Table S4. Protein sequence motifs identified in this study

Protein	Motif	Residue Range (Location)	Description (Possible Role)
Wzx	RHLIESMPVVIG	99 – 110 (PL2$_{\text{X}}$)	RX$_{10}$G (O-Ag subunit recognition)
	GTLGA	15 – 19 (TMS X1)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	ATIFA	49 – 53 (TMS X2)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	AVAIA	90 – 94 (TMS X3)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	ALAVA	115 – 119 (TMS X4)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	AACIA	150 – 154 (TMS X5)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	ATALA	181 – 185 (TMS X6)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	ALWVG	186 – 190 (TMS X6)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GDSAG	243 – 247 (TMS X7)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	AGWFA	246 – 250 (TMS X7)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GEAWA	320 – 324 (TMS X10)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	AWAFS	322 – 326 (TMS X10)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	SGRYA	326 – 330 (TMS X10)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	SIAYA	388 – 392 (TMS X12)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
Wzy	RENQGRRMLVLLS	135 – 147 (CL2$_{\text{Y}}$)	$\underline{\text{R/KXXXGXXXLhhhh}}$hD (Walker B ATPase consensus)
	RRALAREVFAAG	175 – 186 (PL2$_{\text{Y}}$)	RX$_{10}$G (O-Ag subunit recognition)
	RRAFIVPSTLLG	290 – 301 (PL5$_{\text{Y}}$)	RX$_{10}$G (O-Ag subunit recognition)
	AFFSA	20 – 24 (TMS Y1)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	ALICA	59 – 63 (TMS Y2)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GVPLA	107 – 111 (TMS Y4)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	AIAFG	111 – 115 (TMS Y4)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GIVNA	220 – 224 (TMS Y7)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GALLG	321 – 325 (TMS Y10)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	SMLVG	369 – 373 (TMS Y12)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
WaaL	TGYG	158 – 161 (CL3$_{\text{L}}$)	GXS/$\underline{\text{TGXG}}$KS/TS/T (Walker A ATPase consensus)
	RQISEHPWLGHG	273 – 284 (PL5$_{\text{L}}$)	RX$_{10}$G (O-Ag subunit recognition)
	HNIELGVLFAGG	303 – 314 (PL5$_{\text{L}}$–TMS L10)	HX$_{10}$G (Required for O-Ag ligation to lipid A-core)
	ALLTG	29 – 33 (TMS L1)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	AAILA	115 – 119 (TMS L5)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GAVIS	136 – 140 (TMS L6)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	AVISA	137 – 141 (TMS L6)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GLTAA	217 – 221 (TMS L8)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	ALALA	239 – 243 (TMS L9)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GVLFA	308 – 312 (TMS L10)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GGIIG	313 – 317 (TMS L10)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	AVLLA	340 – 344 (TMS L11)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	GLAAG	351 – 355 (TMS L11)	GAS$_{\text{Right}}$ (TMS dimerization/packing)
	ALLYA	378 – 382 (TMS L12)	GAS$_{\text{Right}}$ (TMS dimerization/packing)

$\underline{\text{Underline}}$ represents consensus sequence match with given sequence. Cytoplasmic loop (CL), periplasmic loop (PL). Subscript $_{\text{X}}$, $_{\text{Y}}$, $_{\text{L}}$ denotes Wzx, Wzy, WaaL, respectively.