Supplementary information

Hornerin contains a Linked Series of

Ribosome-Targeting Peptide Antibiotics

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Supplementary Fig. S1 | TEM of *P. aeruginosa*, treated with selected HRNR-peptides.

TEM analyses of 6.25 x 10^7 /ml *P. aeruginosa* ATCC 11446, in 10 mM NaP/ 1 % TSB/ pH 5.5, treated with 667 µg/mL HRNR₁₁₃₂₋₁₁₄₃ (GSGSRQSPSYGR) (**a**, **b**), 667 µg/mL HRNR₁₁₃₂₋₁₁₅₇ (GSGSRQSPSYGRHGSGSGRSSSSGQH) (**c**, **d**) and 667 µg/mL HRNR₂₆₀₆₋₂₆₂₈ (HGSRSGQSSRGERHGSSSGSSSH) (**e**, **f**), respectively, for 1h at room temperature. Note the dodecapeptide HRNR₁₁₃₂₋₁₁₄₃ affecting only a limited number of cells, which are destroyed (**a**, **b**) in a similar fashion as seen with rSUMO3-HRNR₂₅₉₁₋₂₆₈₄ with widespread peeling of the outer membrane and extensive lysis with loss of the cytoplasmic electron-dense material. A limited number of *P. aeruginosa* ATCC 11446, treated with either HRNR₁₁₃₂₋₁₁₅₇ (**c**, **d**) or HRNR₂₆₀₆₋₂₆₂₈ (**e**, **f**) showed large blebs on the outer membrane. Cytoplasmic swelling was observed at the area where the outer membrane appeared to be ruptured. **g**, **h**, Control. Images are representative of two independent experiments, sampling on average 10 images per condition in each experiment.



Supplementary Figure S2 | **TEM of HR 1-18-treated** *P. aeruginosa.* **a**, **b**, TEM of 6.25 x 10^7 /ml *P. aeruginosa* ATCC 10145, in 10 mM NaP/ 0.25 % glucose/ pH 5.5, treated with 167 µg/mL HR1-18 (HRNR₂₅₅₆₋₂₆₇₇)(GRHGSGLGHSSSHGQHGSGSGR) for 1h at ambient temperature. **c**, **d**, control. Note the condensation of electron-dense cytoplasmic material in HR1-18-treated bacteria (**a**, **b**). Images are representative of two independent experiments, sampling on average 10 images.



Supplementary Figure S3 | Ultrastructure kinetics in rSUMO3-HRNR₂₅₉₁₋₂₆₈₄-treated *E. coli*. TEM of 6.25×10^7 /ml *E. coli* ATCC 11775, in 10 mM NaP/ 1% TSB/ pH 5.5, treated with 500 µg/mL rSUMO3-HRNR₂₅₉₁₋₂₆₈₄ for 5min (**a**, **b**), 20min (**c**), 1h (**d**) and 2h (**e**) at RT. **f**, buffer control (2h treatment). Note the absence of membrane perturbation and the presence of few blebs of the outer membrane with an occasional ballooning and some electron-dense cytoplasmic aggregates already after 5 min incubation. After 1h and 2h treatment intracytoplasmic electron-dense aggregates accumulate in rSUMO3-HRNR₂₅₉₁₋₂₆₈₄-treated bacteria (**d**, **e**). At higher magnification, in samples of rSUMO3-HRNR₂₅₉₁₋₂₆₈₄-treated bacteria often nanofiber-like structures were detected (**a** - **e**, red arrows). Images are representative of two independent experiments, sampling on average 10 images per condition in each experiment.



Supplementary Figure S4 | rSUMO3-HRNR₂₅₉₁₋₂₆₈₄ forms amyloid-like nanostructures.

rSUMO3-HRNR₂₅₉₁₋₂₆₈₄ was treated with ultrasound and then analyzed by monitoring thioflavin T fluorescence (a) and light microscopy (b) for amyloid-formation. In a second

experimental series, FITC-labeled rSUMO3-HRNR₂₅₉₁₋₂₆₈₄ was treated with ultrasound and then monitored by light microscopy (**c**, **f**), for DAPI-staining (**d**, **g**) and for fluorescence, after storage for 1 h (**c** - **e**) and 20 h (**f** - **h**), respectively. Scale bar 20 μ m.



Supplementary Figure S5 | **Identification of rSUMO3-HRNR**₂₅₉₁₋₂₆₈₄-**interacting proteins upon SulfoLink®–coupling resin-chromatography.** An *E. coli*-extract was applied to a SulfoLink®–column and bound proteins were eluted with an increasing gradient of NH₄Cl-buffer (**a**). Aliquots of each fraction were analyzed by SDS-PAGE and silver staining (**b**) and by a Far-Western blot (**c**) using rSUMO3-HRNR₂₅₉₁₋₂₆₈₄ as "bait" protein and polyclonal antibodies against HRNR₂₅₉₁₋₂₆₈₄ for visualization of protein interaction. MW: molecular weight standards; MIX: crude *E. coli*-extract; X1 -X3: unbound material; A1 - A7: bound material.



Supplementary Figure S6 | **rSUMO3-HRNR**₂₅₉₁₋₂₆₈₄ **binds to** *E. coli* **ribosomal proteins.** SulfoLink[®]– column-bound proteins of an *E. coli*-extract were separated on a **Jupiter**[®] **300Å C18-RP-HPLC column** and eluted with an increasing gradient of **2-propanol (Prp) in aqueous 0.1 % TFA (a)**. Aliquots of UV-absorbing peak fractions were analyzed in a Far- SUMO3-HRNR₂₅₉₁₋₂₆₈₄-dotblot analysis (b) and dotblot-positive fractions (highlighted as boxes) were subjected to a Far-rSUMO3-HRNR₂₅₉₁₋₂₆₈₄-Westernblot analysis (c). Note the presence of the most intensive band at 37 kDa (D13 and D14), and ~20 more or less intensive bands corresponding to a MW between 12 and 34 kDa.

Supplementary Figure S7a, b



Supplementary Figure S7a, b | Identification of *E. coli* 50S ribosomal protein L28 in rSUMO3-HRNR₂₅₉₁₋₂₆₈₄-Far-Westernblot-positive HPLC fractions. In fraction D3 (Supplementary Figure S6) the *E. coli* 50S ribosomal protein L28 was identified (Mascot search reveals amino acid sequences of matching peptide fragments (a, b). MS-analysis of the D3 fraction before digestion revealed a major 8876,092 Da mass (average [Mr+H] mass) corresponding to an NH₂-terminally truncated version of L28 (residues 9-85).

Supplementary Figure S7c – g

C					
Mascot Search Results					
Database 1 : SwissFrot 2014 08 (546238 sequences; 194363168 residues) Taxonomy 1 : Escherichia coli (22963 sequences) Database 2 : NCBInr 20140521 (20589704 sequences; 17795984493 residues) Taxonomy 2 : Escherichia coli (105901 sequences) : Error tolerant search of all simificant protein hits	Mascot Score Histogram				
Protein hits : 1::RSI1 ECO24 305 ribosomal protein S11 05=Escherichia coli 0139:H28 (strain E243) 1::RSI0 ECO24 305 ribosomal protein S10 05=Escherichia coli 0139:H28 (strain E243) 2::eji445945422 305 ribosomal protein S10 05=Escherichia coli 0139:H28 (strain E243) 1::RSI0 ECO24 305 ribosomal protein S10 Escherichia coli 0139:H28 (strain E243) 1::RSI0 ECO24 305 ribosomal protein S20 05=Escherichia coli 0139:H28 (strain E243) 1::RSI0 ECO24 305 ribosomal protein S20 05=Escherichia coli 0139:H28 (strain E243)	377A / ETEC) GN=rpaK FE=3 SV=1 Individual ions scores 50 indicate identity or extensive homology (p=0.05). 377A / ETEC) GN=rpaK FE=3 SV=1 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits. 377A / ETEC) GN=rpaF FE=3 SV=1 377A / ETEC) GN=rpaF FE=3 SV=1				
2::gi]446057343 305 ribosomal protein S18 (Escherichia coli) 2::gi]446057343 305 ribosomal protein S18 (Escherichia coli) 5 30- 15- 10- 10- 10- 10- 10- 10- 10- 10					
d 30S ribosomal protein S11	e ^{30S ribosomal protein S18}				
Protein sequence coverage: 51%	Protein sequence coverage: 48%				
Matched peptides shown in magenta. 1 MAKAPIRARK RVRKQVSDGV AHIHASFNNT IVTITDRQGN ALGWATAGGS 51 GFRGSRKSTP FAAQVAAERC ADAVKEYGIK NLEVMVKGPG PGRESTIRAL 101 NAAGFRITNI TDVTPIPHNG CRPPKKRRV	Matched peptides shown in blue. 1 MARYFRRAKF CRETAEGVQE IDYKDIATLK NYITESGKIV PSRITGTRAK 51 YQRQLARAIK RARYLSLLPY TDRHQ				
Start- End Observed Nr (capt) Nr (calc) Delta N Score Expect Rank 0 Peptide 15 - 37 832.7853 2495.3342 2494.2565 1.0777 0 124 2.5e-09 1 K. QVEDOVABLEASENDITIVITIER.0 38 - 53 775.640 1348.7934 1348.7433 0.5051 0 78 9.6e-05 1 R. QOBLOGVABLEASENDITIVITIER.0 38 - 543.440 1246.7734 1246.506 0.423 0 K. STFYDAQVABER.C 50 - 69 500.7740 1058.5309 -0.0174 0 61 1 T. FIPAQVAABR.C 51 - 67 410.724 12542 0.0210 0 8.112.4996.0 0 59 - 610 410.2440 818.4399 0.0336 0 34 2.3 1 R.ADRAGER.I	Start- End Observed Mc (expt) Mr (calc) Dalta M Score Expect Rank U Peptide 13 - 24 700.3640 1398.7134 1398.6667 0.0467 0 109 8e-08 1 U R.FTAECOVGEIDYK.D 13 - 24 700.3640 1398.134 1398.6667 0.0467 0 109 8e-08 1 U R.FTAECOVGEIDYK.D 13 - 24 701.8740 1401.7334 1400.6799 1.0625 6 9 1 U R.FTAECOVGEIDYK.D 13 - 30 681.3853 2041.1342 2040.0415 1.0927 1 49 0.071 1 U R.FTAECOVGEIDYKD.IATLK.N 25 - 30 330.7140 659.4134 659.3854 0.0231 0 46 1.094.7 R.FTAECOVGEIDYKD.IATLK.N 31 - 38 911.4700 910.4627 910.4356 0.0231 0 41.9 1 R.NITTESKK.I 44 - 73 452.840 910.4326				
f 305 ribosomal protein S19	g 305 ribosomal protein S20				
Protein sequence coverage: 48%	Protein sequence coverage: 43%				
Matched peptides shown in green. 1 MPRSLKKGPF IDLHLLKKVE KAVESGDKKP LRTWSRRSTI FPNMIGLTIA 51 VHNGRQHVFV FVTDEMVGHK LGEFAPTRTY RGHAADKKAK KK	Matched peptides shown in o <u>range</u> . 1 MANIKSAKKR AIQSEKARKH NASRRSMMRT FIKKVYAAIE AGDKAAAQKA 51 <mark>FNEMQPIVDR</mark> QAAKGLIHKN KAARHKANLT AQINKLA				
Start- End Observed Mr (expt) Mr (calc) Delta M Score Expect Rank U Peptide 7 -17 427.6153 1279.8242 1279.7652 0.0589 1 1 3.4e+02 1 U K.KGPFIDLHLLK.K 8 -17 384.9153 115.7242 1151.6703 0.0589 0 8 8e+02 1 U K.KGPFIDLHLLK.K 22 -32 400.5753 1198.7042 1198.6670 0.0372 1 9 0.0088 1 U K.AUPFIDLHLK.K 56 -70 574.9853 17.1942 151.8650 0.702 0 70 R.OWPVPVTDENVORK.L 56 -70 580.3253 1737.9542 1737.8509 0.1033 0 1 4.2 1 U R.OWPVPVTDENVORK.L 71 - 78 445.7640 889.5134 889.4658 0.0477 0 45 0.21 1 U K.LGEFAPTR.T <th>Start- End Observed Mr (expt) Mr (calc) Delta M Score Expect Rank U Peptide 10 - 16 416,7440 831,4734 830,4610 1.0125 1 3 3.5+402 4 KRUDSEK.A 34 - 44 389,2533 1163,6166 1.0125 1 3 3.5+402 4 KRUDSEK.A 35 - 44 518,7840 1035,5237 1035,5237 0.0298 0 2 0.2 1 K.VYAAIEADOK.A 50 - 60 660.3440 1318,6734 1318,6340 0.0395 0 9 9 1 U K.ATMEMODYNR.Q 50 - 60 661.3540 1320.6934 1319,6310 1.6625 6 1 U K.ATMEMODYNR.Q 50 - 60 669.3440 1334,6289 0.0446 78 9.8e-05 1 U K.ATMEMODYNR.Q 50 - 60 669.</th>	Start- End Observed Mr (expt) Mr (calc) Delta M Score Expect Rank U Peptide 10 - 16 416,7440 831,4734 830,4610 1.0125 1 3 3.5+402 4 KRUDSEK.A 34 - 44 389,2533 1163,6166 1.0125 1 3 3.5+402 4 KRUDSEK.A 35 - 44 518,7840 1035,5237 1035,5237 0.0298 0 2 0.2 1 K.VYAAIEADOK.A 50 - 60 660.3440 1318,6734 1318,6340 0.0395 0 9 9 1 U K.ATMEMODYNR.Q 50 - 60 661.3540 1320.6934 1319,6310 1.6625 6 1 U K.ATMEMODYNR.Q 50 - 60 669.3440 1334,6289 0.0446 78 9.8e-05 1 U K.ATMEMODYNR.Q 50 - 60 669.				

Supplementary Figure S7c-g | Identification of the *E. coli* 30S ribosomal proteins S11, S18, S19 and S20 in SUMO3-HRNR₂₅₉₁₋₂₆₈₄-Far-Westernblot-positive HPLC fractions. In fraction D6 (Supplementary Figure S6) the *E. coli* 30S ribosomal proteins S11, S18, S19 and S20 were identified. Amino acid sequences of identified peptide fragments from digested D6 fraction are shown separately for each 30S ribosomal protein using separate colors for different ribosomal proteins (c - g).

Supplementary Figure S7h, i



Supplementary Figure S7h, i I Identification of the 50S *E. coli* ribosomal protein L2 in rSUMO3-HRNR₂₅₉₁₋₂₆₈₄-Far-Westernblot-positive HPLC fractions. In fraction D13 (Supplementary Figure S6) the *E. coli* 50S ribosomal protein L2 was identified (h, i). MS-analysis of the D13 fraction before digestion revealed 2 major constituents (i). The 29748.428 da (average [M_r+H]) mass matches most closely to the calculated M_r mass for the entire L2 amino acid sequence lacking the aminoterminal methionine. The most intense 13044.289 da mass signal most probably represents an internal L2 fragment (i).



Supplementary Figure S8 I **HRNR**₂₅₉₁₋₂₆₈₄ **binds to 30S and 50S** *E. coli* **ribosomal proteins.** SulfoLink[®]column-bound proteins of an *E. coli*-extract were separated on a **Jupiter**[®] **300Å C18-RP-HPLC column** and were eluted with an increasing gradient of **acetonitrile (ACN) in aqueous 0.1 % TFA (a)**. Aliquots of selected, in a HRNR-Far-Dotblot analysis positive HPLC fractions (C4 - D4) as well as SulfoLink[®]column-bound proteins as control (Mix), were subjected to a HRNR-Far-Westernblot and analyzed with HRNR₂₅₉₁₋₂₆₈₄ antibodies (**b**). Some bands seen in the crude ribosome extract (mix) are missing in HPLC fractions (e.g. at 20, 24 and 25 kDa). MW: Molecular weight marker.



Supplementary Figure S9 | Identification of 50S *E. coli* ribosomal proteins L22 and L13 in HRNR₂₅₉₁. ₂₆₈₄-Far-Westernblot-positive HPLC fractions. SulfoLink®–column-bound proteins of an *E. coli*extract, separated on a Jupiter 300Å C18-RP-HPLC column, eluted with acetonitrile, showing band(s) upon HRNR₂₅₉₁₋₂₆₈₄-Far-Westernblot (Supplementary Figure S8), were subjected to reduction, alkylation and tryptic digestion with subsequent MS/MS analysis at a QTOF-2 ESI-MS. Whereas in fraction D4 the *E. coli* 50S ribosomal protein L22 was identified (a), MS/MS analyses revealed the *E. coli* 50S ribosomal protein L13 in fraction C11 (b).



Supplementary Figure S10 | LC-MS/MS analyses identify a wide range of 50S and 30S *E. coli* ribosomal proteins with apparent HRNR-binding properties. SulfoLink®–column-bound proteins of an *E. coli*-extract were separated on a Aeris® widepore RP-HPLC column with a gradient of Prp in aqueous 0.1 % TFA (a) and fractions were analyzed for rSUMO3-HRNR₂₅₉₁₋₂₆₈₄-binding proteins in a HRNR-Far-dot blot system (b). Note strongest dots in fractions C5, D10, D11, E5 and E12.

Accession	Description	Score
W1G3Y5	30S ribosomal protein S10 OS=Escherichia coli ISC11 GN=rpsJ PE	22,27
W1G5N2	30S ribosomal protein S11 OS=Escherichia coli ISC11 GN=rpsK PE	12,95
W1FQT2	30S ribosomal protein S12 OS=Escherichia coli ISC11 GN=rpsL PE	16,63
W1FUI0	30S ribosomal protein S2 OS=Escherichia coli ISC11 GN=rpsB PE=	130,12
W1G3V3	30S ribosomal protein S3 OS=Escherichia coli ISC11 GN=rpsC PE=	121,77
W1G3T6	30S ribosomal protein S4 OS=Escherichia coli ISC11 GN=rpsD PE=	52,04
W1G3W9	30S ribosomal protein S5 OS=Escherichia coli ISC11 GN=rpsE PE=	60,37
W1G2U2	30S ribosomal protein S6 OS=Escherichia coli ISC11 GN=rpsF PE=	39,47
W1G213	50S ribosomal protein L10 OS=Escherichia coli ISC11 GN=rplJ PE=	35,14
W1G1R6	50S ribosomal protein L11 OS=Escherichia coli ISC11 GN=rplK PE	19,38
W1G5Q1	50S ribosomal protein L14 OS=Escherichia coli ISC11 GN=rplN PE	8,93
W1G3U0	50S ribosomal protein L15 OS=Escherichia coli ISC11 GN=rplO PE	37,59
W1G7H8	50S ribosomal protein L17 OS=Escherichia coli ISC11 GN=rplQ PE	11,89
W1G7I8	50S ribosomal protein L18 OS=Escherichia coli ISC11 GN=rplR PE	7,37
W1G7K5	50S ribosomal protein L2 OS=Escherichia coli ISC11 GN=rplB PE=	23,78
W1G2X9	50S ribosomal protein L20 OS=Escherichia coli ISC11 GN=rplT PE	41,15
W1FUZ6	50S ribosomal protein L21 OS=Escherichia coli ISC11 PE=3 SV=1	24,46
W1G611	50S ribosomal protein L23 OS=Escherichia coli ISC11 GN=rplW PE	9,52
W1G3U9	50S ribosomal protein L24 OS=Escherichia coli ISC11 GN=rplX PE	12,00
W1FT83	50S ribosomal protein L3 glutamine methyltransferase OS=Escheri	14,93
W1G5R1	50S ribosomal protein L3 OS=Escherichia coli ISC11 GN=rplC PE=	37,65
W1G3V7	50S ribosomal protein L4 OS=Escherichia coli ISC11 GN=rplD PE=	220,74
W1G602	50S ribosomal protein L5 OS=Escherichia coli ISC11 GN=rplE PE=	95,61
W1G5Z8	50S ribosomal protein L6 OS=Escherichia coli ISC11 PE=3 SV=1 -	5,80
W1G0Z3	50S ribosomal protein L9 OS=Escherichia coli ISC11 GN=rplI PE=	123,48
W1G024	LSU ribosomal protein L1p (L10Ae) OS=Escherichia coli ISC11 PE=	25,49
W1G016	LSU ribosomal protein L7/L12 (P1/P2) OS=Escherichia coli ISC11 F	376,57
W1G3L1	Ribosomal protein OS=Escherichia coli ISC11 PE=3 SV=1 - [W1G3	29,47
W1FWK2	Ribosomal RNA small subunit methyltransferase C OS=Escherichia	12,87
W1FZR0	Ribosomal RNA small subunit methyltransferase E OS=Escherichia	5,62
W1FUM5	Ribosomal silencing factor RsfS OS=Escherichia coli ISC11 GN=rsf	92,69
W1FS83	SSU ribosomal protein S1p OS=Escherichia coli ISC11 PE=4 SV=1	294,85
W1FR69	SSU ribosomal protein S7p (S5e) OS=Escherichia coli ISC11 PE=4	14,31
D ()	B. (1)	
Protein 200 rikes sus slave		Modification(s)
305 ribosomal pr		
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305 ribosomal pr		
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305 riposomal pr		M4(Ovidation)
SUS riposomal pr		ivi4(Oxidation)
305 ribosomal pr		
JUG REDOSOMAL Dr		

Supplementary Figure S11 | All-Fractions-Precursor-Ion-Area.

Fraction	Protein	# Unique Peptides	Sequence Coverage (%)
C5	30S ribosomal protein S12 OS=Escheri	4	20.16%
	30S ribosomal protein S21 OS=Escheri	3	29.58%
	50S ribosomal protein L2 OS=Escheric	3	14.65%
D10	10 kDa chaperonin OS=Escherichia col	2	17,53%
010	30S ribosomal protein S10 OS=Escheri	2	13 59%
	205 ribosomal protein 510 05-Escheri	4	26.64%
	305 ribosomal protein 511 05-Escheri	2	25.61%
	305 ribosomal protein 510 03-Escheric	6	23,01/0
	30S ribosomal protein 55 OS=Eschenic	0	27,4770
	30S ribosomal protein 54 US=Eschenic	0	52,4370
	30S ribosomal protein So US=Escheric	4	13,/470
	50S ribosomal protein L13 US=Escheri	10	//,40%
	50S ribosomal protein L14 OS=Escheri	6	55,28%
	50S ribosomal protein L16 OS=Escheri	3	28,68%
	50S ribosomal protein L17 OS=Escheri	6	37,01%
	50S ribosomal protein L18 OS=Escheri	5	45,30%
	50S ribosomal protein L2 OS=Escheric	19	52,01%
	50S ribosomal protein L3 OS=Escheric	4	21,53%
	50S ribosomal protein L4 OS=Escheric	7	37,81%
	50S ribosomal protein L6 OS=Escheric	2	16,50%
	50S ribosomal protein L9 OS=Escheric	3	24,16%
	Cysteine desulfurase IscS OS=Escheric	2	7,67%
	DNA-binding protein OS=Escherichia c	4	23,36%
	DNA-directed RNA polymerase subuni	8	70,15%
	Ferredoxin, 2Fe-2S OS=Escherichia col	2	18,92%
	FKBP-type peptidyl-prolyl cis-trans iso	2	28,69%
	Pseudouridine synthase OS=Escherich	5	22,13%
	Pseudouridine synthase OS=Escherich	3	15,46%
	Ribosomal protein OS=Escherichia coli	2	17,99%
	ServI-tRNA synthetase OS=Escherichia	2	15,18%
	Signal recognition particle protein OS=	2	5.74%
	Single-stranded DNA-binding protein (2	13,04%
	SSU ribosomal protein S7p (S5e) OS=E	4	53.57%
	SSU ribosomal protein S8p (S15Ae) OS	2	22.83%
	Translation elongation factor Tu OS=E	2	19.40%
D11	205 ribosomal protein \$3 OS=Escheric	2	16.74%
DII	205 ribosomal protein S4 OS=Escheric	2	13 25%
	505 ribosomal protein L13 OS=Escheri	10	48.59%
	505 ribosomal protein L15 05-Escheri	2	40,35%
	505 ribosomal protein L14 OS-Escheri		44,1270 EC 419/
	505 ribosomal protein L18 OS-Escheria		30,4170
	50S ribosomal protein L2 US=Eschenic		23,0670
ED	305 ribosomai protein 510 US=Escherid		21,3070
	30S ribosomal protein S3 US=Escheric	10	48,50%
	30S ribosomal protein S4 OS=Escheric	4	37,09%
	30S ribosomal protein S6 OS=Escheric	8	67,18%
	50S ribosomal protein L14 OS=Escheri	2	30,08%
	50S ribosomal protein L22 OS=Escheri	3	35,45%
	50S ribosomal protein L23 OS=Escheri	4	39,00%
	50S ribosomal protein L5 OS=Escheric	3	18,44%
	50S ribosomal protein L9 OS=Escheric	2	22,15%
E12	30S ribosomal protein S2 OS=Escheric	2	19,92%
	30S ribosomal protein S3 OS=Escheric	4	34,76%
	30S ribosomal protein S4 OS=Escheric	2	23,84%
	30S ribosomal protein S6 OS=Escheric	10	73,28%
	50S ribosomal protein L14 OS=Escheri	2	30,08%
	50S ribosomal protein L5 OS=Escheric	5	34,64%
	50S ribosomal protein L9 OS=Escheric	3	27.52%
F14	30S ribosomal protein S10 OS=Escheri	4	35,92%
	30S ribosomal protein S11 OS=Escheri	3	36.64%
	30S ribosomal protein S12 OS=Escheri	3	41,13%
	30S ribosomal protein S2 OS=Escheric	13	60.59%
\vdash	305 ribosomal protein S3 OS=Escheric	13	56.65%
<u> </u>	305 ribosomal protein S4 OS=Escheric	6	44 37%
<u> </u>	205 ribosomal protein S5 OS=Escheric	4	34.13%
<u> </u>	305 ribosomal protein 55 05-Escheric		22 92%
<u> </u>	505 - hosomal protein 50 05-Escheric	6	28 70%
<u> </u>	50S ribosomal protein L10 OS=Escheri	4	33,7570
<u> </u>	505 ribosomal protein L11 OS=Escheri		30,00%
	505 ribosomai protein L14 OS-Escher		50,08%
<u> </u>	50S ribosomal protein L15 OS=Escheri		D9,0370
	50S ribosomal protein L17 US=Escheri		20,7770
	50S ribosomal protein L18 OS=Escheri		17,95%
	50S ribosomal protein L2 OS=Escheric	3	15,38%
	50S ribosomal protein L20 OS=Escheri	0	30,51%
	50S ribosomal protein L21 OS=Escheri	4	56,25%
	50S ribosomal protein L23 OS=Escheri	3	33,00%
	50S ribosomal protein L24 OS=Escheri	3	39,42%
	50S ribosomal protein L3 glutamine m	3	8,71%
	50S ribosomal protein L3 OS=Escheric	6	35,89%
	50S ribosomal protein L4 OS=Escheric	18	79,60%
	50S ribosomal protein L5 OS=Escheric	9	44,13%
	50S ribosomal protein L6 OS=Escheric	2	9,71%
	50S ribosomal protein L9 OS=Escheric	10	63,76%

Supplementary Figure S12 | Data Base Research Results Edited.

Supplementary Tables

Supplementary Table S1 | Amino acid sequences of HRNR fragments generated as HRNR polypeptides or SUMO3-(His)₆-fusion proteins

rHRNR₁₉₅₉₋₁₁₇₂ THGQHGSTSGQSSSCGQHGASSGQSSSHGQHGSGSSQSSGYGRQGSGSGQSPGHGRGSGSRQSPSYGRHGSGSGRSSSSGQHGSGLGESSGFGHHES rHRNR₂₅₉₁₋₂₈₈₄ SQHGSGSGHSSGYGQHGSRSGQSSRGERHGSSGSGSSSHYGQHGSGSRQSSGHGRQGSGSGQSPSRGRHGSGYGHSSSHGQHGSGSGRSSSRGPY

Supplementary Table S2 | HRNR-primer-sequences used in this study

Name	Oligonucleotide-Sequence	A.T.1	A.T.2	vector
SUMO-hrnr-2-F	ACCCATGGGCAACACGGTTC	71,3°C		pET-Sumo
SUMO-hrnr-2-R	TCAAGACTCGTGGTGACCAAAGC	69,6°C		
pSu-hr3-b-2591-f (Bsal)	AAGGTCTCAAGGTAGCATGGGTCTGGCT	60°C	77,1°C	pSumo3
pSu-hr3-b-2684-r (BamHI)	AAGGATCCTTAATATGGGCCACGGCTGGAA	60°C	77,4°C	

A.T.1: Annealing temperature underlined sequence; A.T.2: Annealing temperature whole

sequence. The complementary coding sequence is underlined.