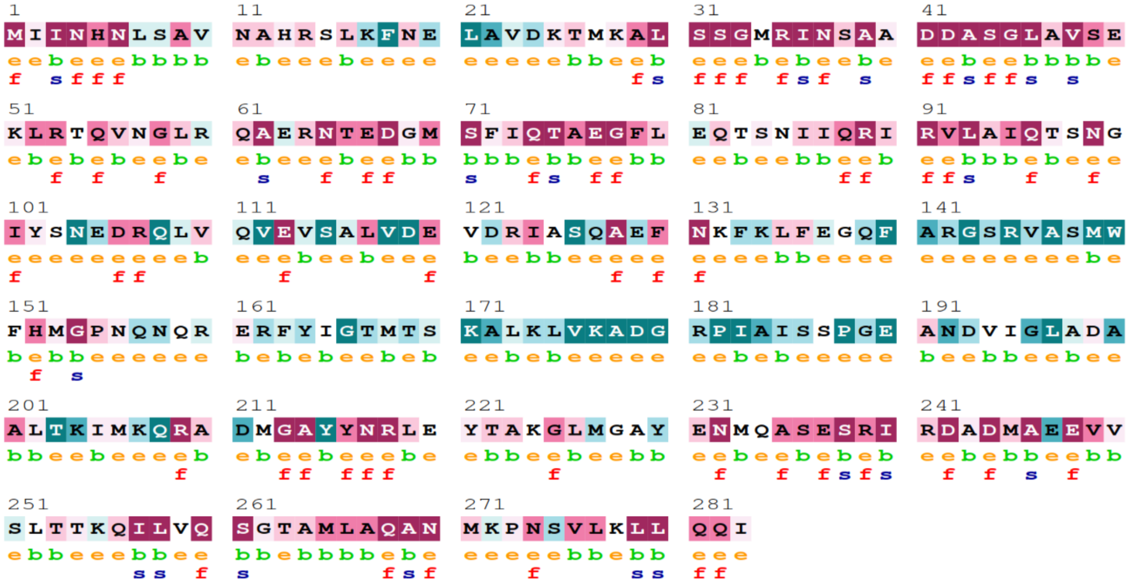
(A)


1
MIINHNLSAV
eebeeebbbb
f sfff
11
NAHRSLKFNE
ebeeebeeee
21
LAVDKTMKAL
eeeeebbeeb
fs
31
SSGMRINSAA
eeebebeebe
fff fsf s
41
DDASGLAVSE
eebeebbbbe
ffsffs s
51
KLRTQVNGLR
ebebebeebe
f f f
61
QAERNTEDGM
ebeeebeebb
s f ff
71
SFIQTAEGFL
bbbebbeebb
s fs ff
81
EQTSNIIQRI
eebeebbeeb
ff
91
RVLAIQTSNG
eebbbebeee
ffs f f
101
IYSNEDRQLV
eeeeeeeeeb
f ff
111
QVEVSALVDE
eeebeebeee
f f
121
VDRIASQAEF
beebbeeeee
f f
131
NKFKLFEGQF
eeeebbeeee
f
141
ARGSRVASMW
eeeeeeeebe
151
FHMGPNQNQR
bebbeeeeee
f s
161
ERFYIGTMTS
bebebeebeb
171
KALKLVKADG
eebebeeeee
181
RPIAISSPGE
eebebeeeee
191
ANDVIGLADA
beebbeebee
201
ALTKIMKQRA
bbeebeeeeb
f
211
DMGAYYNRLE
ebeebeeebe
ff fff
221
YTAKGLMGAY
ebbeebeebb
f
231
ENMQASESRI
eebeebebeb
f f fsfs
241
RDADMAEEVV
eebebbeebb
f f s f
251
SLTTKQILVQ
ebbeeebbee
ss f
261
SGTAMLAQAN
bbebbbbebe
s fsf
271
MKPNSVLKLL
eeeeebbebb
f ss
281
QQI
eee
ff

(B)


1
RINSAADDAS
eeeeeeeebe
fff f ffsf
11
GLAVSEKLRT
ebbbbeebee
fs ss
21
QVNGLRQAER
ebeebeebee
f f s
31
NTEDGMSFIQ
ebeebbbbbe
f f s f
41
TAEGFLEQTS
bbeebbeebe
ssff f
51
NIIQRIRVLA
ebbeebeebb
ff ffs
61
IQTSNGIYSN
bebeeeeeee
f f f
71
EDRQLVQVEV
eeeeebeeeb
ff f
81
SALVDEVDRI
eebeeebeeb
s f f
91
ASQAEFNKFK
beeeeeeeee
f ff
101
LFEGQFARGS
bbeeeeeeee
111
RVASMWFHMG
eeeebebebb
f s
121
PNQNQRERFC
eeeeeebebe
131
IGTMTSKALK
beebebeebe
141
LVKADGRPIA
beeeeeeebe
151
ISSPGEANDV
beeeeebeeb
161
IGLADAALTK
beebeebbee
171
IMKQRADMGA
beeeeeebee
f ff
181
YYNRLEYTAK
beeebeebbe
fff
191
GLMGAYENMQ
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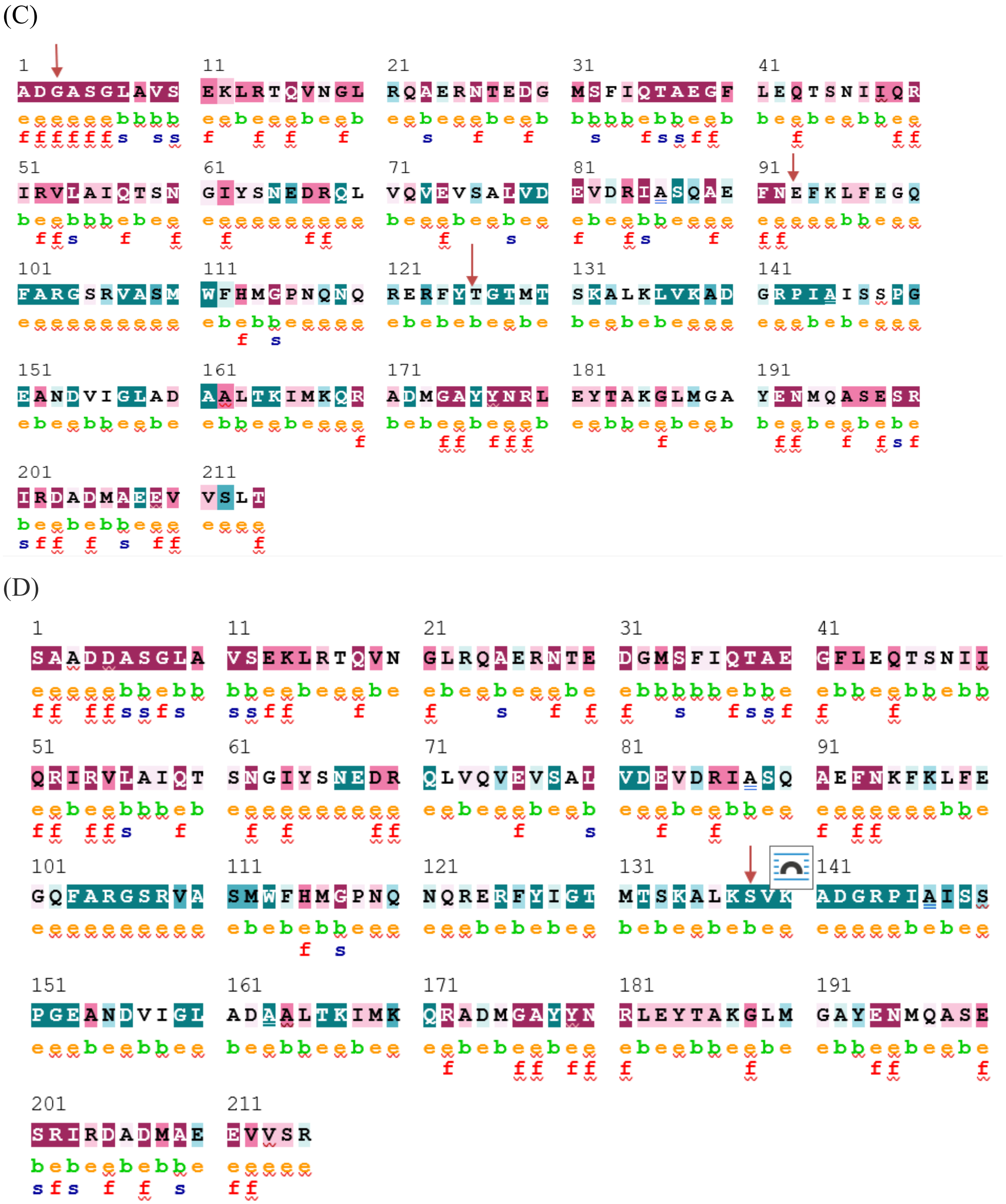
f ff
201
ASESRIRDAD
ebeeebeebe
f fffs f f
211
MAEEVVS
bbeeeee
s ff f

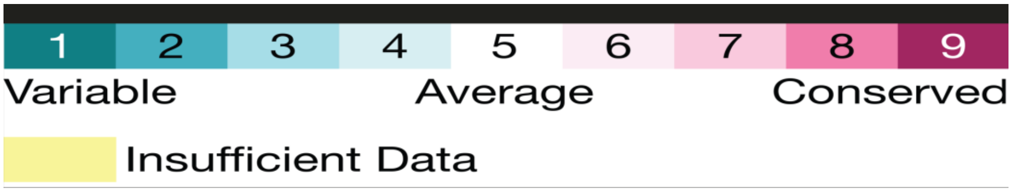


Additional File 3: Figure S1: FlaB protein of L. interrogans (A) (WP_000586170, template), variant protein sequences of NHSL13SL215 (B) (WKR44734) NHSL13ML092 (C) (WKR38874), and NHSL13ML506 (D) (WKR38873). Conserved regions of *L.interrogans* FlaB protein sequence and partial FlaB variant protein sequences of the patient sample created by the ConSurf web server (https://consurf.tau.ac.il/consurf_index.php).

Amino acid sequence (WKR38874) deduced from the nucleotide sequence of patient number, NHSL13ML092 (WKR38874). The variant D3G (D42G in wild type) is located in a highly conserved region. The other two variants K93E and I126T (K132E and I165T in template) are located in variable regions.

Amino acid sequence (WKR44734 and WKR38873) deduced from the nucleotide sequence of patient number, NH SL13SL215 and NHSL13ML506. The mutation Y130C (Y164C in wild type) and L138S (L175S in wild type) are located in variable regions.

↓ Mutation positions



e - An exposed residue according to the neural network algorithm.

b - A buried residue according to the neural network algorithm.

f - A predicted functional residue (highly conserved and exposed).

s - A predicted structural residue (highly conserved and buried).