

1 Geräte

Gerät	Typ	Hersteller
Absauganlage	Manuell	Sartorius, Göttingen
Analysenwaage	CP64	Sartorius, Göttingen
Autoklav	Varioklav 400 EP	H+P Labortechnik, Oberschleißheim
Brutschrank	B5042	Heraeus/Kendro, Osterode
Elektrophoresekammern	Agagel Mini	Biometra, Göttingen
	Mini-Sub Cell GT	Bio Rad, München
	Mini-Protean II	Bio Rad, München
Geldokumentationsanlage	Gel Doc 2000	Bio Rad, München
Gefriertrockner	Beta A mit Speed Vac Concentrator	Heraeus Christ Savant
Geltrockner	Unigeldryer 4050D	UniEquip, Leipzig
Inkubationsschüttler	Thermomixer 5436	Eppendorf, Hamburg
Magnetrührer	IKA Combimag RCT	Janke & Kunkel, Staufen
Mikrowellenofen	ER-7720 DC	Toshiba
Netzgeräte	ECPS 3000/150	Pharmacia/Amersham
pH-Meter	761 Calimatic	Knick, Berlin
Phosphorimager	Storm 840	Molecular Dynamics/Amersham
Pipetten	Pipetman P2, 10, 20, 100, 200, 1000	Gilson, Bad Camburg
Reinstwasseranlage	Milli-Q	Millipore, Eschborn
Rotoren	JA-14, JA-17	Beckman, München
Scanner	Snapscan 1212U	Agfa, Köln
Schüttler	Vortex Genie 2	Bender & Hobein, Zürich
Spektralphotometer	UV-260	Shimadzu, Duisburg
Szintillationszähler	LS 6000 SC	Beckman, München
Thermozykler	PCT-100 PCR Sprint	MJ Research, Inc Hybaid, Heidelberg
Ultraschallbad	Sonorex RK 102	Bandelin, Berlin
UV-Transilluminator	Reprostar II	Camag, Berlin
Waage	1401 MP8	Sartorius, Göttingen
Wasserbäder	1002	GFL, Burgwedel
Zentrifugen	Mikrocentrifuge 5415 C Biofuge A J2-21 Optima TL Ultracentrifuge	Stratagene, Heidelberg Eppendorf, Hamburg Heraeus/Kendro, Osterode Beckman, München Beckman, München

2 Enzyme, Proteine, Nukleinsäuren und Chemikalien

Alkalische Phosphatase	Roche, Mannheim
Anorganische Pyrophosphatase	Sigma Aldrich, Taufkirchen
Aprotinin	Roche, Mannheim
Bulk-tRNA	Roche, Mannheim
DNA-Längenstandards:	
100-1000 bp	Bioline, Luckenwalde
200-10000 bp	Bioline, Luckenwalde
50-2000 bp	Bioline, Luckenwalde
DNA Oligomere	IBA, Göttingen; Metabion, Martinsried
DNase I	Roche, Mannheim
DNase I (RNase frei)	Roche, Mannheim
Exonuclease III	Promega, Mannheim
Leupeptin	Roche, Mannheim
M-MLV Reverse Transkriptase (RNase H)	Promega, Mannheim
Mung Bean Nuclease	Promega, Mannheim
Proteinase K	Gibco/ Invitrogen
Protein-Molekulargewichtsstandard:	
LMW-6 (14,4-94 kDa)	Amersham Bioscience, Freiburg
¹⁴ C-Marker (2,5-30 kDa)	Amersham Bioscience, Freiburg
<i>Pfu</i> -, <i>Pwo</i> -Polymerase	Roche, Mannheim
Pyruvatkinase	Roche, Mannheim
Radioaktivität:	
³⁵ S-CTP	Amersham Bioscience, Freiburg
¹⁴ C-Leu	Amersham Bioscience, Freiburg
Restriktionsendonukleasen	NEB, Frankfurt a. M.; Roche, Mannheim; Gibco; Promega, Mannheim
Rinderserumalbumin	Roche, Mannheim
RNase Inhibitor	Promega, Mannheim
Superscript III reverse Transcriptase (RNase H)	Invitrogen
T4 DNA-Ligase	Roche, Mannheim
T4 Polynukleotidkinase	Stratagene, Heidelberg
T7 RNA Polymerase	Stratagene, Heidelberg
<i>Taq</i> DNA Polymerase	Promega, Mannheim
tRNA aus <i>E. coli</i> MRE 600	Roche, Mannheim
dNTPs	Bioline, Luckenwalde
NTPs	Roche, Mannheim
Heparin	Roth, Karlsruhe

Nonidet P40	Roche, Mannheim
Sialyl-Lewis X	Calbiochem/ VWR, Bad Soden/Berlin
Streptomycin	Roth, Karlsruhe; Sigma Aldrich, Taufkirchen

Alle Chemikalien halten den Reinheitsgrad p.A. und wurden von folgenden Unternehmen bezogen.

Fluka Chemie AG, Heidelberg
 Merck, Darmstadt
 Roth, Karlsruhe
 Sigma Aldrich, Deisenhofen
 Serva, Heidelberg
 VWR, Darmstadt

Kits

Plasmid-Isolierung

PRM Turbo	QBiogene, Heidelberg
Plasmid DNA Purification	Macherey&Nagel, Düren
JET Star Plasmidprep Kit	Genomed, Löhne

DNA-Extraction/Purification

High Pure PCR Purification Kit	Roche, Mannheim
GFX	Amersham Bioscience, Freiburg
Quick Clean	Bioline, Luckenwalde Macherey&Nagel, Düren

RNA Isolation

High Pure RNA Purification Kit	Roche, Mannheim
--------------------------------	-----------------

Ligation

pGEM-T Easy Vector SystemII	Promega, Mannheim
-----------------------------	-------------------

Sonstiges

Epoxyaktivierte Sepharose 6B	Amersham Bioscience, Freiburg
Glasfilter GF/C	Whatman, Merck, Darmstadt
Heparin-Sepharose CL-6B	Amersham Bioscience, Freiburg
Filterpapier DE 81	Whatman
Filterpapier 3MM	Whatman
Minisäulen mit Fritten Mobicols	MoBiTec, Göttingen
NAP-5 Column	Amersham Bioscience, Freiburg
Quarzküvette 104-QS	Hellma, Müllheim
Szintillationsvials Minis 2000	Zinsser Analytik, Fankfurt/a.M

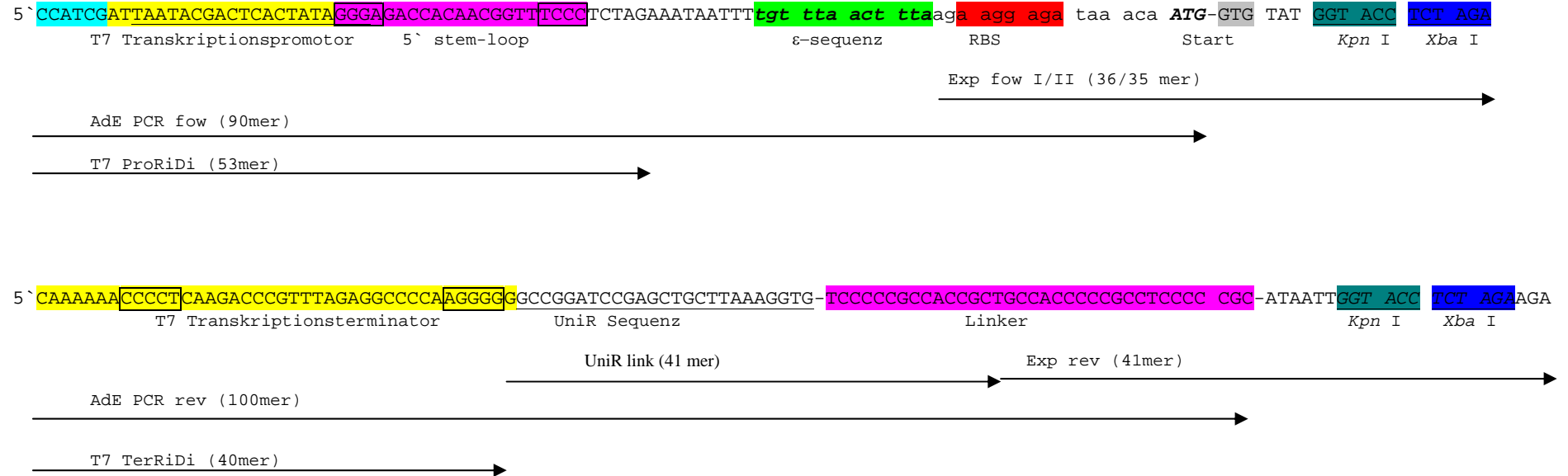
3 Primersequenzen

Name	Sequenz 5'-3'	Nukleotidanzahl	T _m in °C
Bst fd	ATG GAC AAA AAG AAA GCA G	19	50,2
Bst rev	TTA CGA TGC TGA TTT TGT TCC	21	54
Aki fd	ATG AAG AAC CTC AAA AAG TTA ATA	24	52,5
Aki rev	TAT TAT TGT ACT ATT TCT ATT AC	23	48,2
Bsph fd	GCC GGG TTT TCG GAT GTT G	19	58,8
Bsph rev	TAG ATG AG CGA ATT GTC CG	20	55,3
Thth fd	ATG AAG AAA AGG CTG GTC	18	51,4
Thth rev	TTA GAA CTT TAC GGT GTA	19	50,2
Eac fd	CCG GAA ACG CCT AAG ACG GCT GC	23	67,8
Eac rev	CTA CTG GTT GTC ATC TAC CCA TAT TG	26	61,6
Aki fXbaSLH	TCT AGA AAG AAC CTC AAA AAG TTA ATA	27	59,6
Aki rXbaSLH	TCT AGA TTA TGC AAC TTT TGA AAT GAG	27	66,3
Aki fKpnSLH	ATA TAT GGT ACC TCT AGA AAG AAC CTC AAA	30	63
Aki rKpnSLH	TTA ATT GGT ACC TCT AGA TTA TGC AAC TT	29	63,4
Ea fXbaSLH	TCT AGA CCG GAA ACG CCT AAG ACG G	25	55,8
Ea rXbaSLH	TCT AGA TTA CTC GTT CTG GCC GAA G	25	57,4
Ea fKpnSLH	ATA TAT GGT ACC TCT AGA CCG GAA ACG	27	61,3
Ea rKpnSLH	TTA ATT GGT ACC TCT AGA TTA CTC GTT CTG	30	62,7
Bsph fXbaSLH	TCT AGA GCC GGG TTT TCG GAT GTT	24	62,7
Bsph rXbaSLH	TCT AGA TTA TAG ATG AAG CGA ATT GTC	27	58,9
Bsph fKpnSLH	ATA TAT GGT ACC TCT AGA GCC GGG TTT	27	63,4
Bsph rKpnSLH	TTA ATT GGT ACC TCT AGA TAG ATG AAG	27	58,9
Th th f2	TCA CAC TGC TGG CAG GGC	18	60,5
Th th rev2	TG AGC TGA TCT TGA AGG CCT	21	57,9
Bst fXbaSLH	TCT AGA GCA ACG GAC GTG GCG AC	23	66
Bst rXbaSLH	TCT AGA TTA AGT TAC AGT AGC AGT TAA	27	57,5
Bst fKpnSLH	ATA TAT GGT ACC TCT AGA GCA ACG GAC GTG	30	66,8
Bst rKpnSLH	TTA ATT GGT ACC TCT AGA TTA AGT TAC AGT	30	59,9
Th fXbaSLH	TCT AGA GTC ACA CTG CTG GCA GGG	24	66,1
Th rXbaSLH	TCT AGA TTA GAA CTC CTG GAC GGC	25	64,6
Th fKpnSLH	ATA TAT GGT ACC TCT AGA GTC ACA CTG CTG	30	65,4
Th rKpnSLH	TTA ATT GGT ACC TCT AGA TTA GAA CTC C	28	60,7
Aki rXbaSlp	TCT AGA TTA TTG TAC TAT TTC TAT TAC	27	54,3
Aki rKpnSlp	TTA ATT GGT ACC TCT AGA TTA TTG TAC	27	57,4
Th rXbaSlp	TCT AGA TTA GAA CTT TAC GGT GTA G	25	58,1
Th rKpnSlp	TTA ATT GGT ACC TCT AGA TTA GAA CTT TAC	30	59,9
Ea rXbaSlp	TCT AGA CTA CTG GTT GTC ATC TAC C	25	61,3
Ea rKpnSlp	TTA ATT GGT ACC TCT AGA CTA CTG G	25	59,7
Bst rXbaSlp	TCT AGA TTA CGA TGC TGA TTT TGT ACC	27	60,4
Bst rKpnSlp	TTA ATT GGT ACC TCT AGA TTA CGA TGC	27	60,4

VII ANHANG

T7 pBsk	GTA ATA CGA CTC ACT ATA GGG C	22	58,4
T3 pBsk	AAT TAA CCC TCA CTA AAG GG	20	53,2
ThDNAPol fKpn	CAC GGT ACC GAG GCG ATG CTT CCG	24	69,6
ThDNAPol rEco	TTA ATT GAA TTC CTA ACC CTT GGC GGA	27	61,9
Shuffel	ATA TGG TAC CTC TAG A	16	44,1
pBsk SK	CGC TCT AGA ACT AGT GGA TC	20	57,3
pBsk KS	TCG AGG TCG ACG GTA TCG	18	58,2
pASK2 Seq f	GAG TTA TTT TAC CAC TCC C	19	52,4
pASK2 Seq r	CGC AGT AGC GGT AAA CG	17	55,2
Exp fow.I	AGA AGG AGA TAA ACA ATG GTG TAT GGT ACC TCT AGA	36	
Exp fow.II	AGA AGG AGA TAA ACA ATG GTG ATG GTA CCT CTA GA	35	
Exp.rev	GCC ACC CCC GCC TCC CCC GCA TAA TTG GTA CCT CTA GAA GA	38	
AdE-PCR fow	CCA TCG ATT AAT ACG ACT CAC TAT AGG GAG ACC ACA ACG GTT TCC CTC TAG AAA TAA TTT TGT TTA ACT TTA AGA AGG AGA TAA ACA ATG	90	
AdE-PCR rev	CAA AAA ACC CCT CAA GAC CCG TTT AGA GGC CCC AAG GGG GGC CGG ATC CGA GCT GCT TAA AGG TGT CCC CCG CCA CCG CTG CCA CCC CCG CCT CCC CCG C	100	
T7 ProRiDi	CCA TCG ATT AAT ACG ACT CAC TAT AGG GAG ACC ACA ACG GTT TCC CTC TAG	51	
T7 TerRiDi	CAA AAA ACC CCT CAA GAC CCG TTT AGA GGC CCC AAG GGG G	40	
UniR Link	GGC CGG ATC CGA GCT GCT TAA AGG TGT CCC CCG CCA CCG CT	41	
AS-Oligo	TTA AGC TGC TAA AGC GTA GTT TTC GTC GTT TGC GAC TA	38	

4 Übersicht über die Primer der Expressions-PCR und des „*Ribosome Display*“



5 SLH- und Slp-Sequenzen aus:

5.1 *Acetogenium kivui*

1 ATGAAGAACC TCAAAAAGTT AATAGCAGTG GTCTCCACCT TCGCATTGGT
 M K N L K K L I A V V S T F A L V
 51 GTTCAGTGCG ATGGCAGTAG GGTTTGCTGC AACGACACCG TTCACCGATG
 F S A M A V G F A A T T P F T D V
 101 TGAAAGATGA TGCACCTTAT GCATCAGCAG TGGCTCGTCT GTATGCTCTT
 K D D A P Y A S A V A R L Y A L
 151 AATATCACGA ATGGTGTAGG AGATCCCAAA TTTGGTGTAG ATCAGCCAGT
 N I T N G V G D P K F G V D Q P V
 201 TACAAGAGCT CAGATGATTA CATTTCGTAAA CAGAATGCTG GGCTATGAAG
 T R A Q M I T F V N R M L G Y E D
 251 ACTTAGCTGA AATGGCTAAG AGCGAGAAAT CAGCATTTAA AGATGTACCA
 L A E M A K S E K S A F K D V P
 301 CAAAATCACT GGGCAGTTGG ACAAATTAAC TTGGCTTACA AATTAGGGCT
 Q N H W A V G Q I N L A Y K L G L
 351 GGCGCAAGGT GTTGAAATG GTAAATTTGA TCCAAATAGC GAGCTGAGAT
 A Q G V G N G K F D P N S E L R Y
 401 ATGCACAAGC ATTGGCATT TATTAAAGAG CACTTGGCTT CAAAGACCTT
 A Q A L A F V L R A L G F K D L
 451 GACTGGCCTT ATGGTTATCT CGCTAAAGCT CAAGACCTCG GACTAGTACA
 D W P Y G Y L A K A Q D L G L V H
 501 TGGCTTAAAT CTTGCCTACA ACGGAGTAAT TAAACGTGGT GACTTGGCAT
 G L N L A Y N G V I K R G D L A L
 551 TAATATTGGA CAGAGCATTG GAAGTACCAA TGGTTAAATA TGTAGATGGC
 I L D R A L E V P M V K Y V D G
 601 AAAGAAGTGC TTGGAGAGCC GCTCATTTC A AAGTTGCAA CAAAGGCAGA
 K E V L G E P L I S K V A T K A E
 651 ATATACAGTA ATAGCTACAA ATGCTCAAGA CAGGTCAGTT GAGGAAGGCA
 Y T V I A T N A Q D R S V E E G K
 701 AAGTTGCAGT ATTAGACAAG GATGGTAAAT TAACTACTAT TAACGCAGGT
 V A V L D K D G K L T T I N A G
 751 CTTGTTGACT TTTCAGAATA TCTTGGCAAA AAAGTAATTG TATACTCAGA
 L V D F S E Y L G K K V I V Y S E
 801 GAGATTTGGT GACCCGGTAT ATGTTGCTGA AGGAGATAAT GATGTTGTAA
 R F G D P V Y V A E G D N D V V S
 851 GCTTTACAGA AGGTCAAGAT TCCGTTGGTA CAACAGTATA TAAGAATGAT
 F T E G Q D S V G T T V Y K N D
 901 GATAATAAAA CTGCTATAAA AGTTGATGAT AATGCGTATG TACTTTACAA
 D N K T A I K V D D N A Y V L Y N
 951 TGGCTATTTG ACAAAGTTT CTAAAGTGAC TGTA AAAAGAA GGTGCGGAAG
 G Y L T K V S K V T V K E G A E V
 1001 TAACAATTAT AAACAACAAC TATCTCATTG TAAATGGTTC TTATGACAAC
 T I I N N N Y L I V N G S Y D N
 1051 TCAACAATTG TGTACAATGA TGTACAAAGT GGTGACAAGT ACCTCAATAG
 S T I V Y N D V Q S G D K Y L N R
 1101 AGATTCTAAT TACGAATTGA AAGGAACAGT AACAGTAACA GGTGCAGTAT
 D S N Y E L K G T V T V T G A V S
 1151 CAAAAGTAAC AGATATTTAAA GCTAATGATT ATATCTACTA TGGCAAGCAA
 K V T D I K A N D Y I Y Y G K Q
 1201 TATGATGTAA ATGGAATGT TGTGGGAACA GTAATATACG TTGTAAGAAA
 Y D V N G N V V G T V I Y V V R N
 1251 TCAGGTAACCT GGTACTGTTA CAGAAAAGTC TGTCAGTGGT TCAACATATA
 Q V T G T V T E K S V S G S T Y K
 1301 AGGCTTCCAT AGATAATGTT TCTTATACTG TAGCTGATAA TAATGTATGG
 A S I D N V S Y T V A D N N V W

VII ANHANG

1351 AATCAGCTTG AACCAGGTAA GAAAGTAACA GTCATACTTA ATAAAGATAA
 N Q L E P G K K V T V I L N K D N
 1401 TGTAATTGTA GGAATATCTT CAACAACACTAC AACCAACAGCT GTAAAT'TATG
 V I V G I S S T T T T T A V N Y A
 1451 CTATATTTAA AGAGAAATCA GATCCATTTA CTGCTTGGTT TGCAAAAGTG
 I F K E K S D P F T A W F A K V
 1501 AAGTTGATCC TGCCAGATGC TGCAGAAAAA GTATTTGATG CGGTGTACAG
 K L I L P D A A E K V F D A V Y S
 1551 CGACGTATAT GATAAAGTCA ACTTAGCGGA AGGTACTATA GTAACCTATA
 D V Y D K V N L A E G T I V T Y T
 1601 CAGTTGATGC AAATGGTAAA TTAAATGACA TACAGAGGGC AAATGATCAA
 V D A N G K L N D I Q R A N D Q
 1651 CCATTTAGCA GTGCTTCATA TAAAGCTGAT GCAAAAAGTAT TAACTGAAGG
 P F S S A S Y K A D A K V L T E G
 1701 TAGTACGACA TACTACATCA CAGACAACAC AGTGCCTTCTT AACACACAA
 S T T Y Y I T D N T V L L N N T S
 1751 GTGATGGTTA TAAAGCATT AACTGACAG ATCTAAAAGA TGCTACAAAC
 D G Y K A L K L T D L K D A T N
 1801 CTGAACGTTA AGATTGTAGC GGATAATTAC AATGTGGCAA AGGTAGTAGT
 L N V K I V A D N Y N V A K V V V
 1851 ATTTAATAAT GCATCTTTTG TATCAACTAC AACATCTACA GTTTATGCAT
 F N N A S F V S T T T S T V Y A Y
 1901 ATGTAACAGG TACAGCAGAT GTGTACGTAA ATGGCTCAAC ATTTACTAGA
 V T G T A D V Y V N G S T F T R
 1951 TTAACAGTTC TTGAAAATGG TCAAACAAAG ACATATGATG CAAATGCACA
 L T V L E N G Q T K T Y D A N A Q
 2001 ATTAGCTACA AATTATACAC ATAAAGCGGT TGTATTAACA TTAAC TAATG
 L A T N Y T H K A V V L T L T N A
 2051 CAAAAATTGC AAACATTGCG TTGCCAACGG TTGCTTCAGG AGTAAAATTA
 K I A N I A L P T V A S G V K L
 2101 ACAAATATTG ATCAAGCTAA TTTAAGAATT ACTGATACTA CCAATAAAGG
 T N I D Q A N L R I T D T T N K G
 2151 ATATCTCTTG GATCCTAACT TTATAGTAGT AGATACAAAT GGTAATCTCA
 Y L L D P N F I V V D T N G N L K
 2201 AAGGATTAAG CGATATTACA AAGGATACAG GAGTTAACCT CTATACTAAC
 G L S D I T K D T G V N L Y T N
 2251 GACGTAGGTA AAGTATTTGT AATAGAAATA GTACAATAA 3'
 D V G K V F V I E I V Q *

Abb. 39: Sequenz des S-layer-Proteins aus *Acetogenium kivui* (DSM 2030), 2289 bp (AC: M31069), 763 Aminosäuren (ID: AAA21930.1). Unterstrichen die putative SLH-Sequenz (3-639).

5.2 *Bacillus sphaericus*

1 ATGGCTAACC AACCAAAGAA ATACAAAAAA TTCGTAGCGA CGGCAGCAAC
 M A N Q P K K Y K K F V A T A A T
 51 GGCAACATTA GTAGCATCTG CTATCGTACC AGTGGCTTCT GCAGCAGGAT
 A T L V A S A I V P V A S A A G F
 101 TTTCAGATGT AGCAGGTAAC GACCACGAAG TAGCAATCAA CGCACTTGCT
 S D V A G N D H E V A I N A L A
 151 GATGCAGGTA TCATCAATGG ATACGCTGAC GGCACATTCA AACCAAACCA
 D A G I I N G Y A D G T F K P N Q
 201 AACAATTAAC CGCGGTCAAG TGGTTAAATT ATTAGGTCGT TATTTAGAAG
 T I N R G Q V V K L L G R Y L E A
 251 CACAAGGCCA AGAAATCCA GCTGACTGGA ATTCAAACA ACGCTTCAAC
 Q G Q E I P A D W N S K Q R F N
 301 GATCTACCAG TAACAGCTGA AGCAGAATTA GTAAAATATG CTGCACTAGC
 D L P V T A E A E L V K Y A A L A

VII ANHANG

351 AAAAGATGCA GCGTATTCA ACGGTTCAAA CGGCAACTTA AACGCTTCAC
K D A G V F N G S N G N L N A S Q
401 AAACAATGCA ACGTCAACAA ATGGCAGTAG TTTTAGTACG TGCTAT'AAA
T M Q R Q Q M A V V L V R A I K
451 GAAATCGCTG GCGTAGACTT AGTAGCTGAG TACAAAAAAG CGAATTTTCGT
E I A G V D L V A E Y K K A N F V
501 AACAGAAAT' GGTGACTTAG ACAAAGCTTA CTCTGCAGAA CAACGCACAG
T E I G D L D K A Y S A E Q R T A
551 CGATCGTTGC TTTAGAATAT GCGGGTATTA CAAATGTTGC TCACTTCAAC
I V A L E Y A G I T N V A H F N
601 CCAGGTAACA GCGTAACACG CGGACAATTC GCTTCATTCT TATACCGCAC
P G N S V T R G Q F A S F L Y R T
651 AATCGAAAAAC GTGGTAAACG CTCCTGAAGC TGGCGCTGCG GCAGTGAAAG
I E N V V N A P E A G A A A V K A
701 CTGTAAACAA CACAAC'GTT GAAGTAACAT TCGACGAAGA AGTAGACAAC
V N N T T V E V T F D E E V D N
751 GTACAAGCTC TTAAC'TTCTT AATCTCTGAT TTAGAAGTGA AAAACGCAGC
V Q A L N F L I S D L E V K N A A
801 TGTA AAAACAA ACTAACAAAA AAGTTGTTGT TTTAACTACT GCACCTCAAA
V K Q T N K K V V V L T T A P Q T
851 CTGCTGACAA AGAGTACACT GTATCTCTTG GCGAAGAAAA AATTGGTACT
A D K E Y T V S L G E E K I G T
901 TTCAAAGGTA TCGCAGCTGT AGTTCCTACT AAAGTAGATT TAGTAGAAAA
F K G I A A V V P T K V D L V E K
951 ATCAGTTCAA GGTAAACTTG GCCAACAAGT AACACTGAAA GCACAAGTAA
S V Q G K L G Q Q V T L K A Q V T
1001 CAGTTGCTGA AGGTCAAACA AAAGCTGGTA TTCCAGTAAC TTTCTTCATC
V A E G Q T K A G I P V T F F I
1051 CCAGGTTCTG CTAATGGTGT GAAATCTCCA GTAACAGTTG AAGCTGTAAC
P G S A N G V K S P V T V E A V T
1101 AGATGAAAAAC GGTGTTGCTT CTTATACTTA CACTCGTTAC GCTGCAACAA
D E N G V A S Y T Y T R Y A A T N
1151 ACGACACAGT AACTGTATAC GCGAACGGTG ACCGTTCTAA ATTCTCAACT
D T V T V Y A N G D R S K F S T
1201 GGTATATGTCT TCTGGGCTGT TGATCAACAT CTAACGATTA CTGAAGTAAC
G Y V F W A V D Q H L T I T E V T
1251 AACTGGTAAT ACAATCAACA ACGGAGCTAA CAAAACGTAT AAAGTCACTT
T G N T I N N G A N K T Y K V T Y
1301 ACAAACACCC GGAAACTGGT AGACCGGTAT CAGGTAAAGT ACTAAACGTT
K H P E T G R P V S G K V L N V
1351 TCTGTA'CTTG AAAACATTGA TGTAACCGTT GATAAATTAC AAAACGTTAC
S V L E N I D V T V D K L Q N V T
1401 GGTGAATGGT GTTGC'GTTAG TTCAAACGAG CGAAAATAAC ATGCGAGCTG
V N G V A V V Q T S E N N M R A A
1451 CACAAATCAC AACTGATTCA AAAGGTGAAG CAACATTCAC AATTT'CAAGT
Q I T T D S K G E A T F T I S G
1501 TCTAACGCTA CAGTTACTCC AGTAGTATTT GAAGCTGCTT CAACTAATGT
S N A T V T P V V F E A A S T N V
1551 TGCAAACACT TACTCTCAA AATATACAGC AGATACTA CAAGCTGTTG
A N T Y S P K Y T A D T L Q A V A
1601 CGTCTAAAAT AACATTTGGT GCTATTCAAG CTGCTTATAC AATTGAAGTA
S K I T F G A I Q A A Y T I E V
1651 ACTCGTGATG GTGGT'GAAAC TGCTGCTACT GGAGTTTTAA ACGGACGTA
T R D G G E T A A T G V L N G R K
1701 ATACAATGTA GTGGTTAAAG ATAAAGATGG TAAAGTAGCT GCTAACGAAA
Y N V V V K D K D G K V A A N E I
1751 TTGTTAACGT GGCATTTAAC GAAGATATTG ATGGCGTAAT TTCTACAGTT
V N V A F N E D I D G V I S T V
1801 ACTTCTGCTC AATTCGTA'AAA AATCGAAAAAC GGTAAACAAG TTGGCTACAA
T S A Q F V K I E N G K Q V G Y N

VII ANHANG

1851 TGGTAAGAAA ATTACGGTTA CAACAAACTC TAAAGGTGAA GCAAGCTTCG
 G K K I T V T T N S K G E A S F V
 1901 TCATCGGAAG TGACGCTGTA AATTCTTACG CTACACCAAT CGTTTGGATT
 I G S D A V N S Y A T P I V W I
 1951 GACATCAATA ACCAAAGTGG TAAAGATGCA AACTTAGACA AAGGTGAGCC
 D I N N Q S G K D A N L D K G E P
 2001 TTCAGCAATT GCACCAATTT CATACTTCCA AGCACCATAT TTAGATGGTT
 S A I A P I S Y F Q A P Y L D G S
 2051 CTA AATTAGT ATCTTACAAA GGTACAACCTG AAACCTGACAA ATTTGTTAGT
 K L V S Y K G T T E T D K F V S
 2101 GGAGAAACTG CAACATTTAA AGTACAACCTT ACGAACCAAA GTGGTAAAGT
 G E T A T F K V Q L T N Q S G K V
 2151 CGTACAGAAT TCTAGTTACA CAACAAAGGA TGTACGTAC ACTGTTTACA
 V Q N S S Y T T K D V T Y T V Y N
 2201 AACTGGTGC TAATAATGTA AAAGTTGGCG ATGTTGAAAT CGCTCCAAAC
 T G A N N V K V G D V E I A P N
 2251 CGCGTGCATA CATTAGTTGC CGCAAACGGG AAATCGACGT TACTACTG
 R V H T L V A A N G K S T L L L ?

Abb. 40: Sequenz des S-layer Proteins aus *Bacillus sphaericus* (DSM 396), 2298 bp (AC: AJ 292964), 766 Aminosäuren (ID: CAC19881.4). Unterstrichen die putative SLH-Sequenz, die am 5. Januar 2001 bekannt war. Nicht vollständig. Veränderung wurde gelb markiert (s.o.).

501 AACAGAAATT GGTGACTTAG ACAAAGCTTA CTCTGCAGAA CAACGCACAG
 T E I G D L D K A Y S A E Q R T A
 551 CGATCGTTGC TTTAGAATAT GCGGGTATTA CAAATGTTGC TCACTTCAAC
 I V A L E Y A G I T N V A H F N
 601 CCAGGTAACA GCGTAACACG CGGACAATTC GCTTCA**TCTA**
 P G N S V T R G Q F A S **S**

5.3 *Geobacillus stearothermophilus*

1 ATGGACAAAA AGAAAGCAGT CAAACTCGCC ACAGCCAGCG CTGTAGCAGC
 M D K K K A V K L A T A S A V A A
 51 GAGCGTTTC GTCGAGCCA ACCCGCATGC TTCCAAGCA GCAACGGACG
 S A F V A A N P H A S Q A A T D V
 101 TGGCGACGGT CGTCAGCCAA GCGAAAGCGC AAATGAAAGA AGCATACTAT
 A T V V S Q A K A Q M K E A Y Y
 151 ACGTACAGCC ATACGGTAAC GGAAACGGGC CAATTCCCAGG ACATTAAGA
 T Y S H T V T E T G Q F P D I K D
 201 TGTATATGCC GCCTACAACA AAGCAAAACA AGCGTATGCA AACGCGGTTG
 V Y A A Y N K A K Q A Y A N A V A
 251 CTGTCGTGAA CAAAGCCGGC GGCGGAAAA AAGACGCGTA TTTGGCTGAT
 V V N K A G G A K K D A Y L A D
 301 TTGCAAGCTA TATACGAAAC GTATGTATTC AAAGCCAACC CGAAATCGGG
 L Q A I Y E T Y V F K A N P K S G
 351 CGAAGCGCGC GTGGCTACGT ACATCGACGC TTACAACCTAT GCGACAAAAT
 E A R V A T Y I D A Y N Y A T K L
 401 TAGACAAAAT GCGCCAAGAA CTCAAAGCAG CCGTCGATGC GAAAGATCTG
 D K M R Q E L K A A V D A K D L
 451 AAAAAGCAG AAGAGCTCTA CCACAAAATT TCGTACGAGC TCAAAACGCG
 K K A E E L Y H K I S Y E L K T R
 501 CACGGTCATT CTCGACCGCG TCTACGGCCA ATCGACGCGC GAACTCCTCC
 T V I L D R V Y G Q S T R E L L R
 551 GTTTCGACGTT CAAAGCCGAT GCTCAAGCAT TGCGCGACAG ATTGATCTAC
 S T F K A D A Q A L R D R L I Y
 601 GACATCACCG TTGCCATGAA AGCGCGTGAA GCGCAAGACG CTGTCAAAGC
 D I T V A M K A R E A Q D A V K A

VII ANHANG

651 CGGCAACTTG GACAAAGCGA AAGCCGCGCT TGACCAAGTC AACCAATACG
 G N L D K A K A A L D Q V N Q Y V
 701 TATCGAAAAGT AACCGATGCG TTCAAAGCCG AACTGCAAAA AGCAGCACAA
 S K V T D A F K A E L Q K A A Q
 751 GACGCCAAGG CGGCGTATGA AGCAGCATTG ACGCCGAAGG TTGAGAGTGT
 D A K A A Y E A A L T P K V E S V
 801 AAGTGCATG GACTCTACAA GCTTCAAAGT TACATTTACT AAGCCTGTAG
 S A I D S T S F K V T F T K P V D
 851 ACAAAGCAAC AGCAATTCCT AAAAACTTCT CTATTACTTT AAAAGGTACT
 K A T A I P K N F S I T L K G T
 901 GAAACTAAAC TTTATCCTAA GTCTGTTGAA GTATCTGAGA GTGGATTAAC
 E T K L Y P K S V E V S E S G L T
 951 TGCTACTGTA ACTCTTTATG ATACATTAGT AGACGGTAAA ACTTACACTG
 A T V T L Y D T L V D G K T Y T V
 1001 TTGTAACATC TGGTTTAAAA GATACAGCTG GTAAAGAATT TGAACTAGC
 V T S G L K D T A G K E F E T S
 1051 ACAAACGAAT TCACTTACAA CAAGCCAGTA CCAGCTTCTA TTACATTCAA
 T N E F T Y N K P V P A S I T F N
 1101 CTTCAATAAG TTACCTGAAG ATAGTGCAGT TGATTTGACT AAATACGTAA
 F N K L P E D S A V D L T K Y V T
 1151 CTGTTAAGGA TGCTGCTGGT AACGTAATTA AATCTGGCTT CGAGTTAGAA
 V K D A A G N V I K S G F E L E
 1201 TTCACTTCAA GTGAAAAATT AACTCAAGGT AAATTCATCA ATACTACTGG
 F T S S E K L T Q G K F I N T T G
 1251 TAAGAAGTCA GTTATTGTTA ACGCTACTGT AAAAGGCACA AATGTTACAA
 K K S V I V N A T V K G T N V T T
 1301 CTGGTAACGT AATCCTTGCA GTTGAGGATG AAAAAAGCTGC AGAAGTTAGT
 G N V I L A V E D E K A A E V S
 1351 GAATTAATAA TAACTAAGGA CAACAAAGAG GTTGTAAGTCT TTTACGCAAA
 E L K L T K D N K E V V T L Y A N
 1401 TGGTAACGCA TTTGATAAAG ATGGTAACCA AATCTCTAGC GGTACTTTAA
 G N A F D K D G N Q I S S G T L T
 1451 CATTAAACAGC TAAGTTCAAA GACCAATATG GTAATGAATT AACTGGAAAA
 L T A K F K D Q Y G N E L T G K
 1501 GTAGCTGGAA CTGACTATAC ATTTGAATCT CTAAATCCTG AAGTGTTAGT
 V A G T D Y T F E S L N P E V L V
 1551 AGTTGCTCCT GATGGTAGCG TAACTCCAAT CGTTCAGGT ACTGCACTGG
 V A P D G S V T P I V P G T A L V
 1601 TTAAGGTTAA ATATGGTGAG GTTACTAAGA CAATCCCTGT GACTGTAA
 K V K Y G E V T K T I P V T V K
 1651 GCTAACCCAG TATTAGAAAC AATTGCAGTC GACAGCACAG GTGTATCCGT
 A N P V L E T I A V D S T G V S V
 1701 TGCTAAAGT CAAAAAGCTA CATTCAAAGT AACATTAATA GACCAATACG
 A K G Q K A T F K V T L K D Q Y G
 1751 GTAACAAAAT CACTGGTAAT GTAAACGTAA CTTCTGACAA AACTGAAACA
 N K F T G N V N V T S D K T E T
 1801 GCTACAGTTT CTGTATCTAA CTCTGGCATT GGTCAAAGTG AGTACACTGT
 A T V S V S N S G I G Q S E Y T V
 1851 AACTGTGAAC GGTGTTGCTG AAGGTTCTAC TACTATCACA ATTAAGAGTG
 T V N G V A E G S T T I T I K S G
 1901 GTECTAAAGA AGTTAAAGTA CCTGTAAATG TAGTTGCTGG CGGACCAGTA
 T K E V K V P V N V V A G G P V
 1951 GCTAACTACC AAATTAAGT TCTTGACGAT GGTAATAATCG ACAAGAGCGC
 A N Y Q I K V L D D G K I D K S A
 2001 AACTGAAAAGT CCAGCTAACA ACGATGTTCA ATTAAAAGTT TATGCTGTAG
 T E S P A N N D V Q L K V Y A V D
 2051 ATGCTAACGG AAATATTGTT GGCGACATCA CTAACGATGT AACTATTACA
 A N G N I V G D I T N D V T I T
 2101 AGTGAAGCAA CTGATACAAA TGGTGTAAATC GTTAATGCAA GTAAATCTAC
 S E A T D T N G V I V N A S K S T

VII ANHANG

```

2151 TGCAAATGGT GATACTGTAT ACGTAATCAC TGACAACGGT AGCAAAAAAG
    A N G D T V Y V I T D N G S K K V
2201 TAGGTAAAAGA AACTTTAACA GTTAAGCTTG GAAGTGTACAC TCTAGGTACT
    G K E T L T V K L G T V T L G T
2251 GTAGATGTTG AAGTCATCGA TACTACATTA AAAGCTACTG TAGTAACTAA
    V D V E V I D T T L K A T V V T K
2301 GAAAGCAGAC CTTATTGAGC TTGATGCTGC TGATAATGGT GATGCTTTAG
    K A D L I E L D A A D N G D A L A
2351 CTAAGTTACT AGCTAACTTA GATATCAAAG ACCAAAACGG TAATCCAATG
    K L L A N L D I K D Q N G N P M
2401 GTTGACTCTG CTGCAACTCC TAACACTAAT GAAAAATTAC AAGCTCTTAA
    V D S A A T P N T N E K L Q A L K
2451 ATCTGTATTA AGCGGCATCG TAAGCAGCGA CACATCTGTA ATTGGTTCTG
    S V L S G I V S S D T S V I G S V
2501 TATCTAATGT TGATAACTTA AAAGATGATG CTAGCATTTT TGGATTAGCT
    S N V D N L K D D A S I S G L A
2551 GTTAAGAAAAG CAGGTACAGT AACATTAACA CTAGTGTTTA ATGAAGATTC
    V K K A G T V T L T L V F N E D S
2601 TAAGATTGCT CCAATCGCAA TCACAGTTAA AGCTCCTGCT GCAACTCAAG
    K I A P I A I T V K A P A A T Q D
2651 ATGGTGTGAC TGTAACTGGT CTAGACTTAG TGCCAGGTGT AACTGGTGTG
    G V T V T G L D L V P G V T G V
2701 GGTAAAACATA AATTTACTGC AACAGATAAAA ATCAAATCTG GTCACAAATT
    G K T K F T A T D K I K S G H K L
2751 ATATTATGCT GTAGACGATT CAGCAGTACC TGCGCCAGCT GTTGGAACATA
    Y Y A V D D S A V P A P A V G T T
2801 CACGTAATTC AACTAAATTT GCAAATGAAA TCACTGTAGG TACAACAGAA
    R N S T K F A N E I T V G T T E
2851 GTTGCTGCAA ATGCTGGCCA AATTATTACT GTTATTGAAG TAGATAGCAG
    V A A N A G Q I I T V I E V D S S
2901 TGATAGAGTT GTTGGCTACA AAACATTTAC AGTTGAAGCA GCTGATTTAA
    D R V V G Y K T F T V E A A D L S
2951 GTGTTGCAGC TGATAAAACA GGTTCCTACTG CAACAGTTAC TCCAACGGT
    V A A D K T G F T A T V T P T G
3001 GGTAACCAAG TTACTACTGG TAAAACACTG TTAGCAGTTT CTGATTTAGC
    G N Q V T T G K T L L A V S D L A
3051 AAATGGTCAT AAATTATATG CAGCAGCGGC TGGTTCAAGT GCAGCAGCAG
    N G H K L Y A A A A G S S A A A A
3101 CTCCAGTAAA AGGTATTGCA TATACTGATA CTAAGTGTACG AACAACCTAT
    P V K G I A Y T D T T V R T T Y
3151 GGTACTGAAG TAAGTAGTGG TACAGTAGAG GTTGATGCGC AAGACGGACA
    G T E V T S G T V E V D A Q D G Q
3201 ACATATCTCA ATTATTGAAG TTGATGAAAA CGGTAAAGTT GTAGTTATA
    H I S I I E V D E N G K V V G Y K
3251 AAGACTATAC TATTACAGGT ATTCAAATTG GTACAAAATC AGCATCGTAA
    D Y T I T G I Q I G T K S A S *

```

Abb. 41: Sequenz des S-layer Proteins aus *Geobacillus stearothermophilus* (DSM 22), 3300 bp (AC: AF 055578), 1100 Aminosäuren (ID: AAC12757.1). Unterstrichen die in Analogie zu den SLH-Sequenzen klonierte Sequenz.

5.4 *Eubacterium acidaminophilum*

```

1 GTGAGACTTA ACAGCAGAAT TAAGCGAGCA GCCATTTGCT CCTTATTGAC
  V R L N S R I K R A A I C S L L T
51 AACAGCCCTG ACTTTTGGTC AGGTGTCATA CGGCCAGGAA GCTGCGCCGG
  T A L T F G Q V S Y G Q E A A P E
101 AAACGCCTAA GACGGCTGCG GAGCAGAAAAG AGGCAGCCTT GGATGAGCCT
    T P K T A A E Q K E A A L D E P

```

VII ANHANG

151 AAGGAGGCTG CGGCCAGGA AGAGGCAGTG CAGGAAGAAC CGGCTAATAA
K E A A A Q E E A V Q E E P A N K
201 AGAGACGGTT TATGCCGTGA GCGCAAAGGC TCAGGAGGCC GCTGATTTTC
E T V Y A V S A K A Q E A A D F L
251 TCATGGGGCT TGGCCTTGCA AACGGAAAGG AGGACGGCAA ATTCCACCCG
M G L G L A N G K E D G K F H P
301 GAGCAGGGCA TAACAAGGGA GGAGTTTGCA AAGCTGCTTG TAGGCGTGCT
E Q G I T R E E F A K L L V G V L
351 GGGACTCGAA AATGCGGCTC TGCTTTCGAA GGGTGAGCAA ATATTCACAG
G L E N A A L L S K G E Q I F T D
401 ACGTTGAAAG GGACAGGTGG TCGCATCACT ATGTGAGCAT GGCAGTAAGC
V E R D R W S H H Y V S M A V S
451 ATGGGGATGA CGAGAGGCTT CGAGGATGGA AGCTTCAGGC CCGCCGAGAG
M G M T R G F E D G S F R P A E S
501 CGTCACAAGA GCCCAGGCGG CGGCCATGCT TGTAAGATGC TTTGGCTACA
V T R A Q A A A M L V R C F G Y N
551 ATGACTCCTA TGTGCAGGGC AGCTGGCCCG CCAACTACAT ATCCAAGGCC
D S Y V Q G S W P A N Y I S K A
601 GCAGAGTTGG GGATACTCTC GGGAGCGGAA GGCGAGCACT CAGCATCTCT
A E L G I L S G A E G E H S A S L
651 CGGCCGGGGA GATGCGGCTC TCATGGTCAA AAACGCCCTT CACGAAAAT
G R G D A A L M V K N A L H G K Y
701 ACCTCTTCGG CCAGAACGAG GGCAGAATGC TTATGACGGA AAAGAGGGGC
L F G Q N E G R M L M T E K R G
751 ATATACCAGA TAAGGGGCGC AAGGCTTATA AGGTCCATGA GCTACCTGGA
I Y Q I R G A R L I R S M S Y L D
801 TGCGCAGAGC ATGGAGTTTG AGATAACAAG CGATTTCGGAG ATTGAAGGCG
A Q S M E F E I T S D S E I E G G
851 GCGCATTA AAA AAGCGGCGAA AAGCAAATAT TCACGAATCC GGAGGGCATA
A L K S G E K Q I F T N P E G I
901 TACATACAGC CCGGGGAGAC GGTGGAATTT TACGTAGACA AGGATGAAAA
Y I Q P G E T V E F Y V D K D E N
951 CATACTTTAC GTATCCAGGG CCAGTTCCTC CGGCTCAGGC AACCCGGCCC
I L Y V S R A S S S G S G N P A L
1001 TGTCAGCAGG CATGAATGAG GTTGA AAAACG CGTACGCTGA GAAGCCATAC
S A G M N E V E N A Y A E K P Y
1051 GGCATGATAA GGCTTAAGGG CGAGGAGGGC TATATCGACG TGGATTGAGA
G M I R L K G E E G Y I D V D S D
1101 CTCTATAGTC ATGCTTGACG GCGAGACTGT AGATCCCGAT GATTATGAAA
S I V M L D G E T V D P D D Y E S
1151 GCGTTCGCGG GGAGGATGCC TGGGGCAGCT TCGTCTGTA AAAGGACAGG
V L G E D A W G S F V V K K D R
1201 CTGGAGTACG CCAATCTGGT ATCATGGGAC TCCGGGGATT TTGTAATAAA
L E Y A N L V S W D S G D F V I K
1251 AAGTCTGGAC GCCCAAGGAA GCAGCGTATC CGGCATTGAC ACAGAGGGCG
S L D A Q G S S V S G I D T E G G
1301 GAGTAGAAGA CAGATTGATT TTAAAAAACG GCAAGACGGC CTATGATTTT
V E D R L I L K N G K T A Y D F
1351 TACGTGGTCT TGGAAAGCGG CGTGCAGAAG GCGGATTTTCG GGGCCCTTCA
Y V V L E S G V Q K A D F G A L Q
1401 GATTGGCGAC GTCATAAGGA TAGGGAGCGA GAACGAGAGC GCTAACTCAA
I G D V I R I G S E N E S A N S K
1451 AGCCTGTCTA CGTGTTCAGG AACAAATTCGG AAGGCACATT CGAGAGGGTG
P V Y V F R N N S E G T F E R V
1501 TCGGGAGGCG CAAACGGCAA AAGCATAACC TTCAGGCTAA AGGGCATTCC
S G G A N G K S I T F R L K G I P
1551 TGATTGATAC CAGCTTGACG AAAGCTTTGC ATACTCTTAC AATGGAGGGA
D S Y Q L A E S F A Y S Y N G G K
1601 AAAGGGTAAG AGCCGGGTCT GAAAGCATCT CTTCAATAGC GTCCAGTCTG
R V R A G S E S I S S I A S S L

VII ANHANG

```

1651 AATGAATTCT ATAACCAAAA GGTCAAAAATA TATGGGAATC ATGCGGGTGA
    N E F Y   N Q K   V K I   Y G N H   A G D
1701 CGTGGTTTAC GTAGAAGGCA ACTTCAGCCT TGTGATTGAC CAGTACGGCG
    V V Y   V E G N   F S L   V I D   Q Y G V
1751 TGCTGCTGGA TTACGGAGAC GCGGTGCGGG GTGAAATAAA GCTCCTGACC
    L L D   Y G D   A V R G   E I K   L L T
1801 CAGACAGGCT CCAAGCGGGT GTTTGCCTTC GAGGATTCCG ACGAATACGA
    Q T G S   K R V   F A F   E D S D   E Y E
1851 ATACCTCAAA GCCAGAGTGG ATGTCGGTAC TATAGTGAAG TACTCCCAGA
    Y L K   A R V D   V G T   I V K   Y S Q I
1901 TAAACACGGG CACCATAAAG AATCTCAGCG ACGACTTCAC CGAAAACATA
    N T G   T I K   N L S D   D F T   E N I
1951 ATATACACGG ATGACATTAG CATAATAAGC TCCGGCGATG ATTTACCCTGA
    I Y T D   D I S   I I S   S G D D   F T E
2001 GGATTCCGTT GAAATAGGCG GCCAGACATA TAAGGTGGAT TCTGACACGG
    D S V   E I G G   Q T Y   K V D   S D T V
2051 TGTTCTTCGA CTACTCGGAG CAGGATCCCG ACCAGGTAAA GCGTCTTAAC
    F F D   Y S E   Q D P D   Q V K   R L N
2101 TGGGACAAAT TCAAAGGCAG ACAGGTCGTT GGCGACGTGG AGGTAATAGC
    W D K F   K G R   Q V V   G D V E   V I A
2151 CGATACGGAC GGCGACTATC TGCTCATGAT GGCCATCTGG AGCAACATAG
    D T D   G D Y L   L M M   A I W   S N I E
2201 AGGGTATCAA GGAGGACACC AAGGTGGGCT ACGTCCTGGA CAACTTCAGC
    G I K   E D T   K V G Y   V L D   N F S
2251 CTTGGGGACT ACAGATACGT CGAGCTCCAG GAATACGGCT CCGAGGGGAT
    L G D Y   R Y V   E L Q   E Y G S   E G V
2301 CAAAAGCTAC AAGCTTGAAG ACGAGTACAA GGATCTGATG CTTTTTGGAA
    K S Y   K L E D   E Y K   D L M   L F G R
2351 GACTCATAGC ATACCAGATA GGCTCCTCTG ACAAGATAAA CATAGTCGAG
    L I A   Y Q I   G S S D   K I N   I V E
2401 GCGGAGGATA TGGAGTTTGT ATCGGGTGAA GTGACATCTG CAGACAATCG
    A E D M   E F V   S G E   V T S A   D N R
2451 CTACATATCC ATCGAAGGGA CAAGGTACAG GATAGGCGAC GATGCCGTGG
    Y I S   I E G T   R Y R   I G D   D A V G
2501 GCTTCGGAGG CGGCAGGAGC ATCAGCCCAC AGGGCCTTGA CAGTGGAGAC
    F G G   G R S   I S P Q   G L D   S G D
2551 ATAATTGCAG CCTACATCGA GGATGGAAAAG ATTGTGGCAT TTGAAGACCT
    I I A A   Y I E   D G K   I V A F   E D L
2601 AGGCGCTCAA ACGGACTCCA AAATCGCCCA GGGCGTTCTC GTAAGCGTGG
    G A Q   T D S K   I A Q   G V L   V S V D
2651 ACCCAACTTC AAGGGAGTGC CTTTTAATAG AGTTAGACGG CAATGAGAGG
    P T S   R E C   L L I E   L D G   N E R
2701 TCGTTTGCAT GCGCCGAGGA CATTGACTTT GTATTCCGAG ACGGCTACAT
    S F A C   A E D   I D F   V F R D   G Y M
2751 GGAAATAGAG GACGAGGGGG TAGACCCTGT TGAGCTGTTT GAAAGTCTAG
    E I E   D E G V   D P V   E L F   E S L A
2801 CAAGGACAGG CACAGCTGTC AAGTTCTCGT ACAACAGATA TACTGACGAG
    R T G   T A V   K F S Y   N R Y   T D E
2851 ATATATTCAA TATGGGTAGA TGACAACCAG TAG
    I Y S I   W V D   D N Q   *

```

Abb. 42: Sequenz des S-layer Proteins aus *Eubacterium acidaminophilum* (DSM 3953), 2883 bp, 961 Aminosäuren (aus Talke 2001). Unterstrichen die putative SLH-Sequenz.

5.5 *Thermus thermophilus* HB8

1 ATGAAGAAAA GGCTGGTCAC ACTGCTGGCA GGGCTCTTGA CCGTCCTCTC
 M K K R L V T L L A G L L T V L S
 51 CATGGGGTTC GGTCTGGCCC AGTTCTCCGA CGTGCCCGCC GGGCACTGGG
 M G F G L A Q F S D V P A G H W A
 101 CCAAGGAGGC CGTGGAGGCC CTGGCGGCCA AGGGCATCAT CCTGGGCTTC
 K E A V E A L A A K G I I L G F
 151 CCGGACGGCA CCTTCCGGGG CAACGAGAAC CTCACCCGCT ACCAGGCGGC
 P D G T F R G N E N L T R Y Q A A
 201 CCTCCTCATC TACCGGCTCT TGCAGCAGAT TGAGGAGGAG CTGAAGACCC
 L L I Y R L L Q Q I E E E L K T Q
 251 AGGGCACCTC CCCACCATG GAGGCCCTGG CCCCCGAGGA CCTCGAGGCC
 G T S P T M E A L A P E D L E A
 301 ATGATGCGCG AGCTCAAGGC CCAGCCCATG CCTGAGCCCG GCATGGACCA
 M I A E L K A Q P M P E P G M D Q
 351 GGCGGCCCTT AAGGACCTCA TGGACCGGGT GGAGGCCGCC TCCATCGCCC
 A A L K D L M D R V E A A S I A A
 401 CCGACACCGC GCTTGCCAG GCCCAGCAGC TCGCCGAGCG GCTGGACGCC
 D T A L A Q A Q Q L A E R L D A
 451 CTGGCCAGG ACGTGGAGGG CGTGAAGGGC GACCTGGCCG GGCTTAGGAG
 L A Q D V E G V K G D L A G L R S
 501 CCAGGTGGAG GCCAACGCCG ACGCCATCCA GGCCCTGAAC GAGCTCGCCG
 Q V E A N A D A I Q A L N E L A V
 551 TCCTCCTGAA CCAGGACGTC CTCTCCCTCC AGGACCGGGT CACCGCCCTG
 L L N Q D V L S L Q D R V T A L
 601 GAGAAGATGG TCTCCGGCGG CCAGGAGCTC CCCGACCTGG AGCAGTTCGC
 E K M V S G G Q E L P D L E Q F A
 651 CACCAAGGAG GACGTGGCCG CCGTCCAGGA GTTCGCCGCC GCCCTGCGCT
 T K E D V A A V Q E F A A A L R S
 701 CCGACCTGGT GGGCCTCTCC GAGAAGGTTT CCAAGCTGGA GGGCACCGTG
 D L V G L S E K V S K L E G T V
 751 GGCGACCTTT CTGGGAAGGT CGCTACCCTG CAGCGCAACG CTTTACCAT
 G D L S G K V A T L Q R N A F T I
 801 CAGCGGGAGC CTGAGCCTCA ACTACAGCGT GTATCGGGCC TGGGGCCCCG
 S G S L S L N Y S V Y R A W G P D
 851 ACGCCTCGGC TGCAGGGCCG GGCACGGCCA ACACTTTTGA CATTGACCGC
 A S A A G P G T A N T F D I D R
 901 CTCTTCTCCA GCAAGTTCAG CACTGGGGAC GGGAACGGGA ATGGCTCTGT
 L F S S K F S T G D G N G N G S V
 951 GGGCGACGAG GCCGACCTGG GCAAGAACAC GGAGGGCGTC ACCAACGCCA
 G D E A D L G K N T E G V T N A T
 1001 CCCTAAGCGT CAGCTTCTCC ACGGGGAAGT TGGATGCGGC TTCCGATCCG
 L S V S F S T G K L D A A S D P
 1051 GGCAAGCTGA ACAGCTACCC CGGCCTGGTC CAGTTCAGCC TGCGCGCGAA
 G K L N S Y P G L V Q F S L R A K
 1101 GCTGACCAAC CCCGGCAAAT ACGACCCCAG CACGGGTGCG CCCACCTACC
 L T N P G K Y D P S T G A P T Y P
 1151 CCATCAACCT CACCCTGGAT GAGTTTTTCCT CCACGCTGGC GGTGGCCAAG
 I N L T L D E F S S T L A V A K
 1201 GACCAGACCC TCTCCTTAG CTTCGGTTCG TCGGTGAGGT CCAAGTTCAC
 D Q T L S F S F G R S V R S K F T
 1251 CGAGTACGTC TTTGACAACG ACTACAACAG CCGCGGGCAC GGTTCGTGG
 E Y V F D N D Y N S R G H G F V A
 1301 CCACCTACAA GCCCGCCTC CTGGGGGCCA CGCTGACCGG GGTTCACGGG
 T Y K P G L L G A T L T G V Y G
 1351 TCCAAGGGGG CCAACAATGG TGACTTCACG TACTTCCGCG GCGCCCGCCT
 S K G A N N G D F T Y F R G A R L
 1401 GGCTTGGAGC CCTGTTGAAG GCATCGCCTT GGGTGGCTCC TTTGTCCAGG
 A L S P V E G I A L G G S F V Q E

VII ANHANG

1451 AGGGCCTGGA CGCCAACCAA GGGACCACGA GTGCCTCCTT CCCCCTCCT
 G L D A N Q G T T S A S F P A P
 1501 ACCACCGTGT ACGGGGTGGA TGCCAGCGTG AAGCTCGGTC CTGTGGGCC
 T T V Y G V D A S V K L G P V G L
 1551 CGCCGGTGAG TACTTCAATT CCGATGCCGC TCCCAACGCG AACGGGTACT
 A G E Y F N S D A A P N A N G Y Y
 1601 ACGTGAAGGC CGACGTGGCC TTGGGGTCTA TCTCCGTGGC GGGGAACTAC
 V K A D V A L G S I S V A G N Y
 1651 CGGAACATCG GCGCCGGGGT TACCGGGGCG AACATGCTCT CCGGGGACGC
 R N I G A G V T G A N M L S G D A
 1701 CACCAGCACC CTGGACCAGG GCGGCTGGGG CGGCGTTGAT TCCAGCGGTA
 T S T L D Q G G W G G V D S S G N
 1751 ACGTCATCAA CGGGGCGCCC TTCCGCTCTA ACCGCCAGGG CTTTGGGGTG
 V I N G A P F R S N R Q G F G V
 1801 AGCGCTTCGG CGGGGCTTGG ACCCATCACG GTCAAGGGCT ACTACGACAG
 S A S A G L G P I T V K G Y Y D S
 1851 CTCCACGGTC CTTGCCAACG AGACCATTAC CAACTCCTAC GGCGCCTTCA
 S T V L A N E T I T N S Y G A F N
 1901 ACTACAGTGC AAACAACCAG CTCGTGGCCT ACGGCGGCCA GGCGGACCTC
 Y S A N N Q L V A Y G G Q A D L
 1951 GCCTTCGGCG GCTTCACGCT GAGCGGCTTC TACCGCATCG CCCAGCTCAA
 A F G G F T L S G F Y R I A Q L N
 2001 TGGCTCCACC ACCCGTTACA TCCTCACC GAAGCCCGCG GAAGCGGTGT
 G S T T R Y I L T E K P A E A V Y
 2051 ACGCCACGGA GTACGGGGCC AAGCTGGCCC ACGATGGGGC CTCTAAGGAC
 A S E Y G A K L A H D G A S K D
 2101 GCTCTGGTGC CCAAGCTCAA CTTCACGGCC GCTTACACCC AGAAGTACGA
 A L V P K L N F T A A Y T Q K Y D
 2151 CAACGCCACC AGCGGCTTCA CCACCCAGGA CATCGCCGTC TACGGTTCCT
 N A T S G F T T Q D I A V Y G S Y
 2201 ACGAGCTGGC CCTCGGGCCT CTGACCCTCA AGCCCATGGG CCGGTACCAC
 E L A L G P L T L K P M G R Y H
 2251 ACCCAGGACG CCGCGGCGGC GAGCACTTCT TCCGACTACA CCACGGTGAA
 T Q D A A A A S T S S D Y T T V K
 2301 GTACGGGGTG GCGGCTTCTA TTGCCCTGGA CCTTCCCTTC AAGCCCAGCC
 Y G V A A S I A L D L P F K P S L
 2351 TTTCCGGGGA GTACTACGCC CGCTCCACCC AGGTAACCTC GGCCAACAGT
 S G E Y Y A R S T Q V T S A N S
 2401 GGTTCCTTCG CCACGGGCAC CATCTCCGAA AGCAAGTACG CTGTGGGGCT
 G S S A T G T I S E S K Y A V G L
 2451 GAAGCTGGGC GAGTTCCTCT TCAAGAATC CTCGGTGGAA GCCAAGTACG
 K L G E F L F K N S S V E A K Y A
 2501 CCTCCTACAC GGGCAGCGGC CTCAACGCC CCATTCTCCT GGGTGTGCT
 S Y T G S G L N A P I L L G V A
 2551 GACGCCGCCA GCTCCACCAC CTCCGACTAC CTCTACAACA ATGCGGTGAG
 D A A S S T T S D Y L Y N N A V S
 2601 CTCGGTGGGG AGCAACCGGG GCAGCGTGAC CGGGTGGTAC TTCACCTGGA
 S V G S N R G S V T G W Y F T W T
 2651 CGTACTGGGA CCTCACCTTC GCCTACGTGG AAGCCGACGT GAACAACAAC
 Y W D L T F A Y V E A D V N N N
 2701 GGCAACCAGA CCCACGGTCA GGCCTTCAAG ATCAGCTACA CCGTAAAGTT
 G N Q T H G Q A F K I S Y T V K F
 2751 CTAA*

Abb. 43: Sequenz des S-layer Proteins aus *Thermus thermophilus* HB8 (DSM 579), 2754 bp (AC: X57333; S4862), 918 Aminosäuren (ID: CAA 40609.1). Unterstrichen die putative SLH-Sequenz.

6 *Tth*-DNA-Polymerase aus *Thermus thermophilus* HB8

1 ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT
 M E A M L P L F E P K G R V L L V
 51 GGACGGCCAC CACCTGGCCT ACCGCACCTT CTTCCGCCCTG AAGGGCCTCA
 D G H H L A Y R T F F A L K G L T
 101 CCACGAGCCG GGGCGAACCG GTGCAGGCGG TCTACGGCTT CGCCAAGAGC
 T S R G E P V Q A V Y G F A K S
 151 CTCCTCAAGG CCCTGAAGGA GGACGGGTAC AAGGCCGTCT TCGTGGTCTT
 L L K A L K E D G Y K A V F V V F
 201 TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG GCCTACAAGG
 D A K A P S F R H E A Y E A Y K A
 251 CGGGGAGGGC CCCGACCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC
 G R A P T P E D F P R Q L A L I
 301 AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA
 K E L V D L L G F T R L E V P G Y
 351 CGAGGCGGAC GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG
 E A D D V L A T L A K K A E K E G
 401 GGTACGAGGT GCGCATCCTC ACCGCCGACC GCGACCTCTA CCAACTCGTC
 Y E V R I L T A D R D L Y Q L V
 451 TCCGACCGCG TCGCCGTCTT CCACCCCGAG GGCCACCTCA TCACCCCGGA
 S D R V A V L H P E G H L I T P E
 501 GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG GTGGACTTCC
 W L W E K Y G L R P E Q W V D F R
 551 GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC
 A L V G D P S D N L P G V K G I
 601 GGGGAGAAAG CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA
 G E K T A L K L L K E W G S L E N
 651 CCTCCTCAAG AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA
 L L K N L D R V K P E N V R E K I
 701 TCAAGGCCCA CCTGGAAGAC CTCAGGCTCT CTTGGAGCT CTCCCGGGTG
 K A H L E D L R L S L E L S R V
 751 CGCACCGACC TCCCCCTGGA GGTGGACCTC GCCAGGGGC GGGAGCCCGA
 R T D L P L E V D L A Q G R E P D
 801 CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC GGCAGCCTCC
 R E G L R A F L E R L E F G S L L
 851 TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC
 H E F G L L E A P A P L E E A P
 901 TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCCTCT CCCGCCCGA
 W P P P E G A F V G F V L S R P E
 951 GCCATGTGG GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG
 P M W A E L K A L A A C R D G R V
 1001 TGCACCGGGC AGCAGACCCC TTGGCGGGGC TAAAGGACCT CAAGGAGGTC
 H R A A D P L A G L K D L K E V
 1051 CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC TTGGCCTCGA GGGAGGGGCT
 R G L L A K D L A V L A S R E G L
 1101 AGACCTCGTG CCCGGGGACG ACCCCATGCT CCTCGCCTAC CTCCTGGACC
 D L V P G D D P M L L A Y L L D P
 1151 CCTCCAACAC CACCCCGAG GGGGTGGCG GGCCTACGG GGGGGAGTGG
 S N T T P E G V A R R Y G G E W
 1201 ACGGAGGACG CCGCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA
 T E D A A H R A L L S E R L H R N
 1251 CCTCCTTAAG CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG
 L L K R L E G E E K L L W L Y H E
 1301 AGGTGGA AAA GCCCTCTCC CGGGTCCTGG CCCACATGGA GGCCACCGGG
 V E K P L S R V L A H M E A T G
 1351 GTACGGCGGG ACGTGGCCTA CCTTCAGGCC CTTCCCTGG AGCTTGC GGA
 V R R D V A Y L Q A L S L E L A E

VII ANHANG

1401 GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG GGCCACCCCT
 E I R R L E E E V F R L A G H P F
 1451 TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT
 N L N S R D Q L E R V L F D E L
 1501 AGGCTTCCCG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG
 R L P A L G K T Q K T G K R S T S
 1551 CGCCGCGGTG CTGGAGGCC TACGGGAGGC CCACCCCATC GTGGAGAAGA
 A A V L E A L R E A H P I V E K I
 1601 TCCTCCAGCA CCGGGAGCTC ACCAAGCTCA AGAACACCTA CGTGGACCCC
 L Q H R E L T K L K N T Y V D P
 1651 CTCCCAAGCC TCGTCCACCC GAGGACGGGC CGCCTCCACA CCCGCTTCAA
 L P S L V H P R T G R L H T R F N
 1701 CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC CCCAACCTGC
 Q T A T A T G R L S S S D P N L Q
 1751 AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC
 N I P V R T P L G Q R I R R A F
 1801 GTGGCCGAGG CGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA
 V A E A G W A L V A L D Y S Q I E
 1851 GCTCCGCGTC CTCGCCACC TCTCCGGGA CGAAAACCTG ATCAGGGTCT
 L R V L A H L S G D E N L I R V F
 1901 TCCAGGAGGG GAAGGACATC CACACCCAGA CCGCAAGCTG GATGTTCCGG
 Q E G K D I H T Q T A S W M F G
 1951 GTCCCCCGG AGGCCGTGGA CCCCTGATG CGCCGGGCGG CCAAGACGGT
 V P P E A V D P L M R R A A K T V
 2001 GAACTTCGGC GTCTCTACG GCATGTCCGC CCATAGGCTC TCCCAGGAC
 N F G V L Y G M S A H R L S Q E L
 2051 TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGCG CTACTTCCAA
 A I P Y E E A V A F I E R Y F Q
 2101 AGCTTCCCCA AGGTGCGGGC CTGGATAGAA AAGACCCTGG AGGAGGGGAG
 S F P K V R A W I E K T L E E G R
 2151 GAAGCGGGC TACGTGGAAA CCCTCTTCGG AAGAAGGCGC TACGTGCCCC
 K R G Y V E T L F G R R R Y V P D
 2201 ACCTCAACGC CCGGTGAAG AGCGTCAGGG AGGCCGCGGA GCGCATGGCC
 L N A R V K S V R E A A E R M A
 2251 TTCAACATGC CCGTCCAGGG CACCGCCGCC GACCTCATGA AGCTCGCCAT
 F N M P V Q G T A A D L M K L A M
 2301 GGTGAAGCTC TTCCCCCGCC TCCGGGAGAT GGGGGCCCCG ATGCTCCTCC
 V K L F P R L R E M G A R M L L Q
 2351 AGGTCCACGA CGAGCTCCTC CTGGAGGCC CCCAAGCGCG GGCCGAGGAG
 V H D E L L L E A P Q A R A E E
 2401 GTGGCGGCTT TGGCCAAGGA GGCCATGGAG AAGGCCTATC CCCTCGCCGT
 V A A L A K E A M E K A Y P L A V
 2451 GCCCTGGAG GTGGAGGTGG GGATGGGGGA GGACTGGCTT TCCCCAAGG
 P L E V E V G M G E D W L S A K G
 2501 GTTAG*

Abb. 44: Sequenz der *Tth*-DNA-Polymerase aus *Thermus thermophilus* HB8, 2505 bp (AC: D28878), 835 Aminosäuren (ID: BAA06033.1).

7 Selektierte Proteinsequenzen nach dem „*Ribosome Display*“

7.1 Proteinsequenzen aus der Selektion gegen Heparin

1 MVM DL*
 2 MVLWYL*
 3 M VYGTL*
 4 MVMVPLGPGF PML*
 5 MVMVPLEPGF PMLQVTTTK*
 6 MVMVPLESGF RVLQVTTTK*
 7 MVMVPLEPGF PMLQVTTTR*
 8 MVMVPLEPVF PMLQVTTTK*
 9 MVMVPLEPGF RMLQVTTTK*
 10 MVMVPLEPGF PMLQVTTTR*
 11 MVMVPLEPGF RMLQVTTTK*
 12 MVMVPLEPGF PMLQVTTME*
 13 MVMVPLEPGF PMLQVTTTK*
 14 M VYGTSSEPGF PMLQVTTAK*
 15 MVMVPLEPGF PMLQVTSTK*
 16 MVMVPLESGF LMLQVTTTK*
 17 MVMVPLEPGF RMFQVTTTK*
 18 MVMVPLEPGF PMLQVTTTR*
 19 MVMIPLGPGF PMLQVTATK*
 20 MVMVPLEPGF RMLQVTRK*
 21 MVMVPLEPGF PMLQVTTTK*
 22 MVMVPLEPGF PVLQVTTTK*
 23 MVMVPLGPGF PMLQVTTTK*
 24 M VYGTSKAGF SDVACNDPRS SNQRTC*
 25 IPLEXGFRMX QVTTREVAIN ALADAGIIXG *
 26 M VYGTSRAGF SDVAGNDHEV AINALADAGI IQ*
 27 M VYGTSRVGF SDVAGNDHEV AINALADAGI IQWIR*
 28 M VYGTARAGF SDVAGNGHEV AINALADAGI IQWIR*
 29 M VYGTSRAGF SDVAGNDHEV AINALADAGI IQWIR*
 30 M VYGTSRVGF SDVAGNDHEV AINALADAGI INGYAGGTFK PN*
 31 M VYGTSRAGF SDVAGIDHEV AINALADAGI INGYADGTFK PNN*
 32 M VYGTSRAGF SDVAGNDHEV AINALADAGI INGYADSTFK PNQTINCGQV VKLLSRYLEA QGQEIPAGWN SKTTLQRSTS NS*
 33 M VYGASRAGF SDVAGNDHEV AINALADAGI INGYADGTFK PNQTINRGQV VKLLGRYLEA QGQEIPADWN SKRRFQRSTS NS*
 34 M VYGTSRAGF SDVAGNDHEV AINALADGGI INGYADGTFK PNQTINPGQV VKLLGRYLEA QGQEIPADWN SKRRFNDLPV TAEAE LVKYA ALAKRCRRIL
 35 M VYGTSRAGF SDVAGNDHEV AINALADGGI INGYADGTFK PNQTINPGQV VKLLGRYLEA QGQEIPADWN SKRRFNDLPV TAEAE LVKYA ALAKRCRRIL

VII ANHANG

36 MVIYGTSRAGF SDVAGNDHEV AINALADAGI INGYADSTFK PNQTINRGQV VKLLGRYLEA QGQIPADWSS KQRFDDLPVT AEAELVEYAA LAKDAGVFNG
37 MVIYGTSRAGF SDVAGNDHEV AISALADAGI INGYADGTFK PNQTINRGQV VKLLGRYLEA QGQEIADRN SKQRFNDLPV TAEAEVKYA ALAKDAGVFN
38 MVIYGTSRGGF SDVAGNDHEV AINALADAGI INGYADGTFE PNQTINRGQV VKLLGRDLEA QGQEIADWN SKQRFNDLPV TAEAEVKYA ALAKDAGVFN
39 MAYGTSRAGF PDVAGNDHEV AINALADAGI TNGYADGTFK PNQTINRGQV VKLLGRYLEA QGQGIADWN SKQRFNDLPV TAEAEVKYA ALAKDAGAFN

34 RFKRQLKRFT NNATSANGSS FSTCY*
35 RFKRQLKRFT NNATSANGSS FSTCY*
36 -NGNLNLSQT MQRQQMAVVL VRAIKEIAGV DLVAEYKKRI S*
37 -SNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NRVTEIGDLD KAYSAEQRTA IVALEYAGIT NVAHFNPGNS ATRGQFVLF*
38 -SNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYRKA NRVTEIGDLD KAYSAEQRTA IVALEYAGIT NVAHFNPGNS VTRGQFASSY*
39 --NGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NRVTEIGDLD KAYPAEQRTA IVALEYAGIT NVAHFNPGNS VTRGQFASSS RGTNYAGRRG

7.2 Proteinsequenzen aus der Selektion gegen Streptomycin

40 MVIYGTSQSRV FGCCR*
41 MVMVPLEPGF PMSR*
42 MVMVPLVPGF RMLQVTTK*
43 MVMVPLEPGF RMSQVTTK*
44 MVMVPLEPGF PMLQVTTK*
45 MVMVPLEPGF PMSQVTTK*
46 MVMVPLEPGF PMLQVTTK*
47 MVMVPLELGF RVLQVTTTR*
48 MVMVPLEPGF RTLQVATK*
49 MVMVPLEPGF RMLQVTTK*
50 MVMVPLEPGF RMLQVTTK*
51 MVMVPLEPGF RMLQVTTK*
52 MVMVPLEPGF PMLQVTTK*
53 MVMVPLEPGF PMSQVTTK*
54 MVMVPLEPGF RMLQVTTK*
55 MVMVPLEPGF PMSQVTTK*
56 MVMVPLEPGF PMLQVTTTR*
57 MVMVPLEPGF PMSQVTTK*
58 MVMVPLEPGF PMLQVATK*
59 MVMVPLEPGF PMLQVTPRSS NQRAC*
60 MVMVPLEPGF SGVAGNDHEE AINALADAGI IQWIR*
61 MVIYGTSRAGF SDVAGDYHEV AINALADAGI IQWMR*
62 MVIYGTSRSGF SDVAGNDHEV AINALADAGI INEYADGTFK PNQTINRGQV VRLLGRY*
63 MVIYGTSRAGF SGVAGNDHEV AINALADAGI INGYADGTFK PNQTINCGQV VKLLVVI*
64 MVIYGTSRAGF SDVAGNDHEV AINALADAGI LNGYAEYKKA PNQTINRGQV VKLLGRYLEA RAKKFQLTGI QNNASTIYQ*

VII ANHANG

65 MUYGTSRAGF SDVAGNDHEV AINALADAGI LNGYAEQTFK PNQITINRGQV VKLLGRYLEA RAKKFQLTGI QNNASTIYQ*
66 MUYGTSRAGF SDVAGNDHEV AINALADAGI INGYADGTFK PNQITINRGQV VKLLGRYLEA QGQEIPADWN SKQRFNDLPV TAEAEVLNMLH*
67 MUYGTSRAGF SDVAGNDHEV AINALADAGI TNGYADGTFK PNQITINRGQV VKLLGRYLEA QGQEIPAGWN SKQRFNDLPI TAEAEVLKYA ALAKDAGVST
68 MUYGTSRARF SDVAGNDHEV AINALADAGI INGYADSTFK PNQITINRSQV VKLLGRYLEA QGQEIPADWN SKQRLNDLPV TAEAEVLKCA ALAKDAGVFN
69 MUYGTSRAGF SDVAGNDHEV AINALADAGI INGYADGTFK PNQITINRGQV VKLLGRYLEA QGQEIPADWN SKQRFNDLPV TAEAEVLKYA ALAKDAGVFN
70 MUYGTPRAGF SDVAGNDHEV AINALADAGI INGYADGTFK PNQITINRGQV VKLLGRYLEA QGQEIPADWN SKQRFNDLPV TAGAEVLKYA ALAKDAGVFN
71 MUYGTSRAGF SDVAGNDHEV AINALADAGI INGYADGTFK PNQITVNRGQV VKLLGRYLEA QGQEIPADWN SKQRLNDLPV TAEAEVLKYA APAKDAGVFN
72 MUYGTSRAGF SDVAGNDHEV AINALADAGI INGYADSTFK PNQITINRGQV VELLDRYLEA QGQEIPADWN SKQRFNDLPV TAEAEVLKYA ALAKDAGVFN
73 MUYGTSRAGF SDVAGNDHEV AINALADAGI INGYADGTFK PNQITISRGQV VKLLGRYLEA QGQEIPADWN SKQRVNDLPV TAEAESVKYA ALAEDAGVFN
74 MUYGTSRAGF SDVAGNDHEV AISAPADAGI INGYADGTFK PNQITINRGQV VKLLSRYLEA QGQEIPADWN SKQRFNDLPV TAEAEVLKYT ALAKGAGVFN
75 MUYGTSRAGF SDVAGNYHEV AINALADAGI INGYADGTFK PNQITINRGQV VKLLGRYLEA QGQEIPADWN SKQRFNDLPV TAEAEVLKYA ALAKAAGVFN
76 MUYGTSRAGF SDVAGNDHEA PINALADAGI INGYADGTSK PNQITINRGQV VKLLGRYLEA QGQEIPADRN SEQRFNDPPV TAEAEVLKYA ALAKDAGVFN

67 VQTAT*

68 GSNGNLNAS*

69 GSNGNLNASQ TMQRQQMAVV LVRAIKKSLA*

70 GSNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NRVTEIGDLD KAYSAEQRTA IAALEYAGIT NVAHSNPGNS VTRGQFVHLL EVPIMRGRRG

71 GSNGNLNPSQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NRVTEIGDSD KAYSAEQRTA IVALEYAGVT NVAHFNLGNS VTRGQFASSS RGTNYAGRGR

72 GSNGNLNASQ TMQRQQMAVV LVRAIKEIVG VDLVAEYKKA NRVTEIGDLD KAYSSEQRTA IVALEYAGIT NVAHFNPGNS VTRGQFASSS RGTNYAGRGR

73 GSNSNLNASQ TMQRQQMAVV LGRAIKEIAG VDLVAEYKKA NRVTEIGDLD KAYSAEQRTA IVALEYAGTT NVAHFNLGNS VTRGQFASSS RGTNYAGRLG

74 GSNGNLNASQ TMQRQQMAVV LVRAIEEIIAG VDLVAEYKKA NRVTEIGDLD KAYSAEQRTA IVALEYAGIT NVAHFNPGNS VTRGQFASIL EVPIMRGRRG

75 GSNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NLVTEIGDLD KAYSAEQRTA TAALEYAGIT NVAHFNPGNN VTRGQFACSS RGTNYAGEAG

76 GSNGNLNASR TMQRQQMAVV LVRAIKEIAG VGLVAEYKKA NRVTEIGDLD KAYSAEQRTA IVALEYAGIT NVARLNPGNS VTRGQFASSS RGTNYAGEAG

7.3 Proteinsequenzen aus der Selektion gegen N-Acetylglucosamin

77 MVVVPLDRVF RCRR*

78 MUYGTSRAGF FRCCR*

79 MVMVPLEPGF PMLQVTITK*

80 MVMVPLEPGF PMLQVTITK*

81 MVMVPLEPGF PMLQVTITK*

82 MVMVPLEPGF PMLQVTITK*

83 MVMVPLEPGF PMLQVTITK*

84 MVMVPLEPGS PMLQVTITK*

85 MVMVLEPSF PMLQVTITK*

86 MVMVPLEPGF PMLQVTITK*

87 MVMVLEPSF PMLQVTITK*

VII ANHANG

88 MVMVPLEPGF PMLQVTTK*
 89 MVMVPLEPGF RMLQVTTM*
 90 MVMVPPEPGF PMLQVTTK*
 91 MVMVPLEPGF RMLLVTTK*
 92 MVMVPLEPGF PMLQVTTK*
 93 MVMVPLEPGF PILQVTTK*
 94 MVMVPLEPVS PMLQVTTK*
 95 MCMVPLEPGF PMLQVTTK*
 96 MVMVPLEPGF PMLRVTTK*
 97 MVYVPLEPGF PDVAGNDHEV AINALADAGI IQ*
 98 MVYGTSRVGF SDAAGSDHEV AINALADAGI IQWIR*
 99 MVYGTSRAGF SDVAGNDHGV AINALADAGI IQWIR*
 100 MVYGTSRAGF SDVAGNDHGV AINALADAGI INGYADGTFK PNQTFNRGRV VKLLGCYLEA QGQEIPADWN SKQRFNDLPV TAEAESVKYA ALARCRRIQR
 101 MVMVPMSRVS DVAGNDHEVA INALADAGII NGYADGTFKP NQ TINRGQVV KLLGRYLEAQ GQEV PADWNS KQRFNDLPVT AEAELVKYAA LAKDAGVFNG
 102 MVYGTSRAGF SDVAGNDHEV AINALADAGI INGYADGTFK PNQAINRGQV VKFLGRYLEA QGQEIPADWN SKQRFNDLPV TAEAELVKYA ALAKDAGVFN
 103 MVYGTSRPGF SDVAGNDHEV AINALADAGI INGYADGTFK PNQ TINRGQV VKLLGRYLEA QGQEIPADWN SKQRFNDLPV TAEAELVKYA ALAKDAGVFN
 104 MVYGTSRPGF SDVAGNDHEV AINALADAGI INGYADGTFK PNQ TINRGQV VKLLGRYLEA QGQEIPADWN SKQRFNDLPV TAEAELVKYA ALAKDAGVFN
 105 MVYGTSRAGF SDVAGNDHEV AINALADAGI INGYADATFK PNQ TINRGQV VKLLGRYLEA QGQEIPADWD SKQRFSDLPV TAEAELVKYA ALAKDAGVFS
 106 MVMVPLEPGS PDAAGNDHEV AINALADAGI INGYADCTFK PNQ TINRGQV VKLLGRYLEA QGQGI PADWN SKQRLNDLPV TAEAELVKYA ALAKDAGVFN
 107 MVYGTSRAGF SDVAGNDHEV AINALADAGI ING FADGTFK PNQ TINRGQV VKLLGRYLEA QGQEIPADWN SKQRFNDLPV TAEAELVKYA ALAKDAGVFN
 108 MVYGTSRAGF SDVAGNDYEV AINALADAGI INGYADGTFK PNQ TINRGQV VKLLGRYLEA QGQETPADWN SKQRSNDLPV TAEAELVKYA ALAKDAGVFN
 109 MVMVPLEPGF SDVAGNDHEV AINALADAGI INGYADSTFK PNQ TINRGQV VKLLGRYLEA QGREILADWN SEQRFNDLPV TAEAELLYKA ALAKDAGVFN
 110 MVYGTSRAGF SDVAGNDYEV AINALADAGI INGYADGTFK PNQ TINRGQV VKLLGRYLEA QGQETPADWN SKQRSNDLPV TAEAELVKYA ALAKDAGVFN
 111 MVYGTSRAGF SDVAGNDHEV AINALADAGI INGYADATFK PNQ TINRGQV VKLLGRYLEA QGQEIPADWD SKQRFSDLPV TAEAELVKYA ALAKDAGVFS
 112 MVYGTSRAGF SDVAGNDHEV AINALADAGI INGYADATFK PNQ TINRGQV VKLLGRYLEA QGQEIPADWD SKQRFSDLPV TAEAELVKYA ALAKDAGVFS
 113 MVYGTSRAGF SDVAGNDHEV AISALADADI INGYADGTFK PIQT TNRGQV VKLLGRYLEA QGQEIPADWY SKQRFNDLPV TAEAELVKYA ALAKGAGVFN

 100 FKRQLKRFTN NATSANGSSF GTCY*
 101 SNGNLNASQT MQRQLMAVVL VRAIKEIAGA DLVAEYKKRI S*
 102 GSNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKS GFRNRNW*
 103 GSNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NFVAENR*
 104 GSNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NFVAENR*
 105 GSNGNLNASQ TMQRQQMAVV LLRAIKEIAG VDLVAEYKRA NFVTEIDDL KAYSAEQRTA IVALEYAGIT NVAHFNPNGNS VTRGQLASSS RGTNYAGEAG
 106 GSNGNLNASQ TMQRQQMAVV LVRAIKEIAS VDLVAEYEKA NFVTEIGDLD KAYSAEQHTA IVALEYAGIT NVAHLNPGNS VTRGQFVHPL EVPIMRGGGG
 107 GSNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NFVAEIGDLD KAYSTEQRTV IVALEYAGIT NVAHFNPNSNS VTRGLFASSS RGTNYAGWRG
 108 GSNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NFVTEIGDLD KAYSAEQRTG IVALEYAGIT NVAHFNPNGNS VTRGHSFFXE VPXXXXXGG.
 109 GSNGNLNASQ TMQRQQTAVV LVRAIKEIAD VDLVAEYRKA NFVTEIGDLD KAYSAEQRTA TVALEYAGIT NVAHFNPNGNS VTRRQSASSS RVPIMRGGGG
 110 GSNGNLNASQ TMQRQQMAVV LVRAIKEIAG VDLVAEYKKA NFVTEIGDLD KAYSAEQRTG IVALEYAGIT NVAHFNPNGNS VTRGQFVSFL XVPIMREAGG
 111 GSNGNLNASQ TMQRQQMAVV LLRAIKEIAG VDLVAEYKRA NFVTEIDDL KAYSAEQRTA IVALEYAGIT NVAHFNPNGNS VTRGQFASSS RGTNYAGEAG
 112 GSNGNLNASQ TMQRQQMAVV LLRAIKEIAG VDLVAEYKRA NFVTEIDDL KAYSAEQRTA IVALEYAGIT NVAHFNPNGNS VTRGQFASSS RGTNYAGEAG
 113 GTNGNLNASQ TMQRQQMAVV LVCAIKEIAG VDLVAEYKKA NFVTEIGDLD KAYSAEQRTA IVALEYAGIT NVTHFNPGNS VTRGQFASSS RGTNYAGEAG

