

OB FOLD DOMAINS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the priority benefit of United States Provisional Patent
5 Application No. 60/809,105 filed May 26, 2006, entitled "OB Fold Domains," which is hereby
incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

Molecular recognition is central to biological processes, from high-affinity protein-ligand
10 interactions to the more transient protein-protein recognition events of signal transduction
pathways. Such events depend on the versatility of proteins, which have been adapted to new
roles as organisms have evolved. As an example, to capture a foreign antigen, a small number of
antibodies from the immune system's naïve library (which contains approximately 10^7 variants)
(1) recognize the antigen and bind to it with moderate affinity. Selection and maturation then
15 introduces further mutations to generate the tight, highly specific binding required to eliminate
the antigen. In this way a staggering array of binding modes can be grafted on to the basic
antibody scaffold, to sequester targets varying from small molecules to whole cells.

This strategy can be replicated in the laboratory to produce very large libraries of
antibody variants ($>10^{10}$ different clones) (2,3) that can then be selected for binding to a
20 particular target. Repeated cycles of amplification and selection for binding can then "discover"
the test-tube antibodies with tight and specific molecular binding characteristics. This *in vitro*
approach can also be applied to other scaffolds. For example, randomization and selection by
phage display have been used to study and improve the binding of growth hormone and the
growth factor heregulin to their respective receptors (4,5), and "affibodies" have been developed
25 from libraries of a three-helix bundle domain from staphylococcal protein A (6,7). This general
area has been the subject of several reviews (8-10).

OB-fold domains are generally small structural motifs found in a variety of proteins and originally named for their oligonucleotide/oligosaccharide binding properties. The OB-fold domain is a five-stranded closed β barrel and the majority of OB-fold domains proteins use the same face for ligand binding or an as active site. Different OB-fold domains use this “fold-related binding face” to bind oligosaccharides, oligonucleotides, proteins metal ions and catalytic substrates. OB-fold domains are described in for example, Arcus, *Curr. Opin. Struct. Biol.*, Vol. 12: 794-801 (2002) and Theobald, *Annu. Rev. Biophys. Biomol. Struct.*, Vol., 32: 115-33 (2003). Canadian Patent Publication No. 2,378,871 describes beta-pleated sheet proteins with binding properties.

The disclosure of all patents, patent applications, patent application publications, scientific publications and other publications cited herein are hereby incorporated by reference in their entirety.

BRIEF SUMMARY OF THE INVENTION

The invention provides for modified OB-fold domains having desired properties and methods of producing libraries of modified OB-fold domains. The invention also provides for the libraries of modified OB-fold domains produced by such methods and methods for screening such libraries of modified OB-fold domains for desired biological activities. In addition, the invention provides for the modified OB-fold domains identified from such libraries. Also provided herein are modified OB-fold domains obtainable from *Pyrobaculum aerophilum* that exhibit modified binding interactions. A modified OB-fold domain can bind to the same substrate as compared to the naturally-occurring OB-fold domain, or can bind to a different substrate as compared to the naturally-occurring OB-fold domain, or can bind to both the same substrate and a different substrate as compared to the naturally-occurring OB-fold domain. Alternatively, a modified OB-fold domain can be prepared where no known substrate binds to the naturally-occurring OB-fold domain, where the modified OB-fold domain binds to a substrate.

Thus, in one aspect, the invention is an isolated modified OB-fold domain, obtainable from a naturally occurring OB-fold domain, wherein the modified OB-fold domain comprises a)

at least one modified amino acid residue in a β - strand of the OB-fold domain binding face as compared to the naturally occurring OB-fold domain, or b) at least one modified amino acid residue in a β - strand of the OB-fold domain binding face and at least one modified amino acid residue in a strand of the OB-fold domain loop region, or c) at least one modified amino acid residue in a strand of the OB-fold domain loop region, and wherein said modified OB-fold domain has altered binding characteristics as compared to the naturally occurring OB-fold domain. In one embodiment, where a binding partner of a naturally-occurring OB-fold domain is known, the invention is a modified OB-fold domain wherein the domain specifically binds to a different binding partner than the naturally occurring OB-fold domain or has modified binding with its naturally occurring binding partner. In another embodiment, the modified binding comprises about at least a 25%, about a 50%, or about a 75% reduction in the dissociation constant of the modified OB-fold domain with its naturally occurring binding partner, as compared to the corresponding naturally occurring OB-fold domain. In another embodiment, the modified binding comprises a decrease in the dissociation constant by a factor of at least about 2, about 3, about 4, about 5, about 6, about 8, about 10, about 15, about 20, about 25, about 50, about 100, about 200, about 500, about 1000, about 5000, about 10,000, about 50,000, or about 100,000 of the modified OB-fold domain with its naturally occurring binding partner, as compared to the corresponding naturally occurring OB-fold domain. In another embodiment, the invention is a modified OB-fold domain wherein the naturally occurring OB-fold domain occurs in a protein or class of proteins selected from the group consisting of Staphylococcal nuclease proteins; Bacterial enterotoxins; TIMP-like proteins; Heme chaperone CcmE protein; Tail-associated lysozyme gp5, N terminal domain protein; nucleic acid-binding proteins; inorganic pyrophosphatase; Mop-like proteins; CheW like proteins; tRNA_anti (OB-fold nucleic acid binding domain); Telo_bind (telomere-binding protein alpha subunit, central domain); SSB (single-stranded binding protein family OB-fold domain); DUF338 OB-fold domain; DNA_ligase_aden_(NAD-dependent DNA ligase OB-fold domain); Stap-Strp-toxin (Staphylococcal/Streptococcal toxin, OB-fold domain); EIF-5a (Eucaryotic initiation factor 5A hypusine, DNA-binding OB-fold domain); GP5_OB(GP5 N-terminal OB-fold domain); CSD; DNA_ligase_OB; DUF388, EFP; eIF-1a; mRNA_cap_C; OB_RNB; Phage_DNA_bind; Rep-A_N; Rho_RNA_bind; Ribosomal_L2; Ribosomal_S12; Ribosomal_S17; RNA_pol_Rpb8;

RuvA_N; S1; TOBE; TOBE_2; and tRNA_bind. In another embodiment, the invention is a modified OB-fold domain wherein the naturally occurring OB-fold domain is from a thermophilic organism. In yet another embodiment, the invention is a modified OB-fold domain wherein the thermophilic organism is *Pyrobaculum aerophilum*. In another embodiment, the invention is a modified OB-fold domain wherein the modified amino acid residue is in a β -strand of the binding face.

The binding partner of a modified OB-fold domain may be selected from the group consisting of nucleic acids, oligosaccharides, proteins, hormones, and small organic molecules.

In another aspect, the invention is a method of obtaining a modified OB-fold domain comprising a) obtaining nucleic acid encoding a naturally occurring OB-fold domain, or encoding a portion thereof comprising a strand of the binding face and/or a strand of the loop, and b) altering the nucleic acid such that it encodes at least one modified amino acid residue on a β -strand of the binding face and/or at least one modified amino acid residue on a strand of a loop as compared to the naturally occurring OB-fold domain, wherein a modified OB-fold domain is obtained and wherein the modified OB-fold domain has altered binding as compared to the naturally occurring OB-fold domain. In another embodiment, where a binding partner of a naturally-occurring OB-fold domain is known, the modified binding comprises at least about a 25%, about a 50%, or about a 75% reduction in the dissociation constant of the modified OB-fold domain with its naturally occurring binding partner, as compared to the corresponding naturally occurring OB-fold domain. In another embodiment, the modified binding comprises a decrease in the dissociation constant by a factor of at least about 2, about 3, about 4, about 5, about 6, about 8, about 10, about 15, about 20, about 25, about 50, about 100, about 200, about 500, about 1000, about 5000, about 10,000, about 50,000, or about 100,000 of the modified OB-fold domain with its naturally occurring binding partner, as compared to the corresponding naturally occurring OB-fold domain. In one embodiment, the method further comprises altering nucleic acid encoding the modified OB-fold domain, and/or altering nucleic acid encoding at least one amino acid of a protein that comprises the modified OB-fold domain.

In another aspect, the invention provides for a method of producing a library of modified OB-fold domain proteins for display comprising a) obtaining nucleic acid encoding an OB-fold domain, or a portion thereof, and b) subjecting the nucleic acid to random alterations, thereby producing a collection of altered nucleic acid encoding modified OB-fold domains having at least one randomized amino acid residue. In one embodiment, the invention provides for a method of producing a library of modified OB-fold domain proteins for display wherein the nucleic acid encodes at least one amino acid residue of a strand of the OB-fold domain binding face and/or a strand of an OB-fold domain loop. In another embodiment, the method further comprises placing the library of altered nucleic acid encoding modified OB fold domains into a population of host cells or viral particles capable of displaying said modified OB-fold domains on their surface.

In another aspect, the invention provides for an isolated nucleic acid encoding the modified OB-fold domain obtainable from a naturally occurring OB-fold domain, wherein said modified OB-fold domain comprises a) at least one modified amino acid residue in a β -strand of the OB-fold domain binding face as compared to the naturally occurring OB-fold domain, or b) at least one modified amino acid residue in a β -strand of the OB-fold domain binding face and at least one modified amino acid residue in a strand of the OB-fold domain loop region, or c) at least one modified amino acid residue in a strand of the OB-fold domain loop region, and wherein said modified OB-fold domain has altered binding characteristics as compared to the naturally occurring OB-fold domain. In another embodiment, where a binding partner of a naturally-occurring OB-fold domain is known, the altered binding characteristics comprise at least about a 25%, about a 50%, or about a 75% reduction in the dissociation constant of the modified OB-fold domain with its naturally occurring binding partner, as compared to the corresponding naturally occurring OB-fold domain. In another embodiment, the altered binding characteristics comprise a decrease in the dissociation constant by a factor of at least about 2, about 3, about 4, about 5, about 6, about 8, about 10, about 15, about 20, about 25, about 50, about 100, about 200, about 500, about 1000, about 5000, about 10,000, about 50,000, or about 100,000 of the modified OB-fold domain with its naturally occurring binding partner, as compared to the corresponding naturally occurring OB-fold domain.

In another aspect, the invention provides for a host cell or viral particle comprising nucleic acid encoding the nucleic acid of the modified OB-fold domain described above. In yet another aspect, the invention provides for a composition comprising nucleic acid encoding the nucleic acid of the modified OB-fold domain described above.

5 In another aspect, the invention provides for a method of screening a library of modified OB-fold domains for binding with a binding partner, comprising a) obtaining a population of host cells or viral particles displaying a library of modified OB-fold domains on their surface; b) contacting the population of host cells or viral particles with the binding partner under conditions suitable for binding of the binding partner to the modified OB-fold domain; and c)
10 determining binding of the binding partner to the modified OB-fold domain. In one embodiment, the host cells or viral particles are phage that display the modified OB-fold domains on their surface.

In another aspect, the invention provides for a phage library of modified OB-fold domains, wherein the modified OB-fold domains are obtainable from *Pyrobaculum aerophilum*.

15 In another aspect, the invention provides for a modified OB-fold domain displayed on the surface of a cell or viral particle. In one embodiment, the cell or viral particle is a phage, bacteria or yeast.

In another aspect, the invention provides for a modified OB-fold domain attached to a solid support. In one embodiment, the support is selected from the group consisting of beads,
20 glass, slides, chips, and gelatin.

In another aspect, the invention provides modified OB-fold domain proteins having the sequences listed in Appendix II and of the designation U1, U2, U3, U4, U5, U6, U7, U8, U9, S68, S81, pMB16, pMB17, pMB12, pMB18, pMB15, D05, D07, D09, D04, L14, L8, L4, L16, L34, L42, L6, L5, or L44. In another aspect, the invention provides proteins having about 90%,
25 about 95%, about 98%, or about 99% sequence homology to the sequences listed in Appendix II and of the designation U1, U2, U3, U4, U5, U6, U7, U8, U9, S68, S81, pMB16, pMB17, pMB12, pMB18, pMB15, D05, D07, D09, D04, L14, L8, L4, L16, L34, L42, L6, L5, or L44. In

another aspect, the invention provides proteins having about 90%, about 95%, about 98%, or about 99% sequence identity to the sequences listed in Appendix II and of the designation U1, U2, U3, U4, U5, U6, U7, U8, U9, S68, S81, pMB16, pMB17, pMB12, pMB18, pMB15, D05, D07, D09, D04, L14, L8, L4, L16, L34, L42, L6, L5, or L44. In all of the above aspects, the protein can be isolated, purified, or isolated and purified.

In another aspect the invention provides a nucleic acid encoding the protein specified by the sequences listed in Appendix II and of the designation U1, U2, U3, U4, U5, U6, U7, U8, U9, S68, S81, pMB16, pMB17, pMB12, pMB18, pMB15, D05, D07, D09, D04, L14, L8, L4, L16, L34, L42, L6, L5, or L44. In another aspect the invention provides a nucleic acid encoding a protein having about 90%, about 95%, about 98%, or about 99% sequence homology to the sequences listed in Appendix II and of the designation U1, U2, U3, U4, U5, U6, U7, U8, U9, S68, S81, pMB16, pMB17, pMB12, pMB18, pMB15, D05, D07, D09, D04, L14, L8, L4, L16, L34, L42, L6, L5, or L44. In another aspect the invention provides a nucleic acid encoding a protein having about 90%, about 95%, about 98%, or about 99% sequence identity to the sequences listed in Appendix II and of the designation U1, U2, U3, U4, U5, U6, U7, U8, U9, S68, S81, pMB16, pMB17, pMB12, pMB18, pMB15, D05, D07, D09, D04, L14, L8, L4, L16, L34, L42, L6, L5, or L44. In all of the above aspects, the nucleic acid can be isolated, purified, or isolated and purified.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A-1C show an OB-fold domain from the Streptococcal superantigen SMEZ-2 (25). Fig. 1A illustrates the concave binding face. Fig. 1B is the schematic structure with beta sheets and loops labelled along with the N- and C-termini. β 2, β 4 and β 5 are interrupted β -strands and have bulges or loops between their components. Fig. 1C is the corresponding topology diagram for this protein (24). Residues are shown as circles and hydrogen bonds are shown as dotted lines. Loops are labelled and the shear number, S , is indicated.

FIGS. 2A-2B provide an overview of oligonucleotides used for library construction of aspRS-OB. Fig. 2A shows the secondary structure elements for aspRS-OB as indicated in boxes above the oligonucleotides. Arrows and numbers below indicate primers used. Crosses indicate the randomized codons. Fragments 1-4 are assembled in the second PCR step. In this figure the assembly of the 13mRL library is shown (also see Table 4). Fig. 2B shows the overview of oligonucleotides used for library construction of IF5A-OB. The assembly of the different libraries is performed in three independent ways for 11m, 9m, 2RL and 2RL+2 libraries. Symbols are as in Fig. 2A.

Fig. 3 illustrates the Initiation Factor IF-5A from *Pyrobaculum aerophilum* (1BKB, (34)). This schematic ribbon diagram of IF-5A shows the OB fold at the C-terminus and separated from the N-terminal domain by a linker. β -strands and α -helices are shown as arrows and helical ribbons, respectively. β -strands 1-3 form the proposed single stranded DNA binding face of the OB fold.

Fig. 4 illustrates the crystal structure of *E. coli* asp-tRNA synthetase (1C0A, (37)). This schematic ribbon diagram shows the structure of aspRS showing the relationship between the OB-fold and the C-terminal enzymatic domain. β -strands and α -helices are shown as arrows and helical ribbons, respectively. The binding face is indicated (36) comprising β -strands 1-3 and the loop 4/5 between β -strands 4 and 5.

Figs. 5A-5C show the sequence alignment of aspRS OB fold domains from different species. Fig. 5A shows the secondary structure of the OB fold (indicated below the sequence) and β -strands are labeled. Residues with arrows are conserved residues on the binding face and have been randomized in some libraries. Note that the human and yeast sequences have long N-termini and do not start at residue 1 in each case. Numbers at right indicate amino acid positions in each protein. Fig. 5B shows the sequence alignment of IF-5A OB fold domains from different species. Fig. 5C shows the sequence alignment of aspRS-OB from *P. aerophilum* (P.a.), *Pyrococcus kodakaraensis* (P. kodak.) and *Escherichia Coli* (E. coli). Sequence identities are indicated by asterisks. The secondary structure of the OB-fold is indicated below the sequence: l=loop between strands 4 and 5, loop 4/5.

Fig. 6 is a schematic drawing of pRPSP2 used for phage display of aspRS-OB and derivatives. Shown are phage shock promotor (psp), pelB leader sequence, cloning site which contains the *NcoI* / *NotI* restriction sites, c-myc tag used for Western analysis and the gIII gene encoding the pIII protein. Phage displayed fusion proteins consist of the gene product of inserted gene into cloning site, the c-myc tag and pIII protein. pRPSP2 also contains a beta-lactamase gene for selection on ampicillin (not shown in Fig. 6).

Fig. 7 is a Western analysis of phage displayed aspRS-OB. Left lane (no insert) represents pIII only as empty vector pRPSP2 was used to prepare TDPs; centre lane shows aspRS-OB fused to pIII displayed on VCSM13; right lane aspRS-OB on gIII deletion phage Vd3. 10^{11} TDPs were boiled in presence of SDS and BME and separated by 10% SDS-PAGE followed by transfer to a 0.45um nitrocellulose membrane. Detection was performed using a mouse anti-c-myc antibody and a HRP-conjugated rabbit anti-mouse antibody.

Fig. 8 shows a mock phage experiment with aspRS-OB displaying TDP and wild-type VCS-M13 phage to show functional display of wild-type OB fold from aspRS by binding to asp-tRNA. Immobilised tRNA was incubated with VCS-M13 (wild-type phage, no display) and aspRS-OB displaying TDP. The ratio of VCS-M13:TDP was >1000:1. After washing bound particles were eluted by RNA digestion by RNaseA. The recovery factor was calculated by dividing output and input for each VCS-M13 and TDP and for beads only or immobilized tRNA. See Table 6 for input and output data.

Fig. 9 is an enrichment (as $-\log(\text{output phage} / \text{input phage})$) of phage from round one to round six of selection of libraries RL (black circles, solid line) on asp-tRNA and 13mRL on either asp-tRNA (black circles, dotted line) or lysozyme (white circles, broken line)

Fig. 10 is a summary of sequence analysis of selected clones from OBRL selected on asp-tRNA. Out of 12 clones, 10 contained an R or K in the first position, 7 a G in pos. 2, 8 a C in pos. 3, and 6 an R in pos. 4. A consensus sequence was suggested to be R/K G C R.

Fig. 11 shows an analysis of binding of selected clones to asp-tRNA by monoclonal phage binding experiments. Biotinylated asp-tRNA was immobilised on streptavidin coated

magnetic beads and incubated with monoclonal phage samples. RNA-bound particles were specifically eluted by RNA digestion and counted by bacterial infection. The Y-axis shows a recovery factor which is calculated using the number of input phage, output phage from beads only and eluted phage from tRNA. Experiments were performed in duplicate, error bars represent $\pm$ standard deviations. pIII: no fusion; OB3wt = wild type aspRS-OB; D07, D09 mutants from 13mRL selected on asp-tRNA; 16, 17 were mutants pMB16 and pMB17 from aspRS-OB RL selected on asp-tRNA; L6 and L33 were mutants from 13mRL selected on lysozyme.

Fig. 12 is a summary of sequences from aspRS-OB libraries before and after selection. A. Before selection, U1-U6 derived from 13mRL library, U8, U9 from RL library. B. Soluble unselected mutants from 13mRL. C. Mutants from RL selected on asp-tRNA. D. Mutants from 13mRL selected on asp-tRNA. E. Mutants 13mRL selected on lysozyme. The asp-OB wild type sequence is given at the top with corresponding residue number and localisation.

Fig. 13 shows a micropanning prescreen for binders to lysozyme. A 96-well plate was coated with lysozyme (black bars) or BSA (white bars) and incubated with monoclonal phage samples from clones picked after 6 rounds of selection. Bound phage were eluted and counted by bacterial infection. Numbers on Y-axis indicate the number recovered phage, on x-axis the clone numbers are shown, pIII indicates no fusion (empty vector) and OBwt the wild-type aspRS-OB displayed.

Fig. 14 shows analysis of binding of selected clones to lysozyme by ELISA. BSA (white), RNaseA (hatched) and hen egg white lysozyme (black) were immobilised and incubated with monoclonal phage samples. Bound particles were detected with a mouse anti-M13 primary antibody and an HRP-conjugated anti-mouse secondary antibody. Experiments were performed in duplicate, error bars represent $\pm$ standard deviations. pIII: no fusion displayed, OBwt, wild-type aspRS-OB fold.

Figs. 15A-15B show pull down assay with purified aspRS-OB mutants selected on lysozyme. Fig.15A: Mutants were immobilised as GST-fusions on glutathione beads and incubated with lysozyme. After washing, beads were analysed on SDS-PAGE. Lane 1:

13mRL81 (unselected mutant, negative control), 2: L5, 3: L16, 4: L4 (L18), 5: L8 (L21), 6: beads only (double negative control). Fig. 15B: L6 (soluble fraction in lane 1) was immobilised and incubated with lysozyme in same way as above. Beads were loaded and analysed on gel after washing with TBS (lane 2), TBS-T (lane 3), TBS-T 500mM NaCl (lane 4).

5 Fig. 16 shows a binding curve using surface plasmon resonance to determine the K_d for binding between a selected OB-fold domain L6 and Lysozyme. The calculated K_d from this experiment was 3.6×10^{-5} M.

Fig. 17 shows the structure of the OBody-Lysozyme complex. The OBody is depicted as a cartoon (at left) showing secondary structure elements. Lysozyme is depicted as a cartoon (at
10 right). Arg39 (from the OBody) is shown as sticks and points towards the active site of lysozyme. This residue forms hydrogen bonds with the active site acidic residues of lysozyme – Glu35 and Asp52 (see figure 20)

Fig. 18 shows examples of hydrogen bonding interactions at the protein-protein interface for the OBody-lysozyme complex. Residues are shown as sticks and are labelled (D36 and Y37
15 are from the Obody; W63, D101 and N103 are from lysozyme). Hydrogen bonds are depicted as dotted lines. Note that the H-bond from D36 to W63 is between the backbone carbonyl of D36 and the side-chain NH group of W63.

Fig. 19 shows the potential for OBody L8 to be a Lysozyme inhibitor. E35 and D52 are the active site catalytic residues for lysozyme and H60 is from the natural inhibitor of lysozyme.
20 His60 makes hydrogen bond to lysozyme Glu35, thus inhibiting the enzyme. R39 from the OBody hydrogen bonds to both E35 and D52 in a similar manner. The backbone of the OBody and the natural inhibitor of lysozyme are depicted as C-alpha traces. The C-alpha trace for lysozyme is omitted for clarity.

BRIEF DESCRIPTION OF SEQUENCE LISTING

Sequence ID No.	Sequence Name
1.	U1
2.	U2
3.	U3
4.	U4
5.	U5
6.	U6
7.	U7
8.	U8
9.	U9
10.	S68
11.	S81
12.	pMB16
13.	pMB17
14.	pMB12
15.	pMB18
16.	pMB15
17.	D05
18.	D07
19.	D09
20.	D04
21.	L14
22.	L8
23.	L4
24.	L16
25.	L34

26.	L42
27.	L6
28.	L5
29.	L44
30.	Oligo 005
31.	Oligo 006
32.	Oligo 011
33.	Oligo 012
34.	Oligo 050
35.	Oligo 054
36.	Oligo 055
37.	Oligo 056
38.	Oligo 057
39.	Oligo 058
40.	Oligo 059
41.	Oligo 060
42.	Oligo 061
43.	Oligo 062
44.	Oligo 068
45.	Oligo 028
46.	Oligo 029
47.	Oligo 032
48.	Oligo 033
49.	Oligo 034
50.	Oligo 035
51.	Oligo 074
52.	Oligo 076
53.	Oligo 078
54.	Oligo 089

55.	Oligo 051
56.	Oligo 052
57.	Oligo 053
58.	Oligo 018
59.	Oligo 019
60.	Oligo 030
61.	Oligo 031
62.	Oligo 073
63.	Oligo 075

DETAILED DESCRIPTION OF THE INVENTION

The inventors discovered that “OB-fold domain(s)” or “OB-fold(s)” or “OB-fold protein domain(s)”, which were originally named for their observed oligosaccharide-oligonucleotide binding properties, can be used as molecular recognition domains or scaffolds for producing modified OB-fold domains, and for creating libraries of modified OB fold domains which can be screened for desired biological activities, such as for example, binding to desired targets, and altered enzymatic properties. While the OB-fold domain was originally named for its oligosaccharide-oligonucleotide binding properties, it has since been observed at protein-protein interfaces as well (Theobald at al., *Annu. Rev. Biophys. Biomol. Struct.*, Vol. 32:115-33(2003)). Accordingly, the present invention relates, in part, to the use of OB-fold domains, or portions thereof, in methods of producing modified OB-fold domains having desired properties; methods of producing libraries of modified OB-fold domains; the libraries of modified OB-fold domains produced by such methods; methods for screening such libraries of modified OB-fold domains for desired biological activities; and the modified OB-fold domains identified from such libraries. For example, such libraries of modified OB-fold domains can be screened for modified OB fold domains, or portions thereof, having increased or decreased binding interactions with a particular target(s) of interest, such as for example, a nucleotide, protein, or carbohydrate; or increased or decreased enzymatic activity.

In illustrative examples disclosed herein, the inventors have demonstrated production of a phage display library of modified OB-fold domains based on the tRNA anticodon binding domain of Aspartate tRNA Synthetase (AspRS) from *Pyrobaculum aerophilum*; stability of the AspRS modified OB-fold domains produced; and proper folding of AspRS modified OB-fold domains produced. In illustrative examples disclosed herein, the inventors have demonstrated the functional display of AspRS modified OB-fold domains on the surface of phage, thus allowing for screening of the library for modified OB-fold domains having desired properties. As demonstrated herein, the inventors were able to produce, screen for and select a modified AspRS OB fold domain that was converted from a nucleic acid binding domain, in its naturally occurring state, into a lysozyme protein binding molecule by using the compositions and methods disclosed herein. In other illustrative embodiments disclosed herein, the initiation factor IF-5A from *Pyrobaculum aerophilum* which contains an OB-fold domain was used to produce libraries of modified OB-fold domains.

The discovery that OB-fold domains of proteins can be used as a platform for producing modified OB-fold domains or libraries of modified OB-fold domains and screening for molecular recognition events has applications in diagnostic and therapeutic methods and, as described herein, has advantages over approaches known in the art using antibodies or other protein scaffolds. As will be understood by one of skill in the art, the methods disclosed herein for preparation of a library of modified OB-fold domains of AspRS or IF5A from *Pyrobaculum aerophilum* can be applied to other OB-fold domains described herein and known in the art. As will be understood by the skilled artisan, additional display and screening methods known in the art can be used to identify modified OB-fold domains having desired properties. It is also contemplated that the modified OB-fold domains could be attached to fixed and/or solid surfaces and used to screen for binding interactions. For example, OB-fold proteins can be covalently coupled to a fixed surface, or could be bound to a surface using an affinity tag (e.g., a 6xHis tag). Methods of covalently coupling proteins to a surface are known by those of skill in the art, and affinity tags that can be used to affix proteins to a surface are known by those of skill in the art. Further, OB-fold proteins can be coupled to a solid surface, including but not limited to, beads, glass, slides, chips and gelatin. Thus, a series of OB-fold proteins can be used to make an array

on a solid surface using techniques known to those of skill in the art. For example, U.S. Patent Application Publication No. 2004/0009530 discloses methods to prepare arrays.

General Techniques

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are within the skill of the art. Such techniques are explained fully in the literature, such as, *Molecular Cloning: A Laboratory Manual*, second edition (Sambrook et al., 1989); *Oligonucleotide Synthesis* (M.J. Gait, ed., 1984); *Animal Cell Culture* (R.I. Freshney, ed., 1987); *Handbook of Experimental Immunology* (D.M. Weir & C.C. Blackwell, eds.); *Gene Transfer Vectors for Mammalian Cells* (J.M. Miller & M.P. Calos, eds., 1987); *Current Protocols in Molecular Biology* (F.M. Ausubel et al., eds., 1987); *PCR: The Polymerase Chain Reaction*, (Mullis et al., eds., 1994); *Current Protocols in Immunology* (J.E. Coligan et al., eds., 1991); *The Immunoassay Handbook* (David Wild, ed., Stockton Press NY, 1994); and *Methods of Immunological Analysis* (R. Masseyeff, W.H. Albert, and N.A. Staines, eds., Weinheim: VCH Verlags gesellschaft mbH, 1993); and Gennaro, et al. 2000, *Remington: the Science and Practice of Pharmacy*, 20th Ed. Lipincott Williams and Wilkins: Baltimore, MD.

Definitions

As used herein, the term “comprising” and its cognates are used in their inclusive sense; that is, equivalent to the term “including” and its corresponding cognates.

As used herein, the singular form “a”, “an”, and “the” includes plural references unless indicated otherwise.

Various proteins characterized as containing OB-fold domains are known in the art and described herein. As described herein in more detail, “OB-fold domain” encompasses family members that share the structural feature of a conserved fold and binding face. OB-fold domain members may also share sequence relatedness. It is contemplated that any OB-fold domain, or portion thereof, can be used to produce a modified OB-fold domain. As used herein, a “naturally

occurring" OB-fold domain refers to an OB-fold domain that has not been genetically engineered to contain nucleic acid or amino acid modifications. As used herein, a "modified OB-fold domain" comprises at least one modified amino acid residue as compared to a naturally occurring OB-fold domain. A modification includes a deletion, substitution, or addition of one or more residues or a combination thereof, as long as the modified OB-fold domain retains the fold-related binding face such that it is available for interaction with a binding partner. It is not required that a "modified OB-fold domain" retain the exact structural features of a naturally occurring OB-fold domain. Modified OB-fold domains may comprise modifications in any amino acid residue including modifications in an amino acid residue of the binding face (the binding face includes the β -sheet and adjacent loops), a loop strand, a core region (a region in the hydrophobic interior of the protein that is not exposed to aqueous solvent), and may further comprise amino acid modifications in any portion of the protein comprising the OB-fold domain, as long as the modified OB-fold domain retains the fold-related binding face such that it is available for interaction with a binding partner. In some examples, a modified OB-fold domain is characterized by an ability to bind a binding partner that the naturally occurring OB-fold domain does not. In other examples, a modified OB-fold domain has modified binding with its naturally occurring binding partner. In some examples, an OB-fold domain is isolated, that is, removed from at least a portion of the naturally occurring protein within which it is contained. In other examples, a modified OB-fold domain is associated with a non-naturally occurring protein. In other examples, a modified OB-fold domain is associated with a naturally or non-naturally occurring protein, to which the naturally-occurring OB-fold domain does not bind or to which the naturally-occurring OB-fold domain binds only non-specifically. In other examples, a modified OB-fold domain can be produced where the naturally-occurring OB-fold domain does not have a known binding partner. It will be appreciated that the binding partner, if any, to a naturally occurring OB-fold domain may not be known a priori when screening a library of modified OB-fold domains for binding to a particular binding partner.

Modified OB-fold domains can be prepared which bind to the natural substrate of a naturally occurring OB-fold domain with altered binding characteristics. Such altered binding characteristics can be demonstrated under the same conditions as the naturally occurring OB-fold

domain. Alternatively, the altered binding characteristic may be one or more of (but not limited to) thermostable binding (e.g., the modified OB-fold domain demonstrates stronger binding to the natural substrate at elevated temperatures than the naturally occurring OB-fold domain), thermolabile binding (e.g., the modified OB-fold domain demonstrates weaker binding to the natural substrate at elevated temperatures than the naturally occurring OB-fold domain), modified binding under different conditions of pH (e.g., the modified OB-fold domain demonstrates stronger binding to the natural substrate at high pH than the naturally occurring OB-fold domain, or demonstrates weaker binding to the natural substrate at high pH than the naturally occurring OB-fold domain, or demonstrates stronger binding to the natural substrate at low pH than the naturally occurring OB-fold domain, or demonstrates weaker binding to the natural substrate at low pH than the naturally occurring OB-fold domain), or modified binding under different conditions of ionic strength (e.g., the modified OB-fold domain demonstrates stronger binding to the natural substrate at high ionic strength than the naturally occurring OB-fold domain, or demonstrates weaker binding to the natural substrate at high ionic strength than the naturally occurring OB-fold domain, or demonstrates stronger binding to the natural substrate at low ionic strength than the naturally occurring OB-fold domain, or demonstrates weaker binding to the natural substrate at low ionic strength than the naturally occurring OB-fold domain). The modified binding or altered binding characteristic can comprise about at least a 25%, about a 50%, or about a 75% reduction in the dissociation constant of the modified OB-fold domain with its naturally occurring binding partner, as compared to the corresponding naturally occurring OB-fold domain (that is, the modified OB-fold domain may bind at least about 1.33, 2, or 3 times more strongly than the naturally occurring OB-fold domain). In one embodiment, the modified binding comprises a decrease in the dissociation constant by a factor of at least about 2, about 3, about 4, about 5, about 6, about 8, about 10, about 15, about 20, about 25, about 50, about 100, about 200, about 500, about 1000, about 5000, about 10,000, about 50,000, or about 100,000 of the modified OB-fold domain with its naturally occurring binding partner, as compared to the corresponding naturally occurring OB-fold domain (that is, the modified OB-fold domain may bind at least about 2, about 3, about 4, about 5, about 6, about 8, about 10, about 15, about 20, about 25, about 50, about 100, about 200, about 500, about 1000,

about 5000, about 10,000, about 50,000, or about 100,000 times more strongly than the naturally occurring OB-fold domain).

A “library” of modified OB-fold domains refers to a collection of OB-fold domains that includes a high ratio of modified OB-fold domains as compared to naturally occurring OB-fold domains. That is, a library of modified OB-fold domains does not imply that the collection contains only modified OB-fold domains. A library of modified OB-fold domains may contain some percentage of unmodified or naturally occurring OB-fold domains. The library may contain OB-fold domains having one or more or multiple amino acid residues randomized. For example, a library of modified OB-fold domains may contain OB-fold domains that contain random modifications in one amino acid residue (which modification may be a single type of modification, such as a single amino acid substitution, or multiple different modifications, such as for example a substitution of a single amino acid with two or more random amino acids) or two or more amino acid residues, which can be in one or more structural regions, such as for example, in the binding face, and/or loop region, and/or core region. A modified OB-fold domain may have additional modifications or the protein comprising the modified OB-fold domain may have modifications in amino acid residues, as long the fold-related binding face is available for interaction with binding partners. A “library” of modified OB-fold domains does not imply any particular size limitation to the number of members of the collection. A library may contain as few as about 10 variants, and may range to greater than 10^{20} variants. In some embodiments the library will have up to about 10^8 variants, and in some embodiments the library will have up to about 10^{12} variants. A “library” of modified OB-fold domains refers to the collection of modified OB-fold domains that are encoded via nucleic acid alterations, that is, at the stage of gene assembly prior to introduction into an expression system as well as the collection that is introduced into an expression system, expressed and/or displayed.

The terms “polynucleotide” and “nucleic acid”, used interchangeably herein, refer to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. These terms include a single-, double- or triple-stranded DNA, genomic DNA, cDNA, RNA, DNA-RNA hybrid, or a polymer comprising purine and pyrimidine bases, or other natural, chemically, biochemically modified, non-natural or derivatized nucleotide bases. The backbone

of the polynucleotide can comprise sugars and phosphate groups (as may typically be found in RNA or DNA), or modified or substituted sugar or phosphate groups. Alternatively, the backbone of the polynucleotide can comprise a polymer of synthetic subunits such as phosphoramidates and thus can be a oligodeoxynucleoside phosphoramidate (P-NH₂) or a mixed phosphoramidate- phosphodiester oligomer. Peyrottes et al. (1996) *Nucleic Acids Res.* 24: 1841-8; Chaturvedi et al. (1996) *Nucleic Acids Res.* 24: 2318-23; Schultz et al. (1996) *Nucleic Acids Res.* 24: 2966-73. A phosphorothioate linkage can be used in place of a phosphodiester linkage. Braun et al. (1988) *J. Immunol.* 141: 2084-9; Latimer et al. (1995) *Molec. Immunol.* 32: 1057-1064. In addition, a double-stranded polynucleotide can be obtained from the single stranded polynucleotide product of chemical synthesis either by synthesizing the complementary strand and annealing the strands under appropriate conditions, or by synthesizing the complementary strand de novo using a DNA polymerase with an appropriate primer. Reference to a polynucleotide sequence (such as referring to a SEQ ID NO) also includes the complement sequence.

The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, mRNA, tRNA, rRNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, uracyl, other sugars and linking groups such as fluororibose and thioate, and nucleotide branches. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. Other types of modifications included in this definition are caps, substitution of one or more of the naturally occurring nucleotides with an analog, and introduction of means for attaching the polynucleotide to proteins, metal ions, labeling components, other polynucleotides, or a solid support. Preferably, the polynucleotide is DNA. As used herein, "DNA" includes not only bases A, T, C, and G, but also includes any of their analogs or modified forms of these bases, such as methylated nucleotides, internucleotide modifications such as uncharged linkages and thioates, use of sugar analogs, and modified and/or alternative backbone structures, such as polyamides.

“Under transcriptional control” is a term well understood in the art and indicates that transcription of a polynucleotide sequence, usually a DNA sequence, depends on its being operably (operatively) linked to an element which contributes to the initiation of, or promotes, transcription. “Operably linked” refers to a juxtaposition wherein the elements are in an arrangement allowing them to function.

A “host cell” includes an individual cell or cell culture which can be or has been a recipient of nucleic acid encoding an OB-fold domain, and in some examples, a modified OB-fold domain. Host cells include progeny of a single host cell, and the progeny may not necessarily be completely identical (in morphology or in total DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation and/or change. A host cell includes cells transfected or infected *in vivo* or *in vitro* with nucleic acid encoding an OB-fold domain. In some examples, the host cell is capable of expressing and displaying the OB-fold domain on its surface, such as for example, phage display. “Expression” includes transcription and/or translation.

A nucleic acid that “encodes” an OB-fold domain, or portion thereof, is one that can be transcribed and/or translated to produce the OB-fold domain or a portion thereof. The anti-sense strand of such a nucleic acid is also said to encode the OB-fold domain.

I. OB-fold protein domains

At the most general level, the OB-fold domain is a five-stranded mixed β barrel. See for example, Arcus, 2002, Curr. Opin. Struct. Biol. Vol 12:794-801. The OB-fold domain is found in all three kingdoms and, as discussed in more detail herein, is represented in both sequence and structural databases. Generally speaking, OB-fold domains have a conservation of fold and functional binding face. Different OB-fold domains use their fold-related binding face to variously bind oligosaccharides, oligonucleotides, proteins, metal ions, and catalytic substrates.

OB-fold domains have a number of features which make them well suited as scaffolds for randomisation of amino acid positions and selection of modified OB-fold domains with desired properties. OB-fold domains are generally small, stable proteins which are easily produced and randomised. Theobald et al., 2003, supra, disclose that OB-fold domains range between 70 and 150 amino acids in length. Additionally, the face of the OB-fold domain protein, already demonstrated through evolution to be versatile, is available for randomization. The OB-fold domain is ubiquitous in all three kingdoms and thus, it is possible to choose an OB-fold domain to suit particular applications. For example, OB-fold domains from thermostable microorganisms are described herein for production of libraries of modified OB-fold domains. Ob-fold domains can be selected for therapeutic application; for example, an enzymatic OB-fold domain can be selected to produce proteins with new enzymatic activities. These features provide an advantage over more traditional antibody and protein scaffolds.

The general structure of OB-fold protein domains is a 5-stranded mixed β -barrel that presents a concave β -sheet as an external binding face flanked by two variable loop regions. In the majority of cases the barrel has a Greek-key topology and one end of the barrel is capped by an α -helix (23). β -barrels are uniquely described by their number of strands n , and the shear number, S (26,27). The shear number describes the degree to which the strands are tilted away from the axis of the barrel. Figs. 1A-1C show a β -barrel with $S=10$. This is the number of residues which are formally part of the β -sheet (thus excluding β -bulges) and are counted along the strand in going from A to A*. There are two possibilities ($S=8$ or $S=10$) for the OB-fold and both of these are observed. As examples, the OB-fold domain of the aspartyl tRNA synthetase (aspRS), which binds tRNA, has $S=10$ whereas the cold-shock OB-fold domain DNA binding domains has $S=8$. The OB-fold domain binding face has at its center β strands 2 and 3, and is bounded at the bottom left by loop 1, at the top by loop 4 and at the top right by loop 2 (see Figs. 1A-1C). In different OB-fold domain structures, loops 2 and 4 show wide variation in both length and sequence. See Arcus, 2002, Curr. Opin. Struct. Biol. Vol 12: 794-801. Modified OB-fold domains can vary in length. For example, loop 2 often varies between 2 to 4 amino acids and loop 4 often varies between 3 to 10 amino acids, and in some cases loop 4 accommodates an insertion of much greater length, up to about 30 amino acids.

A survey of 20 sequenced genomes places the OB-fold domain at 28th in a list of the most prevalent biological architectures (27). The OB-fold domain has been found in a variety of proteins including humans, yeast and bacteria. For example, in bacterial superantigens (Sags), an OB-fold domain mediates protein-protein interactions in the bacterial attack on the human immune system (21 and 22). In these proteins it binds a broad range of ligands, including proteins, oligonucleotides and oligosaccharides (23). Examples of the diversity of OB-fold domain proteins include single stranded DNA binding in the oncogene BRCA2 (Yang H. et al., 2002 Science, Vol . 297, 1837-1848), telomere end binding on chromosomes for the yeast protein Cdc13 (Lei M. et al, 2003 Nature, Vol. 426, 198-203), and cell-surface oligosaccharide binding in pathogenic bacteria (Stein P.E. et al, 1994, Structure, Vol. 2, 45-47). As determined by the Structural Classification of Proteins database (SCOP), the standard in classifying protein structures into related “families” and “superfamilies”, OB-fold protein domains are found in nine related superfamilies. Those OB-fold domains which belong to the same “family” have an evolutionary relationship at the sequence, structural and functional levels and appear to be descended from a common ancestor. The OB-fold domain “families” which belong to the same “superfamily” are evolutionarily related based on similar structural and functional features in the absence of definitive sequence similarities. The SCOP database is comprised of proteins of known structure (i.e. their structures have been experimentally determined using either X-ray crystallography or high resolution NMR). Additional OB-fold domains can be determined by the skilled artisan based on structural relatedness, that is, the presence of the fold-related binding face, or structural relatedness and sequence relatedness to known OB-fold domains described herein and known in the art. There are sequence similarities within superfamilies and families and these can be used to identify additional proteins whose structures have not been previously determined under the OB-fold umbrella. See, for example, the publicly available Pfam database (at <sanger.ac.uk/Software/Pfam>). An additional publicly available database is Superfamily (at <supfam.mrcmb.cam.ac.uk/SUPERFAMILY>) which uses hidden Markov models derived from SCOP to classify protein sequences into superfamilies. For example, the “nucleic acid-binding proteins” comprise a superfamily in SCOP database. There are currently 11 families and 66 individual protein structures in this superfamily in SCOP. From these 11 families and 66 structures, the Superfamily database has derived rules to classify 21,158 protein sequences as

OB-fold proteins belonging to the “nucleic acid-binding protein” superfamily. Similarly, the CheW-like superfamily has just a single family and two protein structures in SCOP whereas this has been expanded to include 898 proteins in the Superfamily database.

i. Classification of OB-fold domains at SCOP

For the class of OB-fold domains characterized by SCOP as all beta, with barrel, closed or partly opened where $n=5$, and $S=10$ or $S=8$; greek-key, SCOP currently identifies the following Superfamilies (the numbers in parenthesis are the SCOP reference numbers):

1. Staphylococcal nuclease (50199)

For Staphylococcal nuclease, there is currently a single member of this family although there are many structures in the database for Staphylococcal nuclease. The OB-fold is a closed beta-barrel, $n=5$, $S=10$.

2. Bacterial enterotoxins (50203)

For bacterial enterotoxins, there are two families in this superfamily: Bacterial AB5 toxins (B subunits) and the N-terminal domain of superantigen toxins. The Bacterial AB5 toxins include the heat labile toxin from *E. coli*, the Cholera toxin and Pertussis toxin. All have a closed beta-barrel topology with $n=5$ and $S=10$ with the single exception of the Cholera toxin whose barrel is slightly opened. The N-terminal domains of the superantigen toxins and superantigen-like toxins are all proteins from *Staphylococcus aureus* and *Streptococcus pyogenes* and have typical $n=5$, $S=10$ closed-barrel topologies. There are a large number of these proteins encoded in the genomes of these organisms. The Staphylococcal proteins have recently been renamed according to: “Standard Nomenclature for the Superantigens Expressed by *Staphylococcus*.” Gerard Lina, Gregory A. Bohach, Sean P. Nair, Keiichi Hiramatsu, Evelyne Jouvin-Marche, and Roy Mariuzza, for the International Nomenclature Committee for Staphylococcal Superantigens *The Journal of Infectious Diseases* 2004; 189:2334–6.

3. TIMP-like (50242)

TIMP-like Proteins are eukaryotic proteins that currently are divided into three families all with $n=5$, $S=10$ closed-barrel topology:

a. Tissue inhibitor of metalloproteinases, TIMP (50243) (contains an irregular alpha+beta subdomain in the C-terminal extension).

b. Netrin-like domain (NTR/C345C module) (89320)

c. The laminin-binding domain of agrin (63767)

5 4. Heme chaperone CcmE (82093)

For the Heme Chaperone, CcmE, there is a single family annotated in this superfamily.

Representative structures are from *E. coli* and *S. putrefaciens*.

5. Tail-associated lysozyme gp5, N-terminal domain (69255)

10 For Tail-associated lysozyme gp5, N-terminal domain, there is a single structure which represents both the family and this superfamily. The protein is from bacteriophage T4 and the N-terminal domain is part of a much larger protein complex which forms the cell-puncturing device of the phage.

6. Nucleic acid-binding proteins (50249)

Nucleic acid binding proteins are a large superfamily that encompasses many proteins.

15 The following are the family demarcations and descriptors:

a. Anticodon-binding domain (50250)

barrel, closed; n=5, S=10

b. RecG "wedge" domain (69259)

c. DNA helicase RuvA subunit, N-terminal domain (50259)

20 *barrel, closed; n=5, S=10*

d. Single strand DNA-binding domain, SSB (50263)

barrel, closed; n=5, S=10

e. Myf domain (50277)

f. Cold shock DNA-binding domain-like (50282)

25 *barrel, closed; n=5, S=8*

g. Hypothetical protein MTH1 (MT0001), insert domain (74955)

h. DNA ligase/mRNA capping enzyme, domain 2 (50307)

i. Phage ssDNA-binding proteins (50315) (4)
barrel, open; $n^=5$, $S^*=8$; the members' structures vary greater than those from cellular organisms*

j. DNA replication initiator (cdc21/cdc54) N-terminal domain (89332)

5 k. RNA polymerase subunit RBP8 (50321)
duplication; contains tandem repeat of two incomplete OB-folds; forms a single barrel; $n=8$, $S=10$

7. Inorganic pyrophosphatase (50324)

10 For Inorganic pyrophosphatase, there is just one family in this superfamily. This family
 has a very deep lineage as there are examples from bacteria, archaea and eukaryotes.

1. Inorganic pyrophosphatase (50325)
barrel, closed; $n=5$, $S=8$

1. Inorganic pyrophosphatase (50326)
eukaryotic enzyme has additional secondary structures at both N- and C-termini

15 a. Baker's yeast (*Saccharomyces cerevisiae*) (50327)

b. Archaeon *Sulfolobus acidocaldarius* (50328)

c. *Escherichia coli* (50329)

d. *Thermus thermophilus* (50330)

8. MOP-like (50331)

20 In the MOP-like grouping, there are three families, all with similar functionality and all
 from bacteria.

a. Molybdate/tungstate binding protein MOP (50332)

b. BiMOP, duplicated molybdate-binding domain (50335)
duplication: tandem repeat of two OB-fold domains with swapped C-terminal strands

25 c. ABC-transporter additional domain (50338)
probably stems out from the biMOP domain

9. CheW-like (50341)

This is represented in a single family with two structures from *Thermotoga maritima*,
 CheW and CheA.

30 ii. Sequence databases Pfam and Superfamily

The descriptions from SCOP relate to OB-fold domains from proteins whose 3-dimensional structures have been determined either by X-ray crystallography or NMR.

Additional OB-fold protein domains identified in the database Pfam based on sequence similarity and in the database Superfamily based on sequence profiles derived from SCOP and then applied to the major sequence data are encompassed within the present invention. The present invention encompasses additional OB-fold domains known to those of skill in the art.

As described below, in Pfam there are many families which together represent OB-fold domains. The annotation is as follows:

Family name

- 10 Annotation
Pfam accession number
Total number of proteins in this family in the Pfam database

tRNA_anti

- 15 OB-fold nucleic acid binding domain
Accession number: PF01336
Number of proteins: 1351

Telo_bind

- 20 Telomere-binding protein alpha subunit, central domain
Accession number: PF02765
Number of proteins: 33

SSB

- 25 Single-strand binding protein family
Accession number: PF00436
Number of proteins: 415

DUF388

- 30 Domain unknown function (DUF388)
Accession number: PF04076
Number of proteins: 49

DNA_ligase_aden

- 35 NAD-dependent DNA ligase OB-fold domain
Accession number: PF03120
Number of proteins: 190

Stap_Strp_toxin

Staphylococcal/Streptococcal toxin, OB-fold domain

Accession number: PF01123

Number of proteins: 180

5 *eIF-5a*

Eukaryotic initiation factor 5A hypusine, DNA-binding OB fold

Accession number: PF01287

Number of proteins: 104

10 *Gp5_OB*

Gp5 N-terminal OB domain

Accession number: PF06714

Number of proteins: 6

15 All of the OB fold domains described herein, known in the art and later identified can be used as a scaffold to prepare modified OB-fold domains and to prepare libraries of modified OB fold domains that can be used for screening for altered binding characteristics and altered functional features.

iii. OB-fold binding face for randomization of amino acids

20 A modified OB-fold domain and/or a library of modified OB-fold domains can be prepared based on the structure of any OB-fold domain, including those described herein, known in the art or later identified. Libraries of modified OB-fold domains can be prepared based on methods described herein and known in the art. For example, for any given OB-fold domain, nucleic acid encoding one or more amino acid residues, such as for example, amino acid residues
25 in the strands of an external binding face and/or amino acid residue in the strands of a loop and/or amino acid residues in other portions of the protein containing the OB-fold domain, can be targeted for amino acid residue randomization (that is, random mutation of the amino acid residue(s) via nucleic acid modifications). In some examples, amino acid residues in strands of the external binding face of an OB-fold domain are targeted for amino acid residue
30 randomization. In other examples, particular structures within the OB-fold domain can be targeted for amino acid residue randomization. For example, one or multiple amino acid residues present in the strands of the binding face of an OB-fold domain can be targeted for randomization. The binding face for OB-fold domains includes the C-terminal half of beta-

strand 1, beta-strand 2, beta-strand 3, the C-terminal half of beta-strand 4 and beta-strand 5. See Figures 1A-1C for reference. In another example, the amino acid residues in the loops between the beta-strands of the core OB-fold domain may be targeted for random mutations. In another example, where there are major insertions in the loop regions flanking the OB-fold core domain (e.g. the inorganic pyrophosphatases) amino acid residues on these inserted loops may be selected for randomization. The present invention also encompasses modified OB-fold domains having portions, that is amino acid residues, of the core modified to produce changes in stability to the protein.

II. Production of modified OB-fold domains and display methods

In illustrative embodiments described herein in the examples, two thermophilic OB-fold protein domains, translation initiation factor, IF-5A (S=8), and the aspartyl tRNA synthetase, aspRS (S=10), onto which mutations were introduced, were used to make libraries of modified OB-fold domains, by randomising amino acid residues in the binding face of the OB-fold protein. Both of these proteins are from the hyperthermophilic chrenarchaeon, *Pyrobaculum aerophilum*. Libraries were generated synthetically using long oligonucleotides with specific amino acid positions in the binding face of the OB-fold domain being randomised, followed by gene assembly using PCR. Libraries were tested for the rates of overexpression of their encoded proteins and estimates were made about the fraction of soluble and heat stable proteins encoded by the library. It is demonstrated herein that the aspRS OB-fold domain (aspRS-OB) can be displayed and selected on the surface of phage. Different libraries of modified OB-fold domains, based on the aspRS scaffold as described herein in the examples, were prepared and subjected to phage display methods to demonstrate that modified OB-fold domains can be produced that are capable of binding to different substrates including tRNA, protein and cellulose ligands. In one illustrative embodiment disclosed herein, a binding interaction between a modified OB-fold domain, which in its natural state was a nucleic acid binding domain, and lysozyme is demonstrated.

As will be understood by one of skill in the art, various methods known in the art for preparing modifications of nucleic acid can be used to prepare (encode) OB-fold domains having

modification in one or more amino acid residues. Nucleic acids encoding OB-fold domains may be obtained using standard methods in the art, such as chemical synthesis, recombinant methods and/or obtained from biological sources. Nucleic acid of interest may be placed under the control of one or more elements necessary for their expression in any particular host cell. A variety of host cells are available to propagate OB-fold domains, and displays methods are known in the art and described herein that may be used in display modified OB-fold domains on their surface. Display methods include without limitation phage display, bacterial display, yeast display, ribosome display, and mRNA display.

i. Display methods

Display technologies involve the screening of large libraries of expressed proteins using an immobilised ligand to characterize or discover new interactions between individual proteins and the target ligand. The most important characteristic of display technologies is the ability to couple the proteins being screened (phenotype) with the genetic information encoding them (genotype). In all display technologies the genetic information is isolated simultaneously with the screened protein. This is generally achieved by displaying proteins or protein fragments on the surface of biological entities, e.g. phage, yeast or bacteria, and employing the replication systems of the organism to amplify the library. As an alternative to these in vivo systems, the whole process can also be carried out in vitro and such technologies called ribosome display or mRNA display. In these cases in vitro-generated transcripts are translated in cell extracts and RT-PCR is used to amplify the genetic information after the ligand-mediated isolation of mRNA-ribosome-protein complexes has taken place.

a. Phage display

The display of foreign peptides and proteins on the surface of filamentous bacteriophages is called 'phage display' and is now a commonly used technique to investigate molecular interactions. Normally the protein library to be screened is expressed as a fusion with the gene III protein product at one end of the bacteriophage particle or as a fusion with the gVIII protein on the surface of the phage particle. Infection of bacteria with such a phage library allows very efficient library amplification (Griffith et al., 1994). A typical phage display protocol involves

the production of phage particles in a bacterial host with each particle displaying the gene product of one member of the gene library as a fusion with one type of its coat proteins (gIII or gVIII proteins). A library of phage particles is taken through a selection process for binding to an immobilised target molecule ('biopanning') involving binding of the phage library to the target, washing steps to remove non-bound phage, and elution of bound particles. Usually several rounds of panning are necessary to select molecules with the desired characteristics involving reamplification of eluted phage in the bacterial host and selection on the immobilised target. In illustrative embodiments disclosed herein in the Examples, phage display methods are used to display and screen modified OB-fold domains.

b. Bacterial display and Yeast display

The Bacterial display and Yeast display technologies allow expression of recombinant proteins on the surface of yeast cells *S. cerevisiae* (Boder and Wittrup, 1997) or bacteria (*E. coli*, *Staphylococcus carnosus*) (Daugherty et al., 1998, Wernerus et al., 2003) as a fusion with the α -agglutinin yeast adhesion receptor or a bacterial outer membrane protein (OMP) respectively.

The expressed fusion proteins also contain tag sequences, allowing quantification of the library surface expression by flow cytometry. Combined with indirect fluorescent labeling of the ligand, anti-tag labeling allows cell sorting by FACS (fluorescence activated cell sorting) and the determination of the binding affinities of the interactions (Feldhaus et al., 2003, Wernerus et al., 2003). The features of yeast expression system that make it valuable beside other display techniques are a correct post-translational modification, processing and folding of mammalian proteins which can be problematic in bacterial or in vitro display systems.

c. Ribosome display and mRNA display

Ribosome display and mRNA display are technologies that enable the selection and evolution of large protein libraries in vitro. The only biological component required is a bacterial cell extract that contains the factors required for the translation of in vitro-generated transcripts encoding the protein sequences. In ribosome display, genotype and phenotype are linked together through ribosomal complexes, consisting of messenger RNA (mRNA), ribosome, and

encoded protein, that are used for selection (Hanes and Pluckthun, 1997). The mRNA display method employs puromycin to link mRNA to the translated protein and thus allows purification of an mRNA-protein conjugate containing genotype and phenotype information. After selection, the isolated mRNAs or mRNA conjugates are amplified by RT-PCR and can be transcribed and translated for another round of selection (Lipovsek and Pluckthun, 2004). References for display methods include the following list all of which are here by incorporated by reference in their entirety: Boder ET and Wittrup KD (1997) *Nat Biotechnol.* 15:553-7; Feldhaus MJ et al. (2003) *Nat Biotechnol.* 21:163-70; Griffiths, AD, et al. (1994) *EMBO Journal* 13, 3245-3260; Hanes J, Pluckthun A., et al (1997) *PNAS* May 13;94(10):4937-42; and Lipovsek D, Pluckthun A., (2004) *J. Immunological Meth.* 290 51-67; Wernerus H, et al. (2003) *Appl Environ Microbiol.* 69(9):5328-35.

Display methods are disclosed in for example: Boder ET and Wittrup KD (1997) *Nat Biotechnol.* 15:553-7; Feldhaus MJ et al. (2003) *Nat Biotechnol.* 21:163-70; Griffiths, AD, et al. (1994) *EMBO Journal* 13, 3245-3260; Hanes J, Pluckthun A., (1997), *PNAS* May 13;94(10):4937-42; Lipovsek D, et al. (2004) *J. Immunological Meth.* 290 51-67; and Wernerus H, et al. (2003) *Appl Environ Microbiol.* 69(9):5328-35.

III. Potential targets for screening modified OB-fold domains

The ligands of naturally occurring OB-fold domains are diverse. The production of libraries of modified OB-fold domains extends the diversity of possible targets for OB-fold domains. Potential targets for screening against libraries of modified OB-fold domains encompass a variety of molecules, including, for example, but not limited to, nucleic acids, proteins, peptides, polypeptides, carbohydrates, oligosaccharides, and hormones.

i. Nucleic acids

A large number of OB-fold domains are involved in binding to single stranded DNA and RNA. These include the single stranded DNA binding domains of the oncogene BRCA2, several domains from human replication protein A and the anticodon binding domain of Aspartyl- and

Lysyl-tRNA synthetases. Accordingly, single stranded DNA and tRNA can be used as ligand targets for screening libraries of modified OB-fold domains.

ii. Protein targets

A variety of proteins can be used for screening libraries of modified OB-fold domains, such as enzymes, regulatory proteins, protein and peptide hormones, transport proteins, etc. In an illustrative embodiment disclosed herein, lysozyme is used as a protein target. Other targets include, but are not limited to, ubiquitin, complement component C4, plasminogen precursor, apolipoprotein A-II, plasma protease C1 inhibitor, transthyretin and serum amyloid P-component.

iii. Oligosaccharide targets

Oligosaccharides play an integral part in the biology of all organisms. Oligosaccharide substrates such as, for example, but not limited to, laminarihexose, mannopentaose and xylopentaose can be used as targets.

iv. Hormones

Hormones such as, for example, the steroid hormones estrogen, testosterone, and cortisol; catecholamines, such as epinephrine, and other such molecules can be used to screen against libraries of OB-fold domains. Currently there is no evidence that the OB-fold domain has a steroid hormone or other cofactor as a natural ligand. In addition, it has been classically difficult to raise highly specific antibodies to steroids and a concave binding face, such as the OB-fold domain binding face may prove better at raising the specificity of binding for a particular hormone.

v. Small organic molecules

Small organic molecules (defined as organic molecules with a molecular weight equal to or less than about 1000 daltons) can also be used as targets for OB-fold domains. The small organic molecule may be a naturally occurring molecule, or a synthetic molecule not found in

nature. A naturally occurring small organic molecule may be associated with a living system (such as the steroid hormones; see above) or may occur abiotically. Small organic molecules include, but are not limited to, pollutants or other undesirable substances, such as DDT or polychlorinated biphenyls (PCB's). Small organic molecules include, but are not limited to, drugs and pharmaceuticals, such as doxorubicin and paclitaxel.

IV. Applications for OB-fold domains

As described herein, the OB-fold domain is a versatile molecular recognition platform. A variety of OB-fold domains are known in the art, disclosed herein, and have been identified in SCOP and other databases such as Pfam and Superfamily. Such OB-fold domains can be used in methods for preparing modified OB-fold domains as well as libraries of modified OB-fold domains which can be screened against targets, such as, for example, nucleic acids, proteins, hormones, carbohydrates and oligosaccharides. Such screening methods can be used to identify modified OB-fold domains with desired properties. For example, a human OB-fold domain can be used as a scaffold for the production of libraries of modified OB-fold domains for the screening against human targets that might have application in human therapeutics. In another example, a yeast OB-fold domain can be used as a scaffold for the production of libraries of modified OB-fold domains that might have application in biotechnology or fermentation applications. In yet another example, an enzymatic OB-fold domain can be used as a scaffold for the production of libraries of modified OB-fold domains with new enzymatic properties.

The potential applications for modified OB-fold domains fall into three broad categories: diagnostic reagents; therapeutic application; and tools.

Modified OB-fold domains can be used in a wide range of molecular biology tools and include, for example, use as protein purification reagents for affinity purification of proteins from either recombinant sources or natural sources such as serum. In such applications, OB-fold domains with specific binding affinity for a protein of choice will be immobilised on beads and then used to affinity purify the target protein. Other applications include the use in protein detection for Western blotting; protein detection using fluorescent-labeled OB-fold domains; and protection agents for single stranded DNA and RNA. A central advantage of OB-fold domains

over antibodies in these contexts is the tailoring of the stability of the modified OB-fold domain to match the reagent. For example, thermostable OB-fold domains, such as those obtainable from *Pyrobaculum aerophilum* may be more effective than antibodies as affinity purification reagents.

Diagnostic applications for modified OB-fold domains include, for example: protein detection in fluids such as serum, culture supernatants, and contaminated water; genotyping (many OB-fold proteins are single stranded DNA binding proteins and these could be developed to detect specific DNA or RNA motifs, for use in methods such as genotyping); and in small molecule detection agents.

Given that recombinant antibodies and their fragments currently represent a large number of all biological proteins undergoing clinical trials for diagnosis and therapy, alternatives to antibody libraries such as libraries of modified OB-fold domains have potential as therapeutic agents. Current examples of recombinant antibodies which have reached the marketplace are the oncology therapeutics Herceptin, Anti-HER2 antibody; Rutuxan (Rutuximab) Anti-CD20 antibody; and Avastin Anti-VEGF antibody. Humanized libraries of modified OB-fold domains may be prepared from which specific ones can be identified having appropriate binding characteristics that can find use in the therapeutic arena.

EXAMPLES

20 *Example 1: Materials and Methods*

Chemicals and biochemicals

Standard oligonucleotides were purchased from Invitrogen and all long randomized oligonucleotides were from MWG (Martinsried, Germany). *Pfx* and *taq* polymerase and all restriction enzymes were from Invitrogen (Carlsbad, USA). Shrimp alkaline phosphatase (SAP) and T4 ligase were from Roche (Basel, Switzerland). The phagemid vector pRPSP2 and phage VCS-M13 and VCSM-13d3 (Vd3) were from Dr. J. Rakonjac (31,32). Streptavidin coated magnetic beads and Protector[®] RNase inhibitor were from Roche, as was hen egg lysozyme.

Bovine Serum Albumine was from Sigma. Biotinylated transfer RNA was prepared using the MEGAscript *in vitro* transcription kit from Ambion (USA) and the biotin RNA labeling mix from Roche. Nitrocellulose membranes for western analysis was from Schleicher & Schuell (Dassel, Germany), and the substrate used was SuperSignal[®] from Pierce (USA).

5

Bioinformatics

Structures were viewed, analyzed or transformed into figures from PDB files (33) using Swiss-pdbViewer and Pymol (at pymol.sourceforge.net). The PDB entry 1bkb (34) was used for structural analysis of IF-5A. For aspRS the PDB files of aspRS homologues 1b8a (35), 1eov (36), 1coa (37) were used.

10

The structural model of aspRS-OB was obtained from SwissModel (38-40) by submitting the amino acid sequence of aspRS-OB from *Pyrobaculum aerophilum*. Alignments were done using ClustalW (version 1.8) online via the EBI service website (<www.ebi.ac.uk/services/>).

15

Cloning

General cloning was carried out according to Sambrook and Russell (41). The wild type genes for aspRS-OB (asp-tRNA synthetase from *Pyrobaculum aerophilum* IM2, bases 1-327, amino acids 1-109, NCBI access number NP_558783) and IF5A-OB (IF-5A from *Pyrobaculum aerophilum* IM2, NP_560668, bases 208-399, amino acids 76-139) were amplified by PCR from *P. aerophilum* IM2 genomic DNA (NC 003364, (42)) using oligonucleotides 005 and 006 for aspRS-OB and 011 and 012 for IF5A-OB. Oligonucleotide sequences are listed in Appendix I. All PCR products for overexpression were digested with *Bam*HI and *Eco*RI and ligated into pProEx-Htb. pProEx-Htb produces the protein as an N-terminal His₆-tagged fusion-protein. For cloning of the aspRS-OB gene into pJARA140, aspRS-OB was amplified by the PCR using the oligonucleotide pair 050/044 and digested using *Nco*I and *Not*I. pJARA140 was also digested with the same enzymes and dephosphorylated prior to ligation. For subcloning, selected mutant genes were amplified using vector specific primers and inserted into donor vector pDONR221 and subsequently into pDEST15, both part of the GATEWAY[®] cloning system (Invitrogen). pDEST15 allows protein expression as a fusion to glutathione-S-transferase (GST).

20

25

30

Escherichia coli

E. coli K12 strain XL1-blue (43) was used for cloning and plasmid preparations of all constructs derived from pProEx and for small scale protein synthesis, *E. coli* JM101 derivative TG1 was used for cloning of all pRPSP2 constructs and for all phage produced with VCS-M13 helper phage. *E. coli* K561 transformed with pJARA131 and pJARA112 (resulted in *E. coli* K1762, (44)) was used for preparation of VCS-M13d3 helper phage for multivalent display. *E. coli* BL21 (DE3) (Novagen) was used for large scale protein production and purification.

Gene libraries construction

Libraries were constructed by incorporation of mutagenic oligonucleotides containing the codon NNK (N=A,C,G or T, K=T or G) in selected positions. AspRS-OB gene fragments carrying incorporated mutations were generated by PCR and then assembled into full-length genes. Long oligonucleotides which introduce randomized positions are listed in Table 1. In a first PCR step, gene fragments were generated using corresponding flanking primers and incorporating the oligonucleotides randomized at selected positions (30 cycles, 94°C for 1 min, 52.5°C for 30 sec, 68°C for 1 min). In a second step, the gene fragments were assembled into a full length gene by an overlap-extension PCR (25 cycles, 94°C for 1 min, 52.5 °C for 30 sec, 68°C for 1 min). The amount of assembled product was calculated by spectrophotometry to be greater than 10^{11} molecules to ensure that a diversity of 10^8 is maintained in the following steps. Assembled products were amplified by PCR (30 cycles, 94°C for 1 min, 52.5°C for 30 sec, 68°C or 1 min) using vector specific primers 005/006 or 011/012 for aspRS-OB and IF5A-OB respectively, digested and ligated into pProEx-Htb. For phage libraries of aspRS-OB primers 050/044 were used for cloning into pRPSP2 (see below). Plasmids containing either the wild type gene or assembled libraries were transformed into *E. coli* XL1-Blue and grown overnight at 37 °C on LB-agar plates complemented with ampicillin (50 µg/ml). Diagnostic PCR was performed by picking individual colonies and growing them in 50 ul LB/Amp for several hours. 1 ul of this culture was used to do a 10 ul PCR amplification (25 cycles, 94°C for 1 min, 52.5 °C for 30 sec, 68°C for 1 min) using diagnostic primers for pProEx-Htb or pRPSP2 respectively. *Pfx* polymerase was used for all preparative PCR reactions whereas *taq* polymerase was used for

diagnostic PCR reactions only. A scheme outlining the assembly strategy for each OB-fold gene is shown in Figures 2A and 2B.

Overexpression profiles of proteins from libraries

5 For each library, transformed bacteria were plated onto agar (containing LB-amp) and single colonies were picked and grown overnight in 100 μ l LB-amp (50 μ g.ml⁻¹) at 37 °C in a 96 deep-well plate with shaking at 1200 rpm in an Eppendorf Thermomixer. The cultures were diluted by adding 900 μ l fresh LB-amp, grown for a further 60 min, and then induced using 1 mM isopropyl-D-thiogalactopyranoside (IPTG) for 4 hrs at 37°C. Bacterial cells were collected
10 by centrifugation, resuspended in 150 μ l Tris- buffered saline (TBS: 50 mM Tris-HCl, pH 7.5, 150 mM NaCl) and analyzed by SDS polyacrylamide gel electrophoresis (SDS-PAGE, 15% polyacrylamide). Table 1 is a list of long oligonucleotides used for aspRS-OB and IF5A-OB library construction. Each randomized codon is defined by NNK: N=A/T/G/C, K= T/G or MNN: M= A/C for the antisense codons. Also see Figures 3A and 3B.

Table 1

OB fold	oligo	DNA sequences 5' to 3'	location in OB	length in bp
aspRS	051	GTT GCC GGT TGG GTA NNK NNK TTG NNK GAC NNK GGG NNK NNK AAG NNK GTG NNK GTG NNK GAT AGG GAG GGG GGC GCG	beta strand 1+2	78
	052	ATC GGG GGT TTT TCC CGC MNN GAG MNN GAC MNN CAC MNN CGC GCC CCC CTC CCT ATC	beta strand 3	57
	053	ATT GTT GAG GCC AGT AAA NNK NNK NNK NNK GGT GTG GAG ATT TTC CCC	loop 4/5	48
IF-5A 9m	018	TTTATAGTCGCGCATGTCKNNTAGKNNNA ATKNNATCTCKNNAACKNNKNNTATKN NCGCCGTGAATTTCTCAAT	beta strand 1+2	75
	019	GACATGCGCGACTATAAANNKATANNKG TGCCGATGAAATACGTC	beta strand 3	54
IF-5A 11m	030	ATT GAG AAA TTC ACG GCG NNK ATA NNK NNK GTT NNK GGA GAT AGC AAC GGC GCG	beta strand 1	54
	031	GTA TTT CAT CGG CAC MNN TAT MNN TTT MNN GTC GCG MNN GTC MNN TAG MNN AAT MNN CGC GCC GTT GCT ATC TCC	beta strand 2+3	75
IF-5A 2RL	073	CTC TCC GTT TCA GGA GAT NNK NNK GGC GCG GTA ATT CAG CTA	Loop 1/2	42
IF-5A 2RL+2	075	CTC TCC GTT TCA GGA GAT NNK NNK AGC AAC GGC GCG GTA ATT	Loop 1/2	42

Resuspended cells were lysed by freeze-thaw and addition of lysozyme (0.5 mg.ml⁻¹) and, after sedimentation of insoluble material, the soluble fraction was also analyzed by SDS-PAGE. A small-scale purification step was conducted by binding soluble proteins using 5 µl Ni-NTA resin (Qiagen, Germany). Ni-NTA beads were washed with TBS and bound proteins were identified using SDS-PAGE.

Protein expression and purification

Wild type OB-fold domains, aspRS-OB, IF5A-OB and the mutants IF5A-OB/A2 and aspRS-OB/13mRL were expressed and purified in milligram quantities. 25 ml overnight

cultures of *E. coli* XL1-Blue in LB-amp (50 $\mu\text{g}.\text{ml}^{-1}$) were used to inoculate 500 ml of LB-amp medium. Cultures were grown at 37 °C to $\text{OD}_{600}=0.6$ and induced by 1 mM IPTG for 4 hrs. Bacteria were collected by centrifugation and stored at -20 °C. Cells were resuspended in 25 ml TBS + 10 mM imidazole and lysed by sonication. OB-fold proteins derived from IF-5A were
5 treated in a heat step which involves incubation for 30 min at 85 °C. This denatures a large portion of *E. coli* proteins. Lysed cells were centrifuged at 16,000 rpm in a Sorvall SS-34 rotor for 30 min. For purification, the lysate was loaded onto a Ni-NTA High trap column (Amersham Pharmacia, Sweden). Elution from the column was performed using an imidazole gradient. Purified protein was dialysed against imidazole-free 20mM Tris-HCl pH7.5, 150 mM NaCl,
10 concentrated and subjected to a second purification step by size exclusion using a Superdex® 200 column (Amersham).

Phage library preparation

General procedures for working with phage were performed according to Barbas *et al.*
15 (45). To prepare stocks of phage aspRS-OB-pIII-Vd3 for selection, $\sim 6 \times 10^9$ *E. coli* TG1 cells harbouring aspRS-OB in pJARA140 were used to inoculate 200 ml, 2 x YT-amp (50 $\mu\text{g}.\text{ml}^{-1}$). This culture was grown for 1 hour with shaking at 37 °C and infected with approximately 1×10^{12} units Vd3 helper phage for 30 min at 37 °C without shaking. The cells were then washed and grown for another 4 hrs in 2 x YT-amp. Phage were then concentrated from the culture
20 supernatant by polyethylene glycol (PEG) precipitation, resuspended in TBS and stored at 4 °C. The phage titre was determined as 3.0×10^{11} TDP. ml^{-1} .

For cloning of aspRS-OB gene libraries into pRPSP2 the oligonucleotide pair 050/044 was used for PCR-amplification of the assembled gene library. PCR product was digested by *NcoI* and *NotI*. Ligation was performed by using approximately 10 μg of *NcoI/NotI*-digested
25 phage vector pRPSP2 and insert, in a molar ratio of 1:5 in a 1 ml reaction followed by purification on spin columns (Roche or Qiagen, Hilden, Germany). Transformation of the 50 μl eluate was performed into $10 \times 50 \mu\text{l}$ electrocompetent *E. coli* TG1 cells by electroporation yielding approximately 1×10^8 transformants. Transformed cells were cultured in 100 ml SOC medium for one hour at 37 °C, before addition of 400 ml LB/Amp and growing for another hour
30 at 37 °C. Samples were taken to estimate the ligation and transformation efficiency by plating a

dilution series on LB/Amp agar plates and analyzing individual clones for correct insert size by diagnostic PCR. Colonies were randomly picked and the number of correct inserts was measured from diagnostic PCR of individual colonies. The number of inserts of the correct size was 89% and the number of colonies calculated to be 9×10^7 resulting in a diversity of $\sim 8 \times 10^7$ different clones carrying an insert of correct size. Once the culture reached $OD_{600} = 0.4$ the culture was then infected with approximately 5×10^{12} pfu VCS-M13 helper phage (Stratagene), left for 20 min at 37°C without agitation, and then shaken for 1 hour. Kanamycin was added to a final concentration of 50 ug/ml culture and the culture was grown overnight at 37°C. Bacteria were sedimented and phage precipitated overnight at 4 °C after dissolving in 20 g PEG8000 (Sigma) and 15 g NaCl. Phage were pelleted by centrifugation, dissolved in 5 ml PBS, filtered through 0.45 filters and used for panning.

Preparation of biotinylated RNA target

Generation of biotin labeled asp-tRNA was carried out by *in vitro* transcription using the MEGAscript kit (Ambion, USA) and the Biotin RNA Labeling mix (Roche, Switzerland) containing biotin-16-UTP. The DNA template was made on the basis of expression-PCR (41) by PCR assembly of synthetic oligonucleotides covering the 78 bp asp-tRNA gene from *P. aerophilum* (Gene_ID: 1464263) and a 150 bp DNA fragment amplified from pET28 (Invitrogen) including the T7 promoter region at the 3' end followed by GG for optimal promoter activity according to recent promoter recognition studies for T7 (42). This resulted in an assembled product of 230 bp which was precipitated by ethanol, dried, resuspended in RNase-free H₂O and used as the template for transcription without further cloning (41). *In vitro* transcription was carried out following the manufacturer's manual (Ambion) and yielded ~ 5 ug biotinylated asp-tRNA from a 25 ul reaction.

Selection of aspRS-OB libraries

Biotinylated asp-tRNA was used as a target in the selection from the libraries 'RL' and '13mRL', and hen egg lysozyme (Roche, Switzerland) was used for selection from '13mRL' only.

For selection on RNA, biotinylated asp-tRNA was immobilised by binding to streptavidin coated paramagnetic beads. 10 ul beads were washed twice with 400 ul PBS-T (PBS, 0.1% Tween) and incubated with 100 ng biotinylated asp-tRNA for 30min at RT with agitation and occasional inverting. Beads were washed 3 times with PBS-T before incubation for 2 hours with 1ml of $\sim 10^{11}$ cfu phage library RL or 13mRL in PBS-T+0.5% BSA. After 6 washes with PBS-T for the first round of panning and 8 washes for the subsequent panning rounds, beads were washed 2 more times with PBS and incubated with 1 ug (5 Kunitz units) RNase A (from bovine pancrease, Roche) for 30min at 37 °C to digest RNA and elute RNA-bound phage. Eluted phage particles were counted by bacterial infection and used for infection of 3 ml of a fresh TG1 culture for TDP production for the next round of panning. Cultures were left for 20 min at 37 °C without agitation, incubated for one hour with shaking before addition of ampicillin and grown overnight. Overnight cultures were used to inoculate 500 ml prewarmed LB/Amp. Helper phage infection and TDP production followed the same procedure as for the phage library preparation outlined above. After 4 rounds of panning individual clones were analyzed.

For selection on lysozyme, 4 ml Immuno Tubes (Nunc, Denmark) were coated with 2.5 ml lysozyme solution (10ug/ml) in 20 mM NaCO_3 pH 9.0 overnight at 4 °C and blocked with 4 ml 1% BSA in PBS for 1 hr at RT. Phage from library 13mRL were added ($\sim 2.5 \times 10^{11}$ cfu in 2.5 ml) and incubated for 2 hrs at RT with gentle agitation and occasional inversion. Washing was performed quickly within 5 min by 8 washing steps with PBS-T 0.1% BSA (for the first round of selection only 6 washes were performed using PBS-T) and 2 steps with PBS. Bound phage were eluted by incubation for 10 min with 2.5 ml elution buffer (0.2M glycine-HCl pH2.2, bromphenol blue) and immediately neutralized using 500ul 1 M Tris-HCl pH 9.0. Eluted phage were counted and used to infect a fresh 3 ml TG1 for TDP amplification and subsequent rounds of panning. Culture growth and TDP production were carried out in the same way as described above for panning on asp-tRNA. After 6 rounds of selection and amplification clones were picked and analyzed.

Western blot for phage display protein detection

A phage sample of aspRS-OB was concentrated by PEG precipitation to 1×10^{11} TDP/ml and 10 μl combined with gel loading buffer (contained SDS and BME), boiled and separated on

a 10% SDS-PAGE gel. After transfer onto a nitrocellulose membrane (Protran, Schleicher & Schuell, Germany) aspRS-OB-pIII fusion protein was detected using a mouse anti-c-myc primary antibody (Zymed, Invitrogen) and a HRP-linked anti-mouse secondary antibody (Amersham-Pharmacia, Sweden). Visualisation was performed using SuperSignal® substrate (Pierce, USA).

Phage ELISA

Phage ELISA experiments were performed to analyse selected clones for binding to lysozyme. Ninety-six-well ELISA plates were coated with 5 ug/ml hen egg lysozyme, 5 ug/ml RNaseA or 1% BSA in PBS at 4°C overnight. After two washes with TBS, plates were blocked with blocking buffer (5% skim milk in TBS) for one hour at RT before phage (10^9 cfu/well, derived from VCS-M13d3) were added in 2.5% skim milk-TBS-T. Plates were incubated for 2 hours at RT with agitation. After 10 washes with H₂O, mouse anti-M13 protein VIII diluted in blocking buffer was added and incubated for 1 h at RT. Plates were washed 4 times with H₂O and horseradish peroxidase (HRP)-coupled rabbit-anti-mouse immunoglobulins (Pierce) in blocking buffer were added to the wells and incubated for 1 h at RT. Wells were washed 4 times with H₂O and 50 ul substrate solution (1 mg/ml o-phenylene-diamine in PBS 0.030% H₂O₂) was added per well. The reaction was stopped after ~ 15 min by addition of 25 ul 2.5 M H₂SO₄ and the absorbance was recorded at 492nm.

For relative phage quantification (quantification of displayed fusion protein) phage samples were used directly to coat plates. After blocking with blocking buffer, phage were detected using mouse anti-c-myc primary antibody (Zymed, Invitrogen) and an HRP-conjugated anti-mouse secondary antibody following the procedure described above.

Monoclonal phage preparations

For phage binding experiments monoclonal phage samples were prepared as multivalent display using a gIII deletion variant of VCS-M13d3 (Vd3) (Rakonjac *et al*, 1999) as helper phage. For the micropanning prescreen monovalent phage were used derived from wtVCS-M13. Helper phage VCS-M13 and Vd3 stocks were prepared from single plaques following general protocols (Barbas III *et al*. 2001) with the exception that VCS-M13 was grown on TG1, Vd3 on

E. coli K1762 (K561 transformed with plasmids pJARA131 (cam^r) and pJARA112 (amp^r)) was used as a host strain to supply pIII for phage assembly. Vd3 samples were heated at 65°C for 20 min to kill λ -lysogen from the bacterial host.

To prepare stocks of phage aspRS-OB on Vd3 or VCS-M13, *E. coli* TG1 transformed with the corresponding pRPSP2 derivative were grown in 100 ml LB/Amp to OD₆₀₀ = 0.4 and infected with 10¹² pfu Vd3 or VCS-M13 respectively. After 20 min incubation at 37 °C without agitation, the culture was incubated for another hour with shaking. Kanamycin (50 ug/ml final concentration) was added and the culture was incubated overnight. Cells were sedimented and phage purified by precipitation using PEG/NaCl following current protocols (Barbas III *et al.*) and as discussed above. TDPs were resuspended in PBS and used for analysis.

Monoclonal phage binding experiments on asp-tRNA

For testing binding of phage displayed protein to asp-tRNA, monoclonal phage samples were used displaying the fusion protein in a multivalent fashion on Vd3. The procedure carried out was essentially as that for the first round of selection outlined above. Biotinylated asp-tRNA was bound to streptavidin coated paramagnetic beads and TDP samples were applied (10⁹ cfu/tube). After incubation and washing steps RNA was digested by addition of RNaseA and eluted TDP were counted by bacterial infection.

GST 'pull down' assay

Mutants selected on lysozyme were subcloned into GATEWAY[®] pDEST15 for expression as GST-fusion proteins. Constructs were transformed into *E. coli* BL21 (DE3) and cultures were grown in 3 ml LB/Amp. Cells were induced by addition of IPTG to a final concentration 1 mM and grown for another 4 hrs at 37°C. Cells were sedimented, resuspended in 300 ul lysis buffer (Tris-HCl 7.5 150mM NaCl) and lysed by sonication. Insoluble material was sedimented and the soluble fraction was incubated with 10 ul glutathion-linked sepharose beads (Amersham) for 1 hr at 4 °C. After two washing steps with TBS-T, beads were incubated with 300 ul TBS-T including 150 ul lysozyme (1mg/ml) and 0.1% BSA for 1 hr at 4 °C. Washing was performed using different buffers: TS (50 mM Tris-HCl pH7.5, 150mM NaCl), TBS-T (20 mM Tris-HCl pH7.5, 150mM NaCl, 0.1% Tween20), TBS-T-500 (TBS-T, 500 mM

NaCl). Beads were resuspended in gel loading buffer (containing SDS and BME), boiled and analyzed by SDS-PAGE.

Biosensor Binding Analysis

5 The ligand lysozyme was coupled to a CM5 *Biacore* sensor chip, at 30 µg/mL in sodium acetate buffer at pH 4.3 *via* the primary amine groups of the protein. The second of four flow cells available on the chip was activated with 35 µL, at 5 µL/min, of a 1:1 mixture of EDC:NHS (commercially available from Biacore). Lysozyme was coupled to the activated surface with successive injections of between 10-20 µL, until an adequate response was seen. Remaining
10 uncoupled active groups on the chip were deactivated with an injection of ethanolamine-HCl. For analysis, OB3 13mRL L6 was organized in a 1:2 dilution series of six concentrations, beginning at 370 µM in running buffer, plus a buffer-only blank. Each of the seven samples were analyzed in duplicate for 1 min @ 25 µL/min, in random order, using the first flow cell as a reference. The response curves were visualized and processed using *BIAevaluation* (Biacore).
15 Relative response at each concentration was averaged and plotted to determine R_{max} and kD using *Sigma Plot* (Systat Software, Inc.).

Example 2: OB-fold domains from Pyrobaculum aerophilum.

To study whether OB-fold domains can be used as a scaffold for generating proteins with
20 specific binding and enzymatic properties, the tolerance of individual OB-fold domain proteins toward mutations across the proposed binding face was studied. Two OB-fold domains from *Pyrobaculum aerophilum*, a hyperthermophilic crenarchaea ($T_{\text{max}} = 104\text{ }^{\circ}\text{C}$, $T_{\text{opt}} = 100\text{ }^{\circ}\text{C}$) were selected. This choice was made following a database search using the Superfamily database (version 1.65 (46)) to find OB-fold proteins in the *P. aerophilum* genome (42). This database
25 uses a library of all proteins of known structure which have been clustered into 1294 SCOP superfamilies (SCOP: Structural classification of proteins) to develop hidden Markov models which are then used as profiles to search sequenced genomes for proteins likely to contain similar folds. This search yielded 14 hits representing protein sequences containing potential OB-fold domains from the genome of *P. aerophilum* IM2.

Each of these sequences were analyzed to find OB-fold proteins which are spatially separated from other domains and thus expected to be independently stable. The sequences were also aligned to a 3-dimensional model representing the superfamily or to available, homologous, three dimensional protein structures, to check the reliability of the OB-fold prediction from the sequence. Of these 14 sequences, 8 fulfilled the criteria (see Table 2). Six of the eight candidates belonged to two functional classes of RNA binding proteins: translation initiation factors (IF) and aminoacyl-tRNA synthetases (aaRS). Two candidates had no functional annotation and were classified as “conserved hypothetical proteins.”

The OB-fold domains from the chosen sequences were cloned. The domain boundaries were identified from sequence alignments and tested for expression and solubility in *E. coli*. OB-fold domains from the aspartyl tRNA synthetase (aspRS-OB) and from the translation initiation factor IF-5A (IF5A-OB) were initially chosen since they expressed well and were soluble and heat stable.

An additional advantage of the IF-5A protein was the availability of the high resolution 3-dimensional structure in the Pfam DataBase (34) from which surface exposed residues could be reliably chosen for randomisation. This structure of IF-5A (Figure 3) shows two domains with the OB-fold at the C-terminus and spatially separated by a linker region, thus satisfying our selection criteria. The proposed binding face (β -strands 1-3) is directed away from the protein centre and toward the solvent. The OB fold of IF-5A has a shear number of $S=8$ and is thus, a representative of one sub-class of the OB-fold domains.

The OB-fold domain of asp-tRNA synthetase (aspRS-OB) was chosen as a representative of the second sub-class of OB-fold proteins with the property, $S=10$. A three dimensional structure of aspRS from *P. aerophilum* is not available, however there are a number of structures in the PDB for aspRS proteins from other organisms. Figure 4 shows the crystal structure of aspRS from *E. coli* (37). A sequence alignment for the OB-fold domain from *P. aerophilum* aspRS and its *E. coli* homologue show that the OB-fold domains have a sequence identity of 30%. Over their full lengths the aspRS proteins are 20% identical at the sequence level. The OB-fold lies at the N-terminus and is clearly spatially separated from the larger C-terminal domain. The binding face points away from the C-terminal domain toward the solvent. While the N-terminal OB-fold domain binds to tRNA and constitutes the anticodon recognition domain,

binding specifically the aspartyl-tRNA anticodon (36), the C-terminal domain constitutes the enzymatic component of the protein. Table 2 shows eight selected sequences from P.

aerophilum with predicted OB folds. NP accession numbers are given along with the predicted size and the proposed shear number. The 3-dimensional structure is available for IF-5A. The predicted size for the conserved hypothetical protein, NP_559846, corresponds to the whole protein. In this case, the boundaries of the OB-fold domain are difficult to accurately predict.

Table 2

Protein annotation containing predicted OB-fold	NP number	size of OB fold	shear number (S)
translation initiation factor IF-5A	(NP_560668)	10 kDa	8
translation initiation factor IF-2 alpha subunit	(NP_560442)	12 kDa	8
translation initiation factor IF-1A	(NP_559055)	14 kDa	8
aspartyl-tRNA synthetase	(NP_558783)	15 kDa	10
asparaginyl-tRNA synthetase	(NP_560397)	14 kDa	10
lysyl-tRNA synthetase	(NP_559586)	18 kDa	10
conserved hypothetical protein	(NP_560727)	11 kDa	-
conserved hypothetical protein	(NP_559846)	29 kDa	-

Each of these OB-fold domains have homologues in all kingdoms offering opportunities for applications in a different physiological contexts (see Figs. 5A-5B for sequence alignments of aspRS (Fig. 5A) and IF-5A (Fig. 5B) from different species). Fig. 5C shows the sequence alignment of aspRS-OB from *P. aerophilum*, *P. kodakaraensis*, and *E. coli*. Sequence identities are indicated by asterisks. The secondary structure of the OB-fold is indicated below the sequence: 1+loop between strands 4 and 5, loop 4/5.

Example 3: Choice of residues for randomization.

The residues for randomization of the two OB-fold domains were chosen on the basis of their three dimensional structures. The structure for IF-5A is available. A structure for the OB fold of aspRS from *P. aerophilum* was generated by modelling using SwissModel (38-40) and

the available structures from *E. Coli* (36,37) and *Pyrococcus kodakaraensis* (35) as structural templates.

On the binding face of the OB-fold domains, surface exposed residues were chosen from β -strands 1-3. Since aspRS and IF5A OB-fold domains have different shear numbers, their structures are slightly different. In particular, the arrangement of the β -strands 4 and 5 along with the loop between these strands is different. In the case of aspRS-OB, the loop between strand 4 and 5 was also included for randomization in one of the libraries. Thus, for aspRS-OB, 13 solvent exposed residues situated on β -strands 1-4 and in the loop between strands 4 and 5 were chosen for randomization. This gives a maximum number of 17 mutation sites and a theoretical variability of $20^{17} = 1.3 \times 10^{22}$ possible mutants.

To assess the tolerance to such mutations, a set of libraries were constructed addressing parts of the binding face independently. For IF5A-OB, libraries were constructed which randomized either 9 or 11 positions on β -strands 1-3 (Figure 8) resulting in two libraries with calculated theoretical variation of $20^9 = 5.12 \times 10^{11}$ and $20^{11} = 2 \times 10^{14}$ variants respectively. Two small libraries (400 variants each) were generated targeting the loop between strands 1 and 2 by randomising two introduced residues, serine-asparagine (2RL) or, by extending the loop using a further two residues (2RL+2). For details of the residues chosen and their locations in the OB-fold domains see Figures 8 and 9.

Example 4: OB-fold libraries

A set of libraries addressing defined regions of each OB-fold domain were constructed. For aspRS-OB-fold domain, the β -strands were mutated individually and in combination with each other. The loop between strands 4 and 5 was separately randomized in the wild type OB-fold domain (that is, the naturally occurring OB-fold domain) and in a fully randomized library. As a result, five libraries of different sizes and different arrangements of randomized positions were constructed (see Tables 3A-3B).

For IF5A-OB, the β -strands 1-3 as well as the loop between strand 1 and 2 were targeted for randomisation. This loop (between strands 1 and 2) was targeted for randomisation to assess its potential to extend the randomized surface area. There are examples of naturally occurring OB-fold proteins which show extended loops in this region which suggests that this loop might

be amenable to extension. In a similar approach used for aspRS-OB-fold domains, libraries with different sets of mutations (see Table 3) were assembled by PCR, cloned into an expression vector and expressed in *E. coli*. Clones representing library members carrying mutations were picked and analyzed for inserts of correct size, expression as a His₆-tagged protein, solubility and binding to Ni-NTA-resin.

Table 3A

aspRS-OB library	randomized area	theoretical size of library	number of mutations
4m	β3	$20^4 = 1.6 \times 10^5$	4
9m	β1-2	$20^9 = 5.1 \times 10^{11}$	9
13m	β1-3	$20^{13} = 8.2 \times 10^{16}$	13
4RL	Loop 4/5	$20^4 = 1.6 \times 10^5$	4
13m4RL	β1-3 + loop 4/5	$20^{17} = 1.3 \times 10^{22}$	17

Table 3B

IF5A-OB library	randomized area	theoret. size of library	number of mutations
9m	β1-3	$20^9 = 5.1 \times 10^{11}$	9
11m	β1-3	$20^{11} = 2.0 \times 10^{14}$	11
2RL	Loop 1/2	$20^2 = 400$	2
2RL+2	Loop 1/2	$20^2 = 400$	2

Tables 3A-3B are a list of gene libraries for aspRS-OB. Suffix 'm' indicates mutation in the β-sheet covering β-strands 1-3. Suffix 'RL' indicates the randomized loop region (Loop 4/5 in case of aspRS-OB and Loop 1/2 in case of IF5A-OB).

Example 5: Library assembly

Libraries were essentially assembled on the basis of overlap extension PCR incorporating synthetic oligonucleotides with degenerate codons at the desired positions. First, gene fragments covering the whole gene and containing overlapping regions were generated by ordinary PCR techniques. Randomized fragments were generated by incorporation of the corresponding long oligonucleotides containing randomized codons. Fragments were assembled by PCR using equimolar amounts of these gene fragments in combination with primers flanking the gene

resulting in amplification of the full length gene incorporating the randomized positions. Using different combinations of degenerate oligonucleotides several libraries containing random mutations in different areas of the binding face were generated. Diversity was created in aspRS-OB at residues on the beta sheet W28, E29, R31, I33, R35, V36, F38, V40, R42, F47, Q49, T51, K53 and in the loop region I85, A86, K87, S88. Library RL (randomized loop) contains 4 randomized positions in the loop region between beta strand-4 and 5. The theoretical diversity for the RL library is $20^4 = 160000$ different variants. After transformation, library RL contained $\sim 10^7$ clones, of which 94% had an insert of correct size resulting in a full coverage of the diversity of the library. The theoretical diversity of 13mRL is very high with $\sim 5 \times 10^{22}$ variants. 10^8 clones were obtained after transformation with 89% correct inserts. Out of 10 sequenced clones 8 had desired mutated sequences whereas 2 clones had frameshifts which would result in non-sense translation. The overall diversity was estimated to be $\sim 8 \times 10^7$ variants in the 13mRL library.

Libraries for IF5A-OB were generated individually. "9m" and "11m" libraries each have a different pair of long oligonucleotides incorporated into the gene. For the 11m library, the loop1/2 was extended by 4 amino acids (Ser-Asn-Gly-Ala) to provide a sufficient overlap of the randomized fragments. For the small libraries 2RL and 2RL+2, randomized sites within the loop region were generated using one oligonucleotide containing randomized positions incorporated into the gene covering the corresponding region. Diversities of IF-5A libraries with 9 and 11 mutations were estimated to be 1×10^7 variants, the theoretical diversity of the small libraries (400 variants) were fully covered.

Example 6: Expression of OB-fold mutant proteins.

Both naturally occurring OB-fold domains expressed well in *E. coli* (10-20 mg.l⁻¹ of culture) and are predominantly soluble after cell lysis. These remain soluble after heat treatment (15 min at 85 °C) and bind quantitatively to Ni-NTA beads. The OB-fold libraries were cloned and expressed as N-terminal His₆-tagged proteins. A set of protein characteristics were recorded addressing protein stability and structural integrity.

PCR libraries were cloned into an expression vector with an efficiency of 90-95% (determined by colony PCR) and genes were expressed as polyhistidine fusion proteins in *E.*

coli. 48 or 96 colonies were screened for expression, solubility and Ni-binding. The results are summarized in Table 4.

Table 4

5

13m library

Fragment	sense oligo	antisense oligo	Template	Gene fragment	mutations	Fragment Size
1	005	054	aspRS-OB wt	N-term	- (wt)	80bp
2	059	006	aspRS-OB wt	C-term	- (wt)	180bp
3	051 055	056 056	no template	β -strands 1 & 2	9	80bp
4	057 057	058 052	no template	β -strand 3	4	50bp
assembly 13m library: fragments 1-4						

4m and 9m libraries

Fragment	sense oligo	antisense oligo	Template	Gene fragment	mutations	Fragment Size
4m						
1	005	056	aspRS-OB wt	N-terminal portion incl. β 1-2	- (wt)	~140bp
2	Fragment 1	052	-	N-terminal portion incl. β 1-3	4 mutations in β 3	~180bp
3	059	006	aspRS-OB wt	C-terminal portion incl. β 1, β 4-5	- (wt)	~180bp
assembly 4m library: fragments 1-3						
9m						
1	005	056	aspRS-OB 13m library	N-terminal portion incl. β 1+2	9 in strand 1+2	~150bp
2	068	006	aspRS-OB wt	C-term incl. β 3-5	- (wt)	~200bp
assembly 9m library: fragments 1-2						

10

4RL and 13m4RL libraries

Fragment	sense oligo	antisense oligo	Template	Gene Portion	mutations	Fragment Size
1	005	060	aspRS-OB wt	N-terminal portion incl. B-strand 1-4	- (wt)	~250bp
2	005	060	aspRS-OB 13m library	N-terminal portion incl. B-strand 1-4	13 mutations in β -sheet	~250bp
3	053* 061	063 063	no template	loop4/5 + β -strand 5	4 mutations in L4/5	~60bp
4	062	006	aspRS-OB wt	C-term	- (wt)	~70bp
assembly 4RL library: fragments 1+3+4						
assembly 13m4RL library: fragments 2+3+4						

Summary of the library construction for aspRS-OB is shown in Table 4. For each library the PCR generated gene fragments, oligonucleotides and templates are listed. Gene fragments were generated by PCR incorporating oligonucleotides. PCR products were then assembled to the full length gene by overlap extension PCR using gene flanking primers (oligos 005 and 006). Also, see Figures 2A-2B. Approximately half of the clones from all libraries of aspRS-OB expressed well in *E. coli*. The number of randomized positions on the β -sheet (i.e., the number of amino acid positions on the binding face that were randomized in order to construct the library) appeared to correlate with the percentage of expressing variants. For both libraries with 13 mutations, 13mRL and 13m, ~45% of the mutant proteins express well. The library containing 9 mutations on β -sheets 1 and 2 show expression in 52% of the clones. The library which targets only loop 4/5 for randomisation had a very high number of expressing clones at 81%. However, the combination of randomized positions on both the face and the extended loop (13mRL+2) dropped the number of expressing clones to just 30%.

In the case of IF5A-OB, libraries with mutations on the β -sheet were expressing at a comparatively low rate, 12%, and of these, 9-25% were soluble. In contrast, 72-81% of the mutants containing randomized positions in just loop1/2 only, were expressed and, of these, ~70% were soluble. All IF5AOB mutants were heat treated at 80°C after lysis. Thus all the soluble and Ni-binding mutants were also heat stable.

A few mutants were picked for preparative expression and purification. In addition, the large scale purification of an aspRS-OB mutant was also performed. Table 5 shows the summary of expression, solubility and Ni-NTA-binding experiments.

Table 5

OB fold	library	screened	expression	express./ screen. [%]	solubility	(%)	Nickel binding
aspRS	13m4RL	48	21	(44)	3/10	(30)	2/2
	13m	96	43	(45)	6/14	(43)	5/5
	9m	48	25	(52)	4/8	(50)	-
	4m	48	38	(79)	-		-
	wtRL	48	35	(73)	-		-
IF-5A	9m	192	21	(11)	2/21	(9)	2/2
	11m	144	16	(11)	4/16	(25)	4/4
	2RL	32	26	(81)	20/26	(77)	13/16
	2RL+2	32	23	(72)	18/26	(69)	14/18

Between 32 and 192 colonies for each library were screened for expression, solubility
 5 and binding to Ni-NTA. Table 5 shows the number of expressing clones, the calculated ratio of
 expressing clones for each library, and presents an estimation of the solubility and Ni-NTA
 binding properties of expressing OB-fold mutants.

Example 7: Analysis of phage displayed aspRS-OB

10 An important criteria for a protein domain as a scaffold for library generation is its
 capacity to be functionally displayed in a chosen display system. The experiments disclosed
 herein used phage display. To assess the viability of this technique for selection of aspRS-OB
 mutants the display of recombinant wild type aspRS-OB as gIII fusions on the surface of
 filamentous bacteriophage M13 was assessed. The presence of a pIII-aspRS-OB fusion in
 15 prepared phage particles by Western blotting was analyzed. Functional display of displayed
 aspRS-OB was studied by a phage binding assay using asp-tRNA as the target ligand.

The gene for wild type aspRS-OB was cloned into phagemid vector pRPSP2 upstream of
 the gIII gene generating a fusion protein with aspRS-OB at the N-terminus and pIII at the C-
 terminus (see Figure 6). This phagemid vector contains gIII under the control of the phage shock
 20 promotor (psp) which is activated upon infection of the *E.coli* host by helper phage (31). Helper
 phage VCS-M13d3, gIII deletion mutant (44) was used which allowed multivalent display of the

target protein. All copies of gIII proteins (3-5 copies) will be fusions to the target protein aspRS-OB. Multivalent display was used to increase sensitivity in binding assays (48).

The construct, pRPSP2 containing the gene for aspRS-OB was transformed into *E. coli* TG1 cells. The resulting culture was infected by the Vd3 helper phage and transducing particles (TDPs) were produced. These recombinant bacteriophage were harvested, tested for display of the target protein by western analysis using an antibody against the c-myc antigen sequence localized between the aspRS-OB and pIII (See figures *infra*). This showed a strong signal at the expected size for the fusion protein pIII-aspRS-OB.

To test whether the displayed wild type OB-fold is still functional on the surface of the phage, a phage binding experiment was performed to immobilised asp-tRNA with this phage sample displaying aspRS-OB. A TDP sample displaying aspRS-OB was incubated with asp-tRNA immobilised on magnetic beads. Unbound phage were washed away and bound phage eluted by tRNA digestion using RNaseA. The number of eluted phage were then counted by bacterial infection and compared with the number eluted from a sample incubated with beads only. To demonstrate specificity of binding, VCS-M13wt in a >1000 fold excess was added to the TDP sample and the number of eluted particles was counted. The ratio of eluted phage from tRNA to input phage was calculated for each sample. The input and results are summarized in the following table.

Table 6

	VCSM13	OB3wtTDP
input	3.0×10^{12}	1.7×10^9
output from beads only	1.2×10^9	2.1×10^5
output from tRNA	1.7×10^9	4.0×10^7
beads only out/in	4.0×10^{-4}	1.2×10^{-4}
tRNA out/in	5.7×10^{-4}	2.4×10^{-2}
quotient beads (out/in) / tRNA (out/in)	7.1×10^{-1}	5.2×10^{-3}
quotient tRNA (out/in) / beads (out/in)	1.42	190.48
TDP / VCS-M13	134.45	

The recovery was about 200-fold higher for phage displaying the aspRS-OB (2.4×10^{-2}) when compared to phage only (5.7×10^{-4} , see Figure 8). This indicated a significant affinity between the displayed aspRS-OB for the immobilised asp-tRNA. In the case of VCS-M13 without displayed protein, the ratio of eluted particles from the beads alone compared to immobilised tRNA was very similar (1:1.42) indicating that the phage bound non-specifically. That ratio was much higher (1:190.48) for aspRS-OB displaying particles demonstrating binding specificity of this domain for asp-tRNA. These results demonstrate that aspRS-OB is functionally intact when displayed on the surface of phage.

Example 8: Library selections

Selection on asp-tRNA

The loop region between beta sheet 4 and 5 in bacterial aspRS anticodon-binding domains is important for binding to the tRNA as well as for specific recognition of the bases in the anticodon (49). Thus asp-tRNA was considered to be good target to test the viability of an aspRS-OB library. The library aspRS-OB RL was used since it contains full coverage of the theoretical diversity and therefore contains copies of the wild-type aspRS-OB fold sequence which was expected to bind well to the tRNA target. Even if none of the mutants bound to the

tRNA, at least the wild-type should be selected by the biopanning process. An aspRS-OB RL gene library was generated as before, cloned into pRPSP2 yielding $\sim 10^7$ clones and monovalently displayed on phage. After four rounds of panning, a significant enrichment was observed as represented by the ratio of output phage to input phage – indicating an enrichment of target-specific binding domains (Figure 9). Clones were randomly picked from the selected fraction and sequenced. The sequences showed the consensus R/K G C R for the 4 amino acids in the loop region for binding to asp-tRNA (Figure 10). Of 12 sequenced clones, 5 fulfilled this consensus completely, 3 out of the remaining 7 agreed in 3 of the 4 amino acid positions. The consensus sequence is in striking contrast to the wild-type sequence (IAKS) which suggests that the new consensus sequence more strongly binds asp-tRNA in comparison to the wild-type domain. This was confirmed in a phage binding experiment with monoclonal phage preparations where two clones have higher affinity for asp-tRNA than wild type aspRS-OB (Figure 16). For this experiment, phage displaying the corresponding mutant domains were incubated with immobilised asp-tRNA. Bound phage were specifically eluted with RNaseA and counted. The recovery rate R was calculated as $[(\text{output/input})_B / (\text{output/input})_{\text{RNA}}]$ where (output/input) refers to the ratio of recovered phage (output) divided by the number of input phage, subscript 'B' refers to beads only, subscript 'RNA' refers to immobilised asp-tRNA. The results indicate that we have enriched a consensus sequence with enhanced binding affinity for immobilised asp-tRNA from a phage library derived from aspRS-OB mutants (Figures 10 and 11).

Selection was performed in the same manner against immobilized tRNA using the larger library '13mRL' which has much greater diversity compared to 'RL'. The enrichment pattern is shown in Figure 9 and indicates significant enrichment after 5 rounds of panning. Sequence analysis is summarized in Figure 12. Selected sequences contained a high proportion of positively charged amino acids suggesting those mutants were selected by binding to the negatively charged asp-tRNA backbone. The mutant with the greatest number of basic residues (D07) was found three times indicating a high abundance in the pool of selected clones. The phage binding experiment on immobilised asp-tRNA monoclonal phage samples prepared from the selected clones D07 and D09 showed that these clones were recovered in a number several times higher than the wild-type aspRS-OB domain suggesting stronger binding of the displayed mutant to asp-tRNA. These phage binding experiments are not precise measurements but

indicate a successful selection process and demonstrate that aspRS-OB libraries can be used to select against an immobilised target using phage display. The full sequences of the selected clones in Figure 12 are listed in Appendix II, and are designated U1, U2, U3, U4, U5, U6, U7, U8, U9, S68, S81, pMB16, pMB17, pMB12, pMB18, pMB15, D05, D07, D09, D04, L14, L8, L4, L16, L34, L42, L6, L5, or L44.

Example 9: Selection on Lysozyme

Lysozyme was selected as a target to demonstrate the proof-of-principle in choosing an OB-fold mutant domain from a naïve library which binds to another protein. Hen egg white lysozyme is a small stable protein which is commercially available and has a number of medically important human homologues. After four rounds of panning on immobilised lysozyme, enrichment of bound phage was observed. A further two more rounds of panning were performed before clones were randomly picked and screened for binding to lysozyme. Monoclonal phage samples were then prepared and studies were undertaken to characterize binding in a 'micropanning' approach on lysozyme immobilised on a 96-well ELISA plate. Bound phage were eluted and counted. Out of 22 clones 9 showed phage recovery numbers above the background of pIII, OB wild-type and BSA (clones L4, L5, L6, L8, L14, L15, L16, L18, L21, Figure 13). These clones were sequenced. Sequences for some of the clones were identical (L14 and L15; L4 and L18; L8 and L21) narrowing down the number of unique clones to six. This redundancy indicated a high proportion of clones with the same sequence in the sample due to enrichment. Two more rounds of panning were performed and 6 more clones were sequenced (L32, L33, L34, L42, L43, L44). Three sequences matched sequences of previous clones (L32=L14=L15, L33=L8=L21=L43), while L44 was identical to L5 in the beta-sheet region but showed a different pattern in the loop region. L34 and L42 were new sequences. The number of clones in the selected pool after 6 rounds can be assumed to be very small and covered to a significant extent by the nine sequences shown in Figure 12, panel E. Clones L14 (L32, L15), L8 (L33, L21, L43), L34, L4, L5 and L6 were subjected to binding studies in an ELISA approach using multivalent display (Figure 14). Results showed that all clones bound to lysozyme whereas particles without a displayed aspRS-OB did not (pIII). Other negative controls included the wild type aspRS-OB (OBwt). All analyzed clones bind in higher

numbers (higher OD values in ELISA experiments) to lysozyme than to RNaseA or BSA demonstrating specificity of binding to lysozyme. As shown in Figure 11, clones L6 and L33 did not bind to tRNA.

5 *Example 10: Expression and analysis of purified mutants*

Clones L4 (L18), L5, L6, L16 and L33 (L21) were subcloned into an expression vector and expressed as GST fusion proteins for analysis for lysozyme binding in 'pull-down' assays. As shown in Figs. 15A-15B, immobilised mutants bound lysozyme whereas the unselected mutant 13mRL81 did not bind. This confirmed binding of selected mutants to lysozyme. L6
10 binding to lysozyme was studied in presence of different buffers. Figure 15B shows that L6 binds to lysozyme after washing with 500mM NaCl. Clone L6 was expressed and purified and its binding kinetics on immobilised lysozyme were analyzed using surface plasmon resonance (Biacore). The binding constant was calculated to be 3.6×10^{-5} M (Figure 16).

These experiments demonstrate the production of large, synthetic libraries of OB-fold
15 domains which contain randomized codons and demonstrate that transcribed, mutant proteins from these libraries are stable and folded. Functional display of an OB-fold domain is demonstrated at the surface of phage thus allowing efficient screening of the library for differing functions of choice. Selection of modified OB-fold domains, from OB-fold libraries, using phage display is demonstrated. These variants must have desired characteristics, be they chosen
20 binding interactions or enzymatic activity. As demonstrated herein, the tRNA anticodon binding domain of Aspartate tRNA Synthetase (AspRS) from *Pyrobaculum aerophilum* was chosen as an OB-fold scaffold to demonstrate the applicability of OB-folds to serve as carriers of diversity. The results show that this tRNA anticodon binding domain can be converted into a specific protein binding molecule by applying the methods disclosed herein.

25 Each mutation introduced into a protein framework can potentially affect its folding and thus its stability and solubility. To understand the tolerance towards mutations in the protein framework libraries containing different sets, or combinations of mutated areas, were generated and screened for expression and solubility of randomly picked mutants. Libraries with unrestricted diversity were planned and generated. Such naive libraries contain all possible
30 combinations of mutations through randomisation. It is expected that a large number of mutants

will not be tolerated for reasons of either stability, folding or solubility due to unfavorable combinations of amino acids in particular areas in the molecule. A library derived from aspRS-OB containing 17 random amino acid positions in the binding face, 13 on the beta sheet (beta strands 1-3) and 4 in the loop between strands 4 and 5 was generated. Libraries comprising sets of mutations addressing individual beta strands or the loop region only were generated.

After screening libraries of modified OB-fold domains for expression and solubility it was found that ~16% of all mutants in a 17-mutation library of aspRS-OB were overexpressing and soluble and a few selected mutants were proven to fold accurately as demonstrated by NMR and CD spectroscopy. This shows that a significant proportion of this library is usable for selection against a target of interest. AspRS-OB Libraries 13mRL and RL were constructed as phage display libraries. The practical diversity of 13mRL was $\sim 8 \times 10^7$ different clones representing a very small fraction of the $\sim 5 \times 10^{22}$ possible combinations (theoretical diversity) of 17 random positions. The diversity of RL is only 1.6×10^5 (4 random positions) and is expected to be fully covered by $\sim 1 \times 10^7$ clones after transformation. Sequencing of randomly picked clones confirmed the diversity of the library.

Phage display is the most commonly used display technology and thus favorable for display of the aspRS-OB scaffold. There are no reports of the display of an aspRS anticodon binding domain at the surface of a phage, or the display of any other OB-fold domain in general. Display of a protein on a phage requires several steps that might affect the integrity of the displayed protein as well as the growth of the host cell. After synthesis in the cytoplasm the protein has to be stable in the reducing environment of the cell and must be unaffected by fusion to the pIII phage protein. The fusion protein is then targeted through the oxidising environment of the periplasm for phage assembly before the whole phage particle is released into the media. For any protein this process involves interactions with the environment at multiple stages, and in case of a scaffold derived from an anticodon binding domain binding to host nucleic acids must also be considered. Detection of aspRS-OB (by Western analysis) displayed on M13 phage showed good expression. Detection of aspRS-OB libraries RL and the larger 13mRL (also by Western blotting) showed much less efficient display on phage. This observation can be explained by a high degree of unstable mutants in the naive random libraries. These data suggest proteolytic degradation of unfavorable mutants in the cytoplasm or periplasm of *E. coli*, an effect

observed before in studies on the Z-domain from protein A (50). This also correlates with results from the expression and solubility screens. Weaker signals of phage displaying libraries were observed in other scaffolds (carbohydrate binding domain, (51); cellulose binding domain, (52)). Library designs of future libraries would need to take this factor into account to increase the ratio of displayed fusion to degradation. This is a general problem of naive random libraries and not a phenomenon observed in OB-folds only.

Selection on asp-tRNA

Phage binding and selection experiments on the native target asp-tRNA indicated successful and functional display of asp-OB and its derived libraries on M13 phage. From the small RL library a consensus sequence was obtained representing mutants with higher affinity than the wild type as shown in monoclonal panning experiments. The derived consensus sequence R/K G C R was different from the wild-type sequence and contained 2 positively charged amino acids suggesting binding to the negatively charged RNA backbone. The presence of the glycine in this loop region might ensure flexibility of the loop while the function of the cysteine remains unclear.

Sequences of unselected clones showed diversity of the aspRS-OB RL library and sequences from clones matching the consensus sequences after selection showed variation of the corresponding DNA codons demonstrating selection for the phenotype rather than for genotype. Due to a very limited coverage of the diverse library 13mRL, a consensus could not be derived from the small number of sequences of clones selected on asp-tRNA. This is expected since the practical diversity is about 10^8 clones but the theoretical diversity is approximately 10^{22} . Thus, the diversity coverage of the phage library is only a very small fraction of that theoretically possible. A significant number of positively charged residues was observed in all sequenced clones (9 in D07, 5 in D05, 6 in D09) indicating a selection for positively charged residues through binding to the negatively charged RNA backbone. The motif R X G S occurring in two mutants (D07, D04) suggests an important role of the loop in tRNA binding as it is the case for the wild-type aspRS-OB. Binding experiments with monoclonal phage samples showed stronger binding to asp-tRNA than the wild-type domain. This supported the conclusion that a selection

upon binding to the immobilised target occurred and indicated that our OB-fold scaffold is well suited for display on phage and the biopanning process.

Selection on lysozyme

5 The 13mRL library was selected on hen egg lysozyme. After several rounds of panning a number of clones were isolated and analyzed for sequence and for binding to the target molecule. Out of 22 clones in a pre-screen, 6 finally showed detectable binding to lysozyme in a phage ELISA experiment. Examination of sequences of 14 clones revealed that two were detected twice, one even four times. This suggests a reasonably small number of different clones in the
10 selected fraction. Sequences of 9 different clones indicated similarities in their composition. A few positions showed some interesting similarities, for example position 29, which is an acidic residue (D or E) in 6 clones out of 9, position 31 is a valine in 5 out of 9 sequences, in position 35 a positively charged residue appears in 4 clones, position 38 is an aromatic residue (Y, F, W) in 5 cases and finally position 85 is glycine in 5 clones. Also, in beta strand 3, there are
15 noticeable patterns ETET and PETE occurring in clones L16 and L34, and in beta strand 1 D V/L A/L in L32, L2, L6, L5, L44. Also striking is the identity of L5 and L44 in the beta sheet whereas the loop region is different. There are no cysteines in all mutants except L6. However, more obvious consensus sequences could not be derived probably due to poor coverage of the very large library and the small number of sequences obtained. Several clones were expressed
20 and purified as GST fusion proteins and analyzed by pull down experiments showing binding of the clones to lysozyme. Clone L6 bound even in the presence of 500 mM sodium chloride indicating binding of reasonable affinity. Clone L6 was expressed and purified and the kinetics and thermodynamics of binding were analyzed by surface plasmon resonance showing a K_d of $\sim 3.6 \times 10^{-5}$ M. Considering the small size and the composition of this naive library a binding
25 constant in μ M range is a very significant result and offers an excellent starting point for optimization by affinity maturation procedures.

Example 11: Three dimensional structure of the OBody L8 in complex with lysozyme

30 L8 was cloned using Gateway (Invitrogen) into pDONR221 then subcloned into the expression vector pDEST15 which was transformed into BL21 (DE3) *E. coli* cells. These cells

were inoculated into 500 mL of auto-induction media and shaken at 37 °C in 2 L baffled flasks. The fusion protein GST-L8 was purified from bacterial lysate using a GSH affinity column (GE Biosciences). The GST tag was removed using rTEV protease and separated from L8 by size exclusion chromatography (S75 16/60 prep-grade, GE Biosciences). L8 was then purified a third
5 time to improve monodispersion in solution, again by size exclusion (S75 10/300 analytical grade, GE Biosciences).

The purified protein was combined with *Gallus gallus* egg white lysozyme (Roche) in an approximate 1:1 molar ratio, to a final concentration of L8 at 37.5 mg/mL and lysozyme at 42.9 mg/mL, in TBS (25 mM TRIS, pH 7.5, 137 mM NaCl, 3 mM KCl). The complex in
10 solution was screened against 480 crystallisation conditions using custom screens and a sitting drop format.

A single large crystal grew from an equal mixture of protein in TBS and precipitant (7% MPEG 5K, 0.2 M HEPES pH 7.8). This crystal was then gathered in a nylon loop, coated in cyroprotectant, and frozen under a stream of cold N₂ gas (110 K). A dataset of 700 images was
15 collected using a rotating anode X-ray generator and Mar345 detectors giving diffraction to 2.8 Å. Images were indexed using DENZO and data were scaled using Scalepack. For data collection statistics see table. The structure was solved using molecular replacement (AMoRe) incorporating both lysozyme (PDB entry 193L) and the OB-fold codon recognition domain from the *Pyrococcus kodakarensis* aspartyl tRNA synthase (PDB entry 1B8A) as models. Two
20 molecules of lysozyme were found in the asymmetric unit along with one OB-fold domain. A second OB-fold was placed by replicating the complex in the asymmetric unit based on the position of the second lysozyme molecule. The structure was iteratively built and refined using COOT, CCP4 and PHENIX. A second dataset was collected using the same crystal at the SSRL, to 2.69 Å resolution. It was indexed in the same space group and phased by molecular
25 replacement using the complete unit cell from the previous structure. Building and refinement was done using COOT, CCP4 and PHENIX.

Table 7**Statistics for X-ray crystallographic structure of L8 in complex with lysozyme.**

	Home Source Data	Synchrotron Data
<i>Crystal Properties</i>		
Space Group	P4 ₁ 2 ₁ 2	P4 ₁ 2 ₁ 2
Unit Cells Axes (a, b, c)	76.585, 76.585, 166.150	76.759, 76.759, 166.344
Unit Cell Angles (α , β , γ)	90, 90, 90	90, 90, 90
<i>Data Collection</i>		
Resolution	50-2.8 (2.872-2.8)	34.85-2.69 (2.76-2.69)
Total Reflections	267,952	144,772
Unique Reflections	12,301	16,010
Completeness	95.3 (54.75)	99.15 (92.80)
Redundancy	21	9
R_{merge}	4.2 (59.0)	7.3 (54.3)
Wilson B Factor	85	65
Mosaicity	0.6	0.6
I/ σ I	50.14 (1.6)	32.50 (4.22)
<i>Molecular Replacement</i>		
Correlation Coefficient	66.2	71.2
R	52.7	38.9
<i>Refinement</i>		
Resolution	25-2.8 (2.872-2.8)	27.5-2.75 (2.82-2.75)
R	26.5 (35.0)	22.5 (26.5)
R_{free}	34.0 (50.7)	29.6 (37.6)
Protein Atoms	3338	3384
rmsd, bond lengths	0.012	0.013
rmsd, bond angles	1.541	1.452

B factors, average	66.942	51.146
--------------------	--------	--------

Table 8. Protein-protein interface data for L8 in complex with lysozyme

Buried surface area	840 Å ²
Average antibody/antigen buried surface area	950 Å ²
H-bonds at interface	7
Salt bridges at interface	2
Polar:Non-polar atoms at interface	43%:57%
Gap Volume Index	2.94
Average Gap Volume Index (antibody/antigen)	3.0
K_d (surface plasmon resonance)	36 μM

Appendix I

OB fold	Oligo	5' – 3' sequence
aspRS	005	CAC C AGT GGA TCC GTG TAT CCT AAA AAG ACC
	006	ACC CGG GAA TTC TCA GTC TAT TGG AAG CGG CTT
IF-5A	011	CAC C AGT GGA TCC ATT GAG AAA TTC ACG GCG
	012	ACC CGG GAA TTC TCA CTA TTT AAC TCT AAT AAT

- 5 Oligonucleotides for PCR amplification of the wild type OB-folds of aspRS and IF-5A from *Pyrobaculum aerophilum*.

Oligo	5' – 3' sequence
050	GGT GAC CTA CCA TGG CCC AGG TGG TGT ATC CTA AAA AGA CCC AC
054	TAC CCA ACC GGC AAC AAC
055	GTT GTT GCC GGT TGG GTA
056	CGC GCC CCC CTC CCT ATC
057	GAT AGG GAG GGG GGC GCG
058	ATC GGG GGT TTT TCC CGC
059	GCG GGA AAA ACC CCC GAT
060	TTT ACT GGC CTC AAC AAT
061	ATT GTT GAG GCC AGT AAA
062	GGT GTG GAG ATT TTC CCC
068	GAG GGG GGC GCG TTT GTG CAA GTC ACG CTC AAG G

Oligonucleotides for PCR assembly of libraries based on aspRS-OB from P. aerophilum

028	GGAGATAGCAACGGCGCGGTAATTCAGCTAATGGAC
029	CGCGCCGTTGCTATCTCCTGAAACGGAGAGTATTTG
032	GTGCCGATGAAATACGTC
033	GACGTATTTTCATCGGCAC
034	CGCGCCGTTGCTATCTCC
035	GGAGATAGCAACGGCGCG
074	ATCTCCTGAAACGGAGAG
076	TAGCTGAATTACCGCGCC
078	CTCTCCGTTTCAGGAGA
089	GGCGCGGTAATTCAGCTA

Oligonucleotides for PCR assembly of libraries based on IF5A-OB from P. aerophilum

5 Appendix II

Amino Acid Sequences of Various Obodies. The numbering for the sequences is consistent with the numbering in Figure 10 and Figure 12.

Design- ation	Amino Acid Sequence
U1	VYPKKTHWTAETPNLHGTEVVVAGWVECLADTGIEKGVLVVDREGGACVRVHLQAGKTPDH LFKVFAELSREDVVVIKGIVEASKGYKSGVEIFPSEIWILNKAKPLPID
U2	VYPKKTHWTAETPNLHGTEVVVAGWVGALRDLGLGKGVSVFDREGGAVVTNLLAGKTPDH LFKVFAELSREDVVVIKGIVEASKSRVGGVEIFPSEIWILNKAKPLPID
U3	VYPKKTHWTAETPNLHGTEVVVAGWVAALGDAGDSKTVTVNDREGGAPVHVQLDAGKTPDH LFKVFAELSREDVVVIKGIVEASKYRLKGVEIFPSEIWILNKAKPLPID
U4	VYPKKTHWTAETPNLHGTEVVVAGWVDPLDRGLAKGVSVRDREGGASVPVTLLAGKTPDH LFKVFAELSREDVVVIKGIVEASKQRYVGVEIFPSEIWILNKAKPLPID
U5	VYPKKTHWTAETPNLHGTEVVVAGWVKVLPDGGFCKYVRVEDREGGASVLVALSAGKTPDH LFKVFAELSREDVVVIKGIVEASKLGHFGVEIFPSEIWILNKAKPLPID
U6	VYPKKTHWTAETPNLHGTEVVVAGWVISLDRGGTKLVEVIDREGGAIVVQLLAGKTPDH LFKVFAELSREDVVVIKGIVEASKRLVNGVEIFPSEIWILNKAKPLPID
U7	VYPKKTHWTAETPNLHGTEVVVAGWVFXLLDXGMGKLVRVPDREGGAPVDVDLPAGKTPDH LFKVFAELSREDVVVIKGIVEASKCGGGGGEIFPHEIWILNKAGKPLPID

U8	VYPKKTHWTAETIPNLHGTEVVVAGVWVELRDIGKVKFVVVRDREGFVQVTLKAGKTPDHLF KVFAELSREDVVVIKGIVEASKVGLGVEIFPSEIWILNKAKPLPID
U9	VYPKKTHWTAETIPNLHGTEVVVAGVWVELRDIGKVKFVVVRDREGFVQVTLKAGKTPDHLF KVFAELSREDVVVIKGIVEASKGDCGVEIFPSEIWILNKAKPLPID
S68	VYPKKTHWTAETIPNLHGTEVVVAGVWVRS�VDGGRVKAVNVQDREGGAKVEVLLEAGKTPDH LFKVFAELSREDVVVIKGIVEASKGEWSGVEIFPSEIWILNKAKPLPID
S81	VYPKKTHWTAETIPNLHGTEVVVAGVWVGLVDMGLLKGVTVGDREGGASVLVRLTAGKTPDH LFKVFAELSREDVVVIKGIVEASKLVPQGVVEIFPSEIWILNKAKPLPID
pMB16	VYPKKTHWTAETIPNLHGTEVVVAGVWVELRDIGKVKFVVVRDREGFVQVTLKAGKTPDHLF KVFAELSREDVVVIKGIVEASKRGCRGVEIFPSEIWILNKAKPLPID
pMB17	VYPKKTHWTAETIPNLHGTEVVVAGVWVELRDIGKVKFVVVRDREGFVQVTLKAGKTPDHLF KVFAELSREDVVVIKGIVEASKKGCRCGVEIFPSEIWILNKAKPLPID
pMB12	VYPKKTHWTAETIPNLHGTEVVVAGVWVELRDIGKVKFVVVRDREGFVQVTLKAGKTPDHLF KVFAELSREDVVVIKGIVEASKRGCAGVEIFPSEIWILNKAKPLPID
pMB18	VYPKKTHWTAETIPNLHGTEVVVAGVWVELRDIGKVKFVVVRDREGFVQVTLKAGKTPDHLF KVFAELSREDVVVIKGIVEASKRSCRGVEIFPSEIWILNKAKPLPID
pMB15	VYPKKTHWTAETIPNLHGTEVVVAGVWVELRDIGKVKFVVVRDREGFVQVTLKAGKTPDHLF KVFAELSREDVVVIKGIVEASKLSLVGVEIFPSEIWILNKAKPLPID
D05	VYPKKTHWTAETIPNLHGTEVVVAGVWQRLYDRGKRKSVSVVDREGGAPVTVCLRAGKTPDH LFKVFAELSREDVVVIKGIVEASKWNCGXVEIFPSEIWILNKAKPLPID
D07	VYPKKTHWTAETIPNLHGTEVVVAGVWRKLRDRGPAYVWVRDREGGATVRVRLQAGKTPDH LFKVFAELSREDVVVIKGIVEASKRKGSGVEIFPSEIWILNKAKPLPID
D09	VYPKKTHWTAETIPNLHGTEVVVAGVWVRLRDWGLAKTVRVKDRREGGASVRVTLRAGKTPDH LFKVFAELSREDVVVIKGIVEASKWVWVGVEIFPSEIWILNKAKPLPID
D04	VYPKKTHWTAETIPNLHGTEVVVAGVWSCLDAGKRKWVYVVDREGGAPVAVRLRAGKTPDH LFKVFAELSREDVVVIKGIVEASKRAGSGVEIFPSEIWILNKAKPLPID
L14	VYPKKTHWTAETIPNLHGTEVVVAGVSDLLDAGRAKYVFVYDREGGAEVMVTLAAGKTPDH LFKVFAELSREDVVVIKGIVEASKGWRDGVVEIFPSEIWILNKAKPLPID
L8	VYPKKTHWTAETIPNLHGTEVVVAGVVASLGDYGRVKIVKVS DREGGAAPVYLEAGKTPDH LFKVFAELSREDVVVIKGIVEASKGVGRGVEIFPSEIWILNKAKPLPID
L4	VYPKKTHWTAETIPNLHGTEVVVAGVVGELADFGDMKTVAVRDREGGAEPVPTLLAGKTPDH LFKVFAELSREDVVVIKGIVEASKGSTSGVEIFPSEIWILNKAKPLPID
L16	VYPKKTHWTAETIPNLHGTEVVVAGVVASLVDGGPRKWVVRDREGGAEVTVELTAGKTPDH LFKVFAELSREDVVVIKGIVEASKGLRWGVEIFPSEIWILNKAKPLPID
L34	VYPKKTHWTAETIPNLHGTEVVVAGVVGMLDEGALKGVEVRDREGGAPVEVTLEAGKTPDH LFKVFAELSREDVVVIKGIVEASKGYSGVEIFPSEIWILNKAKPLPID
L42	VYPKKTHWTAETIPNLHGTEVVVAGVVDLVDLGRNKLQVSDREGGARVLVNLAAAGKTPDH LFKVFAELSREDVVVIKGIVEASKIQRSGVEIFPSEIWILNKAKPLPID
L6	VYPKKTHWTAETIPNLHGTEVVVAGVVEDLVDAGTKWVFC DREGGAQVIVELVAGKTPDH LFKVFAELSREDVVVIKGIVEASKSRAVGVEIFPSEIWILNKAKPLPID
L5	VYPKKTHWTAETIPNLHGTEVVVAGVVDLVDAGTWKFVQVADREGGANVWVSLVAGKTPDH LFKVFAELSREDVVVIKGIVEASKLPSYGVVEIFPSEIWILNKAKPLPID
L44	VYPKKTHWTAETIPNLHGTEVVVAGVVDLVDAGTWKFVQVADREGGANVWVSLVAGKTPDH LFKVFAELSREDVVVIKGIVEASKPGAAGVEIFPSEIWILNKAKPLPID

References

1. **Rajewsky, K.** 1996. Clonal selection and learning in the antibody system. *Nature* **381**: 751-758.
- 5 2. **Griffiths, A. D., S. C. Williams, O. Hartley, I. M. Tomlinson, P. Waterhouse, W. L. Crosby, R. E. Kontermann, P. T. Jones, N. M. Low, T. J. Allison, and et al.** 1994. Isolation of high affinity human antibodies directly from large synthetic repertoires. *EMBO Journal* **13**: 3245-3260.
- 10 3. **Nissim, A., H. R. Hoogenboom, I. M. Tomlinson, G. Flynn, C. Midgley, D. Lane, and G. Winter.** 1994. Antibody fragments from a 'single pot' phage display library as immunochemical reagents. *EMBO Journal* **13**: 692-698.
4. **Atwell, S., M. Ultsch, A. M. De Vos, and J. A. Wells.** 1997. Structural plasticity in a remodelled protein-protein interface. *Science* **278**: 1125-1128.
- 15 5. **Ballinger, M. D., J. T. Jones, J. A. Lofgren, W. J. Fairbrother, R. W. Akita, M. X. Sliwkowski, and J. A. Wells.** 1998. Selection of heregulin variants having higher affinity for the erbb3 receptor by monovalent phage display. *Journal of Biological Chemistry* **273**: 11675-11684.
6. **Gunneriusson, E., K. Nord, M. Uhlen, and P. A. Nygren.** 1999. Affinity maturation of a taq DNA polymerase specific affibody by helix shuffling. *Protein Engineering* **12**: 873-878.
- 20 7. **Nord, K., J. Nilsson, B. Nilsson, M. Uhlen, and P. A. Nygren.** 1995. A combinatorial library of an alpha-helical bacterial receptor domain. *Protein Engineering* **8**: 601-608.
8. **Binz, H. K., P. Amstutz, and A. Pluckthun.** 2005. Engineering novel binding proteins from nonimmunoglobulin domains. *Nature Biotechnology* **23**: 1257-1268.
- 25 9. **Binz, H. K., and A. Pluckthun.** 2005. Engineered proteins as specific binding reagents. *Current Opinion in Biotechnology* **16**: 459-469.
10. **Hosse, R. J., A. Rothe, and B. E. Power.** 2006. A new generation of protein display scaffolds for molecular recognition. *Protein Science* **15**: 14-27.
11. **Sidhu, S. S., H. B. Lowman, B. C. Cunningham, and J. A. Wells.** 2000. Phage display for selection of novel binding peptides. *Methods in Enzymology* **328**: 333-363.
- 30 12. **Stemmer, W. P. C.** 1994. DNA shuffling by random fragmentation and reassembly: In vitro recombination for molecular evolution. *Proceedings of the National Academy of Sciences of the United States of America* **91**: 10747-10751.
13. **Sidhu, S. S.** 2000. Phage display for selection of novel binding peptides. *Methods in Enzymology* **328**: 333-363.
- 35 14. **Stemmer, W. P. C.** 1994. Rapid evolution of a protein in vitro by DNA shuffling. *Nature* **370**: 389-391.
15. **Zhao, H., and F. H. Arnold.** 1997. Optimisation of DNA shuffling for high fidelity recombination. *Nucleic Acids Research* **25**: 1307-1308.
- 40 16. **Zhao, H., L. Giver, Z. Shao, J. A. Affholter, and F. H. Arnold.** 1998. Molecular evolution by staggered extension process (step) in vitro recombination.[see comment]. *Nature Biotechnology* **16**: 258-261.
17. **Volkov, A. A., and F. H. Arnold.** 2000. Methods for *in vitro* DNA recombination and random chimeragenesis. *Methods in Enzymology* **328**: 447-456.
- 45 18. **Coco, W. M., W. E. Levinson, M. J. Crist, H. J. Hektor, A. Darzins, P. T. Pienkos, C. H. Squires, and D. J. Monticello.** 2001. DNA shuffling method for generating highly

recombined genes and evolved enzymes.[see comment]. *Nature Biotechnology* **19**: 354-359.

19. **Hemminki, A., S. Niemi, A. M. Hoffren, L. Hakalahti, H. Soderlund, and K. Takkinen.** 1998. Specificity improvement of a recombinant anti-testosterone Fab fragment by CDRIII mutagenesis and phage display selection. *Protein Engineering* **11**: 311-319.
20. **Jermutus, L., A. Honegger, F. Schwesinger, J. Hanes, and A. Pluckthun.** 2001. Tailoring in vitro evolution for protein affinity or stability. *Proceedings of the National Academy of Sciences of the United States of America* **98**: 75-80.
21. **Hanes, J., L. Jermutus, and A. Pluckthun.** 2000. Selecting and evolving functional proteins in vitro by ribosome display. *Methods in Enzymology* **328**: 404-430.
22. **Boder, E. T., and K. D. Wittrup.** 2000. Yeast surface display for directed evolution of protein expression, affinity and stability. *Methods in Enzymology* **328**: 430-445.
23. **Altamirano, M. M., J. M. Blackburn, C. Aguayo, and A. R. Fersht.** 2000. Directed evolution of a new catalytic activity using the a/b-barrel scaffold. *Nature* **403**: 617-622.
24. **Arcus, V.** 2002. Ob-fold domains: A snapshot of the evolution of sequence, structure and function. *Current Opinion in Structural Biology* **12**: 794-801.
25. **Arcus, V. L., T. Proft, J. A. Sigrell, H. M. Baker, J. D. Fraser, and E. N. Baker.** 2000. Conservation and variation in superantigen structure and activity highlighted by the three-dimensional structures of two new superantigens from streptococcus pyogenes. *Journal of Molecular Biology* **299**: 157-168.
26. **Murzin, A. G.** 1993. Ob(oligonucleotide/oligosaccharide binding)-fold: Common structural and functional solution for non-homologous sequences. *EMBO Journal* **12**: 861-867.
27. **Qian, J., B. Stenger, C. A. Wilson, J. Lin, R. Jansen, S. A. Teichmann, J. Park, W. G. Krebs, H. Yu, V. Alexandrov, N. Echols, and M. Gerstein.** 2001. Partslist: A web-based system for dynamically ranking protein folds based on disparate attributes, including whole-genome expression and interaction information. *Nucleic Acids Research* **29**: 1750-1764.
28. **Zhang, C., and S. H. Kim.** 2000. A comprehensive analysis of the greek key motifs in protein beta-barrels and beta-sandwiches. *Proteins* **40**: 409-419.
29. **Murzin, A. G., A. M. Lesk, and C. Chothia.** 1994. Principles determining the structure of beta-sheet barrels in proteins. I. A theoretical analysis. *Journal of Molecular Biology* **236**: 1369-1381.
30. **Murzin, A. G., A. M. Lesk, and C. Chothia.** 1994. Principles determining the structure of beta-sheet barrels in proteins. II. The observed structures. *Journal of Molecular Biology* **236**: 1382-1400.
31. **Beekwilder, J., J. Rakonjac, M. Jongsma, and D. Bosch.** 1999. A phagemid vector using the e. Coli phage shock promoter facilitates phage display of toxic proteins. *Gene* **228**: 23-31.
32. **Rakonjac, J., G. Jovanovic, and P. Model.** 1997. Filamentous phage infection-mediated gene expression: Construction and propagation of the gIII deletion mutant helper phage R408d3. *Gene* **198**: 99-103.

33. **Berman, H. M., J. Westbrook, Z. Feng, G. Gilliland, T. N. Bhat, H. Weissig, I. N. Shindyalov, and P. E. Bourne.** 2000. The protein data bank. *Nucleic Acids Research* **28**: 235-242.
- 5 34. **Peat, T. S., J. Newman, G. S. Waldo, J. Berendzen, and T. C. Terwilliger.** 1998. Structure of translation initiation factor 5A from pyrobaculum aerophilum at 1.75 Å resolution. *Structure* **6**: 1207-1214.
35. **Schmitt, E., L. Moulinier, S. Fujiwara, T. Imanaka, J. C. Thierry, and D. Moras.** 1998. Crystal structure of aspartyl-tRNA synthetase from pyrococcus kodakaraensis kod: Archaeon specificity and catalytic mechanism of adenylate formation. *EMBO Journal* **17**: 5227-5237.
- 10 36. **Moulinier, L., S. Eiler, G. Eriani, J. Gangloff, J. C. Thierry, K. Gabriel, W. H. McClain, and D. Moras.** 2001. The structure of an AspRS-tRNA(Asp) complex reveals a tRNA-dependent control mechanism. *EMBO Journal* **20**: 5290-5301.
- 15 37. **Rees, B., G. Webster, M. Delarue, M. Boeglin, and D. Moras.** 2000. Aspartyl tRNA-synthetase from Escherichia coli: Flexibility and adaptability to the substrates. *Journal of Molecular Biology* **299**: 1157-1164.
38. **Guex, N., and M. C. Peitsch.** 1997. SWISS-MODEL and the Swiss-PdbViewer: An environment for comparative protein modeling. *Electrophoresis* **18**: 2714-2723.
39. **Peitsch, M.** 1995. Protein modeling by e-mail. *Bio/Technology*: 658-660.
- 20 40. **Schwede, T., J. Kopp, N. Guex, and M. C. Peitsch.** 2003. SWISS-MODEL: An automated protein homology-modeling server. *Nucleic Acids Research* **31**: 3381-3385.
41. **Sambrook, J., and D. W. Russel.** (2001) *Molecular cloning a laboratory manual*, 3rd Ed., Cold Spring Harbor Laboratory Press, New York
- 25 42. **Fitz-Gibbon, S. T., H. Ladner, U. J. Kim, K. O. Stetter, M. I. Simon, and J. H. Miller.** 2002. Genome sequence of the hyperthermophilic crenarchaeon pyrobaculum aerophilum. *Proceedings of the National Academy of Sciences of the United States of America* **99**: 984-989.
43. **Bullock, W. O., J. M. Fernandez, and J. M. Short.** 1987. Xl1-blue - a high-efficiency plasmid transforming recA Escherichia-coli strain with beta-galactosidase selection. *Biotechniques* **5**: 376-&.
- 30 44. **Rakonjac, J., J. Feng, and P. Model.** 1999. Filamentous phage are released from the bacterial membrane by a two-step mechanism involving a short C-terminal fragment of pIII. *Journal of Molecular Biology* **289**: 1253-1265.
45. **Barbas III, C., D. Burton, J. Scott, and G. Silverman.** (2001) *Phage display a laboratory manual*, Cold Spring Harbor Laboratory Press, New York
- 35 46. **Gough, J., K. Karplus, R. Hughey, and C. Chothia.** 2001. Assignment of homology to genome sequences using a library of hidden Markov models that represent all proteins of known structure. *Journal of Molecular Biology* **313**: 903-919.
47. **Bogden, C. E., D. Fass, N. Bergman, M. D. Nichols, and J. M. Berger.** 1999. The structural basis for terminator recognition by the Rho transcription termination factor. *Molecular Cell* **3**: 487-493.
- 40 48. **Hoogenboom, H. R., A. P. de Bruine, S. E. Hufton, R. M. Hoet, J. W. Arends, and R. C. Roovers.** 1998. Antibody phage display technology and its applications. *Immunotechnology* **4**: 1-20.

49. **Brevet, A., J. Chen, S. Commans, C. Lazennec, S. Blanquet, and P. Plateau.** 2003. Anticodon recognition in evolution - switching tRNA specificity of an aminoacyl-tRNA synthetase by site-directed peptide transplantation. *Journal of Biological Chemistry* **278**: 30927-30935.
- 5 50. **Wahlberg, E., C. Lendel, M. Helgstrand, P. Allard, V. Dincbas-Renqvist, A. Hedqvist, H. Berglund, P. A. Nygren, and T. Hard.** 2003. An affibody in complex with a target protein: Structure and coupled folding. *Proceedings of the National Academy of Sciences of the United States of America* **100**: 3185-3190.
- 10 51. **Gunnarsson, L. C., E. N. Karlsson, A. S. Albrekt, M. Andersson, O. Holst, and M. Ohlin.** 2004. A carbohydrate binding module as a diversity-carrying scaffold. *Protein Engineering Design & Selection* **17**: 213-221.
- 15 52. **Berdichevsky, Y., E. Ben-Zeev, R. Lamed, and I. Benhar.** 1999. Phage display of a cellulose binding domain from *Clostridium thermocellum* and its application as a tool for antibody engineering. *Journal of Immunological Methods* **228**: 151-162.

CLAIMS

What is claimed is:

1. An isolated modified OB-fold domain, obtainable from a naturally occurring OB-fold domain, wherein said modified OB-fold domain comprises
 - a) at least one modified amino acid residue in a β - strand of the OB-fold domain binding face as compared to the naturally occurring OB-fold domain, or
 - b) at least one modified amino acid residue in a β - strand of the OB-fold domain binding face and at least one modified amino acid residue in a strand of the OB-fold domain loop region, or
 - c) at least one modified amino acid residue in a strand of the OB-fold domain loop region,and wherein said modified OB-fold domain has altered binding characteristics as compared to the naturally occurring OB-fold domain.
2. The modified OB-fold domain of claim 1 wherein said domain specifically binds to a different binding partner than the naturally occurring OB-fold domain or has modified binding with its naturally occurring binding partner.
3. The modified OB-fold domain of claim 1 or claim 2 wherein said naturally occurring OB-fold domain occurs in a protein or class of proteins selected from the group consisting of Staphylococcal nuclease proteins; Bacterial enterotoxins; TIMP-like proteins; Heme chaperone CcmE protein; Tail-associated lysozyme gp5, N terminal domain

protein; nucleic acid-binding proteins; inorganic pyrophosphatase;
 Mop-like proteins; CheW like proteins; tRNA_anti (OB-fold nucleic
 acid binding domain); Telo_bind (telomere-binding protein alpha
 subunit, central domain); SSB (single-stranded binding protein family
 5 OB-fold domain); DUF338 OB-fold domain;
 DNA_ligase_aden_ (NAD-dependent DNA ligase OB-fold
 domain); Stap-Stp-toxin (Staphylococcal/Streptococcal toxin, OB-fold
 domain); EIF-5a (Eucaryotic initiation factor 5A hypusine, DNA-
 binding OB-fold domain); GP5_OB (GP5 N-terminal OB-fold
 10 domain), CSD, DNA_ligase_OB, DUF388, EFP, eIF-1a,
 mRNA_cap_C, OB_RNB, Phage_DNA_bind, Rep-A_N,
 Rho_RNA_bind, Ribosomal_L2, Ribosomal_S12, Ribosomal_S17,
 RNA_pol_Rpb8, RuvA_N, S1, TOBE, TOBE_2, and tRNA_bind.

4. The modified OB-fold domain of claim 1 or claim 2 wherein said
 15 naturally occurring OB-fold domain is from a thermophilic organism.
5. The modified OB-fold domain of claim 4, wherein said thermophilic
 organism is *Pyrobaculum aerophilum*.
6. The modified OB-fold domain of any of claims 1-5 wherein said
 20 modified amino acid residue is in a β -strand of the fold-related
 binding face.
7. The modified OB-fold domain of any of claims 1-6, wherein the
 binding partner of the modified OB-fold domain is selected from the
 group comprising nucleic acids, oligosaccharides, proteins, hormones,
 and small organic molecules.
8. A method of obtaining a modified OB-fold domain of any of claims 1-
 25 7, comprising:

- a) obtaining nucleic acid encoding a naturally occurring OB-fold domain, or encoding a portion thereof comprising a strand of the binding face and/or a strand of the loop, and
- b) altering the nucleic acid such that it encodes at least one modified amino acid residue on a β -strand of the binding face and/or at least one modified amino acid residue on a strand of a loop as compared to the naturally occurring OB-fold domain, wherein a modified OB-fold domain is obtained and wherein said modified OB-fold domain has altered binding as compared to said naturally occurring OB-fold domain.
9. The method of claim 8 further comprising, altering nucleic acid encoding said modified OB-fold domain, and/or altering nucleic acid encoding at least one amino acid of a protein that comprises said modified OB-fold domain.
10. A method of producing a library of modified OB-fold domain proteins for display comprising,
- a) obtaining nucleic acid encoding an OB-fold domain, or a portion thereof, and
- b) subjecting said nucleic acid to random alterations, thereby producing a collection of altered nucleic acid encoding modified OB-fold domains having at least one randomized amino acid residue.
11. The method of claim 10 wherein said nucleic acid encodes at least one amino acid residue of a strand of the OB-fold domain binding face and/or a strand of an OB-fold domain loop.

12. The method of claim 10 or claim 11, further comprising placing the library of altered nucleic acid encoding modified OB fold domains into a population of host cells capable of displaying said modified OB-fold domains on their surface.
- 5 13. An isolated nucleic acid encoding the modified OB-fold domain of any of claims 1-7.
14. A host cell comprising a nucleic acid encoding the modified OB-fold domain of any of claims 1-7.
- 10 15. A phage comprising a nucleic acid encoding the modified OB-fold domain of any of claims 1-7.
16. A composition comprising a nucleic acid encoding the modified OB-fold domain of any of claims 1-7.
17. A method of screening a library of modified OB-fold domains for binding with a binding partner, comprising:
- 15 a) obtaining a population of host cells or viral particles displaying a library of modified OB-fold domains on their surface;
- b) contacting said population of host cells or viral particles with said binding partner under conditions suitable for binding of said binding partner to said modified OB-fold domain; and
- 20 c) determining binding of said binding partner to said modified OB-fold domain.
18. The method of claim 17 wherein said host cells or viral particles are phage that display the modified OB-fold domains on their surface.

19. A phage library of modified OB-fold domains of any of claims 1-7,
wherein said modified OB-fold domains are obtainable from
Pyrobaculum aerophilum.
- 5 20. A modified OB-fold domain of any of claims 1-7 displayed on the
surface of a cell or viral particle.
21. The modified OB-fold domain of claim 20 wherein said cell or viral
particle is a phage, bacteria or yeast.
23. A modified OB-fold domain of any of claims 1-7 attached to a solid
support.
- 10 24. The modified OB-fold domain of claim 23 wherein said support is
selected from the group consisting of beads, glass, slides, chips, and
gelatin.