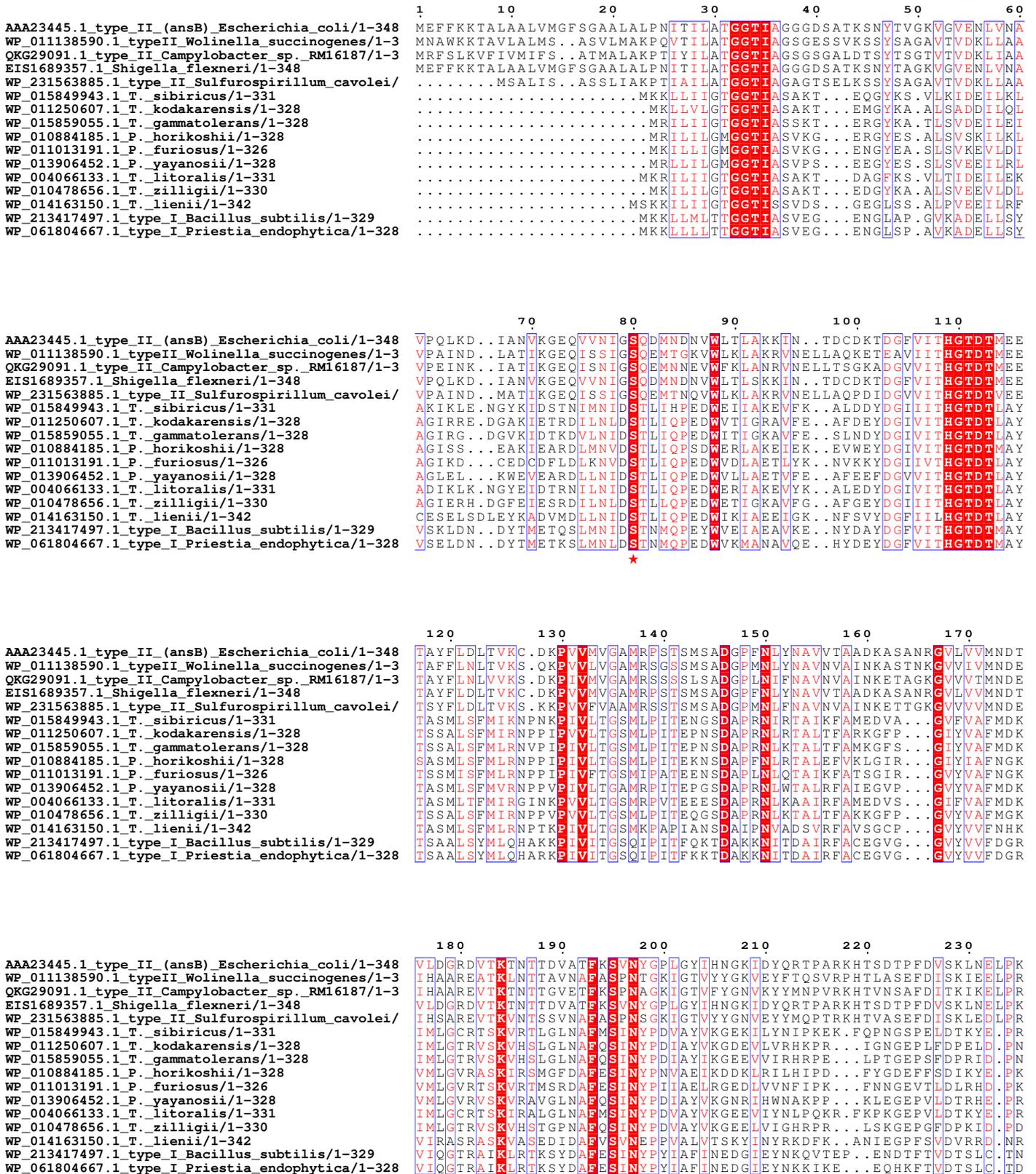


Figure S1. Amino acid sequence comparison of mesophilic and thermophilic L-asparaginases



	240	250	260	270	280	290																																																				
AAA23445.1_type_II_(ansB)_Escherichia_coli/1-348	V	G	I	V	Y	N	A	N	S	D	L	P	A	K	A	L	V	D	A	G	I	V	S	A	V	G	N	G	N	L	...																											
WP_011138590.1_typeII_Wolinella_succinogenes/1-3	V	D	I	L	Y	A	H	P	D	D	T	D	V	L	V	N	A	A	L	Q	A	G	A	K	G	I	I	H	A	G	M	G	N	G	N	P	...																					
QKG29091.1_type_II_Campylobacter_sp._RM16187/1-3	V	D	I	I	Y	S	H	S	N	D	N	P	D	F	A	N	I	S	I	K	N	G	A	K	G	I	I	S	A	G	M	G	N	G	N	P	...																					
EIS1689357.1_Shigella_flexneri/1-348	V	G	I	V	Y	N	Y	A	N	S	D	L	P	A	K	A	L	V	D	A	G	I	V	S	A	V	G	N	G	N	L	...																										
WP_231563885.1_type_II_Sulfurospirillum_cavolei/	V	D	I	V	Y	A	H	P	S	D	T	D	V	M	V	K	A	A	V	A	A	G	A	K	G	I	I	H	A	G	M	G	N	G	N	P	...																					
WP_015849943.1_T._sibiricus/1-331	V	V	L	R	V	T	P	G	L	G	E	I	D	A	V	L	D	A	G	Y	K	G	I	V	L	E	G	Y	G	A	G	L	P	Y	R	K	S	N	L	L	S	K	I	K	E	I	T	P	K	I	P	V	I	M	T			
WP_011250607.1_T._kodakarensis/1-328	V	V	H	I	R	L	T	P	G	L	S	P	E	V	L	R	A	V	A	R	A	T	D	G	I	V	L	E	G	Y	G	A	G	I	P	Y	R	G	R	N	L	L	E	V	V	S	E	T	A	R	E	K	P	V	M	T		
WP_015859055.1_T._gammatolerans/1-328	V	A	Y	L	R	L	T	P	G	L	S	P	E	V	F	L	A	V	A	E	K	V	H	G	I	V	L	E	G	Y	G	A	G	I	P	Y	R	G	R	N	L	L	E	A	V	S	R	V	A	R	E	K	P	V	M	T		
WP_010884185.1_P._horikoshii/1-328	V	L	V	I	K	L	I	P	G	L	S	G	D	I	V	R	E	A	L	R	L	G	Y	K	G	I	I	L	E	G	Y	G	V	G	I	P	Y	R	G	T	D	L	F	E	V	V	S	S	I	S	K	R	I	P	V	V	L	T
WP_011013191.1_P._furiosus/1-326	V	L	V	I	K	L	I	P	G	L	S	G	D	I	F	R	A	A	V	E	L	G	Y	R	G	I	V	I	E	G	Y	G	A	G	I	P	Y	R	G	S	D	L	L	Q	T	I	E	E	L	S	K	E	I	P	I	V	M	T
WP_013906452.1_P._yayanosii/1-328	V	L	V	L	R	L	V	P	G	M	E	G	D	V	L	E	A	A	L	E	L	G	Y	R	G	I	V	L	E	G	Y	G	V	G	I	P	Y	R	G	R	D	L	L	D	V	V	R	R	V	A	T	E	I	P	V	V	M	T
WP_004066133.1_T._litoralis/1-331	V	V	F	I	R	L	T	P	G	L	D	G	N	A	I	D	A	L	V	K	A	A	H	R	G	I	V	L	E	G	Y	G	A	G	I	P	Y	R	K	R	D	I	L	S	K	R	E	I	T	P	O	I	P	V	V	M	T	
WP_010478656.1_T._zilligii/1-330	V	A	Y	L	R	L	T	P	G	L	S	P	E	V	F	L	A	V	A	N	K	A	H	G	I	I	L	E	G	Y	G	A	G	I	P	Y	R	G	R	D	L	L	S	A	V	S	E	R	E	K	P	V	M	T				
WP_014163150.1_T._lienii/1-342	V	F	V	L	K	I	F	P	G	L	E	P	S	I	V	E	T	V	I	E	R	D	I	S	G	L	I	V	E	S	F	G	A	G	L	P	Y	R	G	R	N	L	D	I	L	S	K	A	A	Q	I	P	V	V	L	T		
WP_213417497.1_type_I_Bacillus_subtilis/1-329	V	C	L	L	K	L	H	P	G	L	K	P	E	M	F	D	A	L	K	S	M	Y	K	G	I	V	I	E	S	Y	G	S	G	V	P	F	E	G	R	D	I	L	S	K	V	N	E	L	I	E	S	G	I	V	V	I	T	
WP_061804667.1_type_I_Priestia_endophytica/1-328	V	L	L	R	L	H	P	G	L	K	P	E	M	F	D	A	L	K	G	L	Y	K	G	I	V	I	E	S	Y	G	S	G	V	P	F	E	E	R	N	I	L	E	K	R	I	N	E	L	V	E	S	G	V	V	I	T		

	300	310	320	330	340																																																							
AAA23445.1_type_II_(ansB)_Escherichia_coli/1-348	S	R	V	P	T	G	A	...	T	T	Q	E	A	E	V	D	D	A	K	Y	G	F	V	A	S	G	T	L	N	P	Q	K	A	R	V	L	Q	L	A	L	T	Q	T	K	D	P	Q	Q	I	Q	T	F	N	Q	Y	.				
WP_011138590.1_typeII_Wolinella_succinogenes/1-3	S	R	V	G	S	G	S	...	T	T	Q	E	A	E	V	D	D	K	K	L	G	F	V	A	T	E	S	L	N	P	Q	K	A	R	V	L	M	L	A	L	T	K	T	S	D	R	E	A	I	Q	K	I	F	S	T	Y	.			
QKG29091.1_type_II_Campylobacter_sp._RM16187/1-3	S	R	V	G	S	G	E	...	T	T	I	N	G	E	V	D	D	K	K	L	G	F	L	A	S	D	N	L	N	A	Q	K	A	R	V	L	M	L	A	L	T	Q	T	N	D	K	A	K	I	Q	E	F	F	Y	T	H	.			
EIS1689357.1_Shigella_flexneri/1-348	S	R	V	P	T	G	A	...	T	T	Q	E	A	E	V	D	D	A	K	Y	G	F	V	A	S	G	T	L	N	P	Q	K	A	R	V	L	Q	L	A	L	T	Q	T	K	D	P	Q	Q	I	Q	T	I	F	N	Q	Y	.			
WP_231563885.1_type_II_Sulfurospirillum_cavolei/	S	R	V	G	S	G	S	...	T	T	L	E	G	E	V	D	D	A	K	Y	G	F	I	A	T	T	L	N	P	Q	K	A	R	V	L	M	L	G	L	T	K	T	N	D	K	K	A	L	Q	R	L	F	L	E	Y	.				
WP_015849943.1_T._sibiricus/1-331	T	Q	A	L	Y	D	G	V	D	L	T	R	Y	E	V	G	R	R	A	L	E	A	G	I	P	A	K	D	M	T	K	E	A	T	I	T	K	L	M	W	A	L	G	H	T	K	D	V	E	K	I	R	E	I	M	H	T	N	Y	
WP_011250607.1_T._kodakarensis/1-328	T	Q	A	L	Y	D	G	V	D	L	T	R	Y	E	V	G	R	R	A	L	E	A	G	I	P	A	K	D	M	T	K	E	A	T	L	T	K	L	M	W	A	L	G	H	T	R	D	L	E	E	I	R	K	I	M	E	R	N	Y	
WP_015859055.1_T._gammatolerans/1-328	T	Q	A	L	Y	D	G	V	D	L	T	R	Y	E	V	G	R	R	A	L	E	A	G	I	P	A	K	D	M	T	K	E	A	T	L	V	K	L	M	Y	A	L	G	R	T	N	G	L	E	E	V	R	R	I	M	E	K	N	L	
WP_010884185.1_P._horikoshii/1-328	T	Q	A	I	Y	D	G	V	D	L	T	R	Y	K	V	G	R	I	A	L	E	A	G	V	I	P	A	K	D	M	T	K	E	A	T	I	T	K	L	M	W	I	L	G	H	T	K	N	I	E	E	V	K	Q	L	M	G	K	N	I
WP_011013191.1_P._furiosus/1-326	T	Q	A	M	Y	D	G	V	D	L	T	R	Y	K	V	G	R	L	A	L	R	A	G	V	I	P	A	K	D	M	T	K	E	A	T	V	T	K	L	M	W	I	L	G	H	T	N	N	V	E	E	I	K	V	L	M	R	K	N	L
WP_013906452.1_P._yayanosii/1-328	T	Q	T	L	Y	D	G	V	D	L	T	K	Y	K	V	G	R	K	A	L	E	V	G	V	I	P	A	K	D	M	T	K	E	A	T	I	T	K	L	M	W	I	L	G	H	T	R	D	V	G	E	V	R	L	M	L	T	N	M	
WP_004066133.1_T._litoralis/1-331	T	Q	A	L	Y	D	G	V	D	L	T	K	Y	E	V	G	R	K	A	L	E	A	G	I	P	A	K	D	M	T	K	E	T	T	I	T	K	L	M	W	A	L	G	H	T	K	N	V	E	E	V	K	E	I	M	H	T	N	Y	
WP_010478656.1_T._zilligii/1-330	T	Q	A	L	H	G	V	D	L	M	K	Y	E	V	G	R	R	A	L	E	A	G	V	I	P	A	K	D	M	T	K	E	A	T	L	V	K	L	M	W	A	L	G	H	T	K	N	V	D	V	R	E	I	I	L	T	N	V		
WP_014163150.1_T._lienii/1-342	S	Q	V	L	I	N	G	V	N	L	H	T	Y	E	V	G	I	R	A	L	K	A	G	V	I	S	A	E	D	M	S	K	E	A	A	V	T	K	L	M	W	V	L	G	H	T	K	N	I	D	E	I	R	R	L	F	K	T	P	I
WP_213417497.1_type_I_Bacillus_subtilis/1-329	T	Q	C	L	E	E	G	E	D	M	S	I	Y	E	V	G	R	R	V	N	Q	D	L	I	I	R	S	R	N	M	N	T	E	A	I	V	P	K	L	M	W	A	L	G	O	S	S	D	L	P	V	K	R	I	M	E	T	P	I	
WP_061804667.1_type_I_Priestia_endophytica/1-328	T	Q	C	L	E	E	G	E	D	M	S	I	Y	E	V	G	R	R	V	N	Q	D	L	I	I	R	S	R	N	M	N	T	E	A	I	V	P	K	L	M	W	A	L	G	O	S	S	D	L	P	V	K	R	I	M	E	T	P	I	

AAA23445.1_type_II_(ansB)_Escherichia_coli/1-348
WP_011138590.1_typeII_Wolinella_succinogenes/1-3
QKG29091.1_type_II_Campylobacter_sp._RM16187/1-3
EIS1689357.1_Shigella_flexneri/1-348
WP_231563885.1_type_II_Sulfurospirillum_cavolei/
WP_015849943.1_T._sibiricus/1-331	VNEIKS.....
WP_011250607.1_T._kodakarensis/1-328	AGEITGS.....
WP_015859055.1_T._gammatolerans/1-328	AGELSSAF.....
WP_010884185.1_P._horikoshii/1-328	TGELTRVS.....
WP_011013191.1_P._furiosus/1-326	VGELRD.....
WP_013906452.1_P._yayanosii/1-328	VGEIGKSA.....
WP_004066133.1_T._litoralis/1-331	ADEIEG.....
WP_010478656.1_T._zilligii/1-330	SDEIGKES.....
WP_014163150.1_T._lienii/1-342	AGEIKQHKIYYRTPQR
WP_213417497.1_type_I_Bacillus_subtilis/1-329	ADDVVL.....
WP_061804667.1_type_I_Priestia_endophytica/1-328	ADDVVL.....

Identical amino acid residues are marked in red. The substrate-binding Ser residue is marked by a red star.
 ESPrnt 3.0 was used for multiple sequence alignments [28].