aliquot libraries and store them at -80ºC for an undetermined period of time and thaw them only once. Beyond those limits, we recommend adding glycerol 10% to the phage preparations.

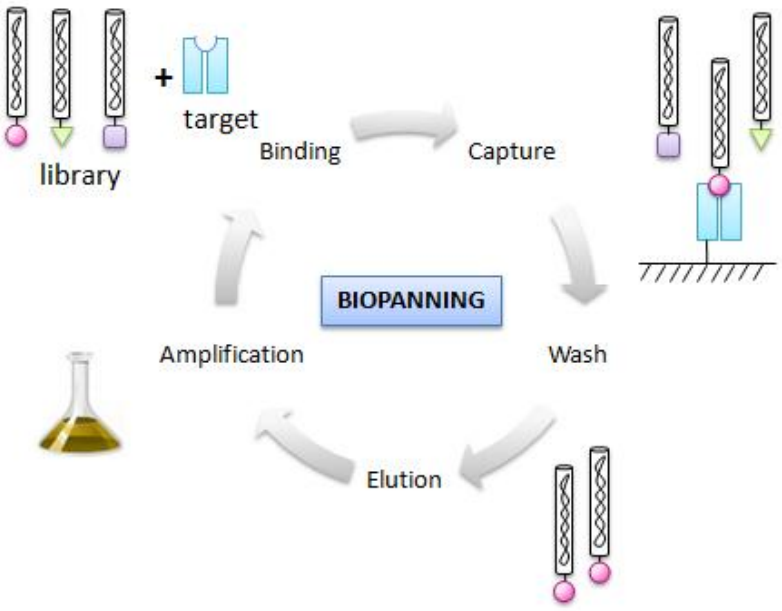
Contaminations

The possibility of contaminations by other phages, wild-type filamentous phages, helper phages or even fADL-1 phages from another library should always be in mind. Two reasons favor contaminations; first fd-tet-derived vectors are relatively constrained and make stable superinfections with other phages, in particular ubiquitous wild-type filamentous phage; second contaminations are easily transmitted along successive rounds of screen.

The best treatment of contamination is prevention. Follow precisely the guidelines for working with phages to keep contaminations away; separate vessels and plasticware using other phage systems from the one using fADL-1 vector; always use an F^- strain such as MC1061 to build the primary libraries.

Sometimes deeper analyses are necessary to diagnostic a contamination. You can try to make plaques with your phage preparation (fADL-1 makes tiny plaques) or you can prepare RF DNA on an F' recA1 bacterial strain and analyze dsDNA. We find simpler to analyze circular ssDNA from purified phage preparation to verify for the absence of contamination. Please, consult **Antibody Design Labs** online technical resources at http://www.abdesignlabs.com/technical-resources/ for a protocol for analyzing filamentous phage ssDNA by electrophoresis.

Library Screening Workflow



Biopanning was a term created by George Smith (7) to designate a selection procedure where “binders” are progressively enriched through iterative rounds of selection. In this process, binder/target complexes are captured on a solid surface and selectively eluted after a thorough wash to eliminate non-specific clones; elution and amplification of the bound phage allows further rounds of selection and enrichment.

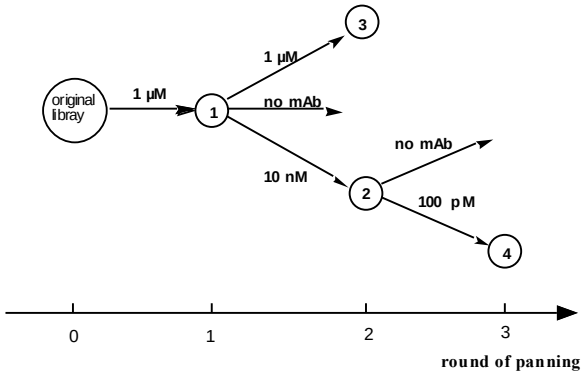
It is useful to distinguish varied phage populations to adjust screening conditions; thus one often considers non-binding phages, non-specific binding phages, low-affinity binding phages and high affinity binding phages (8). Because biopanning is a dynamic and competitive process, the preferential enrichment of one population may inhibit competitively the growth of the others. During a biopanning experiment, the primary goal will be to control non-specific phages in order to identify the first positive, specific clones; if the stringency is too high from the initial round of panning, binders may get definitively lost.

In “solid-phase capture”, the target is attached to the solid phase; target binding and capture occur at the same time in a process intrinsically multivalent. This method of screening is particularly well-adapted for the first round of selection of fADL-1 -based libraries to enrich even the lowest affinity binders. fADL-1 is a multivalent type-3 phage vector mainly used for the isolation of low-to-moderate affinity binders, typically found in peptide libraries. The use of a phage vector has also been reported to improve the screening antibody libraries in some cases (9).

In “solution-phase capture”, the target is incubated with the target in solution followed by the capture of the phage/target complexes on a solid surface. Binding in solution can be helpful to prevent selection of non-specific binders. Varying the concentration of the target during binding is a way to control selection stringency. The biotin/streptavidin system is often used for capture. This opens many possibilities to control selection; for example adding an excess of non-biotinylated target can be used during affinity maturation to prevent re-binding and operate K_{0ff} selection or adding an excess of molecules where binding is not desired can be helpful for negative selection.

A classical screening of a fADL-1 library will start with a high-avidity solid-phase capture to insure all binders present in the primary library at very low concentrations are enriched and not lost. This round will be followed by multiple rounds of solution-phase captures at varied target concentrations to guide the selection toward the highest affinity binders.

Enrichment of a population of selective binders is often seen by an increase in the number of eluted phage (selection yield = total eluted phage / total input phage). Here is a typical tree made during the selection of a peptide library with a monoclonal antibody; the first round was done on a plastic surface; rounds 2 and 3 were done by solution-phase capture with an anti-isotypic antibody.



Biopanning Protocols

The following guidelines are general recommendations and not a substitute for the multiple books, chapters, reviews and publications on the matter.

Solid-capture surfaces

Small Petri dishes have been used with success for the first round. We prefer high-binding capacity surfaces found on ELISA plates; multiple wells can be combined if a large surface is desired. Immunotubes (Nunc™ Maxisorp 444202 Immuno Tubes) are extremely popular for solid phase-capture assays.

Solution-capture surfaces

The use of the interaction between biotin and strepavidin is the preferred option for solution capture. Streptavidin can be adsorbed on a plastic surface but pre-coated magnetic beads offer elegant alternatives. A classical solution to the problem of non-specific binders is to alternate capture surfaces between rounds to prevent their enrichment.

Blocking and wash buffers

Most protocols recommend PBS or TBS for blocking and during binding with either BSA (1 - 3%) or milk (3% - 5%) with Tween 20 (0.5‰ – 1.5‰). Tween 20 is usually incompatible with screening on cell surface. Washing is usually extensive (5-10 times) using the same buffer base without blocking agent. We recommend washing 5 times with a buffer containing Tween 20 followed by 5 times without Tween 20. Many non-specific plastic binders exhibit a Tween-dependent binding and the use of different washing conditions helps eliminate them.

Phage input

There are 3 ways to count virions, virions, phage OD and TU. Transducing units (TU) count successful transduction events during infection, either as plaques (pfu) or colonies (cfu) as with fADL-1. If we know the infectivity I of a phage, we can deduce the exact number of virions: v = TU/I. Unfortunately, infectivity may vary with display, especially on pIII; on the other hand getting a precise knowledge of infectivity during screening is time consuming and not very informative. It is more convenient to assume infectivity, e.g. 5% for fADL-1, to convert TU into virions and *vise versa* on a routine basis. Since virions are made of DNA and protein in a ratio that mostly depends on the length of the virions and therefore on the size of

the phage genome, it is possible to estimate phage concentration by spectrophotometry (phage OD) (consult **Antibody Design Labs** online technical resources at http://www.abdesignlabs.com/technical-resources/ for a protocol for phage concentration determination using spectrophotometry and references herein). Practically, we recommend around 0.1 - 0.2 phage OD or 7.5E11 – 1.5E12 virions/ml or 4E10 – 8E10 cfu/ml for input; these numbers are concentrations and the absolute number of virions in your biopanning experiment will vary with the volume of incubation.

Elution

Multiple methods have been reported for elution.

- Direct infection. Phages are not eluted and transduction is done directly at the capture surface. Multivalent interactions may interfere with infection and this method is not recommended with fADL-1.
- Acidic elution. This is the most frequently used technique, classically by incubation for 10 min with shaking in the presence 0.1 M glycine/HCl buffer, pH 2.5 with BSA 1 mg/ml. The eluate is neutralized with Tris buffer 1 M, pH 8.0 – 8.5. Use pH paper and different volumes of Tris buffer to determine the best conditions for neutralization.
- Basic elution. Usually done with TEA; note that exposure to basic conditions tend to denature phages rapidly.
- Trypsin elution. Elution with a protease is getting more and more popular. This method is more specific since phages not interacting through the fusion protein will not be released; also binders not eluted at low pH will be now recovered. Noticeably, removal of the display will eliminate bias during transduction created by the interference of fusion proteins with the infection process. Elution conditions must be carefully established with positive controls.
- Others, system specific.

Amplification

The neutralized eluat is stable in liquid state several days at 4ºC or frozen several months at -20ºC. Typically the entire eluat is used for re-amplification after the first round and only part of it during the next rounds. Analysis of single clones is preferably done on colonies prepared directly from the eluate rather than on colonies obtained after re-amplification of the library. For amplification, mix part of the eluat or all of it with a volume equal or superior of SS320 bacterial culture in mid to late log phase (OD_{600} between 0.5 and 1.0); incubate with shaking at 37ºC for 45 min to 1 h; mix with a volume of 2xYT at least 20 times larger, supplement with kanamycin 50 µg/ml and incubate o/n at 37ºC. Prepare virions the morning after. fADL-1 makes very small plaques and therefore will not amplify properly if too many non-infected cells are present in the culture to the contrary of wild type bacteriophages.

To count virions in the eluat, proceed to appropriate dilutions in 2xYT after the 45 min initial incubation, plate on 2xYT/agar plate supplemented with kanamycin 50 µg/ml and incubate o/n at 37ºC.

Pre-made, stabilized, Phage Competent™ SS320 bacteria are available from **Antibody Design Labs** under the catalog number PC002. Phage Competent bacteria are ready for transduction and can be thawed and frozen multiple times without loss of infectivity. Their use brings reliability, eliminates contaminations and shortens experimental time drastically.

Appendix

MSDS Information

MSDSs (Material Safety Data Sheets) are available on the **Antibody Design Labs** website at the corresponding product page.

Quality Control

Specifications and quality control are detailed on the online product page. **Antibody Design Labs** certifies that the product will perform according to these specifications.

Technical Support

Visit **Antibody Design Labs'** website at **www.abdesignlabs.com** for technical resources, including manuals, vector maps and sequences, application notes, FAQs, etc.

For more information or technical assistance, call, write, fax, or email us at:

Antibody Design Labs
4901 Morena Blvd, Suite 203

San Diego, CA 92117

Phone: 1-877-223-3104 (TOLL-FREE)
Fax: 1-858-272-6007 (24 hour)
(Monday – Friday 9:00 AM – 5:00 PM PST)
Email: support@abdesignlabs.com

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