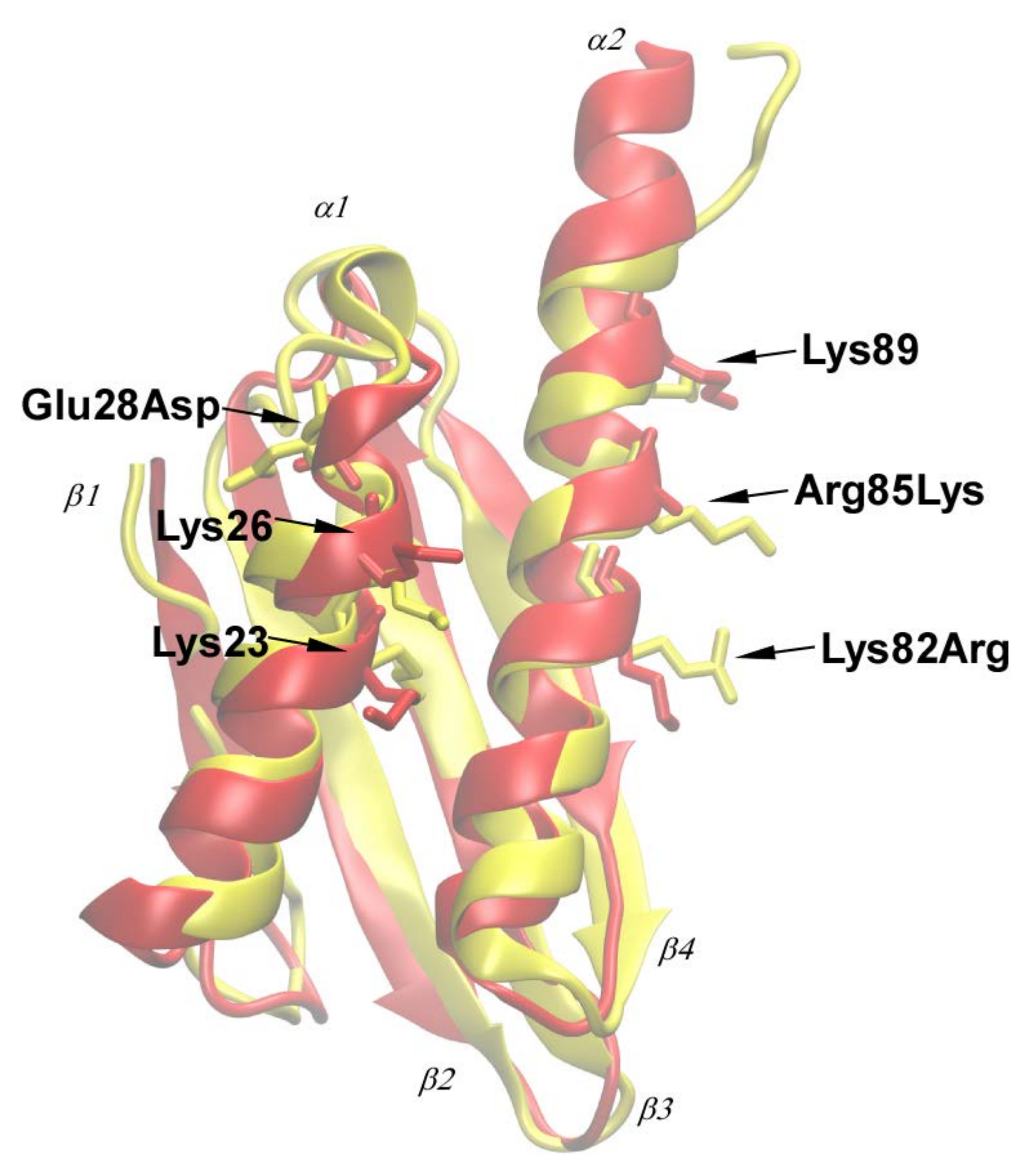
α2
α1
Lys89
Glu28Asp
β1
Arg85Lys
Lys26
Lys23
Lys82Arg
β4
β2
β3

Table S1. Oligonucleotides used in this study.

No.	Name	Sequence (5' -> 3')[a]
PCR primers		
1	bb0449 up	TTTTATGTTGATCCAGATAT
2	bb0449a forward out BglII	**AGATCT**TAGGTTCCATAATATGTTCTC
3	bb0449 reverse out BglII	**AGATCT**GATAGGTAAAAAATGCAAGA
4	bb0449 down	CCAAAGGCATTCGGACTTAG
5	bb0449b forward out BglII	**AGATCT**AATATGTTCTCCCTTTCTCA
6	$flaB_p$ forward BamHI	CGC**GGATCC**TGTCTGTCGCCTCTTGTGGCTTCCGG
7	kan reverse BamHI	**GGATCC**GAGCTTGCGCCGTCCCGT
8	bb0449 reverse BglII	**AGATCT**TTATTTGTTGTTTTTTTTCTCTTTCTCTTTGG
9	flg_p forward BamHI	**GGATCC**TACCCGAGCTTCAAGGAAG
10	aacC1 reverse BamHI	**GGATCC**CGATCTCGGCTTGAACG
11	$flaB_p$ reverse NdeI	**CATATG**TAATCATATGTCATTCCTCCATG
12	bb0449 forward NdeI	**CATATG**ATGGAACCTAAAATTCAAAC
13	bb0449 reverse PstI	**CTGCAG**TTATTTGTTGTTTTTTTTCTCTTTCTCTTTGG
14	bb0449 forward BamHI	**GGATCC**ATGGAACCTAAAATTCAAAC
15	bb0447mid	AAGTCAGTTTCAAGTCCTGCTGT
qRT-PCR primer/probe sets[b]		
16	bb0449 forward	AGACGCACATATTCACT
17	bb0449 reverse	GCTGTTTTGTAAAGTCTT
18	bb0449 probe	[6FAM]CTTCTTAATCTTATTGATAGTGCAAT[TAM]
19	flaB forward	TCTTTTCTCTGCTGAGGGAGCT
20	flaB reverse	TCCTTCCTGTTGAACACCCTCT
21	flaB probe	[6FAM]AAACTGCTCAGGCTGCACCGGTCC[TAM]

[a]Bold type indicates restriction sites.
[b]qRT-PCR probes used 6-Fam™ and TAMRA™ fluorescent dyes.

Table S2. Mass spectrometry identification of proteins in the ribosome protein fraction.

Band no.	Band size (kDa)	Proteins identified[a] (in alphabetical order)
1	59	ApeA, ApeB, GroEL, OppAIV, OspA, P66
2	37	BB0195, BBJ41, BmpA, Eno, Fla, FlaA, Gap, RpoA, **RpsB**[b]
3	24	BB0144, BB0158, BB0215, BB0238, BB0323, BBA69, BBG08, BBJ34, Ldh, NapA, OspD, **RplA**, **RplB**, **RpsC**
4	22	AtpE, BB027, BB0239, BB0334, BB0405, BB0543, BBH32, BBK13[b], BBL35, BBO27, CspA, OspB[c], OspC, PhoU, PncA, **RplC**, **RplD**, **RplU**, **RpsD**
5	18	BBA03, BBI39, BBK40, DbpA, FliL, NapA, P22, **RplE**, **RplF**, **RplI**, **RplY**, **RpsF**
6	16	ErpA, **RplM**, **RplO**, **RpsE**, **RpsG**
7	15	BB0689, CoaD, RevA1, **RplJ**, **RplK**, **RplP**, **RplQ**, **RplR**, **RplS**, **RplT**, **RplV**, **RpmD**, **RpsI**, **RpsL**, **RpsM**, **RpsR**
8	13	BB0651, BBF20, RbfA, **RplN**, **RplW**, **RplX**, **RpmB**, **RpmI**, **RpsH**, **RpsJ**, **RpsK**, **RpsO**, **RpsP**, **RpsS**, **RpsT**, **RpsU**, SpoVG
9	12	BB0162, BB0324, BB0696, EbfC, GroES, P13, **RplA**, **RplL**, **RpmC**, **RpmE2**, **RpmF**, **RpmG**, **RpsQ**, **RpsZ**, RsfS, TrxA

[a] Proteins present in multiple sequential protein bands were presumed to be contaminants resulting from incomplete column washing and were assigned to bands in which the protein was most highly represented, according to protein spectral counts**.** Contaminants were removed from bands subsequent to initial identification.

[b]Bold font indicates ribosomal proteins.

[c] All identified peptides are included in the truncated form of OspB protein present in B31-S9.

References

1. **Ueta M, Ohniwa RL, Yoshida H, Maki Y, Wada C, Wada A.** 2008. Role of HPF (hibernation promoting factor) in translational activity in *Escherichia coli*. J. Biochem. **143:**425-433.

Figure S1. Protein secondary structure comparison of modeled BB0449 and crystallized HPF proteins. Yellow protein represents modeled *B. burgdorferi* BB0449, while red protein represents HPF co-crystallized with ribosomes from *T. thermophilus* (PDB:3V26). The identified amino acid residues are ribosome-protein interaction sites (1), with amino acid substitutions in the modeled BB0449 as indicated. Small italics font indicates β-sheet and α-helix numbering.